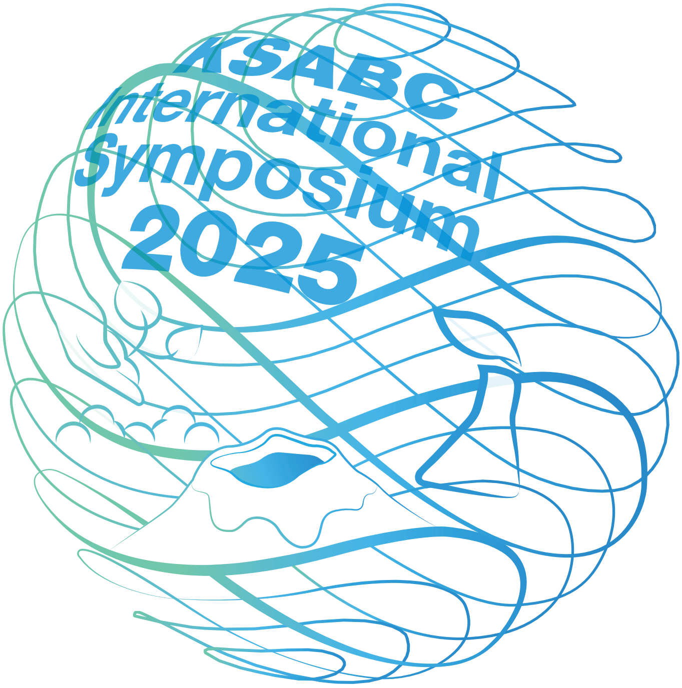
KSABC International Symposium 2025

KSABC
International Symposium
2025

Applied Biological Chemistry
- The key solutions for life and the environment

June 29 - July 1, 2025
ICC JEJU, Jeju, Korea



한국응용생명화학회
The Korean Society for Applied Biological Chemistry

한국응용생명화학회
The Korean Society for Applied Biological Chemistry

Since 2012

풍기과학

실험기자재, 소모품 및 시약

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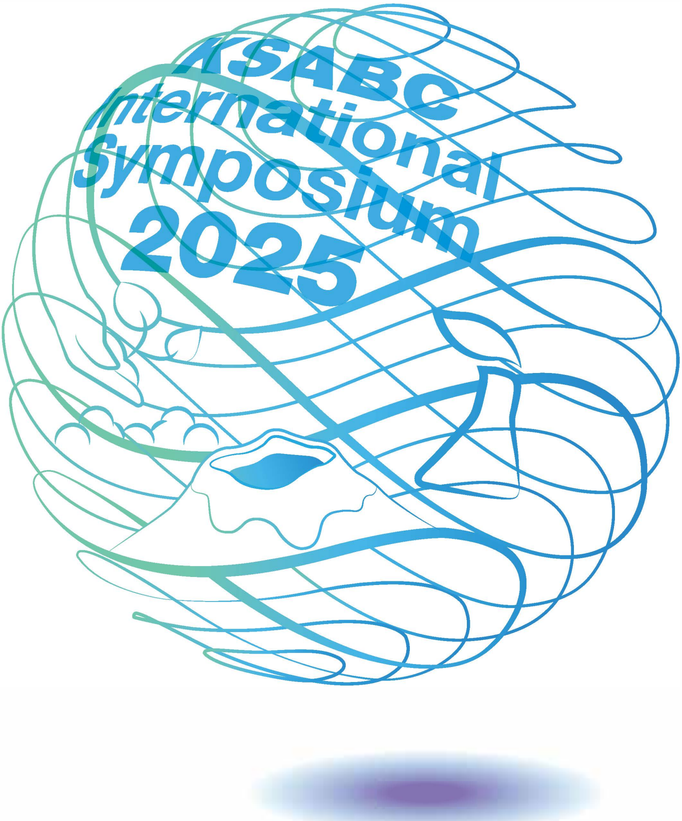

한국응용생명화학회
The Korean Society for Applied Biological Chemistry

KSABC
International Symposium 2025

Hosted by

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한국응용생명화학회
The Korean Society for Applied Biological Chemistry

Co-organized by

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한국과학기술연구원 강릉
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강원 천연물소재
전주기 표준화 허브
(강원도, 강릉시)

경북대학교
농산물품질·안전성평가연구소

경북대학교
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조선대학교 G-LAMP 사업단
CHOSUN UNIVERSITY G-LAMP

항노화 바이오소재 세포공장 지역혁신연구센터
Anti-aging Bio Cell factory RLRC (ABC-RLRC)

전북대학교
농업과학기술연구소

제주대학교
제주지역혁신클러스터육성사업단

This work is supported by the ‘Lottery Fund’ of the ‘Ministry of Strategy and Finance’ and the ‘Science and Technology Promotion Fund’ of the ‘Ministry of Science and ICT’, contributing to the realization of social value and the development of national science and technology.

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Korea Natural Product Institute of Science and Technology

G.O.research

SKYGENe
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Microalgae Ask Us
(주)마이크로알지 에스크 어스

Cell care for Health care
HAN BIO

biodot

JEJU CHUNJI
Agricultural Corporation

ATNT |주| 분석기술과 미래
Analysis Technology and Tomorrow

This work is supported by the 'Lottery Fund' of the 'Ministry of Strategy and Finance' and the 'Science and Technology Promotion Fund' of the 'Ministry of Science and ICT', contributing to the realization of social value and the development of national science and technology.

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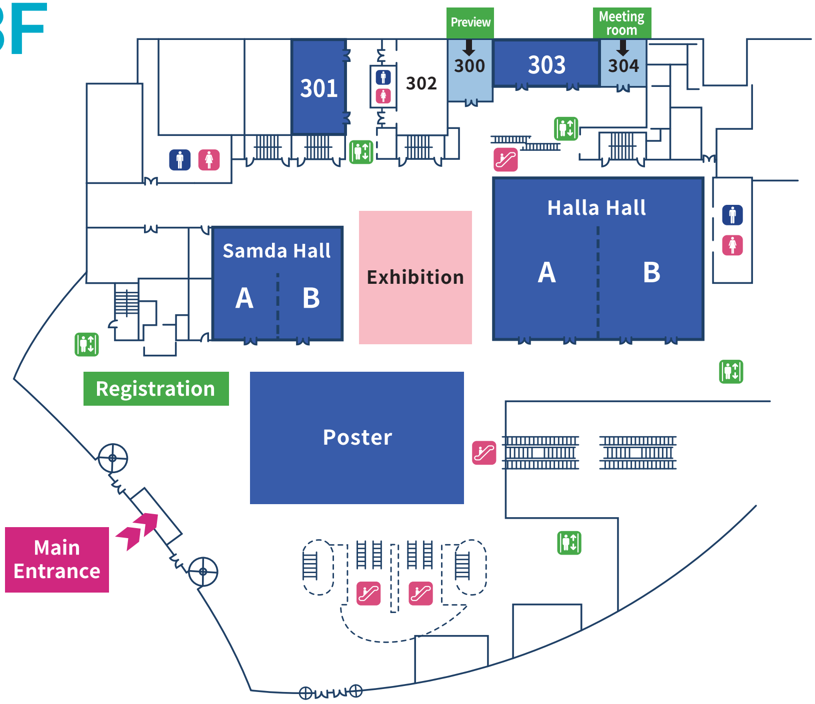
Contents

Floor Plan

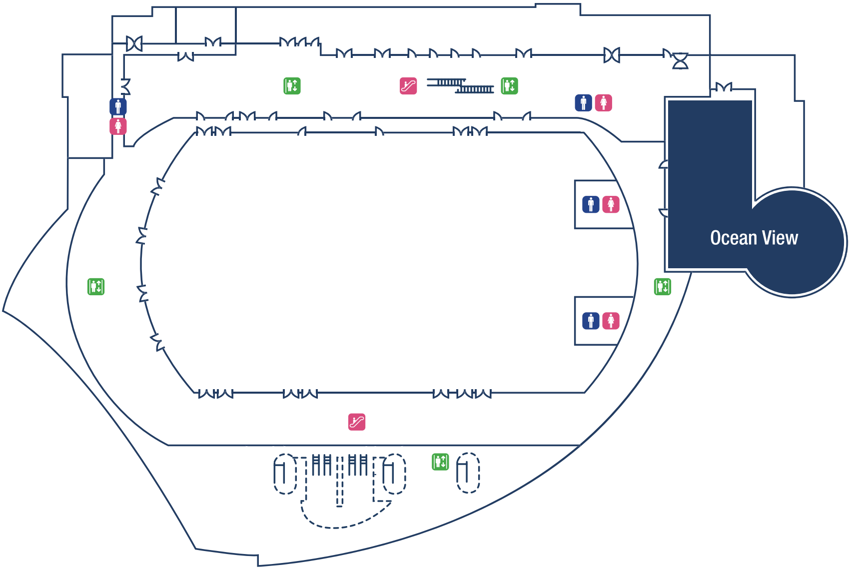
3F



Samda Hall	SL-1, Closing Ceremony
Halla Hall	Award Ceremony, PL, SL-2, AL
Halla Hall A	S1
Halla Hall B	S2
Samda Hall A	S3, S4, YS1, GS1
Samda Hall B	S5, S6, YS2, GS2
303	S7, S8, S10, K-Inno:Ven Star Audition
301	S9
Lobby	Poster, Exhibition

Floor Plan

5F



Ocean View	Networking Ⅰ, Ⅱ

Program at a Glance

June 29 (Sun)

Venue / Time	Samda Hall A	Samda Hall B	Lobby
13:00-	Registration		Poster
14:00-14:50	**SL-1**		
15:10-17:50	**GS1**	**GS2**	
18:00-19:30	**Networking** I **(for Graduate Student) / Ocean View, 5F**		

PL	Plenary Lecture	AL	Award Lectures
SL	Special Lectures	S	Symposia
YS	Young Scientist Presentation	GS	Graduate Student Presentation
K	K-Inno:Ven Star Audition	🟥	Poster Presentation

Program at a Glance

June 30 (Mon)

Venue *Time*	Halla Hall A	Halla Hall B	Samda Hall A	Samda Hall B	303	301	Lobby
09:00-10:40	**S1** Biochemistry · Molecular Biology – Synthetic Biology Based on Structural Biology (AlphaFold)	**S2** Natural Products · Bioactive Materials · Biomedical Sciences / KIST	**S3** Environmental Sciences	**S5** 식품오염물질과 미세플라스틱	**S7** 미래선도 그린바이오 융합기술 및 인재양성	**S9** Natural Bioactives for Disease Modulation and Metabolic Regulation	Poster & Exhibition
10:50-12:30			**S4** Applied Microbiology	**S6** 산업바이오	**S8** 한국생명공학연구원 천연물 클러스터		
12:30-14:00	Lunch						
14:00-14:20	Award Ceremony						
14:20-15:00	**PL**						
15:00-15:40	**SL-2**						
15:40-15:50	*Break*				**S10** 천연물소재의 건강기능식품 사업화 전략		
15:50-16:50	**AL**						
16:50-17:40	Poster Presentation						
17:40-18:00	General Assembly						
18:00-19:30	Networking Ⅱ (for PI) / Ocean View, 5F						

July 1 (Tue)

Venue *Time*	Samda Hall A	Samda Hall B	303	Lobby
09:10-11:40	**YS1**	**YS2**	K-Inno:Ven Star Audition (대학원생 창업경진대회)	Exhibition
11:40-12:00	Closing Ceremony			

Plenary Lecture

June 30 (Mon), Halla Hall

Chair: **Moonjae Cho** (Jeju Nat'l University)

PL 14:20-15:00

Chemical modifications on RNAs: a potent mechanism of gene regulation

Hunseung Kang

Department of Applied Biology, Chonnam National University, Gwangju 61186, Republic of Korea

Special Lectures

June 29 (Sun), Samda Hall

Chair: **Yeon Jong Koo** (Chonnam Nat'l University)

SL-1 14:00-14:50

Integrating Generative AI in Academic Research: From Idea Generation to Data Analysis Automation

Hyun-Soo Ahn

R&BD Partners, Yong-In, Republic of Korea

June 30 (Mon), Halla Hall

Chair: **Hyung Won Ryu** (Korea Research Institute of Bioscience and Biotechnology)

SL-2 15:00-15:40

Knowing, Synthesizing, Applying Bugs for Creativity

Eungbin Kim

Department of Systems Biology, Yonsei University, Seoul 03722, Republic of Korea

Award Lectures

June 30 (Mon), Halla Hall
Chair: Tatsuya Unno (Chungbuk Nat'l University)

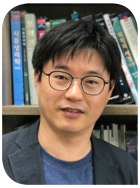
학술상 1967년도 제정

AL-1 15:50-16:10

Happiness from the Art of Natural Products

Sanghyun Lee

Department of Plant Science and Technology, Chung-Ang University, Anseong 17546, Republic of Korea



기창(基倉)과학상 기창(基倉) 한태룡 전임회장의 후원으로 2010년도 제정

AL-2 16:10-16:30

Recent Trends and Technological Advancements in Plant Proteomics: From DDA to 4D-DIA

Sun Tae Kim

Department of Plant Bioscience, Life and Industry Convergence Research Institute, Pusan National University, Miryang 50463, Republic of Korea

HAN BIO Award 한바이오 그룹 후원으로 2022년도 제정

AL-3 16:30-16:50

Protopanaxadiol Attenuates Palmitate-Induced Lipotoxicity and Restores Pancreatic β-Cell Function in INS-1 Cells

Ki Sung Kang

College of Korean Medicine, Gachon University, Seongnam 13120, Republic of Korea

Symposia

S1 Biochemistry · Molecular Biology – Synthetic Biology Based on Structural Biology (AlphaFold)

June 30 (Mon), Halla Hall A

Chair: Bong-Gyu Mun (Chungbuk Nat'l University)

S1-1 **09:00-09:30**

Machine learning-based sequence optimization for protein structures

Keunwan Park

Center for Natural Product Systems Biology, Korea Institute of Science and Technology, Gangneung 25451, Republic of Korea

S1-2 **09:30-10:00**

Daily Rhythms in Metabolism and Sleep Cycle Are Made by a Phosphotimer

Choogon Lee

Department of Biomedical Sciences, Program in Neuroscience, College of Medicine, Florida State University, Tallahassee, USA

S1-3 **10:00-10:30**

Glycan-Mediated Host-Pathogen Interactions: How *Salmonella* AB Toxins Adapt to Hosts

Sohyoung Lee

[1]*Department of Biology, University of Louisiana at Lafayette, Lafayette, LA 70503, USA,* [2]*Department of Microbiology and Immunology, Cornell University, Ithaca, NY 14853, USA*

June 30 (Mon), Halla Hall A

Chair: Young Hun Song (Seoul Nat'l University)

S1-4 **10:50-11:15**

Uptake characterization of soil arsenic species and its effects on nitrogen cycle in Soybean (*Glycine max*(L.) Merrill) Cultivation: A Comparison with Cadmium

Goon-taek Lee

[1]Department of Agricultural Biotechnology, [2]Department of Applied Biology and Chemistry, College of Agricultural and Life Sciences, Seoul National University, Seoul 08826, Republic of Korea

S1-5 **11:15-11:40**

Gene Discovery and Functional Insights to Improve Plant Nitrogen Utilization

Jun Sung Seo

Crop Science and Biotechnology, Dankook University, Cheonan 31116, Republic of Korea

S1-6 **11:40-12:05**

Transcriptomic Approach to Elucidate Molecular Targets of Humic Acid and Their Biological Functions in Plants

Joon-Yung Cha

Division of Applied Life Science(BK21four), Plant Biological Rhythm Research Center, Research Institute of Life Science, Gyeongsang National University, Jinju 52828, Republic of Korea

S1-7 **12:05-12:30**

Daytime-Specific Mechanisms of *FT* Regulation in Photoperiodic Flowering: Morning or Evening?

Young Hun Song

Department of Agricultural Biotechnology, Seoul National University, Seoul 08826, Republic of Korea

S2 Natural Products · Bioactive Materials · Biomedical Sciences / KIST

Co-organized by KIST 한국과학기술연구원 강릉 천연물연구소 제주한의약연구원 JEJU INSTITUTE OF KOREAN MEDICINE

June 30 (Mon), Halla Hall B

Chair: Dae-Geun Song (Korea Institute of Science and Technology)

S2-1 **09:00-09:30**

Identification of novel genes and Korean medicine as regulators of the p53-MDM2 feedback loop

Ji Hoon Jung

College of Korean medicine, Kyung Hee University, Seoul 02447, Republic of Korea

S2-2 **09:30-10:00**

Synthetic Biology-Based Precision Fermentation CDMO: Accelerating Bio-Material Innovation

Eun Ji Kim

Team of Foundry, Division of Strategy & Planing, CJ CheilJedang, Seoul 04560, Republic of Korea

S2-3 **10:00-10:30**

Medicinal plants from Nepal as potential inhibitors of Aβ-aggregation and BACE1

Bishnu Prasad Pandey

[1]*Department of Chemical Science and Engineering, Kathmandu University, PO Box No. 6250, Dhulikhel, Kavre, Nepal,* [2]*Department of Pharmacy, College of Pharmacy, Sunchon National University, Suncheon 57922, Republic of Korea*

S2-4 **10:30-11:00**

Development of medicinal plants for herbal medicine and plant derived drugs from traditional to modern approaches

Elfahmi

School of Pharmacy, Bandung Institute of Technology, Jl. Ganesha 10 Bandung, West Java Indonesia, Indonesia

June 30 (Mon), Halla Hall B

Chair: Jin-Soo Park (Korea Institute of Science and Technology)

S2-5 **11:10-11:40**

Enzymatic Tailoring and Bioengineering of Aromatic Polyketides

Robin Teufel

Department of Pharmaceutical Sciences, University of Basel, 4056 Basel, Switzerland

S2-6 **11:40-12:10**

Elucidating Biochemical Pathway of Neoclerodane Diterpene, Salvinorin A, in *Salvia divinorum*

Dae-Kyun Ro

Department of Biological Sciences, University of Calgary, Calgary, Alberta, Canada

S2-7 **12:10-12:40**

Efficient Synthesis of AMF from Biomass-Derived Carbohydrate via Heterogeneous Flow Chemistry

Se Won Bae

Department of Chemistry, Jeju National University, Jeju 63243, Republic of Korea

S3 Environmental Sciences

June 30 (Mon), Samda Hall A

Chair: **Eun Hea Jho** (Chonnam Nat'l University)

S3-1 09:00-09:25

When Biorefinery Meets Evolutionary Engineering: Integrated Valorization of Defatted Microalgal Biomass

Jin-Ho Yun

[1]Cell Factory Research Center, Korea Research Institute of Bioscience and Biotechnology, Daejeon 34141, Republic of Korea,
[2]Department of Environmental Biotechnology, KRIBB School of Biotechnology, University of Science & Technology (UST), Daejeon 34113, Republic of Korea,
[3]Department of Integrative Biotechnology, College of Biotechnology and Bioengineering, Sungkyunkwan University, Suwon, Gyeonggi-do 16419, Republic of Korea

S3-2 09:25-09:50

Hydrogen Production and Real Wastewater Treatment in Zero-gap Bipolar Membrane Microbial Electrolysis Cell (BPM-MEC)

Eunjin Jwa

Convergence Research Center of Sector Coupling & Integration, Korea Institute of Energy Research, Jeju 63359, Republic of Korea

S3-3 09:50-10:15

Fe-Mn biochar design for reducing environmental burden of wastewater treatment

Daniel C. W. Tsang

Department of Civil and Environmental Engineering, The Hong Kong University of Science and Technology, Clear Water Bay, Hong Kong, China

S3-4 10:15-10:40

Environmental Benefits of Microalgal Biotechnology: Bioremediation and Potential Applications

Sang-Ah Lee

[1]Faculty of Biotechnology, College of Applied Life Sciences, [2]Bio-Health Materials Core-Facility Center, [3]Interdisciplinary Graduate Program in Advance Convergence Technology and Science, Jeju National University, 102 Jejudaehak-ro, Jeju 63243, Republic of Korea

S4 Applied Microbiology

June 30 (Mon), Samda Hall A

Chair: **Tatsuya Unno** (Chungbuk Nat'l University)

S4-1 10:50-11:15

Unveiling Hidden Worlds: Single-Cell Multi-Omics in Environmental Microbiology

Haruko Takeyama

Department of Life Science and Medical Bioscience, Waseda University, Waseda Center for a Carbon Neutral Society, Research Organization for Nano & Life Innovation, Waseda University, Japan

S4-2 11:15-11:40

Application of eDNA in Ecological Surveys of Marine Microbiomes

Dukki Han

*Department of Marine Bioscience, Gangneung-Wonju National University,
7, Jukheon-gil, Gangneung-si, Gangwon-do 25457, Republic of Korea*

S4-3 11:40-12:05

Prevention of Shiga toxin production in enterohemorrhagic *Escherichia coli*

Masayuki Hashimoto

Institute of Molecular Medicine, College of Medicine, National Cheng Kung University, Tainan 70456, Taiwan

S4-4 12:05-12:30

Understanding aerosolization of indoor bacterial communities and antibiotic resistomes in swine farms

Keunje Yoo

Department of Environmental Engineering, Korea Maritime and Ocean University, Busan 49112, Republic of Korea

S5 식품오염물질과 미세플라스틱

June 30 (Mon), Samda Hall B
Chair: **Hae Won Jang** (Sungshin Women's University)

S5-1 **09:00-09:25**

The Content of Nitrosamines in Processed Food and the Health Risk Associated with N-nitrosodimethylamine (NDMA)

Cao-Son Tran

[1]Vietnam Center for Food Safety Risk Assessment, National Institute for Food Control, Hanoi, Vietnam, [2]Department of Toxin and Drug Testing, Hanoi University of Pharmacy, Hanoi, Vietnam

S5-2 **09:25-09:50**

Microplastics in the Environment: Occurrence, Transport, and Ecotoxicological Concerns

Eun-Hee Lee

[1]Department of Microbiology, [2]Institute for Future Earth, Pusan National University, Busan 46241, Republic of Korea

S5-3 **09:50-10:15**

Polystyrene Nanoplastics Promote Premature Cellular Senescence through Skeletal Myoblast Dysfunction in Myoblasts

Yung Hyun Choi

[1]Basic Research Laboratory for the Regulation of Microplastic-Mediated Diseases, [2]Department of Biochemistry, College of Korean Medicine, Dong-eui University, Busan 47227, Republic of Korea

S5-4 **10:15-10:40**

The effects of microplastics on neurodevelopment in mice

Eui-Man Jung

[1]Department of Molecular Biology, College of Natural Sciences, [2]Institute for Future Earth, Pusan National University, Busan 46241, Republic of Korea

S6 산업바이오

Co-organized by 강원 천연물소재 전주기 표준화 허브 (강원도, 강릉시)

June 30 (Mon), Samda Hall B

Chair: Moonhyuk Kwon (Gyeongsang Nat'l University)

S6-1 10:50-11:15

Plant Cell Culture-Driven Breakthroughs in Reverse Aging

Sang Hyun Moh

Plant Cell Research Institute, BIO-FD&C Co., Ltd, Incheon 21990, Republic of Korea

S6-2 11:15-11:40

Antioxidant foods derived from microalgae

Cheol-Ho Pan

Microalgae Ask Us Co. Ltd., 30 Hanam-gil, Gangneung 25441, Republic of Korea

S6-3 11:40-12:05

딥테크 창업기업의 성공적인 성장 전략 (초기 기업 중심)

최고

시너지IB투자㈜

S6-4 12:05-12:30

New Concept of Aeroponic System

Sang-June Nam

Aalsmeer Lab, Agricultral Corporation JEJU-CHUNJI, Jeju 63036, Republic of Korea

S7 미래선도 그린바이오 융합기술 및 인재양성

June 30 (Mon), 303

Chair: **Ki-Ho Son** (Gyeongsang Nat'l University)

S7-1 09:00-09:25

Fermented aged mountain cultivated ginseng sprout and compound K alleviate allergic asthma and acute lung injury through macrophage polarization modulation

Dawon Kang

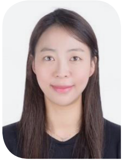
[1]Department of Physiology, College of Medicine, [2]Department of Convergence Medical Science, [3]Department of GreenBio Science and Agri-Food Bio Convergence Institute, Gyeongsang National University, Jinju 52727, Republic of Korea

S7-2 09:25-09:50

Protective effects of *Lonicerae Flos* against OGD-induced damage in bEnd.3 cells with active ingredient prediction via network pharmacology

Ki Sung Kang

College of Korean Medicine, Gachon University, Seongnam 13120, Republic of Korea



S7-3 09:50-10:15

Green Bio-Based Integration of Quality Grading and Smart Distribution for Horticultural Products

Sooyeon Lim

Postharvest Technology Division, National Institute of Horticultural Herbal Science, RDA, Wanju 55365, Republic of Korea

S7-4 10:15-10:40

Patent Acquisition and Commercialization Strategy for Biomaterials

Chan-Joo Kim

Korean Patent Attorney, IPON Co., Ltd, Daejeon 35233, Republic of Korea

S8 한국생명공학연구원 천연물 클러스터

June 30 (Mon), 303
Chair: 최상호 (한국생명공학연구원)

S8-1 **10:50-11:00**

The role of Natural Product Cluster in Korea

Sei-Ryang Oh

Natural Product Central Bank, Korea Research Institute of Bioscience and Biotechnology, Cheongju-si, Chungcheongbuk-do 28116, Republic of Korea

S8-2 **11:00-11:10**

A Base Bank for Korean Native Plants

Jaeyoung Kwon

KIST Gangneung Institute of Natural Products, Korea Institute of Science and Technology, Gangneung 25451, Republic of Korea

S8-3 **11:10-11:20**

Plant-derived natural product resource base bank

Jun Lee

Herbal Medicine Resources Research Center, Korea Institute of Oriental Medicine (KIOM), Naju 58245, Republic of Korea

S8-4 **11:20-11:30**

A Base Bank for Plant-derived Food Resources

Sang Yoon Choi

Korea Food Research Institute, Wanju 55365, Republic of Korea

S8-5 **11:30-11:40**

Establishment of the cooperation center for securing characteristic information of natural compounds to advance Natural Product Cluster and maximize utilization of strategic materials

Young-Won Chin

College of Pharmacy and Research Institute of Pharmaceutical Sciences, Seoul National University, Seoul 08826, Republic of Korea

S8-6 11:40-11:55

Advancing natural product data management platform to be more user-friendly by implementing AI-driven efficacy prediction service

Heejae Yang

Cocoon Inc., Cheongju 28161, Republic of Korea

S8-7 11:55-12:10

Application Strategy of an AI-Based Support Program for Analyzing the Relationships Among Natural Product Components, Diseases, and Targets

Daesik Jeong

Sangmyung University, 5works Inc., Seoul 06094, Republic of Korea

S8-8 12:10-12:25

Korea Forest Plant Essential Oil Bank

Hwan Myung Lee

Department of Biotechnology, College of Life and Health Sciences,
Hoseo University, Asan 31499, Republic of Korea

S9 Natural Bioactives for Disease Modulation and Metabolic Regulation

June 30 (Mon), 301

Chair: **Young-Ok Son** (Jeju Nat'l University)

S9-1 **09:00-09:25**

4-Methylthiobutyl isothiocyanate Potentiates the Efficacy of Chemotherapy in Drug-Resistant Breast Cancer Cells

Ji Soo Kim

Interdisciplinary Graduate Program in Advanced Convergence Technology and Science, Jeju National University, Jeju 63243, Republic of Korea

S9-2 **09:25-09:50**

Distinctive ecophysiological Traits of *Nitrosocosmicus* Ammonia-Oxidizing Archaea

Seongwook Kim

Interdisciplinary Graduate Program in Advance Convergence Technology and Science, Jeju National University, Jeju 63243, Republic of Korea

S9-3 **09:50-10:15**

NOX-derived ROS hyperstabilize HIF-1α under normoxia, revealing a target in pulmonary fibrosis

JinHyuk Choi

Department of Biochemistry, College of Medicine, Jeju National University, Jeju 63241, Republic of Korea

S9-4 **10:15-10:40**

ACF-1: A Novel Small Molecule for Targeted Inhibition of HIF-1α in Idiopathic Pulmonary Fibrosis

Hiruni Nilshi Indeevarie Abeysiriwardhana

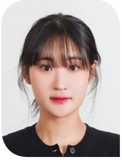
Department of Advanced Convergence Technology and Science, Jeju National University, Jeju-Si 63241, Republic of Korea

S9-5 10:50-11:15

Toward Optimizing Growth Medium for *Haematococcus lacustris*: Effects of Different Media on Growth and Microbial Dynamics

Mehwish Taj

Interdisciplinary Graduate Program in Advanced Convergence Technology and Science, Jeju National University, Jeju 63243, Republic of Korea



S9-6 11:15-11:40

Exploring the Anti-Inflammatory Properties of *Tetragonia tetragonoides* (Pall.) Kuntz in Mouse Macrophages

Yoon-A Kang

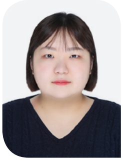
College of Pharmacy and Jeju Research Institute of Pharmaceutical Sciences, Jeju National University, Jeju 63243, Republic of Korea

S9-7 11:40-12:05

p-Coumaric acid prevents hepatic inflammation and fibrosis by suppressing NLRP3 inflammasome activation involved in TLR4 knockout fed a high-fat and high-sucrose diet

Thi My Tien Truong

[1]Interdisciplinary Graduate Program in Advanced Convergence Technology and Science, [2]Department of Food Science and Nutrition, Jeju National University, Jeju 63243, Republic of Korea



S9-8 12:05-12:30

Investigation of Antioxidant Activities and Chemical Profiles of *Idesia polycarpa* Leaves for Potential Applications

Minseo Jeon

Interdisciplinary Graduate Program in Advanced Convergence Technology & Science, Jeju National University, Jeju 63243, Republic of Korea

S10 천연물소재의 건강기능식품사업화 전략

June 30 (Mon), 303

Chair: Min Young Um (Korea Food Research Institute)

S10-1 **15:20-15:45**

Introduction and Outcomes of Technical Support for Smart Commercialization of Health Functional Ingredients

Eunju Kim

International Life Science Institute of Korea, Seoul 04778, Republic of Korea

S10-2 **15:45-16:10**

Organoid-Based Platforms for Functional Food Development: Applications and Future Perspectives

Sang Keun Ha

Functional Food Platform Research Group, Food Functionality Research Division, Korea Food Research Institute, Wanju 55365, Republic of Korea

S10-3 **16:10-16:35**

Advancing Natural Product Research with FloraGenesis: Large-Scale Spectral Databases and Deep Learning-Based Functional Analysis

Sangwon Lee

Bioinformatics & Molecular Design Research Center, 209, Veritas A Hall, Yonsei University, 85 Songdogwahak-ro, Yeonsu-gu, Incheon, Republic of Korea

S10-4 **16:35-17:00**

R&D of a Sleep-Promoting Ingredient Derived from Lime Peel for Global Commercialization

Suengmok Cho

Major of Food Science & Technology, Pukyong National University, Busan 48513, Republic of Korea

Young Scientist Presentation

YS1 Biochemistry · Molecular Biology / Natural Products · Bioactive Materials · Biomedical Sciences

July 1 (Tue), Samda Hall A

Chair: **Choonkyun Jung** (Seoul Nat'l University)

YS1-1 09:10-09:30

Type Ⅰ IFN receptor blockade alleviates the liver fibrosis through the macrophages derived STAT3 signaling

Soo-Jeung Park

Beirne B. Carter Center for Immunology Research, University of Virginia, Charlottesville, Virginia, USA

YS1-2 09:30-09:50

TrkB-Mediated Neuritogenic and Synaptogenic Potential of Coriandrum sativum: An Integrated *In Vitro* and Network Pharmacology Study

Yeasmin Akter Munni

[1]Department of Anatomy, Dongguk University College of Medicine, [2]Department of Physiology, College of Korean Medicine, Dongguk University, Gyeongju 38066, Republic of Korea

YS1-3 09:50-10:10

Evolution and diversification of the ACT-like domain associated with plant basic helix–loop–helix transcription factors

Yun Sun Lee

[1]Department of Biochemistry and Molecular Biology, Michigan State University, East Lansing, MI 48823, USA, [2]Crop Biotechnology Institute, Institutes of Green-bio Science and Technology, Seoul National University, [3]Department of International Agricultural Technology, Seoul National University, Pyeongchang 25354, Republic of Korea

July 1 (Tue), Samda Hall A

Chair: Jongmin Ahn (Korea Research Institute of Bioscience and Biotechnology)

YS1-4 **10:20-10:40**

Flavonoid profiling of Freshwater Bioresources Culture Collection (FBCC) extracts using LC-MS/MS and their anti-obesity properties by regulating hypothalamic neuropeptides

Tae Jin Kim

Using Technology Development Department, Bio-resources Research Division, Nakdonggang National Institute of Biological Resources, Gyeongsangbuk-do 37242, Republic of Korea

YS1-5 **10:40-11:00**

Furanocoumarin enriched *Angelica acutiloba* by metabolite farming based on ethylene and their monoamine oxidase inhibition

Yong Hyun Lee

Division of Applied Life Science (BK21 four), Institute of Agricultural and Life Science (IALS), Gyeongsang National University, Jinju 52828, Republic of Korea

YS1-6 **11:00-11:20**

Sustainable extraction of antioxidant and anti-inflammatory compounds from *Polygonum multiflorum* using natural deep eutectic solvents (NADES)

Kyeong-Ok Choi

Herbal Medicine Resources Research Center, Korea Institute of Oriental Medicine (KIOM), 111 Geonjae-ro, Naju-si, Jeollanam-do 58245, Republic of Korea

YS1-7 **11:20-11:40**

Anti-Inflammatory Dimeric and Trimeric Flavonoids from the Roots of *Pistacia weinmannifolia*

Hyoung-Geun Kim

Natural Product Research Center and Natural Product Central Bank, Korea Research Institute of Bioscience and Biotechnology, Chungcheungbuk-do 28116, Republic of Korea

YS2 Environmental Sciences / Applied Microbiology / Food Sciences

July 1 (Tue), Samda Hall B

Chair: Youri Yang (Kangwon Nat'l University)

YS2-1 **09:10-09:30**

Unlocking Carbon Pathways: Integrating Soil Biochemistry and Physical Structure as the Basis for Carbon Farming

Kyungmin Kim

Department of Agricultural Biotechnology, Seoul National University, Seoul 08826, Republic of Korea

YS2-2 **09:30-09:50**

Genomic Insights into the Dissemination of Antibiotic Resistance Genes in *E. coli* from Veterinary Clinics and Animal Farms in South Korea

Hokyung Song

Department of Environmental Engineering, Chosun University, Gwangju 61452, Republic of Korea

YS2-3 **09:50-10:10**

Environmental Hazards of Cement Production: Alterations in Soil Microbiomes Due to Heavy Metal Contamination

Ve Van Le

Faculty of Biotechnology, College of Applied Life Sciences, Jeju National University, 102 Jejudaehak-ro, Jeju 63243, Republic of Korea

July 1 (Tue), Samda Hall B

Chair: Min Jung Kim (Korea Food Research Institute)

YS2-4 **10:20-10:40**

Navigating the Aquatic Microbial Universe: Absolute Quantification of Microbial Communities through Advanced Metagenomic Approaches

Min-Ji Kim

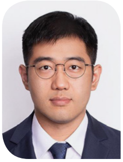
NGS Core Facility, Kyungpook National University, Daegu 41566, Republic of Korea

YS2-5 **10:40-11:00**

Crosstalk Between Long-Chain Fatty Acids and Taste GPCRs: Distinct Modulatory Effects on Bitter, Sweet, and Umami Signaling Pathways

Dong-Uk Shin

Division of Food Functionality Research, Korea Food Research Institute, Wanju-gun 55365, Republic of Korea



YS2-6 **11:00-11:20**

Saccharomyces cerevisiae GILA induces the alleviation of intestinal inflammation in mouse with colitis

Bum Ju Kil

[1]Biomodulation Major, and Center for Food and Bioconvergence, Seoul National University, Seoul 08826, Republic of Korea, [2]Department of Agricultural Biotechnology, and Research Institute of Agriculture and Life Sciences, Seoul National University, Seoul 08826, Republic of Korea, [3]Department of Food and Nutrition, and Bionanocomposite Research Center, Kyung Hee University, Seoul 02447, Republic of Korea

YS2-7 **11:20-11:40**

Exploring the Potential of Food By-products for the Prevention of Cardiovascular Disease

Hana Lee

Department of Food Science and Biotechnology, Chungbuk National University, Cheongju 28644, Republic of Korea

Graduate Student Presentation

GS1 Biochemistry · Molecular Biology / Natural Products · Bioactive Materials · Biomedical Sciences

June 29 (Sun), Samda Hall A

Chair: Su Yeon Seo (Korea Institute of Oriental Medicine)

GS1-1 **15:10-15:20**

Inhibition of glutamate-induced cell death in HT22 cells by mixed extracts of *Dioscorea batatas* and *Zingiber officinale*

Seung-Woo Im[1,2], Tea-Woo Oh[1,2]*

[1]Korean Medicine (KM)-Application Center, Korea Institute of Oriental Medicine (KIOM), Daegu 41062, Republic of Korea, [2]Department of Korean Convergence Medical Science, University of Science & Technology (UST), 1672 Yuseongdae-ro, Yuseong-gu, Daejeon 34054, Republic of Korea

GS1-2 **15:20-15:30**

Enhancing Plant Stress Tolerance through Subcellular Targeting of Catalase

Euyeon Kim, Yeonjong Koo*

Department of Agricultural Chemistry, Chonnam National University, Gwangju, Republic of Korea

GS1-3 **15:30-15:40**

Non-secreted peptide OsRALF5 regulate pollen tube growth in *Oryza sativa*

Hyo-Jeong Kim[1], Ji-Hyun Kim[1], Eui-Jung Kim[2], Ye-Jin Son[1], Ki-Hong Jung[2], Yu-Jin Kim[1]*

[1]Department of Life Science and Environmental Biochemistry, and Life and Industry Convergence Research Institute, Pusan National University, Miryang 50463, Republic of Korea, [2]Graduate School of Green Bio Science & Crop Biotech Institute, Kyung Hee University, Yongin 17104, Republic of Korea

GS1-4 **15:40-15:50**

Tongue tissue endoplasmic reticulum stress response in a DSS-induced colitis model from an oral-gut axis perspective

Young Ju Do[1,2], Su Yeon Seo[1,2*]

[1]Department of Oriental Medicine Research Division, Korea Institute of Oriental Medicine, Republic of Korea, [2]Department of Korea Convergence Medical Science, University of Science & Technology (UST), Republic of Korea

GS1-5 **15:50-16:00**

Development of a Method to Discriminate the Geographical Origins of Peanut (*Arachis hypogaea*) Using Physicochemical and Metabolomic Analyses

Sanghwa Kang, Jiyoung Shin, Junho Yang, Beom-Su Cho, Gangmi Nam, Yeonhwa Park, Jisoo Han, Ji-Young Yang*

Department of Food Science and Technology, Pukyong National University, Busan 48513, Republic of Korea

GS1-6 **16:00-16:10**

Integrated CPC–QM–qNMR Platform for Evaluation of Antibacterial Synergy among the Coumarins from *Cnidium monnieri*

Sangmin Lee[1,2], Young Ho Seo[2], Yerim Joo[1,2], Eunbeen Shin[1,2], Mi Kyeong Lee[3], Saemee Song[4*], Seon Beom Kim[1,2,5*]

[1]Department of Food Science and Technology, College of Natural Resources and Life Science, Pusan National University, Miryang 50463, Republic of Korea, [2]Institute for Future Earth, Pusan National University, Busan 46241, Republic of Korea, [3]College of Pharmacy, Chungbuk National University, Cheongju 28160, Republic of Korea, [4]Department of Infectious Diseases Research, Korea Research Institute of Chemical Technology, Daejeon 34114, Republic of Korea, [5]Food Tech Innovation Center, Life and Industry Convergence Research Institute, Pusan National University, Miryang, Republic of Korea

GS1-7 **16:10-16:20**

Development of Quarantine Disinfestation Methods for *Carposina sasakii* in Fresh Apples

Hwee-Seung Ji[1], So-Yeon Kim[1], Jae-Won Yoon[2], Min-Goo Park[2*]

[1]Department of Agricultural Chemistry, Jeonbuk National University, Jeonju 54896, Republic of Korea, [2]Department of Bioenvironmental Chemistry, Jeonbuk National University, Jeonju 54896, Republic of Korea

June 29 (Sun), Samda Hall A
Chair: **Jihye Kim** (Hannam University)

GS1-8 **16:30-16:40**

Exploring the molecular mechanism that mediates N-induced stem growth in tomato plants

So-hyun Kim, Zion Lee, Seung-won Park, Min-seo Kim, Jae-Sung Shim*

School of Biological Sciences and Technology, Chonnam National University, Gwangju 61186, Republic of Korea

GS1-9 **16:40-16:50**

Anti-inflammatory and Antioxidant Activities of *Platycodon grandiflorum* Root Extract Fermented with *Weissella cibaria* HY207

Min-Jung Park, Sun-Chul Kang*

Department of Biotechnology, Daegu University, Gyeongsan 38453, Republic of Korea

GS1-10 **16:50-17:00**

Isolation and identification of chemical constituents from aerial part of *Lespedeza cyrtobotrya* Miq.

Su-Ah Lee[1,2], Hyoung-Geun Kim[1], Taehoon Oh[3], Sung-Kyun Ko[3], Jung-Hee Kim[1], Su-Yeon Lee[1], In-Seo Heo[1], Seon Min Oh[1], Jongmin Ahn[1], Hyung Won Ryu[1], Dongho Lee[4]*, Sei-Ryang Oh[1]*

[1]Natural Product Research Center and Natural Product Central Bank, KRIBB, 30-Yeongudanji-ro, Ochang-eup, Cheongwon-gu, Cheongju-si, Chungbuk 28116, Republic of Korea, [2]College of Pharmacy, Graduate School of Pharmaceutical Sciences, Ewha Womans University, 52, Ewhyeodae-gil, Seodaemun-gu, Seoul 03760, Republic of Korea, [3]Chemical Biology Research Center, Korea Research Institute of Bioscience and Biotechnology (KRIBB), Cheongju 28116, Republic of Korea, [4]Department of Plant Biotechnology, Collede of Life Sciences and Biotechnology, Korea University, Seoul 02841, Republic of Korea

GS1-11 **17:00-17:10**

Applying *in vitro* propagation and smart farming for the conservation and sustainable production of *Polygonum multiflorum*

Kenneth Happy[1,2], Youngmin Kang[1,2]*

[1]Korean Medicine Convergence Science Major of KIOM School, University of Science and Technology (UST), Daejeon 34113, Republic of Korea, [2]Herbal Medicine Resources Research Center, Korea Institute of Oriental Medicine (KIOM), 111 Geonjae-ro, Naju-si, Jeollanam-do 58245, Republic of Korea

GS1-12 **17:10-17:20**

Schisandrin C Originating from *Schisandra chinensis* Alleviates Depression by Modulating Gut-Brain Axis

Son Hung Tran[1,2], Hyeonseong Lee[1], Siqi Zhang[1,2], Keunwan Park[1], Emmanuel Hitayezu[1], Won Kyu Kim[1,2], Uyen Tran Tu Nguyen[1,2], Sohyun Lee[1,2], Kwanghyun Cha[1,2], Jaeyoung Kwon[1,2], Joonki Kim[1,2], Kyungsu Kang[1,2*]

[1]Gangneung Institute of Natural Products, Korea Institute of Science and Technology, Gangneung, Gangwon-do 25451, Republic of Korea, [2]Natural Product Applied Science, KIST School, University of Science and Technology (UST), Gangneung, Gangwon-do 25451, Republic of Korea

GS1-13 **17:20-17:30**

Anti-Inflammatory Effect of Fermented and Aged Mountain-Cultivated Ginseng Sprout and Its Major Component, Compound K, in an LPS-induced Acute Respiratory Distress Syndrome Mouse Model

Dang Long Cao[1,2], Min-Seok Woo[1], Eun-Jin Kim[1], Sang Soo Kang[2,3], Kye Man Cho[4], Dawon Kang[1,2*]

[1]Department of Physiology and Institute of Medical Sciences, College of Medicine, Gyeongsang National University, Jinju 52727, Republic of Korea, [2]Department of Convergence Medical Science, Gyeongsang National University, Jinju 52727, Republic of Korea, [3]Department of Anatomy and Institute of Health Sciences, College of Medicine, Gyeongsang National University, Jinju 52727, Republic of Korea, [4]Department of GreenBio Science and Agri-Food Bio Convergence Institute, Gyeongsang National University, Jinju 52727, Republic of Korea

GS1-14 **17:30-17:40**

Development of an Alginate-based Hydrogel Incorporating Alginate Oligomers and Antibacterial Peptides for Wound Healing Applications

Yu Bin Kim, Yeon Jong Koo*

Department of Agricultural Chemistry, Chonnam National University, Gwangju 61186, Republic of Korea

GS1-15 **17:40-17:50**

Optimization of Peanut Sprout Extract for its potential lipid-lowering effects via AMPK activation in murine and canine adipose tissue derived mesenchymal stem cells

Jihye Choi[1], Hyun-jin Jang[1], Fang Feng[1], Sujin Kim[1], Thi My Tien Truong[1,2], Sihoon Park[3], Hyun Jung Kim[4], Ji Hee Lim[5], Inhae Kang[1,2*]

[1]Department of Food Science and Nutrition, Jeju National University, Jeju 63243, Republic of Korea, [2]Interdisciplinary Graduate Program in Advanced Convergence Technology and Science, Jeju National University, Jeju 63243, Republic of Korea, [3]Department of Food and Nutrition, Chosun University, Gwangju 61452, Republic of Korea, [4]Department of Food Bioengineering, Jeju National University, Jeju 63243, Republic of Korea, [5]OLAOLAB, Jeju 63359, Republic of Korea

GS2 Environmental Sciences / Applied Microbiology / Food Sciences

June 29 (Sun), Samda Hall B

Chair: **Sang-Ah Lee** (Jeju Nat'l University)

GS2-1 **15:10-15:20**

Perfluorooctanoic Acid Alters Ligand Affinity in Human Serum Albumin Without Structural Unfolding

Jihye Ahn[1], Moonsung Choi[2*]

[1]Department of Optometry, Seoul National University of Science & Technology, Seoul 01811, Republic of Korea, [2]Department of Biomedical Sciences, SeoulTech-KIRAMS Graduate Medical Sciences, Seoul National University of Science & Technology, Seoul 01811, Republic of Korea

GS2-2 **15:20-15:30**

Effect of co-digestion and thermal hydrolysis pretreatment on methane production from cow feces and tomato waste

Jae Gyeong Kim[1], Jeong Min Heo[1], Xin Zhao[3], Jin-Kyung Hong[4],
Eun Hea Jho[1,2*]

[1]Department of Agricultural Chemistry, Chonnam National University, Gwangju 61186, Republic of Korea, [2]Department of Agricultural and Biological Chemistry, Chonnam National University, Gwangju 61186, Republic of Korea, [3]Department of Civil and Environmental Engineering, Seoul National University, Seoul 08826, Republic of Korea, [4]Department of Environment and Energy Engineering, Chonnam National University, Gwangju 61186, Republic of Korea

GS2-3 **15:30-15:40**

Production of Poultry Manure Biochar and Evaluation of Its Potential as an Organic Fertilizer

Ikhyeong Lee[1], Han-Na Cho[1], Chang-Gon Lee[2], Ji-Min Song[2], Se-Won Kang[1,2*]

[1]Department of Agricultural Chemistry, Sunchon National University, Suncheon 57922, Republic of Korea, [2]Department of Agricultural Life Science, Scunchon National University, 57922, Republic of Korea

GS2-4 15:40-15:50

Development of Biochar Treatment Technology for Cyanobacteria Control

Jung-Mok Lee, Jae-Hoon Lee, Jun-Suk Rho, Seul-Rin Lee, Seung-Hoon Lee, Dong-Cheol Seo*

Division of Applied Life Science(BK21 Four) & Institute of Agricultural and Life Sciences, Gyeongsang National University, Jinju 52828, Republic of Korea

GS2-5 15:50-16:00

Can Ammonium Sulfate Reduce Ammonia Volatilization from a Rice Paddy Soil Compared to Urea

Jasmin Melendez[1], Yeomyeong Lee[1], Sohee Yoon[1], Sang Yoon Kim[1,2*]

[1]Department of Agricultural Chemistry & Interdisciplinary Program in IT-Bio Convergence System, Sunchon National University, Suncheon 57922, Republic of Korea, [2]Department of Agricultural Life Science, Sunchon National University, Suncheon 57922, Republic of Korea

GS2-6 16:00-16:10

Machine Learning-Based Prediction of Soil Nutrients Levels from Electrical Conductivity

Seung Jun Lee, Han Na Kim, Jeong Yeon Kim, Su Kyeong Shin, Ye Eun Lee, Jin Hee Park*

Department of Environmental Biological Chemistry, Chungbuk National University, Cheongju 28644, Republic of Korea

GS2-7 16:10-16:20

Suppression of Fusarium Wilt of *Cnidium officinale* Using Biocontrol Agents

Seok Hui Lee, Jun Yeong Park, Jun Won Kang*

Department of Forestry, Kyungpook National University, Daegu 41566, Republic of Korea

June 29 (Sun), Samda Hall B
Chair: **Ji-Hoon Lee** (Jeonbuk Nat'l University)

GS2-8 16:30-16:40

Impact Of Soil Amendments on Soil Microbiota and Plant Defense System: A Study on Beneficial Bacterium and Salicylic Acid in Cucumber Cultivation

Sandamali Harshani Kumari Hathurusinghe[1], Anushree Joshi[1], Tino Bashizi[1], Minsoo Jeong[1], Min-Ji Kim[1], Jae-Ho Shin[1,2*]

[1]Department of Applied Biosciences, Kyungpook National University, Daegu 41566, Republic of Korea, [2]NGS Core Facility, Kyungpook National University, Daegu 41566, Republic of Korea

GS2-9 16:40-16:50

Laccase-producing Bacterium *Pseudomonas palmensis* strain MSK1 isolated from a Plastisphere and its Potential for Decolorization of Synthetic Dyes

Miso Kim[1], Haeun Kim[2], Youri Yang[1,2*]

[1]Department of Food Biotechnology and Environmental Science, Kangwon National University, Chuncheon 24341, Republic of Korea, [2]School of Natural Resources and Environmental Sciences, Department of Biological Environment, Kangwon National University, Chuncheon 24341, Republic of Korea

GS2-10 16:50-17:00

Exploration of Nitrogen-fixing and Nitrous oxide-reducing Bacteria from Legume Roots and Soils

Seung Hwa Jeong[1], Hyeyeon Park[1], Yejin Seon[1], Sujin Lee[2], Yeonjong Koo[1*]

[1]Department of Agricultural Chemistry, Chonnam National University, Gwangju 61186, Republic of Korea, [2]Department of Environment and Energy Engineering, Gwangju Institute of Science and Technomogy, Gwangju, Republic of Korea

GS2-11 17:00-17:10

Microbial Community Dynamics in Municipal Wastewater and Livestock Manure Treatment Plants

Geon Choi[1], Hokyung Song[2], TatsuyaUnno[1*]

[1]Department of Biological Sciences and Biotechnology, Chungbuk National University, Seowon-Gu, Cheongju 28644, Republic of Korea, [2]Department of Environmental Engineering, Chosun University, Chosundae 5-gil 60, Dong-gu, Gwangju 61452, Republic of Korea

GS2-12 17:10-17:20

Metabolomic Insights into Korean Red Peppers across Cultivars and Postharvest Conditions

Hahyeong Yu[1], Kyung-Hyung Ku[2], Jeong-Ho Lim[3], Jihyun Lee[4*]

[1]Department of Food Science and Technology, Chung-Ang University, Anseong 17546, Republic of Korea, [2]Enterprise Solution Research Center, Korea Food Research Institute, Wanju 55365, Republic of Korea, [3]Smart Manufacturing Research Group, Korea Food Research Institute, Wanju 55365, Republic of Korea, [4]Department of Food and Nutrition, Seoul National University, Seoul 08826, Republic of Korea

GS2-13 17:20-17:30

Characterization and Immunomodulatory Effects of Alginate and *Sargassum fulvellum* Oligosaccharides Degraded by Crude Enzymes from *Shewanella oneidensis* PKA 1008

Ha-Young Lee, Dong-Hyun Ahn[*]

Department of Food Science and Technology, The Graduate School, Pukyong National University, Busan 48513, Republic of Korea

GS2-14 17:30-17:40

Comprehensive Evaluation and Field Validation of Chlorine Dioxide Washing Technology for Safety and Quality Maintenance in Red Pepper Powder

Jae-Yun Jo, In-Ung Jeong, Hyang-Hee Kim, Hyo-Sub Lee[*]

Chemical Safety Division, Agro-Food and Crop Protection Department, NAS, Wanju, Republic of Korea

GS2-15 17:40-17:50

Optimization of Heat-Moisture Treatment for Manufacturing Resistant Starch from Red Bean (*Vigna angularis* var. *nipponensis*)

Gangmi Nam, Jiyoung Shin, Junho Yang, Beom-Su Cho, Sanghwa Kang, Jisoo Han, Yeonhwa Park, Ji-Young Yang[*]

Department of Food Science and Technology, Pukyong National University, Busan 48513, Republic of Korea

K-Inno:Ven Star Audition

July 1 (Tue), 303

Chair: Moonsung Choi (Seoul Nat'l University of Science &Technology)

K-1 09:10-09:30

Upcycling Fish Processing By-Products into Functional pet food for Companion Animals

김욱철, 이윤수, 정서린

MBEL (순천향대학교 의료과학과)

K-2 09:30-09:50

팽미(米)

정종빈, 장무연, 김다현, 방도윤, 김혜림, 정예림

Space G (경상국립대학교 생명자원과학과)

K-3 09:50-10:10

식물 조직배양 기반 커피 내 생리활성 물질 생산 연구

김효정, 김지현, 이상민

Cellffee (부산대학교 생명환경화학과)

K-4 10:20-10:40

망팜 (망을 이용한 수경재배)

김혜민, 차형호, 박나윤

CKP (UST-KIST스쿨 천연물응용과학 전공)

K-5 10:40-11:00

정유성분/화산석을 활용한 천연항균 수건 건조기

이상윤

혼저 옵서예 (중앙대학교 식물생명공학과)

Poster Presentation

Poster Category

PBM	Biochemistry · Molecular Biology
PNB	Natural Products · Bioactive Materials · Biomedical Sciences
PES	Environmental Sciences
PFS	Food Sciences
PAM	Applied Microbiology
PBD	Bio-health/Drug development

Posting Time

Posting time for all Posters
June 29 (Sun) 14:00 ~ June 30 (Mon) 18:00

Poster Session

Category *Date*		**PBM**	**PNB**	**PES**	**PFS**	**PAM**	**PBD**
June 30 (Mon)	16:50-17:40	1-54	1-130	1-75	1-23	1-44	1-33
Place		**Lobby (3F)**					

각 세션의 제목을 클릭하면 해당페이지로 이동합니다.

PBM Biochemistry · Molecular Biology

PBM-1

Neuroprotective of Isoflavone-Enriched Soybean Leaves (Glycine Max) on the Scopolamine-Induced Memory Deficits in C57BL6 Mice via Antioxidative Mechanisms

Tae Woo Oh[1,2*], Seung-Woo Im[1,2]

[1]Korean Medicine (KM) Application Center, Korea Institute of Oriental Medicine (KIOM), [2]Korean Convergence Medicine Major KIOM, University of Science and Technology (UST)

PBM-2

Neuroprotective Effects of Dioscorea bulbifera L. Extract Against Glutamate-Induced Oxidative Stress and Apoptosis in HT22 Hippocampal Cells

Tae Woo Oh[1,2*], Seung-Woo Im[1,2]

[1]Korean Medicine (KM)-Application Center, Korea Institute of Oriental Medicine (KIOM), [2]Department of Korean Convergence Medical Science, University of Science & Technology (UST)

PBM-3

Tissue-Specific Expression and Developmental Regulation of *FAD2* and *FAD3* Genes Involved in Fatty Acid Biosynthesis in Milk Thistle

Hyun Uk Kim[*], Je-Hyeong Hong

Bioindustry and Bioresource Engineering, Sejong University

PBM-4

Study on the production of foot-and-mouth disease recombinant vaccine candidates using plant expression systems

Juho Lee[*], Woo-Hyun Jeong, Seon-Kyeong Lee, Kyeong-Ryeol Lee

National Institute of Agricultural Sciences, Rural Development Administration

PBM-5

Generation and validation of a LDL receptor reporter cell line for screening small molecules to treat hypercholesterolemia

Heungsop Shin[1*], Choogon Lee[2*], Jisun Lee[1], Jiyoung Park[2]

[1]Department of Chemical Engineering and Biotechnology, Tech University of Korea, [2]Department of Biomedical Sciences, Florida State University

PBM-6

Immunomodulatory potential of gamma-irradiated macrophage-derived exosomes

Hanui Lee[1], Gyeong Han Jeong[1], So-Yeun Woo[1], Hyoung-Woo Bai[1,2*], Byung Yeoup Chung[1*]

[1]Research division for Biotechnology, Advanced Radiation Technology Institute (ARTI), Korea Atomic Energy Research Institute (KAERI), [2]Radiation Biotechnology and Applied Radioisotope Science, University of Science and Technology (UST)

PBM-7

Enhancement of Tomato Fruit Sweetness by Targeted ALS1 Gene Editing

So Hee Yang, Yeonjong Koo[*]

Department of Agricultural Chemistry, Chonnam National University, Gwangju

PBM-8

Quantitative analysis of DNA-binding to UidR by fluorescence spectroscopy

Hyo Jin Song, Che-Hun Jung[*]

Department of Chemistry, Chonnam National University

PBM-9

PEP-associated protein 3 is a Key Regulator of Chloroplast Development in Rice

Deok Hyun Seo, Geupil Jang[*]

School of Biological Sciences and Technology, Chonnam National University

PBM-10

Bacillus velezensis Enhance Drought Tolerance in Rice

Dongryeol Park, Jinwoo Jang, Deok Hyun Seo, Geupil Jang[*]

School of Biological Sciences and Technology, Chonnam National University

PBM-11

Tongue tissue endoplasmic reticulum stress response in a DSS-induced colitis model from an oral-gut axis perspective

Young Ju Do[1,2], Su Yeon Seo[1,2*]

[1]Department of Oriental Medicine Research Division, Korea Institute of Oriental Medicine, [2]Department of Korea Convergence Medical Science, University of Science & Technology

PBM-12

Interactions of Isocitrate Dehydrogenase with DNA and guanine nucleotides

Jimin Min, Che-Hun Jung[*]

Department of Chemistry, Chonnam National University

PBM-13

Effects of Polysaccharide (Polycan) derived from Black Yeast in TNF-α induced Inflammation in the Intestinal Epithelial Cells and Loperamide- induced Constipation Models

Min Jeong Cho[1], Young-Suk Kim[1*], Bon-Hwa Ku[1], Seon Min Lee[2],
Tae Woo Oh[3,4*]

[1]R&D Center, Glucan co., [2]Center for Bio-Health Research, Korea Institute of Toxicology, [3]Korean Medicine (KM)-Application Center, Korea Institute of Oriental Medicine (KIOM), [4]Department of Korean Convergence Medical Science, University of Science & Technology(UST)

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PBM-14

Genetic engineering-driven overexpression of *SlVTE3* resulted in enhanced vitamin E accumulation in tomatoes

Ah Young Kim[1], Han Yong Lee[2]*

[1]Institute of Well-Aging Medicare & Chosun University G-LAMP Project group, Chosun University, [2]Department of Biology Science, College of Natural Science, Chosun University

PBM-15

Regulation of Rice Pollen Tube Growth by S1P-mediated Processing of pollen-expressed OsRALF peptides

Ji-Hyun Kim[1], Hyo-Jeong Kim[1], Ye-Jin Son[1], Eui-Jung Kim[2], Ki-Hong Jung[2], Yu-Jin Kim[1]*

[1]Department of Life Science and Environmental Biochemistry, and Life and Industry Convergence Research Institute, Pusan National University, Miryang 50463, Republic of Korea, [2]Graduate School of Green Bio Science & Crop Biotech Institute, Kyung Hee University, Yongin 17104, Republic of Korea

PBM-16

OsRALF4, a RALF peptide conserved in Poaceae species, functions as a key regulator of rice grain development via CrRLK1L signaling

Ji-Hyun Kim[1], Hyo-Jeong Kim[1], Ga-Young Noh[1], Ye-Jin Son[1], Do-Hyeon Kim[1], Eui-Jung Kim[2], Riya Tari[2], Woo-Jong Hong[2,3], Cheol Woo Min[4], Da Eun Kim[5], Byoung Il Je[5], Sun Tae Kim[4], Wanqi Liang[6], Ki-Hong Jung[2], Yu-Jin Kim[1]*

[1]Department of Life Science and Environmental Biochemistry, Life and Industry Convergence Research Institute, Pusan National University, Miryang 50463, Republic of Korea, [2]Graduate School of Green Bio-Science & Crop Biotech Institute, Kyung Hee University, Yongin 17104, Republic of Korea, [3]Department of Smart Farm Science, Kyung Hee University, Yongin 17104, Republic of Korea, [4]Department of Plant Bioscience, Life and Industry Convergence Research Institute, Pusan National University, Miryang 50463, Republic of Korea, [5]Department of Horticultural Bioscience, College of Natural Resource and Life Science, Pusan National University, Miryang 50463, Republic of Korea, [6]Joint International Research Laboratory of Metabolic & Developmental Sciences, State Key Laboratory of Hybrid Rice, School of Life Sciences and Biotec, Shanghai Jiao Tong University, Shanghai, China

PBM-17

An Albino Seedling-Lethal Mutant Reveals a Key Regulator of Chloroplast Development in *Arabidopsis thaliana*

Jinhyeong Kim, Geupil Jang*

School of Biological Sciences and Technology, Chonnam National University

PBM-18

Non-secreted peptide OsRALF5 regulate pollen tube growth in *Oryza sativa*

Hyo-Jeong Kim[1], Ji-Hyun Kim[1], Eui-Jung Kim[2], Ye-Jin Son[1], Ki-Hong Jung[2], Yu-Jin Kim[1]*

[1]Department of Life Science and Environmental Biochemistry, and Life and Industry Convergence Research Institute, Pusan National University, Miryang 50463, Republic of Korea, [2]Graduate School of Green Bio Science & Crop Biotech Institute, Kyung Hee University, Yongin 17104, Republic of Korea

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PBM-19

Enhancing Plant Stress Tolerance through ROS Control and Subcellular Targeting of Catalase

Yeonjong Koo*, Euyeon Kim

Agricultural Chemistry, Chonnam National University

PBM-20

Exploring the molecular mechanism that mediates N-induced stem growth in tomato plants

So Hyun Kim, Zion Lee, Seung Won Park, Min Seo Kang, Jae Sung Shim*

School of Biological Sciences and Technology, Chonnam National University

PBM-21

An *Ehd1*-independent short-day flowering pathway mediated by OsJAZ11 and OsMYC2 in rice

Gibeom Baek[1], Janghyun Choi[2], Hyeok Chan Kown[2,3], Jinmi Yoon[2,3], Lae-Hyeon Cho[1]*

[1]Department of Plant Bioscience, Pusan National University, Miryang 50463, Korea, [2]Department of Biological Sciences, Inha University, Incheon, Republic of Korea, [3]Department of Biological Sciences and Bioengineering, Inha University/Industry-Academia Interactive R&E Center for Bioprocess Innovation, Inha University, Incheon, Republic of Korea

PBM-22

The Role of the Nitrogen Use Efficiency-Related Gene HNI9 in Regulating Plant Growth under Salt Stress

Juyeon Park, Quang Tri Le, Hojoung Lee*

Department of Plant Biotechnology, College of Life Sciences and Biotechnology, Korea University, Anam-dong 5-ga, Seongbuk-gu, Seoul 136-713, Republic of Korea

PBM-23

Comparative leaf metabolomics of soybeans across seed coat colors and developmental stages

Vimalraj Mani[1], Soyoung Park[1], Sukhee Kim[2], Kong-Sik Shin[1], Kihun Ha[2]*

[1]Plant Biomaterials and Biotechnology division, National Institute of Agricultural Sciences, [2]National Institute of Agricultural Sciences, Plant Biomaterials and Biotechnology division

PBM-24

Physiological and Cytological Responses of Sweet Potato 'Tongchaeru' to Irrigation Water Salinity in the Saemangeum Reclaimed Land

Young Tae Shin[1], Hyeoun Suk Cho[1]*, Gyung Ran Do[2], Mi Nam Chung[3]

[1]Reclaimed Land Agriculture Research Center, National Institute of Crop Science, [2]Postharvest Technology Division, National Institute of Horticultural and Herbal Science, [3]Value Crop Research Institute, National Institute of Crop Science

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PBM-25

UGT74E2 Negatively Regulates Salt Stress Tolerance in Arabidopsis by Modulating IBA Glycosylation

Eun Kyu Ko, Hojoung Lee*

Department of Plant Biotechnology, College of Life Sciences and Biotechnology, Korea University, Anam-dong 5-ga, Seongbuk-gu, Seoul 136-713, Republic of Korea

PBM-26

Neurotrophic Effects of *Foeniculum vulgare* Ethanol Extracts on Hippocampal Neurons: Role of Anethole in Neurite Outgrowth and Synaptic Development

Sarmin Ummey Habiba[1,2*], In-Jun Yang[3], Il Soo Moon[4], Ho Jin Choi[5,6], Yeasmin Akter Munni[7], Tran Khoa Nguyen[7], Mac Gia Linh[3]

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PBM-27

Venom gland profiling of three korean *Gloydius* species and recombinant expression of major toxins

Park Hyo Sun[1], Yeon-Jong Koo[1*], Su-Jin Lee[2]

[1]Agricultural Chemistry, Chonnam National University, [2]Earth Sciences and Environmental Engineering, Gwangju Institute of Science and Technology (GIST)

PBM-28

Natural variation-driven regulation of temperature- and photoperiod-responsive flowering by FLC and FLC family genes: A potetntial regulatory hub for combating climate change

Zeeshan Nasim*, Nouroz Karim, Ji Hoon Ahn, Eunkyoo Oh*

Department of Molecular Life Sciences, Korea University, Seoul, South Korea

PBM-29

Development of Recombinase Polymerase Amplification (RPA) method for detection of Herbicide-resistant GM crops

Su-Jin Song, An-Cheol Chang, Doh-Won Yun, Jong-Chan Park, Sung Dug Oh*

Department of Agricultural Biotechnology, National Institute of Agricultural Sciences

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PBM-30

Mutation of *SlNRTF3* promotes growth under N-limiting conditions through activation of nitrogen assimilation pathway

Zion Lee, So-Hyun Kim, Min-Seo Kang, Seung-Won Park, Jae-Sung Shim*

School of Biological Sciences and Technology, Chonnam National University

PBM-31

CRISPR-Cas9 Genome Editing in Tomato Using In Vivo Cas9/tracrRNA Expression and Exogenous crRNA

Yaerim Lee, Yeonjong Koo*

Department of Agricultural Chemistry, Chonnam National University

PBM-32

Aureimonas Altamirensis DSM 21988 as a Dual-Function Agent: Promoting Rice Growth and Inducing Systemic Resistance Against Bacterial Blight

Navid Iqbal[1], Youngchul Yoo[1], Sang Won Lee[1,2]*

[1]Department of Genetic Engineering and Biotechnology, Kyung Hee University, Yongin 17104, Korea, [2]Department of Green-Bioscience, Kyung Hee University, Yongin 17104, Korea

PBM-33

Enhancement of Growth and Bioactive Compound Accumulation in Licorice Sprouts through Symbiotic Association with the Newly Isolated *Mixta theicola* QC88-366

Yong-Sung Park, Jin Ryeol Jeon, Sang-Mo Kang, In-Jung Lee*

Dep. of Applied Biosciences, Kyungpook National University

PBM-34

Determination of Platydin D Content by Cultivation Period of *Platycodon grandiflorum* through Plug Seedling Transplantation

Dong Yeol Lee[1]*, Yun Sook Kim[2], Sang Eun Lee[2], Won Min Jeong[1], Yeong In Choe[1], Dong Kyu Jeong[1]

[1]Research & Development Team, Gyeongnam Anti-Aging Research Institute, [2]Institute of Medicinal Resources, Gyeongsangnam-do Agricultural Research and Extension Services

PBM-35

Cadmium Stress Alleviation in Soybean(*Glycine max* L.) via Chitosan–Melatonin Nanoparticles: Hormonal and Metabolomic Mechanistic Analysis

Jin Ryeol Jeon, Ji-In Woo, Hye-Jin Kwon, Jun-Hwi Ha, Yong-Sung Park, Sang-Mo Kang, In-Jung Lee*

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PBM-36

Natural antisense transcript *OsDof2NAT* enhances early heading and drought tolerance by activating *Dof2* expression in rice

Choonkyun Jung*

Department of International Agricultural Technology, Seoul National University

PBM-37

Methyl Jasmonate Preharvest Treatment Activates Plant Defense System and Induces Glucosinolate Production in Wasabi (*Wasabia japonica* Matsum) Leaves

To Quyen Truong[1], Yeong Bin Choi[1,2], Phuong Kim Huynh[1,2], Sang Min Kim[1,2]*

[1]Smart Farm Research Center, Korea Institute of Science and Technology (KIST) Gangneung Institute of Natural Products, Gangneung 25451, Republic of Korea,
[2]Natural Product Applied Science, KIST School, University of Science and Technology, Gangneung 25451, Republic of Korea

PBM-38

Stage-Specific Effects of Sulfur Fertilization on Glucosinolate Production in *Wasabia japonica* Leaves

Ye Lin Kim[1], To Quyen Truong[1], Yeong Bin Choi[1,2], Phuong Kim Huynh[1,2], Sang Min Kim[1,2]*

[1]Smart Farm Research Center, Korea Institute of Science and Technology (KIST) Gangneung Institute of Natural Products, Gangneung 25451, Republic of Korea,
[2]Natural Product Applied Science, KIST School, University of Science and Technology, Gangneung 25451, Republic of Korea

PBM-39

In rice, Actin-related protein 2/3 complex 2B subunit (ARPC2B) regulates Gibberellin Biosynthesis, and overexpression of *OsARPC2B* gene increases Grain Yield

Seung Young Choi[1], Tae Young Um[2], Ik-Young Choi[1]*

[1]Department of Smart Farm and Agriculture Industry, Kangwon National University,
[2]Department of Plant Science, Gangneung-Wonju National University

PBM-40

In rice, microRNA171f regulates expression of *SCL6*, which is involved in drought tolerance and flavonoid biosynthesis

Yong Hun Song, Seung Muk Won, Ga Ram Kim, Kyeong Hee Lee, Taeyoung Um*

Department of Plant Science, Gangneung-Wonju National University

PBM-41

Fumigant Efficacy of Sulfuryl Fluoride Against *Sitophiluls zeamias* and Sorption Characteristics by Origin of Wood Pellets

Ga-Eul Lim[1], Na-Ra Choi[1], Hwan Hee Lee[2], Min-Goo Park[2]*

[1]Department of Agricultural Chemistry, Jeonbuk National University,
[2]Department of Bioenvironmental Chemistry, Jeonbuk National University

PBM-42

Efficacy of Phosphine Fumigation Against *Ostrinia furnacalis* in Sweet Pumpkin (*Cucurbita maxima*)

Oyun-Erdene Enkhjargal[1], Na-Ra Choi[1], So-Yeon Kim[1], Hwan Hee Lee[2], Jae Won Yoon[2], Min-Goo Park[2*]

[1]Department of Agricultural Chemistry, Jeonbuk National University, [2]Department of Bioenvironmental Chemistry, Jeonbuk National University

PBM-43

Development of Multiplex PCR Assays for Simultaneous Detection of Fungal and Viral Pathogens in *Cymbidium kanran*

Jiwon Kim[1], Sunyung Yoon[2], Seungtae Kang[3], Ho Bang Kim[4], Kyung-Hwan Boo[1,2*]

[1]Subtropical/Tropical Organism Gene Bank, Jeju National University, Jeju 63243, Republic of Korea, [2]Department of Biotechnology, College of Applied Life Science (SARI), Jeju National University, Jeju 63243, Republic of Korea, [3]Jeju Orchid Gallery, World Heritage Office, Jeju Special Self-Governing Provincial Government, Jeju 63341, Republic of Korea, [4]Department of Environmental Horticulture, School of Equine Science and Horticulture, Cheju Halla University, Jeju 63092, Republic of Korea

PBM-44

In vitro callus induction of *Psoralea corylifolia* and quantification of bakuchiol under varying plant hormone conditions

Na-Gyeol Hwang[1], Ye-Rin Kim[2], Chan-Woo Park[1], Hyo-Jeong Kim[1], Ji-Hyun Kim[1], Yeongju Lee[2], Yu-Jin Kim[1*]

[1]Department of Life Science and Environmental Biochemistry, and Life and Industry Convergence Research Institute, Pusan National University, [2]Department of Chemistry, Pusan National University

PBM-45

Farnesiferol B and kamolonol as potent BACE1 inhibitors with neuroprotective effects

Jong Min Oh[1,2], Woong-Hee Shin[3], Bomi Kim[4], Eonmi Kim[4], Hyun Ju Son[1], Hoon Kim[1*]

[1]Department of Pharmacy, College of Pharmacy, Sunchon National University, Suncheon 57922, Republic of Korea, [2]Korea Institute of Oriental Medicine, Naju 58245, Republic of Korea, [3]Department of Biomedical Informatics, College of Medicine, Korea University, Seoul 02708, Republic of Korea, [4]National Institute for Korean Medicine Development, Gyeongsan 38540, Republic of Korea

PBM-46

Drug Repurposing of D-Cycloserine: A New Approach to Inhibiting Melanogenesis in Cosmetic Science

Ye-Jin Lee, Hyun-Mi Kim, Chang-Gu Hyun[*]

Jeju Inside Agency & Cosmetic Science Center, Department of Chemistry and Cosmetics, Jeju National University

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PBM-47

Melanogenic Inhibitory and Immunoenhancing Effects of a Novel Lysinibacillus sp. JNUCC 51 Isolated from Baengnokdam, Mt. Halla, Jeju Island

Mi-Na Kim[1], Ji-Hyun Kim[1], Jun-Tae Bae[2], Chang-Gu Hyun[1*]

[1]Department of Chemistry and Cosmetics, Jeju Inside Agency and Cosmetic Science Center, Jeju National University, [2]Jeju Research Center, J2K Bio Co., Ltd

PBM-48

Brevibacillus jejuensis sp. nov., a Novel Species Isolated from Baengnokdam, the Summit Crater Lake of Mt. Halla: Complete Genome Sequencing, Taxonomic Characterization, and Potential Cosmetic Applications

Jeong-Ha Lee[1], Mi-Sun Ko[1], Kil-Teak Hwang[2], Chang-Gu Hyun[1*]

[1]Department of Chemistry and Cosmetics, Jeju Inside Agency and Cosmetic Science Center, Jeju National University, [2]Jeju Biotics R&D Center, TwinChem Co., Ltd.

PBM-49

Regulation of Flowering Time under Natural Sunlight Conditions by Multiple Florigens in Plants

Nayoung Lee[1*], Hiroshi Takagi[2,3], Takato Imaizumi[2,3], Moonhyuk Kwon[1,4*]

[1]Research Institute of Molecular Alchemy, Gyeongsang National University, Jinju 52828, Republic of Korea, [2]Department of Biology, University of Washington, Seattle, Washington, 98195-1800, USA, [3]Center for Gene Research, Nagoya University, Nagoya, 464-8602, Japan, [4]Division of Applied Life Science (BK21 Four), ABC-RLRC, Gyeongsang National University, Jinju 52828, Republic of Korea

PBM-50

Impact of Brassicaceae Biofumigation on Cucurbit Growth and Soil Microbiome

Ga-Yeon Nam[1], Dokyung Lee[2*], Jae-Ho Shin[1,2,3,4*]

[1]Department of Applied Biosciences, Kyungpook National University, Daehak-ro 80, Daegu 41566, Republic of Korea, [2]Department of Integrative Biology, Kyungpook National University, Daehak-ro 80, Daegu 41566, Republic of Korea, [3]NGS Core Facility, Kyungpook National University, Daehak-ro 80, Daegu 41566, Republic of Korea, [4]MICROBALANCE Co., Ltd., Kyungpook National University, Daehak-ro 80, Daegu 41566, Republic of Korea

PBM-51

Integrative Meta-Transcriptomic and Machine Learning Reveal Key Genes Conferring Resistance to *Magnaporthe oryzae* in Rice

Babar Usman[1], Gi Hyun Lee[1], Cheol Woo Min[1], Yiming Wang[2], Ravi Gupta[3], Sun Tae Kim[1*]

[1]Department of Plant Bioscience, Life and Industry Convergence Research Institute, Pusan National University, Miryang 50463, Republic of Korea, [2]Department of Plant Pathology, Key Laboratory of Integrated Management of Crop Disease and Pests, Ministry of Education, Nanjing Agricultural University, Nanjing, China, [3]College of General Education, Plant Stress Physiology and Proteomics Laboratory, Kookmin University, Seoul, South Korea

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PBM-52

Genomic insight into Seed Longevity in *Oryza sativa* cultivar. Dharial

Smita Mirsyad Warsadiharja[1], Sung Hoon Kim[2], Soon Ju Park[1]*

[1]Division of Applied Life Science and Plant Molecular Biology and Biotechnology Research Center, Gyeongsang National University, Jinju 52828, Korea, [2]Department of Southern Area Crop Science, National Institute of Crop Science, Rural Development Administration, Miryang 50424, Korea

PBM-53

PVP-Induced Aggregation of Lysozyme with Minimal Structural Change Leads to Enzymatic Inhibition

So-hyeon Park[2], Moonsung Choi[1,2]*

[1]Department of Biomedical Sciences, SeoulTech-KIRAMS Graduate Medical Sciences, Seoul National University of Science and Technology, Seoul 01811, Republic of Korea, [2]Department of Optometry, Seoul National University of Science and Technology, Seoul 01811, Republic of Korea

PBM-54

Structural Variation Alters Spinosyn A and D Binding Sites on B-Form Bovine Serum Albumin

Hayoung Kim[2], Moonsung Choi[1,2]*

[1]Department of Biomedical Sciences, SeoulTech-KIRAMS Graduate Medical Sciences, Seoul National University of Science and Technology, Seoul 01811, Republic of Korea, [2]Department of Optometry, Seoul National University of Science and Technology, Seoul 01811, Republic of Korea

PNB Natural Products · Bioactive Materials · Biomedical Sciences

PNB-1

Modulation of Mitochondrial Apoptosis and Iron Metabolism by 6-Gingerol in Non-Small Cell Lung Cancer Cells

Se Won Bae[1]*, Hyunjoo Lee[2]

[1]Department of Chemistry and Cosmetics, Jeju National University, [2]Department of International Business and Accountancy, Cheju Halla University

PNB-2

Enhanced Antioxidant Activity of Alkylated Protocatechuic Acid Derivatives in Human Dermal Fibroblasts

Se Won Bae[1]*, Hyunjoo Lee[2]

[1]Department of Chemistry and Cosmetics, Jeju National University, [2]Department of International Business and Accountancy, Cheju Halla University

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PNB-3

Davallia mariesii Moore Improves Fc ε RI-Mediated Allergic Responses in the Rat Basophilic Leukemia Mast Cell Line RBL-2H3 and Passive Cutaneous Anaphylaxis in Mice

Hyun Ju Do[1], Tae Woo Oh[2*]

[1]New Drug Development Center, Daegu Gyeongbuk Medical Innovation Foundation (K-MEDIhub), [2]Korean Medicine Application Center, Korea Institute of Oriental Medicine

PNB-4

Effect of Black Raspberry on Lipid Metabolism-Related Gene Expression in High-Fat and Fructose-Fed Rats

Sun Young Park[1*], Seon Beom Kim[1,2], Myunghoo Kim[1,3]

[1]Institute for Future Earth, Pusan National University, [2]Department of Food Science & Technology, Pusan National University, [3]Department of Animal Science, Pusan National University

PNB-5

Hydroxymethylation of Chlorogenic Acid by Radiolysis with Potent Anti-Inflammatory Agent

Gyeong Han Jeong, Hanui Lee, So-Yeun Woo, Hyoung-Woo Bai, Byung Yeoup Chung*

Research division for Biotechnology, Advanced Radiation Technology Institute (ARTI), Korea Atomic Energy Research Institute (KAERI)

PNB-6

The innovated approach from raw materials to final products by co-steam processing: Biological efficacy improvement of KIOM processed *Polygonum multiflorum* as ethnomedicine with enhanced marker compounds

Yeongjun Ban[1], Roggers Gang[1,2], Kenneth Happy[1,2], Mudondo Joyce[1,2], Ariranur Haniffadli[1,2], Kyeong-Ok Choi[1], Subeen Mun[1], Seyoung Im[1], Youngmin Kang[1,2*]

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[2]Korean Convergence Medical Science major, University of Science & Technology (UST), Korea Institute of Oriental Medicine, Daejeon 34054, Republic of Korea

PNB-7

Trichosanthis Radix: Ethnomedicinal Uses, Phytochemistry, Pharmacology, Quality Control, and Toxicology

Joyce Mudondo[1,2], Kenneth Happy[1,2], Ariranur Haniffadli[1,2], Roggers Gang[1,2], Yeoungjun Ban[2], Kyeong-Ok Choi[2], Subeen Mun[2], Seyoung Im[2], Youngmin Kang[1,2*]

[1]Korean Convergence Medical Science major, University of Science & Technology (UST), Korea Institute of Oriental Medicine, Daejeon 34054, Republic of Korea,
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PNB-8

Database of functional activities and flavonoid content of extracts from the Freshwater Bioresources Culture Collection (FBCC)

Su Young Shin[1], Jeong Ho Kim[1], Ye Ji Hwang[1], Young Teak Oh[1],
Young Jin Park[2], Seokjae Park[3*], Tae Jin Kim[1*]

[1]Using Technology Development Department, Bio-resources Research Division, Nakdonggang National Institute of Biological Resources, Gyeongsangbuk-do 37242, Republic of Korea, [2]Division of Life Sciences, College of Life Sciences and Bioengineering, Incheon National University, Incheon 22012, Republic of Korea, [3]Neurometabolomics Research Center, Daegu Gyeongbuk Institute of Science and Technology, Daegu 42988, Republic of Korea

PNB-9

Finger Print Analysis for Quality Assurance of Perilla Leaves and Quality Variations in Korean Products

Hyun-Gyeong Lee[1], Ye-In Joo[1], Soo-Bin Choi[1], Je-Ho Lee[2], Mi-Yeong An[2],
Seong-Ho Ham[1*]

[1]Institute of Phytomedical Research & Development, Korea Syntex Pharm. Co., Ltd, [2]Preclinical Efficacy Department, Daehan Cell Pharm INC

PNB-10

Non-targeted metabolomics reveals anorectic compounds from *Acer pseudosieboldianum* extracts

Jeong Ho Kim[1], Su Young Shin[1], Ye Ji Hwang[1], Young Teak Oh[1],
Young Jin Park[2], Seokjae Park[3*], Tae Jin Kim[1*]

[1]Using Technology Development Department, Bio-resources Research Division, Nakdonggang National Institute of Biological Resources, Gyeongsangbuk-do 37242, Republic of Korea, [2]Division of Life Sciences, College of Life Sciences and Bioengineering, Incheon National University, Incheon 22012, Korea, [3]Neurometabolomics Research Center, Daegu Gyeongbuk Institute of Science and Technology, Daegu 42988, Republic of Korea

PNB-11

Development of an Alginate-based Hydrogel Incorporating Alginate Oligomers and Antibacterial Peptides for Wound Healing Applications

Yu Bin Kim, Yeonjong Koo*

Department of Agricultural Chemistry, Chonnam National University

PNB-12

Physiological Effects of a Cannabidiol-Encapsulated Nanoemulsion for Therapeutic and Nutraceutical Applications

Eui-Baek Byun*, Yuna Lee, Ha-Yeon Song, Bo-Gyeong Yoo, Jaeyoon Lim,
Sang Hoon Kim

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Korea Atomic Energy Research Institute*

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PNB-13

Immunomodulatory Effects of Ethanol-Extracted Ginseng Sprouts via the HO-1/NF-κB Pathway in an LPS-Induced Macrophage Model: Potential for Cytokine Storm Mitigation

Mi-Yeong An[1], Je-Ho Lee[1], Eunji Ko[1], Seongho Ham[2], Hyun-Gyeong Lee[2], Young-Yil Kim[1*]

[1]Preclinical Efficacy Department, Daehan Cell Pharm INC,
[2]Institute of Phytomedical Research & Development, Korea Syntex Pharm. Co., Ltd

PNB-14

Structure-Based Discovery of Anticancer Peptides from Channa argus: A Traditional Bio-Source Applied to In Silico Screening

Sun Young Park, Namhyun Chung*

Department of Biotechnology, College of Life Sciences & Biotechnology, Korea University

PNB-15

Anticancer effect of peptide W-0094 derived from Anoplophoa glabripennis

Se Hoon Kim, Namhyun Chung*

Korea University, Department of Biotechnology

PNB-16

Validation of analytical methods for *Rosa rugosa*'s flower buds water extracts for standardization as functional ingredients

Bo-Ram Kim, Su Hui Seong, Tae-Su Kim, Jin-Ho Kim, Chan Seo, Ha-Nul Lee, Sua Im, Jung Eun Kim, Ji Min Jung, Kyung-Min Choi, Jin-Woo Jeong*

Division of Natural Product Research, Honam National Institute of Biological Resources, Mokpo 58762, Republic of Korea

PNB-17

Evaluation of modified benzaldehyde derivatives as dual α-glucosidase and α-amylase inhibitors: a viable alternative to acarbose

Na-Hyun Lee, Namhyun Chung*

Department of Biotechnology, Korea University

PNB-18

Comparative Analysis of Allithiamine Content in Garlic-Based Grain Mixtures

Chang-Dae Lee[1], Neil Patrick Uy[1], Sang-Yun Lee[1], Jiheong Chae[2], Minju Kim[2], Minah Jang[2], Eunju Ye[2], Jungwook Kim[2], Sanghyun Lee[1,3*]

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PNB-19

Optimization of Quadrupole Type Mass Spectrometer Conditions for the Quantitative Analysis of Platycosides in Divalent Form

Mi-Jeong Lee*, Geun-Hyoung Choi, Si Myoung Lee

Advanced Analysis Team, Planning & Coordination Division, National Institute of Agricultural Sciences, Rural Development Administration, Wanju 55365, Republic of Korea

PNB-20

Elucidating the Mode of Action of Sorgoleone Analogs via Metabolomics

Jung-Hoon Lee[1,2], Min-Ho Song[1], Eun-Song Choi[1,2], Geon-Woo Park[3], Ji-Won Shin[3], Ha-Jin Son[3], Ji-Yeon Lee[3], Hui-Yeon Ahn[4], Young Soo Keum[3], Ji-Ho Lee[1,2]*

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PNB-21

Structural Effects of Ginsenosides on Inhibiting α-Amylase and α-Glucosidases for Regulating the Postprandial Glycemic Response

Oshini N. P. Idigahawala Gamage, Jongbin Lim*

Department of Food Bioengineering, Jeju National University, Jeju 63243, Republic of Korea

PNB-22

The standardization of the RNA content test and the encapsulation percentage test for mRNA vaccine

Tae Hyung Kim, Hyo Eun Kang, Miran Jo, Joon Ik Ahn, Suk-Bae Lee, Kyung Hee Sohn*

Vaccine Division, Biopharmaceuticals & Herbal Medicine Evaluation Department, National Institute of Food and Drug Safety Evaluation

PNB-23

Ameliorative Effects of a Phenolic Glycoside from *Castanopsis echinocarpa* on Sensorineural Hearing Loss and Its Mechanistic Insights via Molecular Docking Analysis

Sunbeom Kwon[1], Sung Woo Shin[1], Youn Hee Nam[2], Tong Ho Kang[1], Seulah Lee[1]*

[1]Department of Convergent Biotechnology and Advanced Materials Science, College of Life Sciences, Kyung Hee University, Yongin 17104, Republic of Korea, [2]Invivotec Co., Ltd., Seongnam 13449, Republic of Korea

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PNB-24

Photosensitizer Candidates from Marine *Streptomyces* sp. ME-0223

Hee-Tae Yeo[1,2], Jun Su Park[1], Na Yul Woo[1,3], Jin-Soo Park[1,2*]

[1]Natural Product Systems Biology Center, Korea Institute of Science and Technology, [2]Natural Product Applied Science, KIST School, University of Science and Technology, [3]Department of Biology, Gangneung-Wonju National University

PNB-25

Evaluation of Natural Red Argan Oil-Based Complex on Skin Barrier Recovery and Elasticity Enhancement

Su Min Son, Hyungwoo Jo, Dong-Geol Lee, Seunghyun Kang[*]

Research and Innovation Center, COSMAX BTI

PNB-26

Identification of molecular targets and therapeutic potential of ginsenosides through proteome-wide profiling

Dohyeon Kim[1,2], Charuvaka Muvva[1], Keunwan Park[1*]

[1]Center for Natural Product Systems Biology, Korea Institute of Science and Technology, Gangneung 25451, Republic of Korea, [2]Department of Bioinformatics and Life Science, Soongsil University, Seoul 06978, Republic of Korea

PNB-27

An undescribed anti-inflammatory meroterpenoid from the brown alga *Sargassum macrocarpum*

Ji-Yul Kim[*], Gun-Woo Oh, Seok-Chun Ko, Kyung Woo Kim, Dongwoo Yang, Mi-Jin Yim, Jeong Min Lee, Du-Min Jo, Grace Choi, Dae-Sung Lee[*]

Department of Biomaterial Research, National Marine Biodiversity Institute of Korea, Seocheon, Republic of Korea

PNB-28

In vitro Screening of Adipogenesis Inhibitory Effect of Halophyte Plant Extracts for Potential Anti-obesity Treatment

Seok-Chun Ko[1], Kyung Woo Kim[1], Ji-Yul Kim[1], Gun-Woo Oh[1], Jung Min Lee[2], Mi-Jin Yim[2], Jae-Young Je[3], Dae-Sung Lee[4*]

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PNB-29

Effects of Fermented Polygonum cuspidatum on the Skeletal Muscle Functions

Young-Seon Kim[1,2,3], Ji-Hong Lim[1,2,4*], Ji-Hye Han[3], Chang-Hoon Lim[1,2,4], Xue-Quan Fang[1,2,4], Hyeock-Soon Jang[3], Sang-Yun Lee[3], Woo-Jong Yim[3]

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PNB-30

Comparative Analysis of Chlorogenic Acid and Eleutheroside E in the Stems of *Eleutherococcus sessiliflorus* from Wild and Cultivated Environments

Yonghwan Son, Dong Hwan Lee, Dae Hui Jeong, Ji Ah Kim*

Forest Medicinal Resources Research Center, National Institute of Forest Science

PNB-31

Isatin derivatives as promising inhibitors of SARS-CoV-2 Main Protease (Mpro)

Md Sofequl Islam Mukim, Dae-Geun Song*

Natural Products Systems Biology Research Center, Korea Institute of Science & Technology (KIST)

PNB-32

Integrated Genomics and Metabolomics for Isoflavone-Enriched Soybean Resource Discovery and Functional Characterization

Soyoung Park*, Kihun Ha, Mani Vimalraj, Mi-Suk Seo, Kong-Sik Shin, Eunchan Lee

Plant Biomaterials and Biotechnology Division, Department of Agricultural Biology, National Institute of Agricultural Sciences, RDA

PNB-33

Anti-Inflammatory Effect of Fermented and Aged Mountain-Cultivated Ginseng Sprout and Its Major Component, Compound K, in an LPS-induced Acute Respiratory Distress Syndrome Mouse Model

Dang Long Cao[1,2], Min- Seok Woo[1], Eun- Jin Kim[1], Sang Soo Kang[2,3], Kye Man Cho[4], Dawon Kang[1,2]*

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PNB-34

Mitigation of Salinity Stress via Improving Growth and Nutrient Uptake in *Raphanus sativus* L. with Biochar

Rathinapriya Periyasamy, Tae-Jun Lim, Byeongeun Kang, Seung Tak Jeong*

Horticultural and Herbal Crop Environment Division, National Institute of Horticultural and Herbal Science

PNB-35

Sex-Specific Behavioral and Sleep Architecture Alterations Induced by Sleep Deprivation in Mice

Mac Gia Linh, Tran Khoa Nguyen, Sarmin Ummey Habiba, Yeasmin Akter Munni, Yang In - Jun*

Department of Physiology, College of Korean Medicine, Dongguk University, Gyeongju, South Korea

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PNB-36

Anti-inflammatory Effects of Plasma-Induced Phloridzin Derivatives in LPS-stimulated RAW 264.7 Macrophages

So-Yeun Woo, Gyeong Han Jeong, Hanui Lee, Hyoung-Woo Bai,
Seung Sik Lee, Jin-Hong Kim, Kwang-Woo Jung, Moon-Soo Chung,
Byung Yeoup Chung*

Division for Radiation Biotechnology, Advanced Radiation Technology Institute (ARTI), Korea Atomic Energy Research Institute (KAERI)

PNB-37

Metabolomic profiling evaluation of drought-tolerant transgenic rice

Gyeong-Min Lee, Sung-Dug Oh, Hyun-Min Park, Seon-Woo Oh,
Sang-Gu Lee, Jong-Chan Park, An-Cheol Chang*

Department of Agricultural Biotechnology, National Institute of Agricultural Sciences

PNB-38

Correlation Analysis between Metabolites and Ginsenosides of Wild-Simulated Ginseng with Different Harvest Times

Myeongbin Park, Yeong-Bae Yun, Yurry Um*

Forest Medicinal Resources Research Center, National Institute of Forest Science

PNB-39

Chemical Profiling of Flavonoid Glycosides in *Quercus mongolica* Pollen Using LC-MS/MS-Based Molecular Networking

Yerim Joo[1,2], Eunbeen Shin[1,2], Seon Beom Kim[1,2,3]*

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PNB-40

Effects of Irrigation Water Salinity on Growth and Bioactive Compound Activity of Sweet Potato (*Ipomoea batatas*) in the Saemangeum Reclaimed Land

Hyeounsuk Cho[1]*, Mija Lee[2], Young Tae Shin[1], Hak-Seong Lee[1],
Kwang-Seung Lee[1], Hyunsoo Jang[1], Bang-Hun Kang[1], Sang-Young Jeong[1],
Hee-Kyoung Ok[1]

[1]Reclaimed Land Agriculture Research Center, National Institute of Crop Science, [2]Fermented and Processed Food Research Division, National Institute of Crop Science

PNB-41

Multifunctional Skin Benefits of Hot Water Extract from the Improved Cultivar of *Camellia japonica* 'Double-Flowered Camellia'

Ho Bong Hyun, So Yeon Oh, Seon-A Yoon, Sung Chun Kim, Jin Hwang,
Boram Go, Hyejin Hyeon, Ji Gwon Park, Young-Min Ham*

Biodiversity Research Institute, Jeju Technopark

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PNB-42

Luteolin-mediated GDH1 inhibition suppresses colon cancer progression via autophagy and angiogenesis pathways

Himanshi Gahlot, Sun Chul Kang*

Department of Biotechnology, Daegu University

PNB-43

Kaempferol induces apoptosis and suppresses proliferation and migration in colon cancer via hypoxia-mediated inhibition of HIF-1α/VEGF and Wnt/β-Catenin signalling

Muhammad Haroon, Sun Chul Kang*

Department of Biotechnology, Daegu University

PNB-44

Comparison of Inflammatory Cytokine Levels in Blood from Patients with Pancreatic Cancer Before and After Surgery/Chemotherapy

Dong Jae Lee[1], Thuy Thi Thanh Phan[1,2], Moonho Kim[3], Dae-Geun Song[1,4]*

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PNB-45

Isolation and Characterization of Megastigmane Derivatives from *Ardisia humilis* Val Leaves Extract

Alfan Danny Arbianto[1,2], Byeongjin Ro[1], Ja-Gyeong Song[1], Jongmin Ahn[1], Hyung Won Ryu[1], Sei-Ryang Oh[1,2]*

[1]Natural Product Research Center, Korea Research Institute of Bioscience & Biotechnology, [2]KRIBB School, University of Science and Technology

PNB-46

Identification and quantification of trans-anethole in *Foeniculum vulgare* Mill. (Fennel) grown in Korea

Soyoung Shin, Jaehee Hyun*, Youngmi Kim, Wookyu Lee, Jaeuk Seo, Changsoo Kim, Jinhee Hwang

National Center for Medicinal Resources Management, Herbal Medicine Research Division, National Institute of Food and Drug Safety Evaluation, Ministry of Food and Drug Safety

PNB-47

Cognitive-enhancing effects of subtropical natural resource extracts

Min Seong Park, Hyejun Jo, Gwang Pyo Ko, Kyung Hwan Boo, Chang Sook Kim*

Department of Biotechnology, Jeju National University, Jeju 63243, Republic of Korea

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PNB-48

Efficient Separation of Spinach-Derived Saponins Using Twin-Column N-Rich Technique

Su-Yeon Lee[1,2], Doo-Young Kim[1], Chan-Yang Lee[3], Bong-Soo Lee[3], Hyung Won Ryu[1*]

[1]Natural Product Research Center and Natural Product Central Bank, KRIBB, [2]College of Pharmacy, Graduate School of Pharmaceutical Sciences, Ewha Womans University, [3]Research Center, YMC Korea

PNB-49

Stage-Specific Anti-Cancer Metabolites from *Paulownia tomentosa* Fruit Identified by UPLC-QTOF/MS

In Seo Heo[1,2], Seon Min Oh[1], Eun-Bin Kwon[1], Myung-Ji Kang[1], Mun-Ock Kim[1], Su-Yeon Lee[1], Hyoung-Geun Kim[1], Doo-Young Kim[1], Hyung Won Ryu[1], Eun Kyoung Seo[2*], Sei-Ryang Oh[1*]

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PNB-50

Inhibitions of monoamine oxidase A and B by new bioactive flavonoid glycosides isolation from aerial part of *Lespedeza cyrtobotrya* Miq.

Su-Ah Lee[1,2], Hyoung-Geun Kim[1], Taehoon Oh[3], Sung-Kyun Ko[3], Jung-Hee Kim[1], Su-Yeon Lee[1], In-Seo Heo[1], Seon Min Oh[1], Jongmin Ahn[1], Hyung Won Ryu[1], Dongho Lee[4*], Sei-Ryang Oh[1*]

[1]Natural Product Research Center and Natural Product Central Bank, KRIBB, [2]College of Pharmacy, Graduate School of Pharmaceutical Sciences, Ewha Womans University, [3]Chemical Biology Research Center, KRIBB, [4]Department of Plant Biotechnology, College of Life Sciences and Biotechnology, Korea University

PNB-51

Discrimination of *Oenothera* Species using UPLC-QTOF/MS-Based Metabolomics

Byeongjin Ro[1,2], Seon Min Oh[1], Jongmin Ahn[1], Jung-Hee Kim[1], Ja-Gyeong Song[1], Jeong-Eun Ahn[1], Sei-Ryang Oh[1], Bang Yeon Hwang[2*], Hyung Won Ryu[1*]

[1]Natural Product Research Center and Natural Product Central Bank, KRIBB, [2]College of Pharmacy, Chungbuk National University

PNB-52

Application of a Validated UPLC-CAD Method to Evaluate Saponin Content Variation in Spinach across Cultivars and Seasons

Su-Yeon Lee[1,2], Seul Beom Yu[1], Doo-Young Kim[1], Hyun-Jae Jang[1], Seon Min Oh[1], Hyoung-Geun Kim[1], Jongmin Ahn[1], In-Seo Heo[1], Heung Joo Yuk[3], Eun Kyoung Seo[2*], Sei-Ryang Oh[1*], Hyung Won Ryu[1*]

[1]Natural Product Research Center and Natural Product Central Bank, KRIBB, [2]College of Pharmacy, Graduate School of Pharmaceutical Sciences, Ewha Womans University, [3]KM Science Research Division, Korea Institute of Oriental Medicine (KIOM)

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PNB-53

Comparative Analysis of the Morphological and Chemical Characteristics of *Carthamus tinctorius* L. from Different Countries

Choi Yunji, Hyun Jaehee*, Cho Eunsol, Kim Youngmi, Shin Soyoung, Wookyu Lee, Jaeuk Seo, Kim Changsoo, Hwang Jinhee

National Center for Medicinal Resources Management, Herbal Medicine Research Division, National Institute of Food and Drug Safety Evaluation, Ministry of Food and Drug Safety, Republic of Korea

PNB-54

Glut-1 Inhibitor Enhanced the Therapeutic Efficacy of ^{64}Cu-DOTA-Trastuzumab in Osteosarcoma Cells

Krishnapriya Devasena, Shrankhala Sinha*, Ilhan Lim*

Department of Nuclear Medicine, Korea Institute of Radiological and Medico Oncological Sciences

PNB-55

GLUT-1 inhibition enhanced therapeutic efficacy of radiolabeled PSMA in prostate cancer cells

Shrankhala Sinha[1,2], Krishnapriya Devasena[1,2*], Ilhan Lim[1,2*]

[1]*Nuclear Medicine, Korea Institute of Radiological and Medical Sciences,*
[2]*The University of Science and Technology, Daejon*

PNB-56

Therapeutic potential of *Staphylea bumalda* leaf extract for obesity and sarcopenia

Kyeong Min Lee[1], Wook-Chul Kim[2], Yun-Su Lee[2], Seo-Rin Jung[2], Ye-Sol Kim[2], Seung-Hong Lee[1,2*]

[1]*Department of Pharmaceutical Engineering, Soonchunhyang University,*
[2]*Department of Medical Science, Soonchunhyang University*

PNB-57

Extraction and Purification of Sulfated Polysaccharides with Anticoagulant Activity from *Sticopus japonicus*

Eunbeen Shin[1,2,3*], Youngho Seo[2], Sangmin Lee[1,2,3], Siwan Kim[1,2,3], Yerim Joo[1,2,3], Minhyuk Jeong[1,2,3], Daeun Kim[1,2,3]

[1]*Department of Food Science and Technology, Pusan National University,* [2]*Institute for Future Earth, Pusan National University,* [3]*Food Tech Innovation Center, Life and Industry Convergence Research Institute, Pusan National University*

PNB-58

Chamaecyparis pisifera Essential Oil: Chemical Composition Analysis and Evaluation of Antioxidant and Skin Whitening Potentia

Do Yoon Kim[1,2*], Yoon Yi Kim[1], Da Yeon Yoo[1], Ji Hye Bae[1], Ji Seong Yun[1], Hwan Myung Lee[1,2]

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PNB-59

A Study on the Analytical Method for Measuring *l*-Menthol in Three Domestically Cultivated *Mentha arvensis* L. Species

Eunsol Cho, Jaehee Hyun*, Soyoung Shin, Yunji Choi, Youngmi Kim,
Wookyu Lee, Jaeuk Seo, Changsoo Kim, Jinhee Hwang

National Center for Medicinal Resources Management, Herbal Medicine Research Division, National Institute of Food and Drug Safety Evaluation, Ministry of Food and Drug Safety

PNB-60

Anti-Melanogenic Potential of Exosomes Derived from *Hordeum vulgare* L in B16F10 Melanoma Cells and Zebrafish Model

Wook-Chul Kim[1], Yun-Su Lee[1], Seo-Rin Jung[1], Seung Hong Lee[1,2]*

[1]Department of Medical Science, Soonchunhyang University, Asan 31538, Republic of Korea, [2]Department of Pharmaceutical Engineering, Soonchunhyang University, Asan 31538, Republic of Korea

PNB-61

Comparison of metabolite accumulation and antioxidant activity in metabolite-enhanced mung bean leaves by ethylene treatments

Du Yong Cho[1], Ae Ryeon Lee[1], Jong Bin Jeong[1] Mu Yeun Jang[1],
Da Hyun Kim[1], Do Yun Bang[1], Hye Rim Kim[1], Ye Rim Jeong[1],
Jin Hwan Lee[2], Kye Man Cho[1]*

[1]Department of GreenBio Science and Agri-Food Bio Convergence Institute, Gyeongsang National University, [2]Department of Smart Green Resources, Dong-A University

PNB-62

Inhibition of Melanin Synthesis in Melanoma Cells and α-MSH Expression in UVA-irradiated Keratinocytes by *Vitex rotundifolia* L.f. cone Essential Oil

Da Yeon Yoo[1], Do Yoon Kim[1,2], Yoon Yi Kim[1], Ji Hye Bae[1], Ji Seong Yun[1],
Hwan Myung Lee[1,2]*

[1]Korea Forest Plants Essential Oil Bank and Department of Biotechnology, College of Life and Health Sciences, Hoseo University, Asan 31499, Republic of Korea, [2]Korea Essential Oil Resource Research Institute, Hoseo University, Asan 31499, Republic of Korea

PNB-63

Study on the Improvement of Atopic Dermatitis through SNARE Protein Expression Inhibition by *Paulownia coreana* Uyeki flower absolute

Da Yeon Yoo[1], Do Yoon Kim[1,2], Yoon Yi Kim[1], Ji Hye Bae[1], Ji Seong Yun[1],
Hwan Myung Lee[1,2]*

[1]Korea Forest Plants Essential Oil Bank and Department of Biotechnology, College of Life and Health Sciences, Hoseo University, Asan 31499, Republic of Korea, [2]Korea Essential Oil Resource Research Institute, Hoseo University, Asan 31499, Republic of Korea

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PNB-64

Inhibitory effects of *Lonicera japonica* Thunb. Absolute on neointimal formation-related activities of rat vascular smooth muscle cells

Yoon Yi Kim[1], Do Yoon Kim[1,2], Da Yeon Yoo[1], Ji Hye Bae[1], Ji Seong Yun[1], Hwan Myung Lee[1,2*]

[1]Korea Forest Plants Essential Oil Bank and Department of Biotechnology, College of Life and Health Sciences, Hoseo University, Asan 31499, Republic of Korea, [2]Korea Essential Oil Resource Research Institute, Hoseo University, Asan 31499, Republic of Korea

PNB-65

Lindera obtusiloba Blume wood essential oil suppresses UVA-induced α-MSH production and melanogenesis: Potential for natural skin-whitening applications

Yoon Yi Kim[1], Do Yoon Kim[1,2], Da Yeon Yoo[1], Ji Hye Bae[1], Ji Seong Yun[1], Hwan Myung Lee[1,2*]

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PNB-66

Modulation of lipid metabolism by ethanol extract of shiitake mushroom in high-fat diet-induced mice

Young Geol Yoon*

Department of Biological Science, Jungwon University

PNB-67

Enhancement of metabolites and biological activities in mung bean roots cultivated under a vertical farming system

Do Yun Bang[1], Du Yong Cho[1], Ae Ryeon Lee[1], Jong Bin Jeong[1], Mu Yeun Jang[1], Da Hyun Kim[1], Hye Rim Kim[1], Ye Rim Jeong[1], Jin Hwan Lee[2], Kye Man Cho[1*]

[1]Department of GreenBio Science and Agri-Food Bio Convergence Institute, Gyeongsang National University, [2]Department of Smart Green Resources, Dong-A University

PNB-68

Elucidation of the protective effect of schisandrin C originating from *Schisandra chinensis* against indomethacin-induced intestinal injury

Son Hung Tran[1,2], Uyen Tran Tu Nguyen[1,2], Mi Ri Kim[1], Hee Ju Lee[1], Esther Youn[1], Ly Phuong Ho[1,2], Won Young Bae[1], Suk Woo Kang[3], Won Kyu Kim[2,3], Ki Young Choi[4], Keunwan Park[1], Kyungsu Kang[1,2*]

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PNB-69

Comparative study on the bioactivities and marker compound contents of *Citrus reticulata* and Jeju-native *Citrus sunki* peels

Ye Eun Cho[1], So-Young Cho[1], So-Yeon Kim[1], Ji-Yeong Bae[2], Sang Ho Lee[2], Jae Hee Hyun[3], Se Jin Park[1*]

[1]Department of Food Biotechnology and Environmental Science, Kangwon National University, Chuncheon 24341, Republic of Korea, [2]College of Pharmacy, Jeju National University, Jeju 38655, Korea, [3]Herbal Medicine Research Division, National Institute of Food & Drug Safety Evaluation, Jeju 63577, Korea

PNB-70

Potential biological activities of *Citrus trifoliata* Flower Essential Oil as a Natural Antioxidant and Skin Whitening Agent

Do Yoon Kim[1,2*], Yoon Yi Kim[1], Da Yeon Yoo[1], Ji Hye Bae[1], Ji Seong Yun[1], Hwan Myung Lee[1,2]

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PNB-71

Protective effect of Polysaccharides from *Halocynthia roretzi* Tunic on Particulate Matter-Induced Skin Damage and its Anti-Melanogenesis Effect *in vivo* and *in vitro* model

Seo-Rin Jung[1], Wook-Chul Kim[1], Yun-Su Lee[1], Kyeong Min Lee[2], Seung-Hong Lee[1,2*]

[1]Department of Medical Science, Soonchunhyang University, [2]Department of Pharmaceutical Engineering, Soonchunhyang University

PNB-72

Comparative analysis of bioactive compounds and the anti-inflammatory and wound-healing properties of *Centella asiatica*

So-Young Cho[1], Ye Eun Cho[1], So-Yeon Kim[1], Ji-Yeong Bae[2], Sang Ho Lee[2], Jae Hee Hyun[3], Se Jin Park[1*]

[1]Department of Food Biotechnology and Environmental Science, Kangwon National University, [2]College of Pharmacy, Jeju National University, [3]Herbal Medicine Research Division, National Institute of Food & Drug Safety Evaluation

PNB-73

Enhancement of Skin Regeneration by Sargassum pallidum-Derived Polysaccharides through Modulation of Wnt/β-Catenin Pathway

Yun-Su Lee[1], Wook-Chul Kim[1], Seo Rin Jung[1], Kyeong Min Lee[2], Seung-Hong Lee[1,2*]

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[2]Department of Pharmaceutical Engineering, Soonchunhyang University*

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PNB-74

Metabolomic Profiling of Ginger (*Zingiber officinale*) from Diverse Geographical Origins and Analytical Validation of Marker Compounds via UPLC

Bo-Ram Choi[1], Dahye Yoon[1], Hyoung-Geun Kim[2], Dae Young Lee[3*]

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PNB-75

Metabolomics-Based Differentiation of Korean ginseng(*Panax ginseng*) and American ginseng(*Panax quinquefolius*) with Molecular Networking, and Method Validation for Marker Compounds of Korean Ginseng

Dahye Yoon[1], Woo Cheol Shin[2], Bo-Ram Choi[1], Jae-Suk Ban[1], Jin-Kyu Jang[2], Hyeon Seon Na[1,2], Dae Young Lee[2*]

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PNB-76

Comparative analysis of secondary metabolites and antioxidant activities in white and red radish (*Raphanus sativus*) hairy roots

Ki Hyun Kim[1], Chan Ung Park[1], Jin Su Lim[1], Hae Jin Kwon[2], Hye Won Seo[2], Min Hwan Lee[1], Sang Un Park[1,2*]

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PNB-77

Neuroprotective Potential of a New Phenolic Compound from *Scrophularia buergeriana* Roots Revealed by Network Pharmacology

Hyeon Seon Na[1,2], Woo Cheol Shin[2], Seon Min Oh[3], Kwan-Woo Kim[1], Dahye Yoon[1], Jin-Kyu Jang[2], Dae Young Lee[2*]

[1]National institute of Horticultural and Herbal Science, Department of Herbal Crop Research, [2]Kyungpook National University, BK21 FOUR KNU Creative BioResearch Group, School of Life Sciences, [3]Korea Reseach Institute of Bioscience and Biotechnology, Natural Product Research Center and Natural Product Central Bank

PNB-78

Antioxidant and Anti-Aging Effects of Panax Ginseng Root Extract and Its Major Compounds in Human Dermal Fibroblast

Minseo Kang[1], Daesik Jang[2*], Sullim Lee[1*]

[1]Department of Life Science, College of Bio-Nano Technology, Gachon University, [2]Department of Biomedical and Pharmaceutical Sciences, Kyung Hee University, Seoul Campus

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PNB-79

The effect of the season and region on the yield and quality of Torreya nucifera essential oil in South Korea

Chanjoo Park, Nahyun Kim, Hyunjeong Na, Mi-Jin Park*

Division of Forest Industrial Materials, Department of Forest Products and Industry, National Institute of Forest Science

PNB-80

Anti-Obesity Effects of Citrus unshiu Leaf Extract in 3T3-L1 Adipocytes and High-Fat Diet-Induced Obese Mice

Jae-Won Kim, Youngmee Kim, Nari Lee, Jungmin Oh, Jungman Kim, Yeji Lee, Young-Jin Choi, Minho Song, Seong-Il Kang*, Hee Chul Ko*

Research and Development, Jeju Institute of Korean Medicine

PNB-81

Anti-inflammatory and anti-atopic effects of *Elaeocarpus sylvestris* leaf extract in LPS-stimulated HaCaT cells and DNCB-induced BALB/c mice

Young-Ju Do[1], So-Yeon Kim[1], Su-Jung Lee[1], Ye-Won Lee[1], Seon-Woo Lee[1], Na-Hyun Lee[1], Ji-Yeong Bae[2], Sang Ho Lee[2], Se Jin Park[1*]

[1]Department of Food Biotechnology and Environmental Science, Kangwon National University, Chuncheon, Republic of Korea, [2]College of Pharmacy, Jeju National University, Jeju 38655, Korea

PNB-82

Comparison of Anti-inflammatory Activities and Chemical Composition of Essential Oils Extracted from Cupressaceae Family

Hyunjeong Na, Nahyun Kim*, Chanjoo Park, Mi-Jin Park, Soo-Kyeong Jang

Forest Industrial Materials Division, National Institute of Forest Science

PNB-83

Novel Cucurbitane-type Terpenoid and Anti-obesity Effects from Chrysosplenium flagelliferum

Bowon Jung, Eun Jin Heo, Seulah Lee*

Department of Convergent Biotechnology and Advanced Material Science, College of Life Sciences, Kyung Hee University

PNB-84

Assessment of Herbicidal Activity of Natural Triketone Compound from Manuka Oil

Ji-Won Shin, Ji-Woo Yu, Geon-Woo Park, Ji-Yeon Lee, Ha-Jin Son, Young-Soo Keum*

Department of Crop Science, Konkuk University

PNB-85

Preclinical Evaluation of the Therapeutic Effect of Bee Venom on Rheumatoid Arthritis Based on TNF-α Inhibition

Jumgmin Oh, Nari Lee, Yeji Lee, Jae-Won Kim, Jungman Kim,
Young-Jin Choi, Seong-Il Kang, Minho Song, Hee Chul Ko, Youngmee Kim*

Research and Development, JEJU INSTITUTE OF KOREAN MEDCINE

PNB-86

Effects of Bee Venom and Its Derived Peptides Against Dexamethasone and Hydrogen Peroxide-Induced Stress in C2C12 Skeletal Muscle Cells

Young-Jin Choi, Jae-Won Kim, Jungman Kim, Jungmin Oh, Yeji Lee,
Minho Song, Seong-Il Kang, Youngmee Kim*, Hee Chul Ko*

Research and Development, Jeju Institute of Korean Medicine

PNB-87

Inhibition of TNF-α-Induced Collagen Degradation and Oxidative Damage by *Centipeda minima* and Brevilin A in Human Dermal Fibroblasts

Yea Jung Choi[1], Soohyun Kim[2], Ki Sung Kang[1*], Sullim Lee[2*]

[1]Department of prevent medicine, College of Korean Medicine, Gachon University,
[2]Department of Life Science, College of Bio-Nano Technology, Gachon University

PNB-88

Potential Natural Modulators of *Schisandra chinensis* and *Citrus unshiu* Extracts on Prostate and Gut Health

Jungman Kim, Young-Jin Choi, Jae-Won Kim, Jungmin Oh, Yeji Lee,
Dong-Eon Kim, Seong-Il Kang, Minho Song, Youngmee Kim*, Hee Chul Ko*

Research and Development, Jeju Institute of Korean Medicine

PNB-89

Organ-Specific Dynamics of Bioactive Compounds and Antioxidant Activity in *Wasabi Japonica* Across Developmental Stages

Yeong Bin Choi[1,2], To Quyen Truong[1], Phuong Kim Huynh[1,2], Ye Lin Kim[1],
Sang Min Kim[1,2*]

[1]Smart Farm Research Center, Korea Institute of Science and Technology (KIST) Gangneung Institute of Natural Products, Gangneung 25451, Republic of Korea,
[2]Natural Product Applied Science, KIST School, University of Science and Technology, Gangneung 25451, Republic of Korea

PNB-90

Quantitative Analysis Using High-Performance Liquid Chromatography (HPLC) for the Stability Evaluation of Ginseng Radix

Hajeong Kim, Sohee Jang, Jaeuk Seo*, Jaehee Hyun, Wookyu Lee,
Changsoo Kim, Jinhee Hwang

National Center for Medicinal Resources Management, Herbal Medicine Research Division, National Institute of Food and Drug Safety Evaluation

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PNB-91

Stability assessment of Reference Medicinal Plant Material and Analytical Marker for *Scutellaria baicalensis*(Scutellaria root) under stressed conditions

So-Hee Jang, Hajeong Kim, Jaeuk Seo*, Jae-Hee Hyun, Wookyu Lee, Changsoo Kim, Jinhee Hwang

National Center for Medicinal Resources Management, Herbal Medicine Research Division, National Institute of Food and Drug Safety Evaluation

PNB-92

Uncaria Rhynchophylla and hirsuteine as TRPV1 agonists inducing channel desensitization

Chunwhan Choi[1*], Yeon Woo Jung[2], Taewoong Ha[2], Gyu-Sang Hong[2]

[1]Biocenter, Gyeonggido Business & Science Accelerator, [2]Brain Science Institute, Korea Institute of Science and Technology

PNB-93

Stable Carbon Isotope Based Honey Protein Analysis Used in Geographic Origin Discrimination of Robinia Honey

Yun Gon Son, Soon Ok Woo, Hyo Young Kim, Hong Min Choi*

Agricultural Biology, National Institute of Agricultural Science, Rural Development Administration

PNB-94

Improves skin barrier and anti-inflammatory effect of exosomes derived *Fructobacillus fructosus* subsp. NSH-1 strain isolated from *Campsis grandiflora* Flower

Byeong-Min Choi[1], Da Som Kim[2], Hyeri Choi[2], Jaehoon Cho[3], Won-Jae Chi[2], Seung-Young Kim[1,4*]

[1]Department of Pharmaceutical Engineering & Biotechnology, Sunmoon University, Asan 31460, Korea, [2]Biodiversity Research Department, Species Diversity Research Division, National Institute of Biological Resources, Incheon 22689, Korea, [3]Low-Carbon Transition R&D Department, Research Institute of Sustainable Development Technology Principal Researcher, Cheonan 31056, Republic of Korea, [4]R&D Center, BaoGen Inc., Cheonan 31212, Korea

PNB-95

Development of a reliable UPLC analytical protocol for purified Apitoxin

Hong Min Choi*, Soon Ok Woo, Hyo Young Kim, Moon Seon Lee, Yun Gon Son

Department of Agricultural Biology, National Institute of Agricultural Science, Rural Development Administration

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PNB-96

Anti-Inflammatory effect of exosomes derived from lactic acid bacteria isolated from the flower of *Aster koraiensis* in LPS-stimulated RAW 264.7 Macrophage cells

Chae-Yeon Lee[1], Da Som Kim[2], Hyeri Choi[2], Won-Jae Chi[2],
Seung-Young Kim[1,3*]

[1]Department of Pharmaceutical Engineering & Biotechnology, Sunmoon University, Asan 31460, Korea, [2]Biodiversity Research Department, Species Diversity Research Division, National Institute of Biological Resources, Incheon 22689, Korea, [3]R&D Center, BaoGen Inc., Cheonan 31212, Korea

PNB-97

Inhibition activity of inflammation of *Borassus flabellifer* fruit extract

Dahee Hwang[1], Dabin Jung[1], Byeong-Min Choi[1], Seung-Young Kim[1,2*]

[1]Department of Pharmaceutical Engineering & Biotechnology, Sunmoon University, Asan 31460, Korea, [2]R&D Center, BaoGen Inc., Cheonan 31212, Korea

PNB-98

Exploring the potential blood pressure regulatory and vasodilatory effects of enzyme-assisted hydrolysate and purified peptides from olive flounder

Hyo-Geun Lee, Ji-Yul Kim, Seok-Chun Ko*

Department of Biomaterial Research, National Marine Biodiversity Institute of Korea

PNB-99

Effect of *Microbacterium esteraromaticum* Extract on anti-inflammation response of LPS-induced RAW 264.7 cells

Dabin Jung[1], Byeong-Min Choi[1], Yun-Jae Kim[2], Seung-Young Kim[1,3*]

[1]Department of Pharmaceutical Engineering & Biotechnology, Sunmoon University, Asan 31460, Korea, [2]Marine Biotechnology Research Center, Korea Institute of Ocean Science and Technology, Busan, Republic of Korea, [3]R&D Center, BaoGen Inc., Cheonan 31212, Korea

PNB-100

Anti-Inflammatory effects of exosomes derived from *Lactococcus* spp. isolated from *Clematis terniflora* flowers in LPS-stimulated RAW 264.7 Macrophage cells

Yeonbo Jang[1], Da Som Kim[2], Hyeri Choi[2], Won-Jae Chi[2],
Seung-Young Kim[1,3*]

[1]Department of Pharmaceutical Engineering & Biotechnology, Sunmoon University, Asan 31460, Korea, [2]Biodiversity Research Department, Species Diversity Research Division, National Institute of Biological Resources, Incheon 22689, Korea, [3]R&D Center, BaoGen Inc., Cheonan 31212, Korea

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PNB-101

Hair growth-promoting properties of Bacillus/Esculetin ferment filtrate(BEFF) derived through biorenovation

Jun Won Choi[1,2], Tae-Jin Park[1], Hyehyun Hong[1,2], Kyung Wan Park[1], Sung Min Hong[1], Seung-Young Kim[1,2*]

[1]R&D Center, BaoGen Inc., Cheonan 31212, Korea, [2]Department of Pharmaceutical Engineering & Biotechnology, Sunmoon University, Asan 31460, Korea

PNB-102

Anti-Inflammatory Activity of *Peziza vesiculosa* Culture Filtrate Extract in LPS-Stimulated RAW 264.7 Cells

Tae-Jin Park[1], Da Som Kim[2], Hyeri Choi[2], Won-Jae Chi[2], Seung-Young Kim[1,3*]

[1]R&D Center, Baogen Inc., [2]Species Diversity Research Division, National Institute of Biological Resources, [3]Department of Pharmaceutical Engineering & Biotechnology, Sunmoon University

PNB-103

Protective Effects of *Trametes hirsuta* mycelia culture Filtrate on H_2O_2-induced oxidative stress in C2C12 myoblast

Hyehyun Hong[1,2,3], Seung-Young Kim[1,3*]

[1]Department of Pharmaceutical Engineering & Biotechnology, Sunmoon University, Asan 31460, Korea, [2]Biodiversity Research Department, Species Diversity Research Division, National Institute of Biological Resources, Incheon 22689, Korea, [3]R&D Center, BaoGen Inc., Cheonan 31212, Korea

PNB-104

Alleviate Drought Stress on Cereals Using Extracts of *Psidium guajava*, *Aloe vera*, *Allium sativum* and *Medicago sativa* plantAlleviate Drought Stress on Cereals Using Extracts of *Psidium guajava*, *Aloe vera*, *Allium sativum* and *Medicago sativa* plants

Ei Ei, Hyunhwa Park, Pyae Pyae Win, Yong In Kuk*

Department of Bio-oriental Medicine Resources, Sunchon National University

PNB-105

BF Root Extract Suppresses Stress-induced Cancer Metastasis by Targeting Src Kinase

Jae-Hoon Jeong, Shin-Hyung Park*

Department of Pathology, College of Korean Medicine, Dong-eui University, Busan 47227, Republic of Korea

PNB-106

Deoxypodophyllotoxin Exerts Anticancer Effects via Inhibition of the Glucocorticoid Receptor in NSCLC Cells

Jae-Hoon Jeong, Shin-Hyung Park*

Department of Pathology, College of Korean Medicine, Dong-eui University, Busan 47227, Republic of Korea

PNB-107

Dual Anti-Angiogenic Action of PP Root Extract in Endothelial and Gefitinib-Resistant Lung Cancer Cells

Hyun-Ji Park, Shin-Hyung Park*

Department of Pathology, College of Korean Medicine, Dong-eui University, Busan 47227, Republic of Korea

PNB-108

Extract of *Lindera aggregata* Root Tuber Suppresses Catecholamine-Induced Metastatic Potential in Cancer Cells

Shin-Hyung Park*, Jae-Hoon Jeong

Department of Pathology, College of Korean Medicine, Dong-eui University, Busan 47227, Republic of Korea

PNB-109

Extract of *Scutellaria baicalensis* Root Inhibits Macrophage Migration and M2 Polarization

Hyun-Ji Park, Shin-Hyung Park*

Department of Pathology, College of Korean Medicine, Dong-eui University, Busan 47227, Republic of Korea

PNB-110

Induction of Apoptosis by a Marine-Derived SM Extract in Lung Cancer Cells

Shin-Hyung Park*, Hyun-Ji Park

Department of Pathology, College of Korean Medicine, Dong-eui University, Busan 47227, Republic of Korea

PNB-111

A Brown Macroalga SR Extract Triggers Apoptosis in Lung Cancer Cells

Shin-Hyung Park*, Hyun-Ji Park

Department of Pathology, College of Korean Medicine, Dong-eui University, Busan 47227, Republic of Korea

PNB-112

Discovery of α-Glucosidase Inhibitors from Paenibacillus sp. JNUCC 31 via Genome Mining, Metabolite Profiling, and In Silico Analysis

Yang Xu, Xuhui Liang, Chang-Gu Hyun*

Jeju Inside Agency & Cosmetic Science Center, Department of Chemistry and Cosmetics, Jeju National University

PNB-113

Ginsenoside MC Modulates Neuroinflammation via the TLR4/MD2 and Nrf2/ARE Pathways in BV2 Microglial Cells

Ji Won Choi, Jin Young Hur*

Functional food materials Research Group, Korea Food Research Institute

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PNB-114

β-sitosterol induces ferroptosis in triple-negative breast cancer cells by modulating the ROR1/YAP/TAZ signaling pathway

Daekyeong Kim[1], Jisoo Kim[1], Tae Hyeon Yoon[1], Sun Hee Yang[1],
Somi Kim Cho[1,2*]

[1]Interdisciplinary Graduate Program in Advanced Convergence Technology and Science, Jeju National University, Jeju 63243, Korea, [2]Faculty of Biotechnology, College of Applied Life Sciences, SARI, Jeju National University, Jeju 63243, Republic of Korea

PNB-115

Acute treatments of *Myristica fragrans* Houtt. essential oil improved depression-like behaviors enhancing GABAB signaling and stress resilience

Khoa Nguyen Tran, Yeasmin Akter Munni, Gia Linh Mac,
Sarmin Ummey Habiba, In-Jun Yang*

Department of Physiology, College of Korean Medicine, Dongguk University, 123 Dongdae-ro, Gyeongju 38066, Republic of Korea

PNB-116

Characterization and Discrimination of *Panax ginseng* Based on Multi-Platform Metabolomics Combined Molecular Networking Analysis

Woo-Cheol Shin[1], Dahye Yoon[2], Jin-Kyu Jang[1], Dae Young Lee[1*]

[1]BK21 FOUR KNU Creative BioResearch Group, School of Life Sciences, Kyungpook National University, Daegu 41566, Republic of Korea, [2]Department of Herbal Crop Research, National institute of Horticultural and Herbal Science, RDA, Eumseong 27709, Republic of Korea

PNB-117

Integrated Metabolomics and Biological Functional Assessment of *Platycodon grandiflorum* Extract in Alcohol-Related Liver Disease

Jin-Kyu Jang[1], Woo-Cheol Shin[1], Dahye Yoon[2], Dae Young Lee[1*]

[1]BK21 FOUR KNU Creative BioResearch Group, School of Life Sciences, Kyungpook National University, Daegu 41566, Republic of Korea, [2]Department of Herbal Crop Research, National Institute of Horticultural and Herbal Science, RDA, Eumseong 27709, Republic of Korea

PNB-118

Neuroprotective Effects of Coumarin derivatives Isolated from *Peucedanum japonicum*

Jeong-Hyun Park[1], Woo-Cheol Shin[1], Jin-Kyu Jang[1], Kwan-Woo Kim[2],
Young-Seob Lee[2], Dae Young Lee[1*]

[1]BK21 FOUR KNU Creative BioResearch Group, School of Life Sciences, Kyungpook National University, Daegu 41566, Republic of Korea, [2]Department of Herbal Crop Research, National institute of Horticultural and Herbal Science, RDA, Eumseong 27709, Republic of Korea

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PNB-119

Isolation and Characterization of Bioactive Compounds from *Phedimus aizoon* for Sleep Quality Improvement

Yong Jae Jeong[1], Jin-Kyu Jang[1], Woo-Cheol Shin[1], Bo Kyung Lee[2], Yi-Sook Jung[2], Young-Seob Lee[3], Dae Young Lee[1*]

[1]BK21 FOUR KNU Creative BioResearch Group, School of Life Sciences, Kyungpook National University, Daegu 41566, Republic of Korea, [2]Department of Pharmacy, Ajou University, Suwon 16499, Republic of Korea, [3]Department of Herbal Crop Research, National institute of Horticultural and Herbal Science, RDA, Eumseong 27709, Republic of Korea

PNB-120

Evaluation of the Antioxidant and Antiaging Effects of the Native Plant Genus *Schisandra* Extracts and Application in Cosmetics

Hye Yoon Park[1], A Reum Jang[1], Do Yeon Lee[1], Hwa Youn Kim[1], Yi Seul Kim[1], Dae Geon Kim[2], Myo-Deok Kim[2], Hang Eui Cho[3*]

[1]Material Research Team, Cosmecca Korea CIR R&D Center, [2]R&D Center, ACTIVON, [3]Technical Research Institute CCS, Cosmecca Korea CIR R&D Center

PNB-121

Inhibitory Effect of *Citrus unshiu* on the Spread of Antibiotic Resistance Genes

Hyejun Jo, Changsook Kim[*], Gwangpyo Ko, Minseong Park

Jeju National University, Faculty of Biotechnology, College of Applied Life Sciences

PNB-122

Generation of Chrysoeriol-Producing Transgenic Lettuce as a Flavonoid Production Platform

Seulgi Lee[1], Moonhyuk Kwon[1*], Saetbuyl Lee[2]

[1]Division of Applied Life Science (BK21 Four), ABC-RLRC, RIMA, Gyeongsang National University, Jinju 52828, Republic of Korea, [2]Metabolic Engineering Division, National Institute of Agricultural Science, Rural Development Administration, JeonJu, Republic of Korea

PNB-123

Investigation of Zinc Finger Proteins (LsZNFPs) in Laticifer Differentiation for Enhanced Rubber Accumulation in Lettuce

Rara Maharani Rusli[1], Nayoung Lee[2], Moonhyuk Kwon[1*]

[1]Division of Applied Life Science (BK21 Four), ABC-RLRC, RIMA, Gyeongsang National University, Jinju 52828, Republic of Korea, [2]Research Institute of Molecular Alchemy (RIMA), Gyeongsang National University, Jinju 52828, Republic of Korea

PNB-124

Phytochemical Constituents of *Glehnia littoralis* Leaves and Their Chemotaxonomic Significance

Sainan Li, Shuo Tian, Minkyun Na[*]

Pharmacognosy Laboratory, College of Pharmacy, Chungnam National University

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PNB-125

Cytotoxic effects of C17 polyacetylenes isolated from the roots of *Glehnia littoralis* against drug resistant colorectal and lung cancer cells

Jisu Park, Sumin Kang, Soomin Lee, Minkyun Na*

Pharmacognosy Laboratory, College of Pharmacy, Chungnam National University

PNB-126

Metabolite Profiling and Antimicrobial Activities of *Brassica rapa* ssp. *narinosa* (Tatsoi), *B. rapa* var. *narinosa* × *chinensis* (Dacheongchae), and *B. rapa* ssp. *chinensis* (Pakchoi)

Minhwan Lee[1], Haejin Kwon[2], Sang Un Park[1,2*]

[1]Department of Crop Science, Chungnam National University, [2]Department of Smart Agriculture Systems, Chungnam National University

PNB-127

Validation of an Analytical Method for Caffeoylquinic Acid Derivatives Content Enhanced in *Aster* × *chusanensis* by UV Irradiation

Ju Yeon kim[1], Sumin Kim[1], Nari Woo[1], Ki-Ho Son[2*], Jeong Yoon Kim[1*]

[1]Department of Pharmaceutical Engineering, ABC-RLRC, IALS, Gyeongsang National University, Jinju 52725, Republic of Korea, [2]Department of GreenBio Science, Gyeongsang National University, Jinju 52725, Republic of Korea

PNB-128

Neotenone from *Pachyrhizus erosus* with Whitening Effects on Tyrosinase Inhibition and Anti-pigmentation Activity

Seung Yu Lee, Yun Gon Son, Na Rae Kang, Jeong Yoon Kim*

Department of Pharmaceutical Engineering, ABC-RLRC, IALS, Gyeongsang National University, Jinju 52725, Republic of Korea

PNB-129

Neutrophil Elastase Inhibitory Furanocoumarins from *Angelica dahurica* Roots

Seungjae Jang, Jae Yeon Park, Na Rae Kang, Jeong Yoon Kim*

Department of Pharmaceutical Engineering, ABC-RLRC, IALS, Gyeongsang National University, Jinju 52725, Republic of Korea

PNB-130

Whitening Effect of lignan derivatives from Anise hyssop (*Agastache foeniculum*)

Na Rae Kang, Seung Yu Lee, Seungjae Jang, Jeong Yoon Kim*

Department of Pharmaceutical Engineering, ABC-RLRC, IALS, Gyeongsang National University, Jinju 52725, Republic of Korea

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PES Environmental Sciences

PES-1

Characterisitics of Variation of Organic Pollutants in Agricultural Water in Gyeongbuk Province(2023~2024)

Hye-Rin Jeong[1,2]*, Jong-Hee Shin[1], Yeong-Gyu Jeong[1], Yun-Kyung Kim[1], Jun-Young Lee[1], Jung-Gi Ryu[1], Hyo-Sub Lee[3]

[1]Agricultural Environment Research Team, Gyeongsangbuk-do Agricultural Research & Extension Services, [2]Department of Applied Biosciences, Kyungpook National University, [3]National Institute of Agricultural Science, Rural Development Administration

PES-2

Predictive modeling of pesticide half-life in soil using machine learning

In Ung Jeong, Hyo Sub Lee*, Jae Yun Jo, Hyang Hee Kim

Residual Agrochemical Assessment Division, Department of Agro-Food Safety and Crop Protection, National Institute of Agricultural Sciences

PES-3

Effects of Biochar Type, Application Rate, and Frequency on Soil Carbon Content in the Saemangeum Reclaimed Land

Kwang Seung Lee*, Young Tae Shin, Hyeoun Su Jang, Bang Hun Kang, Hee Kyoung Ock, Hak Sung Lee, Seo Young Jeong, Hyeoun Suk Cho

Reclaimed Land Agriculture Research Center, Department of Crop Sciences, National Institute of Crop and Food Science, Rural Development Administration

PES-4

Leachability characteristics of heavy metals in contaminated forest soils

Namin Koo*

Division of Forest Ecology, National Institute of Forest Science

PES-5

Impact of Soil Amendments on Soil Microbiota and Plant Defense System: A Study on Beneficial Bacterium and Salicylic Acid in Cucumber Cultivation

Sandamali Harshani Kumari Hathurusinghe[1], Anushree Joshi[1], Tino Bashizi[1], Minsoo Jeong[1], Min-Ji Kim[1], Jae-Ho Shin[1,2]*

[1]Department of Applied Biosciences, Kyungpook National University,
[2]NGS Core Facility, Kyungpook National University

PES-6

Distribution of Soil Microbial Communities in Greenhouse Soils of Gyeongbuk Province

Jeung Woo Ko*, Hyong Rack Sohn, San-Yeong Kim, Jung-Gi Ryu

Division of Agricultural Food and Enviroment Research, Gyeongsangbuk-do Agricultural Research & Extension Services, Daegu 41404, Korea

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PES-7

Effects of Zerovalent Iron Nanoparticles on the Growth and Photosynthesis of *Arabidopsis thaliana* under Elevated CO_2 Concentrations

Juwon Yoo[1], Junyong Hong[2], Hakwon Yoon[3*]

[1]Department of Food Biotechnology and Environmental Science, Kangwon National University, Chuncheon 24341, Republic of Korea, [2]Department of Biological Environment, College of Agriculture and Life Sciences, Kangwon National University, Chuncheon 24341, Republic of Korea, [3]School of Natural Resources and Environmental Science, College of Agriculture and Life Sciences, Kangwon National University, Chuncheon 24341, Republic of Korea

PES-8

A Study on Biochar Production for Recycling of Spent Growing Media

Ji-Min Song[1], Chang-Gon Lee[1], Han-Na Cho[2], Ikhyeong Lee[2], Ju-Sik Cho[1,2], Se-Won Kang[1,2*]

[1]Department of Agricultural Life Science, Sunchon National University, Suncheon 57922, Republic of Korea, [2]Department of Agricultural Chemistry, Sunchon National University, Suncheon 57922, Republic of Korea

PES-9

Crop-Specific Metabolic Differences and Risk Assessment of Sulfoxaflor in Thistle and Olive

Eun-Song Choi[1,2], Min-Ho Song[2], Ji-Woo Yu[3], Jung-Hoon Lee[1,2], Hui-Yeon Ahn[4], Geon-Woo Park[3], Ji-Won Shin[3], Ji-Yeon Lee[3], Ha-Jin Son[3], Young-Soo Keum[3], Ji-Ho Lee[1,2*]

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PES-10

Correlation Analysis Between Leaf Chlorosis and Flooding-Responsive Metabolites Under Waterlogging Stress During Early Growth of Maize

Jungtae Kim[*], Boseong Seo, Yonghwa Lee, Jeongtae Lee

Crop Environment Research Division, National Institute of Crop and Food Science, RDA

PES-11

Synthesis and Characterization of Nutrient-Enriched, Mineral-Like Particles from Wastewater-Activated Sludge

Jun Seo Kang[1], Beom Sik Kim[1], Ji Won Kim[1], Jong-Rok Jeon[1,2,3*]

[1]Division of Applied Life Science (BK21Plus), Gyeongsang National University, [2]Department of Applied Life Chemistry, Gyeongsang National University, [3]Institute of Agricultural and Life Science (IALS), Gyeongsang National University

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PES-12

Synthesis and Characterization of Nutrient-Enriched, Mineral-Like Particles from Wastewater-Activated Sludge

Manar Tag[1], Hyunah So[1], Juyeon Moon[1], Jong-Rok Jeon[1,2,3*]

[1]Division of Applied Life Science (BK21Plus), Gyeongsang National University,
[2]Department of Applied Life Chemistry, Gyeongsang National University,
[3]Institute of Agricultural and Life Science (IALS), Gyeongsang National University

PES-13

Adsorption characteristic of chlorantraniliprole on biochar

Hoo Bin Han[1], Eun Hea Jho[1,2*]

[1]Agricultural Chemistry, Chonnam National University, [2]Agricultural and Biological Chemistry, Chonnam National University

PES-14

Applicability of *Festuca ovina* var. *coreana* for Amendment-Assisted Phytoremediation of Arsenic-Contaminated Soil

Ye-Eun Lee[1], Keum Chul Yang[2], Han Na Kim[1], Jeong Yeon Kim[1], Su Kyeong Shin[1], Yu Jin Kim[2], Seung Jun Lee[1], Jong Geon Oh[1], Jin Seo Lee[1], Ju-Sung Cho[3], Jin Hee Park[1*]

[1]Department of Environmental and Biological Chemistry, Chungbuk National University, [2]Department of Civil and Environmental Engineering, Kongju National University, [3]Division of Animal, Horticultural, and Food Sciences, Chungbuk National University

PES-15

Machine Learning-Based Prediction of Soil Nutrients Levels from Electrical Conductivity

Seung Jun Lee, Han Na Kim, Jeong Yeon Kim, Su Kyeong Shin, Ye Eun Lee, Jin Hee Park*

Department of Environmental Biological Chemistry, Chungbuk National University

PES-16

Deep Soil Contributes to More Reliable Soil Property Estimation

Jeong Chan Lee, Kyung Jin Min*

Department of Agricultural Biotechnology, Seoul National University

PES-17

Soil Heterotrophic Respiration Is More Sensitive to Seasonal Changes in Temperature and Water Content than Autotrophic Respiration in a Monsoon Continental Climate

Hyunjin Kim, Kyungjin Min*

Department of Agricultural Biotechnology, Applied Life Chemistry, Seoul National University

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PES-18

Effect of Biochar Derived from Agricultural Residues and Livestock Manure on Crop Productivity and Soil Properties

Seong Heon Kim*, Kyoung Young Kim, Yu Na Kim, Sin Sil Kim,
Jae Hyuk Park, Jin Ju Yun, Jae Hong Shim, Sang Ho Jeon, Soon Ik Kwon,
Ahn Seing Noh

Soil and Water Environment Division, National Institute of Agricultural Sciences, Rural Development Administration

PES-19

Distribution of Microbial Extracellular Enzymes in Soil

Minsun Kim, Kyungjin Min*

Department of Agricultural Biotechnology, Seoul National University

PES-20

Optimizing the Application of Organic Fertilizers Mixed with Pyrogenic Carbon Materials for Enhanced Crop Growth and Soil Carbon Sequestration

Seong Heon Kim*, Kyeong Young Kim, Yu Na Lee, Sin Sil Kim,
Jae Hyuk Park, Jin Ju Yun, Jae Hong Shim, Sang Ho Jeon, Soon Ik Kwon,
Ahn Sung Noh

Soil and Water Environment Division, National Institute of Agricultural Sciences, Rural Development Administration

PES-21

Evaluation of Fertilizer Usage and Type in Facility Crops Cultivation

Yu Na Lee, Seong Heon Kim*, Kyeong Yeong Kim, Jae Hong Shim,
Sang Ho Jeon, Ahn Sung Noh, Soon Ik Kwon

Soil and Water Environment Division, National Institute of Agricultural Sciences, Rural Development Administration

PES-22

Evaluation of Fertilizer Usage and Nutrient Management Practices in Korean Rice Cultivation

Sin Sil Kim, Seong Heon Kim*, Jae Hong Shim, Sang Ho Jeon,
Ahn Sung Noh, Soon Ik Kwon, Yu Na Lee, Kyeong Yeong Kim

Soil and Water Environment Division, National Institute of Agricultural Sciences, Rural Development Administration

PES-23

Extracellular Enzyme Products Drive a Pulse of Microbial Respiration upon Rewetting of Dry Soil

Sohyun Woo, Minsun Kim, Kyungjin Min*

Department of Agricultural Biotechnology, Seoul National University

PES-24

Influence of Growing Environment on Major Compounds and Growth Characteristics of Wild *Cudrania tricuspidata* Fruit

Dong Hwan Lee, Yonghwan Son, Dae Hui Jeong, Ji Ah Kim*

Forest Medicinal Resources Research Center, National Institute of Forest Science

PES-25

Adsorption characteristics of imidacloprid by two types of microplastics and biochar

Jeong Min Heo[1], So Hui Bae[2], Hyeon Jeong Lee[2], Eun Hea Jho[1,2]*

[1]Department of Agricultural Chemistry, Chonnam National University, Gwangju 61186, Korea, [2]Department of Agricultural and Biological Chemistry, Chonnam National University, Gwangju 61186, Korea

PES-26

A Subsoil-Inclusive Framework for National-Scale Soil Health Assessment

Min-Gi Park, Kyung-Jin Min*

Department of Agricultural Biotechnology, Seoul National University, Seoul 08826, Republic of Korea

PES-27

Effects of Biochar Application on Soil Enzyme Activities under Lettuce Cultivation

Hyeon Jeong Lee, So Hui Bae, Eun Hea Jho*

Department of Agricultural and Biological Chemistry, Chonnam National University, Gwangju 61186 Republic of Korea

PES-28

Effects of Transition Metals on the Digestibility in Rumen System

Kwang-Min Kim, Kyung-Yeol Oh, Wasi Ullah, Jin-Hyo Kim*

Department of Agricultural Chemistry, Division of Applied Life Science, Institute of Agriculture and Life Science (IALS), Gyeongsang National University, Jinju 52727, Republic of Korea

PES-29

Establishment of analytical methods for nicotine, propylene glycol and glycerol content in aerosol of heated tobacco products using GC-FID

Hyoung-Joon Park, Min Soo Kim, Min Kyong Lee, Gyeong Tae Kim,
Woo Jin Jeon, Hyung Soo Kim, Hyun-Kyung Kim*

Advanced Analysis Division, National Institute of Food and Drug Safety Evaluation, Ministry of Food and Drug Safety

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PES-30

Size-Dependent Toxicity of Polyethylene Nano- and Microplastics on the Growth of *Arabidopsis thaliana*

So Hyun An[1], Hak Won Yoon[2*]

[1]Department of Biological Environment, College of Agriculture and Life Sciences, Kangwon National University, Chuncheon 24341, Republic of Korea, [2]School of Natural Resources and Environmental Science, College of Agriculture and Life Sciences, Kangwon National University, Chuncheon 24341, Republic of Korea

PES-31

Investigation of Pesticide Residues in Soil from Facility Cultivation Areas in Gyeongsangnam-do

Dong Kyu Jeong, Dong Yeol Lee*, Won Min Jeong, Hyeon Hee Kim, Gyeong Hwan Lee, Yeong In Choe

Research & Development Team, Gyeongnam Anti-Aging Research Institute

PES-32

Residue Characteristics of Dinotefuran and Methoxyfenozide in Mulberry

Chae Eun Kim, Hyeon Kyu Jeong, Sua Jeong, Joon Kwan Moon*

Department of Plant Resources and Landscape Architecture, Hankyong National University

PES-33

Monitoring of Pesticide Residue on Greenhouse Soil in Jeonnam Province

Sungwoo Kim[1*], Hyeonji Kim[1], Soyoun Lee[1], Kyungjin Kwak[1], Sunkuk Kim[1], Hyosub Lee[2]

[1]Environment-friendly agriculture research center, Jeollanam-do Agricultural Research & Extension Services, [2]National Institute of Agricultural Science, Rural Development Administration

PES-34

Optimization of Shrimp Shell-Derived Biochar Production for Agricultural Utilization

Jae-Hoon Lee, Jun Suk Rho, Seul-Rin Lee, Jung-Mok Lee, Seung-Hoon Lee, Dong-Cheol Seo*

Division of Applied Life Science(BK21 Four) & Institute of Agriculture and Life Science, Gyeongsang National University

PES-35

Screening of Endophytic Bacteria Isolated from Wheat to Control Streptomycin-Resistant phytopathogens

Jinhee Choi[1], Muhammad Fazle Rabbee[1], Myoung-Goo Choi[2], Kwang-Hyun Baek[1*]

[1]Department of Biotechnology, Yeungnam University, Korea, [2]Winter Crop Research Division, National Institute of Crop and Food Science, RDA, Korea

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PES-36

Biochar production using ecosystem-disrupting plants and its heavy metal adsorption

Jungwon Park[1], Ye-Ji Lee[1*], Jeong-Min Lee[1*], Jonghwan Park[2*],
Dong-Cheol Seo[3]

[1]Department of Applied Bioscience, Dong-A Univercity, [2]Department of Smart Green Resources, Dong-A Univercity, [3]Department of Applied Life Chemistry, Gyeongsang National Univercity

PES-37

Adsorption characteristics of methylene blue by rice husk extracted Si

Ye-Ji Lee[1], Jeong-Min Lee[1], Jung-Won Park[1], Dong-Cheol Seo[2],
Jong-Hwan Park[1*]

[1]Department of Applied Bioscience, Dong-A University, [2]Department of Applied Life Chemistry, Gyeongsang National University

PES-38

Agro-Environmental role of biochar derived from spent coffee ground in pepper cultivation

Jeong-Min Lee[1], Ye-Ji Lee[1], Jung-Won Park[1], Dong-Cheol Seo[2],
Jong-Hwan Park[1*]

[1]Department of Applied Bioscience, Dong-A University, [2]Department of Applied Life Chemistry, Gyeongsang National University

PES-39

Early Multi-Omics Insights into *Fusarium proliferatum*-Induced Dysbiosis in Soybean: Microbiome and Metabolome Rewiring Under Pathogen Stress

Tino Bashizi[1], Seung-Yeon Jeong[1], Tae Ho Kim[1], Kyeongmo Lim[1],
Jae-Ho Shin[1,2*]

[1]Department of Applied Biosciences, Kyungpook National University, Daegu 41566, Republic of Korea, [2]NGS Core Facility, Kyungpook National University, Daegu 41566, Republic of Korea

PES-40

Effects of Planting Density on Head Rice Yield under Delayed Transplanting in the Central Plain Region of Korea

Myeond-Na Shin*

Central-Northern Region Crop Research Center, National Institute of Crop and Fodd Science

PES-41

Effect of Phosphogypsum Derived Byproduct Hydrated Lime compost on Crop Safety and Soil Properties

Jinju Yun[1], Ahnsung Roh[1], Sangho Jeon[1], Seongheon Kim[1], Hyucksoo Kim[2],
Woojin Chung[3], Jaehong Shim[1*]

[1]Division of Soil and Water Environment, National Institute of Agricultural Sciences, RDA, [2]Department of Biological Environment, Kangwon National University, [3]Department of Civil & Energy System Engineering, Kyonggi University

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PES-42

Soil Texture Prediction Using Mid-Infrared Spectroscopy: Model Development and Evaluation

So-Hui Kim, Govind Dnyandev Vyavahare, Seong-Heon Kim,
Kyeon-Yeong Kim, Ahn-Sung Roh, Jin-Ju Yun, Yu-Na Kim, Sang-Ho Jeon*

National Institute of Agricultural Sciences, Division of Soil and Water environment

PES-43

Chemical and Heavy Metal Variability in Greenhouse Soils of Jeonnam Province

Hyeon Ji Kim*, Sung Woo Kim, So Yeon Lee, Kyung Jin Kwak,
Sun Kook Kim, Sun Ju Ko

Environment-Friendly Agricultural Reaserch Institute, Jeollanam-do Agricultural Reasearch and Extension Services

PES-44

Establishment of Pre-Harvest Residue Limits (PHRLs) of Novaluron in *Amaranthus mangostanus* L.

Yeong Jae An, Joon Kwan Moon*, Ho Jin Kim, Tae Eun Kim

Department of Plant Resources and Landscape Architecture, Hankyong National University

PES-45

Differential Phytotoxicity of PPO-Inhibiting Herbicides in Monocotyledonous and Dicotyledonous Plants

Hajin Son, Jiwoo Yu, Geonwoo Park, Jiwon Shin, Jiyeon Lee,
Youngsoo Keum*

Department of Crop Science, Konkuk University

PES-46

Sustainable Soil Management Strategy to Enhance Net Ecosystem Carbon Budget and Sequestration by Optimal Woody Biochar Application in Red Pepper Cropping Systems: Three-year Field Experiment

So Hee Yoon[1], Yeo Myeong Lee[1], Jasmin Melendez[1], Sang Yoon Kim[2]*

[1]Agricultural Chemistry & Interdisciplinary Program in IT-Bio Convergence System, Sunchon National University, [2]Agricultural Life Science, Sunchon National University

PES-47

Regional and strain-level distribution of nitrogen-fixing and N_2O-reducing Bradyrhizobium in South Korea

Jaeyoung Ro, Seoyeon Lee, Min Je Kang, Sujin Lee*, Hor gil Hur*

Department of Environment and Energy Engineering, Gwangju Institute of Science and Technology

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PES-48

Insecticide resistance of *Myzus persicae* (Hemiptera: Aphididae) populations collected from kimchi cabbage fields in South Korea

Doo-Hyung Lee*, Joo-Young Kim, Jung-Wook Kho

Life Sciences, Gachon University

PES-49

Effect of Liquid Fertilizer from Rendered Livestock Carcass Residues on Tomato Growth and Productivity

Jae-Hyuk Park[1], Ik-Hyeong Lee[2], Se-Won Kang[2,3], Ju-Sik Cho[2,3]*

[1]Division of Soil and Water environment, National Institute of Agricultural Sciences, Wanju 55365, Republic of Korea, [2]Department of Agricultural Chemistry, Sunchon National University, Suncheon 57922, Republic of Korea, [3]Department of Agricultural Life Science, Sunchon National University, Suncheon 57922, Republic of Korea

PES-50

Development of a Microalgae-Based Carbon Capture System for Cement Industry Flue Gas Mitigation

Dong-Guk Song[1], Van Ve Le[1], Sang-Ah Lee[1,2,3]*

[1]Faculty of Biotechnology, College of Applied Life Sciences, SARI, Jeju National University, Jeju 63243, Republic of Korea, [2]Interdisciplinary Graduate Program in Advanced Convergence Technology and Science, Jeju National University, Jeju 63243, Republic of Korea, [3]Bio-Health Materials Core-Facility Center, Jeju National University, 102 Jejudaehak-Ro, Jeju 63243, Republic of Korea

PES-51

Organic Matter Recycling Enhances Soil Carbon Sequestration: A Comparative Analysis of Paddy and Upland Agroecosystems

Na-Hyun Kwon[1], Chang-Dong Lee[1,2], Jae-Eun Jung[2], Chan-Young Lee[2], Yun-Ji Kim[2], Jeong-Gu Lee[1,2]*

[1]Department of Applied Biosciences, Kyungpook National University, Daegu 41566, South Korea, [2]School of Applied Life Science, College of Agriculture and Life Sciences, Kyungpook National University, Daegu 41566, South Korea

PES-52

Yields and Film Properties of Biodegradable Mulching Films in Onion, Pepper, and Soybean Cultivation across Different Region

Hyunhwa Park[1], Ei Ei[1], Pyae Pyae Win[1], Ji Young Nam[1], Do Jin Lee[2], Yong In Kuk[1]*

[1]Department of Bio-Oriental Medicine Resources, Sunchon National University, [2]Department of Agricultural Education, Sunchon National University

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PES-53

Interactions between polyethylene microplastics and imidacloprid in soil

U jin Song[1], Hoo Bin Han[2], Ji Won Yang[3], Eun Hea Jho[1*]

[1]Department of Agricultural and Biological Chemistry, Chonnam National University, Gwangju 61186, Republic of Korea, [2]Department of Agricultural Chemistry, Chonnam National University, Gwangju 61186, Republic of Korea, [3]Department of Agricultural Biotechnology, Seoul National University, Seoul 08826, Republic of Korea

PES-54

Planting Density Effects on Yield Components of Rice Varieties with Contrasting Nitrogen Response

Mi-Jin Chae*, Dae-Woo Lee, Chung-Kuen Lee, Kangsu Kwak,
Myeong-Na Shin

Central-Northern Region Crop Research Center Department of Crop Science, National Institute of Crop Science

PES-55

Interactions Between Aggregate-Associated Carbon Storage and Soil Biological and Chemical Properties in Organic Upland Fields

Chang-Hoon Lee*, Mun-Hyeong Park

Department of Horticulture, Korea National University of Agriculture and Fisheries

PES-56

Effect of Long-term Fertilization on Intra- and Inter- Particular Carbon in Upland Soils

Chang-Hoon Lee*, Mun-Hyeong Park

Department of Horticulture, Korea National University of Agriculture and Fisheries

PES-57

Optimization of Soil-Based QuEChERS Extraction and Comparative Assessment of Analytical Efficiency by Physicochemical Characteristics of Pesticides

Hyosub Lee[1*], Seojin Ki[2], Hyanghee Kim[1], Sungwoo Kim[3], Dongyeol Lee[4]

[1]Residual Agrochemical Assessment Division, National Institute of Agricultural Sciences, [2]Department of Environmental Engineering, Gyeongsang National University, [3]Jeollanam-do Agricultural Research and Extension Services, [4]Gyeongnam Anti-Aging Research Institue

PES-58

Risk Assessment and Management of Soil Pesticides Using Physicochemical Properties and Statistical Analysis

Sang-Ik Suh[1], Bumseok Lee[2], Dahui Kim[1], Yeji Kim[2], Hyosub Lee[3],
Minho Son[4], Seo Jin Ki[2*]

[1]Department of Energy System Engineering, Gyeongsang National University, Jinju 52725, [2]Department of Environmental Engineering, Gyeongsang National University, Jinju 52725, [3]Chemical Safety Division, NAS, Wanju 55365, [4]Podo inc., Seongnam 13449

PES-59

Analytical Method for Dichlobenil and 2,6-Dichlorobenzamide Residues in Beef, Milk, and Fat Using GC-MS/MS

Hyo-Lyn Kim, Jonghwa Lee[*], Dai An, Hyunmi Koo, Jeong-Im Kim,
So Young Yune, Young Hun Shim

Gyeongin Regional Office of Food and Drug Safety, Ministry of Food and Drug Safety

PES-60

Development of a Sweetness Booster for Fruits with Antimicrobial Function

Juhyun Yu[1*], Hyeran Shin[2], Hyun Gi Kong[3], Hyeyoung Kweon[2], Wongi Min[4],
Youngho Kim[2]

[1]SugarArt Research Institute, [2]SugarArt Research Institute, Biological Testing Team, [3]Chungbuk National University, Department of Plant Medicine, [4]SugarArt Research Institute, Formulation Development Team

PES-61

Temporal Analysis of Soil Physical Properties in Greenhouse Cultivation Areas of Jeollanam-do, South Korea (2016–2024)

Kyungjin Kwak[1*], Hyeonji Kim[1], Sungwoo Kim[1], Soyoun Lee[1], Sunkook Kim[1],
Suengoh Heo[2], Sugju Ko[1]

[1]Jeollanam-do Agricultural Research & Extension Services, Naju 58228, Korea,
[2]National Institute of Agricultural Science, RDA, Wanju 55365, Korea

PES-62

Greenhouse-Based Residue Dissipation Pattern and Age-Specific Dietary Risk of Propamocarb and Chlorfenapyr in Pumpkin

Yeong-Jin Kim[1], Sung-Gil Choi[1], Jin-Woo Park[1], Deuk-Yeong Lee[1],
Jong-Hwan Kim[1,2], Jong-Su Seo[1*]

[1]Center for Environmental Safety Research, Korea Institute of Toxicology, [2]Human and Environmental Toxicology Program, Korea University of Science and Technology

PES-63

Sustainable Option as Shifting Transplanting Date for Reducing Net Annual Global Warming Potential during Cropping and Fallow Seasons in a Mono Rice Paddy Field

Yeomyeong Lee[1], Sohee Yoon[1], Jasmin Melendez[1], Sang Yoon Kim[1,2*]

[1]Department of Agricultural Chemistry & Interdisciplinary Program in IT-Bio Convergence System, Sunchon National University, Suncheon 57922, Korea,
[2]Department of Agricultural Life Sciences, Sunchon National University, Suncheon 57922, Korea

PES-64

A Study on the Analysis of the Impact of Agricultural Environmental Conservation Activities on Resources in the Agricultural Environmental Conservation Program

Jeong-Woo Son[*], Bu-Yeong Oh, Seung-Oh Hur

Division of Soil and Water Environment, National Institute of Agricultural Sciences

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PES-65

Phosphorus Control Using Metal-Modified Biochar Under Algal Bloom Conditions

Seul-Rin Lee, Dong-Cheol Seo*, Jae-Hoon Lee, Jun-Suk Rho,
Jung-Mok Lee, Seung-Hoon Lee

Institute of Agricultural and Life Sciences & Division of Applied Life Science (BK21 Four), Gyeongsang National University

PES-66

Assessment of the leaching potential and residues for pesticides from soils in rainfall simulations

Jong-Wook Song, Yeoung-Jin Kim, Seong-Yeon Park, Jong-Hwan Kim*

Environmental Safety Research Center, Korea Institute of Toxicology

PES-67

Role of Green Manure in Promoting Humification and Soil Structure Stability in Paddy Systems

Jae-Eun Jung[1], Jeong-Gu Lee[1,2]*, Na-Hyun Kwon[2], Chang-Dong Lee[1],
Chan-Young Lee[1], Yun-Ji Kim[1]

[1]School of Applied Life Science, College of Agriculture and Life Sciences, Kyungpook National University, [2]Department of Applied Biosciences, Kyungpook National University

PES-68

Case study: Soil Health in Organic Conversion Vineyards

Hyun Young Hwang*, Yeon Ho Kim, Sang Min Lee

Regenerative Organic Agriculture Division, National Institute of Agricultural Sciences, Rural Development Administration

PES-69

Enhancing Biochar Stability and Nutrient Content through Co-Pyrolysis Utilizing Plant and Animal By-Products

Jun Suk Rho, Jae-Hoon Lee, Seul-Rin Lee, Jung-Mok Lee, Seung-Hoon Lee,
Dong-Cheol Seo*

Division of Applied Life Science(BK21 Four) & Institute of Agriculture and Life Science, Gyeongsang National University

PES-70

Carbon stability to lime (CaO) and silicate (SiO_2) amendments across soil depths under upland conditions

Na-Hyun Kwon[1], Jeong-Gu Lee[1,2]*

[1]Department of Applied Biosciences, Kyungpook National University, [2]School of Applied Life Science, College of Agriculture and Life Sciences, Kyungpook National University

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PES-71

Differential Physiological Responses to Plastoquinone Biosynthesis-Inhibiting Herbicides with Distinct Modes of Action in *Lactuca sativa* and *Lemna minor*

Ji-Yeon Lee, Ji-Woo Yu, Gun-Wo Park, Ji-Won Shin, Ha-Jin Son,
Young-Soo Keum*

Department of Crop Science, Konkuk University

PES-72

Evaluating the Effect of Enhanced Weathering Material on Lettuce Growth

Jae-Hyuk Park, Jin-Ju Yun, Yu-Na Lee, Govind Dnyandev Vyavahare,
So-Hui Kim, Sin-Sil Kim, Kyeong-Yeong Kim, Seong-Heon Kim,
Jae-Hong Shim, Ahn-Sung Roh, Sang-Ho Jeon*

Division of Soil and Water environment, National Institute of Agricultural Sciences, Wanju 55365, Republic of Korea

PES-73

Evaluation of Biochar as a Sustainable Exfoliating Agent for Replacing Microplastics and Natural Abrasives in Cleansing Foam

Yeo-Ji Choi[1], Chae-Won Eom[1], Seul-Rin Lee[2], Jae-Hoon Lee[2], Jun-Suk Rho[2],
Jung-Mok Lee[2], Seung-Hoon Lee[2], Dong-Cheol Seo[1,2]*

[1]*Department of Applied Life chemistry, Gyeongsang National University,* [2]*Division of Applied Life Science (BK21 Four) and Institute of Agricultural and Life Sciences, Gyeongsang National University*

PES-74

Agronomic Effects of Livestock Manure Compost Produced from Biochar-Mixed litter

Seung Hoon Lee[1], Seul Rin Lee[1], Jun Suk Rho[1], Jae Hoon Lee[1],
Jung Mok Lee[1], Dong Cheol Seo[2]*

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PES-75

Comparative Study on Pesticide Exposure Levels According to Formulation Type and Physical State During Mixing and Spraying by Pesticide Operator

Byung Joon Kim, You Mi Jo, So-Hye Hong, Soo-Jin Park, Ji Young Shin,
Min-Kyoung Paik, Si young Yang*

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PFS Food Sciences

PFS-1

Study on the Deodorizing and pH-Buffering Effects of Eggshell-Derived Calcium Carbonate Pads in Meat Storage

Ji Ho Jeon[1*], Ji Soo Lee[2]

[1]Department of Chemistry & Life science, Sahmyook University, [2]Department of Food & Nutrition, Sahmyook University

PFS-2

Preparation and Characterization of Tannase Immobilized Titanium Dioxide Nanoparticles

Hoon Yoo*, Vu Phuong Dong

Department of Pharmacology and Dental Therapeutics, College of Dentistry, Chosun University

PFS-3

Research on Internationally Harmonized Usage of Sweeteners

Minkyoung Lee[1], Taeyang Kim[1], Sojeong Lee[1], Do-Yeong Kim[2], Hyorim Seo[2], Eunjae Oh[2], Shinai Choi[3], Hyun Chung[3], Eunju Kim[1*]

[1]International Life Science Institute of Korea, [2]Division of Food and Nutrition, Chonnam National University, [3]KnA co. Ltd.

PFS-4

Monitoring and Risk Assessment of Pesticide Residues in Shellfish Using GC and LC-MS/MS

Mi-Hyun Cho[1], Chang-Kyo Seo[1], Myung-Heon Kim[1], Jae-Bin Im[1], Chang-Hyeon Park[1], Eu-Nae Suh[1], Do-Yeon Lee[1], Yoon-Mi Lee[2], Mi-Ra Jo[2], Moo-Hyeog Im[1*]

[1]Food Engineering, Daegu University, [2]Food Safety and Processing Research Division, National Institute of Fisheries Science

PFS-5

Effect of drying methods on metaflumizone residues in Welsh onions

Jae-Bin Im, Mi-Hyun Cho, Myung-Heon Kim, Chang-Kyo Seo, Chang-Hyeon Park, Do-Yeon Lee, Eu-Nae Seo, Moo-Hyeog Im*

Food Engineering, Daegu University

PFS-6

Comprehensive analysis of metabolites and bioactivity from different cultivars of radish sprouts (*Raphanus sativus* L.)

Hye Won Seo[1], Chan Ung Park[2], Jin Su Lim[2], Hae Jin Kwon[1], Ki Hyun Kim[2], Min Hwan Lee[2], Sang Un Park[1,2*]

[1]Department of Smart Agriculture Systems, Chungnam National University, [2]Department of Crop Science, Chungnam National University

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PFS-7

Comparison of immunomodulatory from lactic acid bacteria-fermented mountain-cultivated ginseng sprouts

Jongbin Jeong, Du Yong Cho, Ae Ryeon Lee, Mu Yeun Jang, Da Hyun Kim, Do Yun Bang, Hye Rim Kim, Ye Rim Jeong, Kye Man Cho*

Department of GreenBio Science and Agri-Food Bio Convergence Institute, Gyeongsang National University

PFS-8

Changes in metabolites and biological activities of isoflavone-enhanced mung bean leaves by bioprocessing stages

Mu Yeun Jang[1], Du Yong Cho[1], Ae Ryeon Lee[1], Jong Bin Jeong[1], Da Hyun Kim[1], Do Yun Bang[1], Hye Rim Kim[1], Ye Rim Jeong[1], Jin Hwan Lee[2], Kye Man Cho[1]*

[1]*Department of GreenBio Science and Agri-Food Bio Convergence Institute, Gyeongsang National University,* [2]*Department of Smart Green Resources, Dong-A University*

PFS-9

Optimization of fermentation conditions of isoflavone-enriched mung bean leaves with lactic acid bacteria

Hye Rim Kim[1], Du Yong Cho[1], Ae Ryeon Lee[1], Jong Bin Jeong[1], Mu Yeun Jang[1], Da Hyun Kim[1], Do Yun Bang[1], Ye Rim Jeong[1], Jin Hwan Lee[2], Kye Man Cho[1]*

[1]*Department of GreenBio Science and Agri-Food Bio Convergence Institute, Gyeongsang National University,* [2]*Department of Smart Green Resources, Dong-A University*

PFS-10

Comparisons in the nutritional and functional components of brown rice induced by fermentation with mushroom mycelia

Ye Rim Jeong, Du Yong Cho, Ae Ryeon Lee, Jong Bin Jeong, Mu Yeun Jang, Da Hyun Kim, Do Yun Bang, Hye Rim Kim, Kye Man Cho*

Department of GreenBio Science and Agri-Food Bio Convergence Institute, Gyeongsang National University

PFS-11

Comparison of metabolites and biological activities in isoflavone-enriched soybean leaves by bioconversion with different mushroom mycelia

Ae Ryeon Lee[1], Du Yong Cho[1], Jong Bin Jeong[1], Mu Yeun Jang[1], Da Hyun Kim[1], Do Yun Bang[1], Hye Rim Kim[1], Ye Rim Jeong[1], Jin Hwan Lee[2], Kye Man Cho[1]*

[1]*Department of GreenBio Science and Agri-Food Bio Convergence Institute, Gyeongsang National University,* [2]*Department of Smart Green Resources, Dong-A University*

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PFS-12

Comparison of functional components and biological activity in fermented white rice with edible mushroom mycelia

Da Hyun Kim, Du Yong Cho, Ae Ryeon Lee, Jong Bin Jeong, Mu Yeun Jang,
Do Yun Bang, Hye Rim Kim, Ye Rim Jeong, Kye Man Cho*

Department of GreenBio Science and Agri-Food Bio Convergence Institute,
Gyeongsang National University

PFS-13

Effect of adding rice as a secondary ingredient on the hardness, antioxidant activity and aglycone isoflavone content of tempeh

Hye-Young Park*, Hyun-Joo Kim, Hye-Sun Choi, Ji-Young Park,
Eun Yeong Sim, Hong-Sik Kim

National Institute of Crop and Food Science, Rural Development Administration

PFS-14

Species Diversity of *Aspergillus* and *Fusarium* from Onion Bulbs in Korea

Jung-Hye Choi, Miji Kim, Jung Weol Lee, Jung Yeong Lee, Seora Park,
Miri Kim, Ga Ryeong Baek, Jiwon Han*

Allium Vegetable Research Center, National Institute of Horticultural and Herbal
Science, Rural Development Administration

PFS-15

Sustainable Extraction of Anthocyanins from Mulberry (*Morus Alba* L.) By-Products Using Natural Deep Eutectic Solvents (NADES)

Haeun Lee[1], Jongyoon Choi[2]*, Woojin Jang[2]*, Jihyun Lee[1]*

[1]Department of Food and Nutrition, Seoul National University, [2]Department of Food
Science and Technology, Chung-Ang University

PFS-16

Characterization of volatile compounds in edible insect oils at different storage stages using HS-SPME-Arrow-GC/MS

You Rim Min, Hae Won Jang*

Food Science and Biotechnology, Sungshin women's University

PFS-17

Identification of Key Volatile Markers in Commercial Broth

Jin-Kyung Nam, Hae Won Jang*

Department of Food Science and Biotechnology, Sungshin Women's University

PFS-18

Seasonal and Regional Characteristics of Free Sugars and Crude Fat in Potatoes

Ye-Eun Lee[1], Ji Yun Lee[1], Hyang Lan Eum[2], Hae Won Jang[1]*

[1]Department of Food Science and Biotechnology, Sungshin Women's University,
[2]National Institute of Crop Science, Highland Agriculture Research Institute, RDA

PFS-19

Comparative Screening of Antioxidant and Anti-Inflammatory Activities Among Domestically Bred Carica papaya L. Hybrids Using Different Extraction Solvents

Yaejun Kim[1], Kyeoung Cheol Kim[2], Ji-Hyang Kim[2], Su-Lim Kim[2],
Chankyu Lim[3], Seong-Cheol Kim[3], Dong-Sun Lee[1,2,4]*

[1] Interdisciplinary Graduate Program in Advanced Convergence Technology & Science, Jeju National University, Jeju, Republic of Korea, [2] Bio-Health Materials Core-Facility Center, Jeju National University, Jeju, Republic of Korea, [3] Research Institute of Climate Change and Agriculture, National Institute of Horticultural and Herbal Science, Rural Development Administration, Jeju, Republic of Korea, [4] Faculty of Biotechnology, College of Applied Life Sciences, Jeju National University, Jeju, Republic of Korea

PFS-20

Analysis of volatile components in Korean wheat flour with varying levels of added apple pomace based on drying method using an electronic nose

Chae Min Han*, Seong Ran Yoon, Jung A Ryu, Jung Gi Ryu

Division of Agricultural Food and Environment Research, Gyeongsangbuk-do Provincial Agricultural Research & Extension Services

PFS-21

Fermented Mixture of *Saccharina* and *Panax* Ameliorates Gentamicin-Induced Gut Dysbiosis via Modulation of the Gut Microbiota

Gwnag-Pyo Ko[1], Minseong Park[1], Hyejun Jo[1], Eungyeong Lee[2],
Chang Sook Kim[1]*

[1] Faculty of Biotechnology, Jeju National University, [2] BioNewledge Co. Ltd

PFS-22

Ellagic acid, an active compound of Rosa multiflora fruit, attenuates stress hormone-induced depression in mice by inhibiting monoamine oxidase

Minji Kim[1,2], Dong Wook Lim[1], Min-Sun Kim[1], Heejin Nam[3], Sooim Shin[3],
Changho Lee[1], Min Young Um[1]*

[1] Food Functionality Research Division, Korea Food Research Institute, [2] Division of Food Biotechnology, University of Science & Technology, [3] Department of Biotechnology & Bioengineering, Chonnam National University

PFS-23

Functional Analysis of the Ectopically Expressed Olfactory Receptor OR2AT4 in Leukemic Cells

Min Jung Kim*, Yae Rim Choi

Research Division of Food Functionality, Korea Food Research Institute

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PAM Applied Microbiology

PAM-1

Ferrous Ion-Induced Antifungal Activity of *Metschnikowia persimmonesis* Against *Colletotrichum gloeosporioides*

Ariranur Haniffadli[1,2], Joyce Mudondo[1,2], Kenneth Happy[1,2], Roggers Gang[1,2], Yeoungjun Ban[2], Kyeong-Ok Choi[2], Subeen Mun[2], Seyoung Im[2], Youngmin Kang[1,2*]

[1]Korean Convergence Medical Science major, University of Science & Technology (UST), Korea Institute of Oriental Medicine, Daejeon 34054, Republic of Korea, [2]Herbal Medicine Resources Research Center, Korea Institute of Oriental Medicine, 111Geonjae-ro, Naju-si, Jeollanam-do 58245, Republic of Korea

PAM-2

Analysis of the characteristics of Carbapenem-resistant Enterobacterales (CRE) infections in southern Gyeonggi-do

Yeong Eun Jang*, Jong Sup Jeon, Hyun Jue Kim, Chan Mi Lee, So Jung Park, Ju Hee Kwon, Seung Chan Kim

Department of Infectious Disease Research, Gyeonggi-province Institute of Health and Environment

PAM-3

Metagenomic Insight into the Gut Dysbiosis and Its Association with Non-Alcoholic Fatty Liver Disease in Humans

Anushree Joshi[1], Vineet Singh[1], Jae - Ho Shin[1,2,3*]

[1]Department of Applied Biosciences, Kyungpook National University, [2]Department of Integrative Biology, Kyungpook National University, [3]NGS Core Facility, Kyungpook National University

PAM-4

Metatranscriptomic analysis of plant viruses infecting pepper in Indonesia

Andika Suryaningsih[1], Bu-Young Kim[1], Yu Lim Park[2], Eun-Ae Suh[2], Sun-Jung Kwon[2], Jang-Kyun Seo[1,2*]

[1]Department of International Agricultural Technology, Seoul National University, [2]Institutes of Green Bio Science and Technology, Seoul National University

PAM-5

Evolutionary and pathogenic characterization of the cucurbit aphid-borne yellows virus population in Korea

Bu-Young Kim[1], Andika Suryaningsih[1], Yu Lim Park[2], Eun-Ae Suh[2], Sun-Jung Kwon[2], Jang-Kyun Seo[1,2*]

[1]Department of International Agricultural Technology, Seoul National University, [2]Institutes of Green Bio Science and Technology, Seoul National University

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PAM-6

Unraveling Environmental Immunomodulation: Multi-Omics Study of Microbiome-Mediated Plant Disease Suppression using Gnotobiotic Systems

Minsoo Jeong[1], Sook-Min Kwon[2], Seungyeon Jeong[1], Jae-Ho Shin[1,3*]

[1]Department of Applied Biosciences, Kyungpook National University, Daegu, Republic of Korea, [2]Department of Integrative Biotechnology, Kyungpook National University, Daegu, Republic of Korea, [3]NGS Core Facility, Kyungpook National University, Daegu, Republic of Korea

PAM-7

Microbial Network and Functional Analysis in Rhizosphere Soils Cultivated Wild-Simulated Ginseng

Yeong-Bae Yun[1], Myeongbin Park[1], Yurry Um[1*], Seok Hui Lee[2], Jun-Won Kang[2]

[1]Forest Medicinal Resources Research Center, National Institute of Forest Science, [2]School of Forest Science and Landscape Architecture, Kyungpook National University

PAM-8

Exploration of Nitrogen-fixing and Nitrous oxide-reducing Bacteria from Legume Roots and Soils

Seung Hwa Jeong[1], Hyeyeon Park[1], Yejin Seon[1], Sujin Lee[2], Yeonjong Koo[1*]

[1]Department of Agricultural Chemistry, Chonnam National University, [2]Department of Environment and Energy Engineering, Gwangju Institute of Science and Technology

PAM-9

Vesicle-Based Delivery of *Bacillus*-Derived Lipopeptides Improves Stability and Enhances Antifungal Efficacy in Field Application

Beom Ryong Kang[1*], Midam Kim[2], Gwang Rok Ryu[2]

[1]Institute of Environmentally-Friendly Agriculture, Chonnam National University, [2]Department of Agricultural Chemistry, Chonnam National University

PAM-10

Structure-guided Engineering of TtgR-based Whole-cell Biosensors for Selective and Quantitative Detection of Flavonoids

Hae Kang Ji[1], Kyeongseok Song[1], Jiwon Lee[1], Geupil Jang[2*], Youngdae Yoon[1*]

[1]Environmental Health Science, Konkuk University, [2]Biological Sciences and Technology, Chonnam National University

PAM-11

Effect of streptomycin on the growth characteristics of soil-isolated microorganisms

Jae Gyeong Kim[1], Kehinde Caleb Omidoyin[1], Eun Hea Jho[1,2*]

[1]Department of Agricultural Chemistry, Chonnam National University, Gwangju 61186, Republic of Korea, [2]Department of Agricultural and Biological Chemistry, Chonnam National University, Gwangju 61186, Republic of Korea

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PAM-12

Robustness of Cellulase Activity Under Limited Water Condition

Min-Seung Oh, Kyung-Jin Min*

Department of Agricultural Biotechnology, Seoul National University

PAM-13

Activation of plant defense responses by a chitinase-producing rhizobacterium mitigates cobalt stress in soybean (*Glycine max* L.)

Ji-In Woo, Ho-Jun Gam, Jin Ryeol Jeon, Min Young Back, Sang-Mo Kang, In-Jung Lee*

Department of Applied Biosciences, Kyungpook National University, Daegu 41566, Korea

PAM-14

Whole-Genome Sequencing of the Bacterium *Bacillus amyloliquefaciens* PgBE99, with antifungal activities against fungal disease associated with ginseng leaves

Chi Eun Hong[1]*, Sung Yeon Kim[1], Seung Ho Lee[2], Yong Il Kim[1], In Bok Jang[1], Soohong Kim[1], Young Chang Kim[1]

[1]*Industrial Crop Cultivation Division, Department of Herbal Crop Research, National Institute of Horticultural and Herbal Science,* [2]*Technology Service Division, National Institute of Horticultural and Herbal Science*

PAM-15

Microalgae Anaerobic Digestion for Enhanced Methane Production

Seo-Yeon Yang[1], Won-Seok Kim[2,3], Se-Hoon Kim[3], Jiyoung Choi[4], Ji-Hoon Kim[4], Ji-Hoon Lee[1,5,6]*

[1]*Department of Agricultural Chemistry, Jeonbuk National University,* [2]*Division of Advanced Nuclear Engineering, Pohang University of Science and Technology,* [3]*NC Square,* [4]*Marine Geology & Energy Division, Korea Institute of Geoscience and Mineral Resources,* [5]*Department of Bioenvironmental Chemistry, Jeonbuk National University,* [6]*Institute of Agricultural Science & Technology, Jeonbuk National University*

PAM-16

Comparative Analysis of Scalp Microbiome Across Healthy, Problematic, and Alopecic Conditions

Kyeongmo Lim[1], HyungWoo Jo[2], Sook-Min Kwon[3], Jae-Ho Shin[1,3,4,5]*

[1]*Department of Applied Biosciences, Kyungpook National University, Daehak-ro 80, Daegu 41566, Republic of Korea,* [2]*R&I Center, COSMAX BTI, Seongnam 13486, Republic of Korea,* [3]*Department of Integrative Biology, Kyungpook National University, Daehak-ro 80, Daegu 41566, Republic of Korea,* [4]*NGS Core Facility, Kyungpook National University, Daehak-ro 80, Daegu 41566, Republic of Korea,* [5]*MICROBALANCE Co., Ltd., Kyungpook National University, Daehak-ro 80, Daegu 41566, Republic of Korea*

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PAM-17

Transcriptomic Analysis of *Xanthomonas oryzae* pv. *oryzae* Under Microgravity: Insights into Pathogenicity Modulation and Adaptive Strategies

Youngchul Yoo[1], Sang Won Lee[2*]

[1]Genetic Engineering and Biotechnology, Kyung Hee University,
[2]Green-Bioscience, Genetic Engineering and Biotechnology, Kyung Hee University

PAM-18

The Characteristics of Microbial Communities in Greenhouse Cultivation Soils in Jeonnam Province

So Youn Lee[1*], Hyeon Ji Kim[1], Sung Woo Kim[1], Kyung Jin Kwak[1], Sun Kook Kim[1], Sug Ju Ko[1], Do Hyun Kim[2]

[1]Environment-Friendly Agricultural Research Institute, Jeollanamdo Agricultural Research and Extension Services, [2]National Institute of Agricultural Sciences, RURAL DEVELOPMENT ADMINISTRATION

PAM-19

Isolation of Laccase-producing Bacteria from Diverse Environments and Their Application to Decolorize Textile Dyes

Miso Kim[1], Youri Yang[1,2*]

[1]Department of Food Biotechnology and Environmental Science, Kangwon National University, Republic of Korea, [2]Department of Biological Environment, Kangwon National University, Republic of Korea

PAM-20

Characterization of indole-3-acetic acid (IAA)-producing rhizobacteria with potential to alleviate salt stress in plants

Ju-Yeon Ha, Jin Ryeol Jeon, Ji-In Woo, Min Young Back, Sang-Mo Kang, In-Jung Lee*

Department of Applied Biosciences, Kyungpook National University

PAM-21

Effects of Oil Cake Fertilization on Soil Chemistry and Bacterial Communities in a Jujube Orchard

Kiyoon Kim[1], Tongmin Sa[2*]

[1]Korea Forest Service, National Forest Seed Variety Center, [2]Chungbuk National University, Department of Environmental and Biological Chemistry

PAM-22

Bacterial Carbonate Precipitation by Urease-Producing *Priestia* sp. Strain GS1 in Alkaline Conditions

Chaemin Sim[1], Youri Yang[1,2*]

[1]Department of Food Biotechnology and Environmental Science, Kangwon National University, Republic of Korea, [2]School of Natural Resources and Environmental Science, Department of Biological Environment, Kangwon National University, Republic of Korea

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PAM-23

Effect of Organic Fertilizer on Soil Bacterial Community Structure in a Jujube Orchar

Kiyoon Kim[1], Tongmin Sa[2*]

[1]Korea Forest Service, National Forest Seed Variety Center, [2]Chungbuk National University, Department of Environmental and Biological Chemistry

PAM-24

Screening and Characterization of Polyhydroxyalkanoates (PHAs)-producing Bacteria Isolated from Diverse Environments and Their Potential for Bioplastic Production

Jieun Lim[1], Youri Yang[1,2*]

[1]Department of Food Biotechnology and Environmental Science, Kangwon National University, Republic of Korea, [2]School of Natural Resources and Environmental Science, Department of Biological Environment, Kangwon National University, Republic of Korea

PAM-25

Exploration of Laccase-producing Bacteria from Alkaliphilic Environments and Their Decolorizing Activity against Industrial Synthetic Dyes

Haeun Kim[1], Miso Kim[2], Youri Yang[1,2*]

[1]School of Natural Resources and Environmental Science, Department of Biological Environment, Kangwon National University, Republic of Korea, [2]Department of Food Biotechnology and Environmental Science, Kangwon National University, Republic of Korea

PAM-26

Silicate-solubilizing rhizobacteria enhance drought resilience in wheat (*Triticum aestivum* L.)

Min Young Back, Ho-Jun Gam, Ji-In Woo, Jin Ryeol Jeon, Sang-Mo Kang, In-Jung Lee*

Department of Applied Biosciences, Kyungpook National University, Daegu 41566, Korea

PAM-27

Increasing Fucoxanthin Concentration in *Phaeodactylum tricornutum* by Optimization of Culture Conditions Using Response Surface Methodology

Phuong Kim Huynh[1,2], To Quyen Truong[2], Sang Min Kim[1,2*]

[1]Natural Product Applied Science, Korea Institute of Science and Technology (KIST) School, University of Science and Technology, Gangneung 25451, Republic of Korea, [2]Smart Farm Research Center, KIST Gangneung Institute of Natural Products, Gangneung 25451, Republic of Korea

PAM-28

Integrated Biocontrol and Abiotic Stress Tolerance via *Bacillus*-Derived Lipopeptides and Functional Genomic Trait

Beom Ryong Kang[1*], Midam Kim[2], Gwang Rok Ryu[2], Jun Seok Choi[3]

[1]Institute of Environmentally-Friendly Agriculture, Chonnam National University, [2]Department of Agricultural Chemistry, Chonnam National University, [3]National Institute of Crop Science, Rural Development Administration

PAM-29

Valorization of sulfonated polyethylene via Bio-Fenton reaction supported by *Desemzia* sp. strain C1

Yongseok Ko, Sujin Lee, Minje Kang, Seoyeon Lee, Hor-Gil Hur*

Department of Environment and Energy Engineering, Gwangju Institute of Science and Technology

PAM-30

Conferring non-strain-specific resistance to a potyvirus via overexpression of mutant potyviral coat proteins in soybean

Sun-Jung Kwon[1], Myung-Hwi Kim[2], Young-Soo Chung[3], Kook-Hyung Kim[2], Jang-Kyun Seo[1,4*]

[1]Institutes of Green Bio Science and Technology, Seoul National University, [2]Department of Agricultural Biotechnology, Seoul National University, [3]Department of Genetic Engineering, Dong-A University, [4]Department of International Agricultural Technology, Seoul National University

PAM-31

Agricultural Applications of Pyrrolnitrin-Producing Burkholderia sp.: Effects on Plant Growth and Fungal Suppression

Geon-Woo Park, Ji-Woo Yu, Ji-Won Shin, Ji-Yeon Lee, Ha-Jin Son, Young-Soo Keum*

Department of Crop Science, Konkuk University

PAM-32

Microbial carbon availability decreases, but the degree of carbon limitation remains invariant along soil depth profiles

Seungwon Kim, Kyungjin Min*

Department of Agricultural Biotechnology, Seoul National University

PAM-33

A Novel Secreted Effector MGG40 from *Magnaporthe oryzae* Triggers Immune Responses and Cell Death in Rice

Gi hyun Lee[1], Cheol Woo Min[1], Ju soon Yoo[1], Yiming Wang[2], Jong-Seong Jeon[3], Ravi Gupta[4], Sun Tae Kim[1*]

[1]Department of Plant Bioscience, Life and Industry Convergence Research Institute, Pusan National University, [2]Department of Plant Pathology, Nanjing Agricultural University, [3]Graduate School of Green-Bio Science and Crop Biotech Institute, Kyung Hee University, [4]College of General Education, Kookmin University

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PAM-34

Co-application of a Silicate-Solubilizing *Burkholderia* Strain and Slag Silicate Fertilizer Boosts Maize Biomass and Restructures the Rhizosphere Microbiome

Sihyun Park[1], Ikwhan Kim[2], Sook-Min Kwon[2], Na-Hyun Kwon[1], Hyungwoo Jo[3], Jeong-Gu Lee[1], Jae-Ho Shin[1,2*]

[1]Department of Applied Biosciences, Kyungpook National University, Daegu 41566, Republic of Korea, [2]Department of Integrative Biology, Kyungpook National University, Daegu 41566, Republic of Korea, [3]R&I Center, COSMAX BTI, Seongnam 13486, Republic of Korea

PAM-35

Comparison Growth and Antioxidant Activity of *Lysimachia mauritiana* Lam. by IAA Pruduction Optimized *Bacillus toyonensis* WS2-2

Min Ju Kim, Seung Hee Ham, Sooin Jang, Hayeon Byun, Eun Young Bae, Youn-Bong Ku, Yoo Gyeong Park*

Biological Resources Utilization Department, National Institute of Biological Resources (NIBR)

PAM-36

Effect of *Rahnella bruchi* DSM 27398^T Cultured for Maximum IAA Production on *Lysimachia mauritiana* Lam. Growth

Min Ju Kim, Seung Hee Ham, Sooin Jang, Hayeon Byun, Eun Young Bae, Youn-Bong Ku, Yoo Gyeong Park*

Biological Resources Utilization Department, National Institute of Biological Resources (NIBR)

PAM-37

Microbial Engraftment and Symptom Improvement Following FMT in Dogs with Chronic Enteropathy

Heejoo Hwang[1], Hyunwoo Son[2], Jae-Ho Shin[1,2,3*]

[1]Department of Integrative Biology, Kyungpook National University, Daegu 41566, Republic of Korea, [2]Department of Applied Biosciences, Kyungpook National University, Daegu 41566, Republic of Korea, [3]Next Generation Sequencing (NGS) Core Facility, Kyungpook National University, Daegu 41566, Republic of Korea

PAM-38

Comparative Analysis of Microbial Community Structure and Pathogen Persistence in Municipal Wastewater and Livestock Manure Treatment Facilities

Geon Choi[1], Hokyung Song[2], Cheongnyeong Jin[1], Hanbit Hwang[1], Tatsuya Unno[1*]

[1]Department of Environmental and Biological Chemistry, Chungbuk National University, [2]Department of Environmental Engineering, Chosun University

PAM-39

The Crosstalk between Vaginal, Urinary, and Anal Microbiome in Female Urogenital Tract Health

Da-Ryung Jung[1], Se Young Jeon[2], Gun Oh Chong[2], Jae-Ho Shin[1,3*]

[1]Department of Applied Biosciences, Kyungpook National University, Daegu 41566, Republic of Korea, [2]Department of Obstetrics and Gynecology, Kyungpook National University Chilgok Hospital, Daegu 41404, Republic of Korea, [3]NGS Core Facility, Kyungpook National University, Daegu 41566, Republic of Korea

PAM-40

Time Course for Solubility of Imipenem as an Antibiotic against *Pseudomonas aeruginos*

Gu-Hae Kim[1], Jeongeon Kim[1], Dawon Kang[2*], Jeong Yoon Kim[1*]

[1]Department of Pharmaceutical Engineering, ABC-RLRC, IALS, Gyeongsang National University, Jinju 52725, Republic of Korea, [2]Department of Physiology, Institute of Health Sciences, School of Medicine, Gyeongsang National University, Jinju 52725, South Korea

PAM-41

Chronic PET-Microplastic Exposure Triggers Hyperphagia and Gut Microbiome Perturbation: Implications for Metabolic Health

Gyudae Lee, Seungjun Lee[*], Jae-Ho Shin[*]

Department of Applied Biosciences, Kyungpook National University, Daegu 41566, Republic of Korea

PAM-42

Differential Impacts of Dietary Fibers on the Human Gut Microbiome in an *In Vitro* Fermentation Model

Yujin Hyun[1], Min-Ji Kim[2], Jae-Ho Shin[2,3*]

[1]Department of Integrative Biology, Kyungpook National University, Daegu 41566, Republic of Korea, [2]NGS Core Facility, Kyungpook National University, Daegu 41566, Republic of Korea, [3]Department of Integrative Biology, Kyungpook Natioal University, Daegu 41566, Republic of Korea

PAM-43

First-Crop or Replant? Microbial Fingerprints Decode Ginseng Soil History and Rusty Root Risk

Sook-Min Kwon[1], Minsoo Jeong[2], Jae-Ho Shin[1,2,3*]

[1]Department of Integrative Biology, Kyungpook National University, Daegu 41566, Republic of Korea, [2]Department of Applied Biosciences, Kyungpook National University, Daegu 41566, Republic of Korea, [3]NGS Core Facility, Kyungpook National University, Daegu 41566, Republic of Korea

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PAM-44

Soil Microbial Community Responses to Biofumigation Using *Brassica juncea*: A Temporal Comparison Based on the Presence or Absence of Glucosinolates

Mu-Hyeok Kwon[1], Sihyun Park[1], Jae-Ho Shin[1,2*]

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PBD Bio-health/Drug development

PBD-1

Distinct Microglial Responses to Non-Neurotropic and Neurotropic Influenza A Virus Strains Under Innate Immune Priming

Thi Len Ho[1], Eun-Ju Ko[2*]

[1]Interdisciplinary Graduate Program in Advanced Convergence Technology & Science, Jeju National University, [2]Department of Veterinary Medicine, College of Veterinary Medicine, Jeju National University

PBD-2

Avian Diversity in Ephemeral and Permanent Wetlands of Jeju Island

Young Hun Jeong, Hong Shik Oh*

Interdisciplinary Graduate Program in Advanced Convergence Technology and Science, Jeju National University, Jeju-si 63243, Jeju-do, Republic of Korea

PBD-3

Selective Thyroid Uptake of Technekitty injection (Tc-99m) in Feline Hyperthyroidism

Jaecheong Lim*, So-Young Lee, Seung Jae Lee

Radioisotope Research Division, Korea Atomic Energy Research Institute

PBD-4

Predicting the Fine-scale Habitat Suitability of an Endemic Species, Jeju Striped Field Mouse (*Apodemus chejuensis*) in Jeju Island, South Korea

Binod Kunwar, Hong-Shik Oh*

Interdisciplinary Graduate Program in Advanced Convergence Technology and Science, Jeju National University

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PBD-5

pH-Dependent Modulation of Nitrous Oxide Emission in *Nitrospira inopinata*

Yun Ji Choi[1], Man Young Jung[2*]

[1]Interdisciplinary Graduate Program in Advance Convergence Technology and Science, Jeju National University, [2]Interdisciplinary Graduate Program in Advance Convergence Technology and Science, Department of Biology Education, Jeju National University

PBD-6

Bisphenol A Drives Exosome-Mediated Neuron-to-Glia Mitochondrial Transfer, Accelerating Neurodegeneration

Duy Vu Ba Le[1,2], Gee Euhn Choi[1,2*]

[1]Laboratory of Veterinary Biochemistry, College of Veterinary Medicine and Veterinary Medical Research Institute, Jeju National University, Jeju 63243, Republic of Korea, [2]Interdisciplinary Graduate Program in Advanced Convergene Technology & Science, Jeju National University, Jeju 63243, Republic of Korea

PBD-7

Hepatocyte TonEBP promotes metabolic dysfunction-associated steatohepatitis by transcriptionally activating multiple neutrophil-attracting chemokines

Hana Song, Ye-Seul Jeong, Seung Mi Ko, Mi Gyeong Jang, Soo Youn Choi*

Department of Biology, Jeju National University

PBD-8

Polymethoxyflavones from *Citrus sunki* Leaves Attenuate Renal Dysfunction in Oxidative Stress-Induced Acute Kidney Injury

Hana Song, Ye-Seul Jeong, Seung Mi Ko, Mi Gyeong Jang, Soo Youn Choi*

Department of Biology, Jeju National University

PBD-9

Optimization of Estrogen Analysis Using Liquid–Liquid Extraction and Derivatization Protocol

Min-Ho Song[1], Ji-Woo Yu[2], Jung-Hoon Lee[1,3], Eun-Song Choi[1,3], Ji-Ho Lee[1,3*]

[1]School of Natural Resources and Environment Science College of Agriculture and Life Sciences, Kangwon National University, [2]Department of Crop Science, Konkuk University, [3]Department of Food Biotechnology and Environmental Science, Kangwon National University

PBD-10

ZjGIGANTEA Negatively Regulates Osmotic Stress Tolerance in *Zoysia japonica*

Yueyue Yuan[1], Jin Hee Kim[2*]

[1]Interdisciplinary Graduate Program in Advanced Convergence Technology and Science, Jeju national University, [2]Subtropical Horticulture Research Institute, Jeju National University

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PBD-11

ZjWRKY75 Transcription Factors Mediate Stress-Induced Leaf Senescence via Hormonal Regulation in *Zoysia japonica*

Lanshuo Wang[1], Jeongsik Kim[2*]

[1]Interdisciplinary Graduate Program in Advanced Convergence Technology and Science, Jeju National University, [2]Faculty of Science Education, Jeju National University

PBD-12

Benchmarking AI Applications in Screening: Evaluating AlphaFold3 as a Tool for Drug Discovery

Young Joon Ko, Keunwan Park[*]

Natural Product Research Center, Korea Institute of Science and Technology

PBD-13

Polygonum cuspidatum Extract Containing Emodin Suppresses Lung Cancer-Induced Cachexia by Suppressing TCF4/TWIST1 Complex-Induced PTHrP Expression

Ji-Hye Han[1], Young-Seon Kim[1,2,3], Hyeock-Soon Jang[1], Sang-Yun Lee[1], Xue-Quan Fang[2,3], Chang-Hoon Lim[2,3], Seong-Sil Hong[4], Min-Gu Ko[4], Min-Woo Han[4], Woo-Jong Yim[1], Ji-Hong Lim[2,3,5*]

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PBD-14

Functional study of Fermented Silk Sericin by Marine Extremophiles from the High Seas

Sang-Jae Lee[1], Yu Jeong Yeom[1], Sung Tae Kim[2,3], Il Kwon Bae[4], Yong-Jik Lee[5], Mi Hwa Park[6*]

[1]Department of Food Biotechnology, Research Center for Extremophiles & Marine Microbiology, Silla University, Republic of Korea, [2]Department of Nanoscience and Engineering, Inje University, Gimhae 50834, Republic of Korea, [3]Department of Pharmaceutical Engineering, Inje University, Gimhae 50834, Republic of Korea, [4]Department of Companion Animal Health and Science, Silla University, Busan 46958, Republic of Korea, [5]Department of Bio-Cosmetics, Seowon University, Chung-Ju 28674, Republic of Korea, [6]Department of Food and Nutrition, College of Human Ecology, Silla University, Busan 46958, Republic of Korea

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PBD-15

Bacillus licheniformis CP6 fermented *Abelmoschus Manihot* ameliorates bone loss in ovariectomized rats and promotes osteoblast differentiation through BMP/Runx2 signaling pathway

Mi Hwa Park[1], Joo Young Yang[2], Ji Yeong Park[2], Sondor Ganbat[2], Dariimaa Ganbat[2], Yong-Jik Lee[3], Gaewon Nam[4], Sang-Jae Lee[2*]

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PBD-16

Role of bean yellow mosaic virus P1 and HC-Pro in enhancing gene expression and suppressing RNA silencing in *Nicotiana benthamiana*

Sunmee Choi[1], Suk Hyun Kwon[1], Gi Seok Kwon[1], Ho Seong Choi[2], Young Soon Kim[1], Jeong Hun Lee[1], Won Kyong Cho[1], Sang Hyun Moh[1*]

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PBD-17

Development of Reverse-Aging Cosmetic Ingredients Using Plant Cell Library and SMART-RC^2 Bioreactor System

Eui Hyun Kim, Ji Hyeon Jang, Ji Hyeok Song, Hyo Hyun Seo, Jeong Hun Lee, Sang Hyun Moh[*]

Plant Cell Research Institute of BIO-FD&C Co., Ltd., Incheon 21990, Republic of Korea

PBD-18

Inhibitory Effect of Ganoderma Lucidum Spore Oil Extracted by CO2 Supercritical fluid on Osteoarthritis

Myeong Yeon Shin[1], Yun Ji Heo[1], Min Hye Kim[2*], Godagama Gamaarachchige Dinesh Suminda[2], Yun Hui Min[2], Young Ok Son[1,2*]

[1]Animal Biotechnology, Jeju National University, [2]Interdisciplinary Graduate Program in Advanced Convergence Technology and Science, Jeju National University

PBD-19

PARP-1 activation prevents OA pathogenesis by inhibiting apoptosis in chondrocytes

Min Hye Kim[1], Yun Hui Min[1*], Godagama Gamaarachchige Dinesh Suminda[1*], Yun Ji Heo[2*], Myeong Yeon Shin[2*], Young Ok Son[1,2*]

[1]Interdisciplinary Graduate Program in Advanced Convergence Technology and Science, Jeju National University, [2]Animal Biotechnology, Jeju National University

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PBD-20

Phytochemical composition and antioxidant activity of fermented extracts from *Olea europaea* L. leaves

Yuji Yang[1], Ji-Yeong Bae[1]*, Yoon-A Kang[1], Minseo Jeon[2], Ye-Sol Kang[1]

[1] Jeju Research Institute of Pharmaceutical Sciences, College of Pharmacy,
[2] Interdisciplinary Graduate Program in Advanced Convergence Technology & Science, Jeju National University, Jeju 63243, Korea

PBD-21

Comparative Analysis of Phytochemicals and Antioxidant Activity in *Hibiscus hamabo* plant parts

Ye-Sol Kang[1], Ji-Yeong Bae[1]*, Yoon-A Kang[2], Min-Seo Jeon[3], Yu-Ji Yang[2]

[1] Jeju Research Institute of Pharmaceutical Sciences, Colleage of Pharmacy,
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[3] Interdisciplinary Graduate Program in Advanced Convergence Technology & Science, Jeju National University, Jeju 63243, Korea

PBD-22

Investigation of the Anti-Inflammatory Properties of *Tetragonia tetragonoides* (Pall.) Kuntz in Mouse Macrophages

Yoon A Kang, Ji Yeong Bae*

Jeju Research Institute of Pharmaceutical Sciences, College of Pharmacy

PBD-23

Targeting the SARS-CoV-2 Nsp3 Macrodomain with Evolutionary Chemical Binding Similarity (ECBS): Insights from the CACHE#3 Challenge

Charuvaka Muvva, Keunwan Park*

Center for Natural Product Systems Biology, Korea Institute of Science and Technology (KIST)

PBD-24

Phytochemical analysis and biological activities of *Idesia polycarpa*

Minseo Jeon, Ji-Yeong Bae*

Interdisciplinary Graduate Program in Advanced Convergence Technology & Science, Jeju National University, Jeju 63243, Republic of Korea

PBD-25

Immune-Enhancing Screening of Proteins from a gut bacterium, BP, in RAW 264.7 Macrophages

Thuy Thi Thanh Phan[1,2], Jessica Winarto[1,2], Dong- Jae Lee[1],
Kwang Hyun Cha[1,2], Young- Tae Park[2,3], Choong- Gu Lee[1,2],
Dae- Geun Song[1,3]*

[1] Center for Natural Product Systems Biology, Natural Products Research Institute, Korea Institute of Science & Technology (KIST), Gangneung 25451, Republic of Korea, [2] Natural Product Applied Science, KIST School, University of Science and Technology (UST), Seoul, Republic of Korea, [3] Center for Natural Product Efficacy Optimization, Natural Products Research Institute, Korea Institute of Science & Technology (KIST), Gangneung 25451 Republic of Korea

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PBD-26

Synthesis of Novel Carboxylic Acid Derivatives Targeting the ROS-TGFβ1-HIF-1α Axis for Idiopathic Pulmonary Fibrosis Treatment

Joshua Miguel Anandappa[1], Hiruni Nilshi Indeevarie Abeysiriwrdhana[1], Ayusha Malla[2], Jin-Hyuk Choi[3], Moonjae Cho[3*]

[1]Advanced Convergence Science and Technology, Jeju National University, [2]Biochemistry, ACHEMBIO Inc., [3]Biochemistry, Jeju National University

PBD-27

Application of a Genotoxicity Assessment Framework to Pesticide Evaluation: Case Studies

Youmi Jo[1*], Soo-Jin Park[1], Ji-Young Shin[1], So-Hye Hong[1], Si-Young Yang[1], Min-Kyoung Paik[1], Ahmad Sleiman[2], Bradley Lampe[2], Jessica Evans[2], Kelly A Magurany[3]

[1]Toxicity and Risk Assessment Division, National Institute of Agricultural Sciences, Rural Development Administration, Wanju 55364, Republic of Korea, [2]NSF International, Ann Arbor, Michigan, 48105, USA, [3]Verto Solutions LLC, Washington, DC, 20036, USA

PBD-28

ACF-01 downregulates HIF-1α and potentiates the antitumor effect of Lenvatinib by inducing apoptosis in hepatocellular carcinoma

Tae Hyeon Yoon[1], Dae Kyeon Kim[1], Ji Soo Kim[1], Sun Hee Yang[1], Moonjae Cho[1,2,3], Somi Kim Cho[1,4*]

[1]Interdisciplinary Graduate Program in Advanced Convergence Technology and Science, Jeju National University, Jeju 63243, Republic of Korea, [2]Department of Biochemistry, School of Medicine, Jeju National University, Jeju 63243, Republic of Korea, [3]ACHEMBIO Inc, Jeju 63169, Republic of Korea, [4]Faculty of Biotechnology, College of Applied Life Sciences, SARI, Jeju National University, Jeju 63243, Republic of Korea

PBD-29

Daphne jejudoensis leaf extract Attenuate Psoriatic symptoms by Mitochondrial modulation of Th17 cells

Eunjung Kim[1], Youngjun Park[1,2*]

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PBD-30

High-fat diet alters Colonic CD4+ T Cells with Reprogramming of Inflammatory and Metabolic gene signatures

Umar Manzoor[1], Youngjun Park[1,2*]

[1]Interdisciplinary Graduate Program in Advanced Convergence Technology and Science, Jeju National University, Jeju 63243, Republic of Korea, [2]Jeju Research Institute of Pharmaceutical Sciences, College of Pharmacy, Jeju National University, Jeju 63243, Republic of Korea

PBD-31

Sobrerol (NRM-331) Alleviates Ischemic Stroke and Cognitive Disorder via Multi-Target Mechanisms

A-Ra Goh, Abuzar Ansari, Geon-Seok Park, Soo-Jeong Park, Kang-Hoon Je*

R&D Unit, #302, Neurolmed Co., Ltd., 91, Changnyong-daero 256beon-gil, Suwon 16229, Republic of Korea

PBD-32

A novel compound ACF-01 synergistically enhances the anticancer effects of doxorubicin in MDA-MB-231 cell variants with stem cell properties

Sun Hee Yang[1], Ji Soo Kim[1], Dae Kyeong Kim[1], Tae Hyeon Yoon[1],
Vo Thi Ngoc Tram[2], Moonjae Cho[1,3,4], Somi Kim Cho[1,5*]

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PBD-33

Antiviral Activity Analysis of *Abies nephrolepis* Extract

JungWoo Chae[1*], HuiSeon Jo[1], KyeongSoon Kim[2], Moongyu Jung[2]

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Plenary Lecture

PL

Chemical modifications on RNAs: a potent mechanism of gene regulation

Hunseung Kang

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Epitranscriptomic chemical RNA modifications have recently emerged as a new layer of post-transcriptional gene regulation. Recent advancements in methylated RNA immunoprecipitation sequencing (m^6A-seq) and mass spectrometry have revealed widespread chemical modifications on diverse RNAs, including mRNA, tRNA, rRNA, microRNA, and long-noncoding RNA. Currently, > 170 RNA modifications have been identified in living organisms. Among them, N6-methyladenosine (m^6A) is the most prevalent modification found in eukaryotic mRNAs. In recent years, cellular factors adding, deleting, and interpreting m^6A marks, designated as “writers” (methyltransferases), “erasers” (demethylases), and “readers” (m^6A-binding proteins), respectively, have been identified in plants and animals. An emerging body of evidence shows that methylation on mRNAs affects diverse aspects of RNA metabolism, including stability, splicing, nucleus-to-cytoplasm export, alternative polyadenylation, and translation. In particular, the roles of writers, readers, and erasers in plants are rapidly uncovered, which clearly demonstrates that they are essential for plant growth and abiotic stress responses. In this talk, I will introduce several key findings via analyzing the mutants of m^6A writers, erasers, and readers, which emphasizes the crucial roles of epitranscriptomic chemical mRNA methylation in the plant growth, development, and stress responses.

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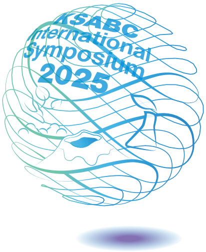


Special Lectures

SL-1

Integrating Generative AI in Academic Research: From Idea Generation to Data Analysis Automation

Hyun-Soo Ahn*, Min-Soo Shin, Seung-In Lee, Dae-woo Shin

R&BD Partners, Yong-In, Republic of Korea

The rapid advancement of generative AI technologies has significantly transformed the landscape of academic research. This lecture aims to provide a comprehensive overview of how researchers can strategically incorporate AI tools throughout the entire research process—from ideation and literature review to writing, data analysis, and automation.

The first half of the curriculum focuses on **research ideation and academic writing using generative AI**. Participants will explore how AI models such as GPT can assist in the initial stages of research design by facilitating idea generation, topic refinement, and research planning. Through case-based demonstrations, attendees will learn to outline a research proposal, create a logical table of contents, and draft abstracts using AI assistance. Emphasis will be placed on the use of AI tools like Perplexity and Consensus for literature search, and Markdown for structuring academic documents. Practical sessions will guide participants through the process of creating a research topic and draft outline using AI prompts.

In the second half, attention shifts toward **data analysis and automation using AI and Python**. The session begins with foundational data handling techniques, where GPT is applied for spreadsheet-based tasks such as cleaning, normalization, and pattern analysis. The curriculum then delves into advanced statistical analysis, including regression and correlation, with an introduction to Python libraries like Pandas and Matplotlib for visualization and computation. Finally, the lecture covers **Google Colab integration**, demonstrating how researchers can automate data workflows—loading, preprocessing, modeling, and saving results—by combining Colab notebooks with GPT-generated code snippets.

Throughout the session, real-time demonstrations and hands-on activities will provide participants with the skills necessary to apply generative AI tools effectively in their own academic research. By the end of the lecture, attendees will gain not only technical know-how but also strategic insights into the ethical and practical use of AI in scholarly environments.

This session is ideal for early-career researchers, graduate students, and academic professionals seeking to leverage AI for enhanced productivity, creativity, and data-driven insight in their research processes.

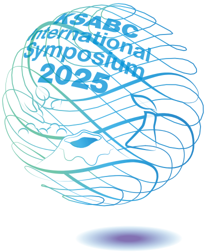
SL-2

Knowing, Synthesizing, Applying Bugs for Creativity

Eungbin Kim

Department of Systems Biology, Yonsei University, Seoul 03722, Republic of Korea

Microorganisms are increasingly recognized not only as subjects of scientific investigation but also as catalysts for creative expression across disciplines. This presentation explores how microbiological knowledge and techniques are being integrated into artistic, educational, and design contexts, reframing microbes as active participants in cultural production. Recent developments in synthetic biology and microbial engineering have enabled novel applications such as agar art, which utilizes pigment-producing bacteria as living media, and bacterial sound research, which translates microbial activity into auditory forms through biosensing and sonification. These examples highlight the potential of microorganisms to serve as both material and metaphor in creative processes. By emphasizing the role of microbes in transdisciplinary innovation, this work proposes a new paradigm that bridges science and the arts. Such convergence not only broadens the scope of microbiological engagement but also encourages new ways of thinking about sustainability, collaboration, and the invisible networks that shape life and culture.



Award Lectures

AL-1

Happiness from the Art of Natural Products

Sanghyun Lee

Department of Plant Science and Technology, Chung-Ang University, Anseong 17546, Republic of Korea

Throughout history, humans have long sought answers in nature to cure diseases and ensure survival. Natural product research is an academic journey aimed at scientifically identifying biological resources and applying them to sustain life and promote healing. My scientific journey is what I call *Natural Product Research*. Groundbreaking drugs such as penicillin, streptomycin, and tamoxifen were derived from natural products and have become major drivers of modern pharmacology and drug discovery. Since the 1980s, advances in isolation and structural identification techniques—especially LC-MS/MS and HPLC—have enabled the identification of natural compounds and the discovery of new drugs. My research has focused on developing foods, nutraceuticals, and medicinal materials by discovering bioactive compounds with antioxidant, anti-inflammatory, anti-diabetic, and immune-enhancing properties from short-cycle forest plants.

However, large pharmaceutical companies have come to prefer synthetic compounds or biologics due to the complex structures of natural products, their low yields, and challenges in commercialization. In addition, the overexploitation of natural resources and the decline in biodiversity threaten the sustainability of natural product research. Furthermore, the gap between mechanistic analysis and clinical application remains a major challenge. The convergence of omics technologies and AI is enabling more precise analysis of in vivo mechanisms of action and accelerating drug discovery in terms of both speed and accuracy. Meanwhile, the rise of synthetic biology is dramatically enhancing the potential for the commercialization of natural products. The climate crisis and the need to conserve biodiversity now point the way forward for natural product research: sustainable resource utilization, ethical extraction, and collaboration with local traditional communities.

Today's natural product researchers must adopt an integrated perspective that encompasses advanced analytical technologies and bioethics. This is essential not only for scientifically grounded functional validation and international credibility but also for bridging the gap between industrialization and public health. Natural products still hold great promise. To realize their full potential, deeper research, greater social empathy, and strategic technological convergence must come together. The K-Milk Thistle localization project involved years of research to domesticate milk thistle and led to the development of a high-silydianin variety called *Silyqueen,* for which a plant patent has been registered. The launch of K-Milk Thistle as a national brand—alongside K-Pop and K-Beauty—laid the foundation for entering both domestic and global markets. By identifying interactions and genetic diversity among silymarin complex components, the project succeeded in differentiating high value-added functionalities.

Natural Product Chemistry is a science, an art, and a way of life. I read nature’s messages and translate them into health, industry, and human well-being. My research leads to industrialization, my success is returned to society, and my work serves as a key to unlocking the future for younger generations.

AL-2

Recent Trends and Technological Advancements in Plant Proteomics: From DDA to 4D-DIA

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Proteomics has become a vital tool in plant science, providing critical insights into the molecular mechanisms governing growth, development, and stress responses. Traditional data-dependent acquisition (DDA) mass spectrometry enabled deep protein identification but suffers from limited reproducibility and a bias toward abundant peptides. The advent of data-independent acquisition (DIA) has addressed these limitations by systematically fragmenting all peptide ions, allowing for highly reproducible and quantitative proteome profiling. In rice (*Oryza sativa*), DIA has significantly improved the detection of low-abundance regulatory proteins involved in stress signaling and adaptation. The recent development of four-dimensional DIA (4D-DIA), which integrates ion mobility as an additional separation dimension, further enhances resolution, sensitivity, and proteomic coverage. This approach enables the quantification of over 10,000 proteins in a single run and supports detailed analysis of post-translational modifications, such as phosphorylation, which are crucial in plant immunity and environmental stress responses. When combined with advanced computational tools, these next-generation technologies are transforming plant proteomics, accelerating systems-level understanding of plant biology. Together, DDA, DIA, and 4D-DIA are enabling precision breeding strategies for developing climate-resilient and high-yielding plant cultivars, offering new avenues for sustainable agriculture.

Award Lectures

AL-3

Protopanaxadiol Attenuates Palmitate-Induced Lipotoxicity and Restores Pancreatic β-Cell Function in INS-1 Cells

Ki Sung Kang

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Free fatty acid (FFA)-induced lipotoxicity plays a critical role in the dysfunction of pancreatic β-cells, a key factor in the development of diabetes. In this study, we evaluated the protective effects of ginsenosides against palmitic acid (PA)-induced β-cell death and impaired glucose-stimulated insulin secretion (GSIS) using INS-1 pancreatic β-cells. Through screening, we identified protopanaxadiol (PPD) as a potent therapeutic candidate that effectively prevented PA-induced cytotoxicity and GSIS dysfunction. The protective effects of PPD appeared to result from the reduction of apoptosis and intracellular lipid accumulation. Mechanistically, PPD attenuated the PA-induced increase in apoptotic markers, including B-cell lymphoma-2-associated X protein (Bax), B-cell lymphoma 2 (Bcl-2), cleaved poly (ADP-ribose) polymerase (PARP), and cleaved caspase-3. Furthermore, PPD restored insulin secretion by enhancing the activation of key signaling molecules such as phosphatidylinositol 3-kinase (PI3K), peroxisome proliferator-activated receptor γ (PPARγ), insulin receptor substrate-2 (IRS-2), protein kinase B (Akt), and pancreatic and duodenal homeobox-1 (PDX-1). Collectively, these findings suggest that PPD alleviates PA-induced lipotoxicity and β-cell dysfunction by modulating apoptotic pathways and promoting critical insulin signaling cascades. Therefore, PPD holds promise as a therapeutic agent for preventing or mitigating β-cell dysfunction in metabolic diseases such as type 2 diabetes.

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Symposia

S1-1

Machine learning-based sequence optimization for protein structures

Keunwan Park

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Synthetic biology relies on modular biological components such as proteins, enzymes, and DNA elements to enable the rational design of systems for biotechnological and industrial applications. Nonetheless, the optimization of these various components remains non-trivial due to the intrinsically high-dimensional and epistatic nature of sequence to function relationships. Conventional directed evolution and rational design approaches often require extensive experimental screening and structure-guided modeling. To overcome these constraints, we propose an iterative, machine learning (ML)-driven framework for the systematic exploration and optimization of protein sequence space. The workflow uses supervised ML models trained on existing sequence–property data to prioritize sequence variants of high predicted scores. Incorporation of experimental feedback into subsequent model retraining cycles enables progressive refinement of predictive accuracy and design efficiency. We demonstrate the utility of this framework using glutamine binding protein (QBP) as a case study. A combination of genetic algorithms and structure-based energy calculations with Alphafold was employed to identify sequence variants exhibiting improved ligand binding affinity and high structural stability.

S1-2

Daily Rhythms in Metabolism and Sleep Cycle Are Made by a Phosphotimer

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The circadian clock generates time cues that regulate daily expression of almost entire genome and physiology including our sleep cycles. Although ample evidence suggests that a phosphotimer consisting of the substrate PER and the kinase CK1 somehow generates these time cues through a series of phosphorylation reactions, how time cues are encoded by these phosphorylation reactions has not been identified. Because previous studies indicated that sleep cycles and chronotypes are dramatically affected by kinetics of this timing device, it would be imperative to understand how the pacemaker PER phosphorylation is translated into timing cues. Here we show that timing cues are generated by trans-phosphorylation through PER-PER dimerization. When PER dimerization is disrupted, PER phosphorylation and circadian rhythms are severely compromised. In mouse models with point mutations in PER dimerization domain, sleep or circadian cycles are dramatically shortened up to ~20 hrs. More significantly, phase of wake/sleep cycles is dramatically advanced switching a nocturnal animal to a half diurnal animal. In addition, the circadian timer can be even more dramatically modulated if the kinase CK1 is mutated. Our studies suggest that the circadian system is highly adaptable to different environment by simple mutations probably because environmental niche for any species needed to be changed frequently for survival during evolution.

S1-3

Glycan-Mediated Host-Pathogen Interactions: How *Salmonella* AB Toxins Adapt to Hosts

Sohyoung Lee[1,2], Yi-An Yang[2], Shawn K. Milano[3], Tri Nguyen[2], Changhwan Ahn[2], Ji Hyun Sim[2], Andrew J. Thompson[4], Eric C. Hillpot[3], Gyeongshik Yoo[2], James C. Paulson[4], Jeongmin Song[2*]

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Glycosylation, the process by which sugar residues are added to macromolecules to form glycoconjugates, is a common post-translational and co-translational modification of many membrane proteins and lipids. Glycans play essential roles in various biological processes, including protein folding, stability, and cell-to-cell adhesion. More importantly, glycans are key players in host-pathogen interactions. Our research reveals that the *Salmonella* toxins have switched their host glycan receptor preferences, leading to distinct clinical manifestations. Typhoidal and non-typhoidal *Salmonella* (NTS) species cause typhoid fever and gastroenteritis, respectively, in humans. While *Salmonella* typhoid toxin contributes to typhoid disease progression and chronic infection, the role of its NTS ortholog remains poorly understood. The binding subunit (PltB) of each toxin exhibits distinct glycan-binding preferences that correspond to the glycan expression patterns of host cells at the primary site of infection or intoxication. By analyzing co-crystal structures of PltB subunits bound to specific glycan receptor moieties, we demonstrate that these structural differences drive variations in glycan recognition and virulence outcomes. Furthermore, immunization with the NTS *S.* Javiana or its toxin provides cross-reactive protection against lethal-dose typhoid toxin challenge. Cumulatively, these findings offer new insights into the evolution of host adaptations in *Salmonella* AB toxins, their cell and tissue tropisms, and the design for improved typhoid vaccines and therapeutics.

S1-4

Uptake characterization of soil arsenic species and its effects on nitrogen cycle in Soybean (*Glycine max*(L.) Merrill) Cultivation: A Comparison with Cadmium

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This study aimed to investigate the effects of arsenic (As) species and cadmium (Cd) on nitrogen cycling, particularly nitrification and nitrogen fixation, in soybean (Glycine max (L.) Merrill) cultivation. To this end, metal uptake, nitrogen transformation in porewater, nitrogen fixation capacity, and nitrogen-associated microbial communities were analyzed. As was oxidized to arsenate (As(V)) by manganese oxides and soil microbes, predominantly accumulated in this form, especially in roots and nodules. The bioconcentration factor (BCF) of As exceeded 1, while that of Cd remained below 1. In As-contaminated pots, Nitrosospira (ammonia-oxidizing bacteria) and Pseudomonas (As(III)-oxidizing bacteria) were dominant, maintaining partial nitrification and promoting hazardous nitrite (NO_2^-) accumulation. In contrast, Cd markedly reduced Nitrosospira abundance, resulting in up to a 52% reduction in nitrification compared to the control. This indicates that Cd severely impaired AOB and disrupted nitrification. Furthermore, As(V) interfered with the uptake of molybdenum(Mo) and iron(Fe) through structural mimicry and oxidative stress, it ultimately reduced nitrogenase activity. Although symbiotic nitrogen-fixing bacteria such as Bradyrhizobium and Ensifer remained in the rhizosphere under As stress, they failed to infect roots and form nodules. Our multi-scale approach, which includes the analysis of soil, porewater, plant tissues, and microbial communities, revealed that As(V) significantly inhibited nitrogenase activity by interfering with the uptake of molybdenum and iron, both of which are essential cofactors for nitrogen fixation. In contrast, Cd selectively suppressed ammonia-oxidizing bacteria (AOB), thereby impairing nitrification. These findings provide valuable mechanistic insights and offer a scientific basis for contaminant-specific soil restoration strategies aimed at mitigating nitrogen loss, reducing N_2O emissions, and maintaining crop productivity in metal(loid)-contaminated farmlands.

S1-5

Gene Discovery and Functional Insights to Improve Plant Nitrogen Utilization

Jun Sung Seo[1*], **Se-jun Oh**[2], **Yeon-Hee Lee**[2], **Ju-Kon Kim**[2]

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[2]Lacemilla Co. Ltd., Pyeongchang 25354, Republic of Korea

Nitrogen (N) is an essential macronutrient for plant growth and development, with a significant influence on crop yield and biomass. However, excessive use of N-based fertilizers leads to serious environmental issues, including greenhouse gas emissions and eutrophication, while also increasing production costs. Enhancing nitrogen use efficiency (NUE) is therefore a critical goal in crop biotechnology to promote sustainable agriculture. Using a reverse genetics approach, we selected 100 nitrogen-responsive genes from our previous RNA-seq transcriptome data obtained under nitrogen-starvation conditions. Gene-specific guide RNAs were designed for each target, and over 1,000 CRISPR-Cas9 knockout mutants were generated. To date, we have successfully established a mutant pool for 75 genes. Several mutants exhibited distinct phenotypes compared to wild-type plants under N-deficient conditions. Functional characterization of selected genes is ongoing, and promising candidates will be applied toward the development of crop varieties with improved NUE.

S1-6

Transcriptomic Approach to Elucidate Molecular Targets of Humic Acid and Their Biological Functions in Plants

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Division of Applied Life Science (BK21four), Plant Biological Rhythm Research Center,
Research Institute of Life Science, Gyeongsang National University, Jinju 52828, Republic of Korea

Humic acid (HA) is a complex supramolecular association formed through the humification of organic matter in soil environments. HA is known not only to stimulate plant growth but also to improve soil properties. Although various bioactivities of HA in plants have been reported, its direct molecular targets and underlying mechanisms remain largely unknown. Here, we conducted transcriptomic analysis to identify the molecular targets through which HA enhances stress tolerance and seed germination in Arabidopsis. Gene ontology enrichment analysis revealed that HA upregulates a broad set of stress-related genes. Notably, HA increased the expression of genes encoding HEAT-SHOCK PROTEINs, thereby enhancing thermotolerance. Additionally, HA upregulated genes involved in maintaining reactive oxygen species homeostasis, contributing to improved oxidative stress tolerance in both Arabidopsis and oilseed rape. These findings suggest that HA exerts a priming effect, protecting plants against various abiotic stresses. In contrast, HA downregulated genes involved in the phenylpropanoid biosynthetic pathway. Previous studies have shown that Arabidopsis mutants defective in this pathway, known as transparent testa (*tt*) mutants, exhibit light-brown seed-coats with reduced tannin level and enhanced seed germination. Similarly, we found that HA suppressed the expression of multiple *TT* genes and promoted seed germination even under inhibitory conditions induced by abscisic acid and paclobutrazol. Collectively, our transcriptomic analysis identifies key molecular targets of HA and provides new insights into how HA regulates plant development and enhances tolerance to abiotic stresses.

S1-7

Daytime-Specific Mechanisms of *FT* Regulation in Photoperiodic Flowering: Morning or Evening?

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Plants monitor photoperiodic changes to optimize flowering time, thereby maximizing reproductive success. In *Arabidopsis thaliana*, the day-length-dependent induction of *FLOWERING LOCUS T (FT)*, encoding a mobile floral inducer, is crucial for proper flowering timing. The transcriptional activation of *FT* under long-day conditions is primarily regulated by CONSTANS (CO), which binds to the *FT* promoter and promotes its expression. CO protein accumulates in the late afternoon of long days, ensuring peak *FT* transcript levels. Although CO directly associates with the *FT* promoter, its recruitment is facilitated by transcription factors with DNA-binding domains. *FT* gene shows two peak expressions under natural long-day (LD) conditions. While only the peak expression in the evening is typically observed under typical laboratory LD conditions, morning *FT* expression is detected in natural environments, in addition to the evening. The morning-specific FT expression is induced by far-red light, which involves a high irradiance response mediated by the far-red light photoreceptor phytochrome A (phyA). In contrast, the effect of far-red light in evening *FT* induction is less pronounced. The external coincidence mechanism, which integrates circadian clock signals and light cues, regulates evening *FT* expression. Many regulators involved in evening *FT* induction have been identified, and their functions are relatively well understood. In contrast, the mechanisms underlying morning *FT* expression have remained largely unknown. This presentation will focus on molecular mechanisms recently discovered that regulate *FT* expression in the morning and evening. These mechanisms are crucial for understanding how the timing of photoperiodic flowering is controlled in a time-of-day-specific manner under natural conditions.

S2-1

Identification of novel genes and Korean medicine as regulators of the p53-MDM2 feedback loop

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The tumor suppressor p53, often referred to as the “guardian of the genome”, is a crucial tumor suppressor gene involved in maintaining cellular integrity. It plays a key role in responding to various forms of cellular stress, such as DNA damage, ribosomal stress, etc., by regulating cell cycle arrest, apoptosis, ferroptosis and cellular senescence. p53 target genes include p21, which mediates cell cycle arrest, BAX and PUMA, which promote apoptosis, and MDM2, which provides negative feedback regulation of p53 itself. The precise modulation of these target genes is essential for maintaining genomic stability and preventing tumorigenesis, highlighting the critical role of p53 in cellular homeostasis and cancer prevention. The p53-MDM2 feedback loop constitutes a critical regulatory axis essential for maintaining cellular homeostasis by controlling the stability and activity of the tumor suppressor p53. Disruption of this loop is a hallmark of various malignancies, underscoring the need for novel therapeutic strategies targeting this pathway. Our research team focuses on identifying novel genes that regulate p53 and the p53-MDM2 feedback loop in cancer cells, and on elucidating their underlying mechanisms. In addition, we investigate the potential of traditional Korean medicinal herbs as anticancer agents by screening for active compounds and studying their related mechanisms to evaluate their applicability in cancer therapy.

S2-2

Synthetic Biology-Based Precision Fermentation CDMO: Accelerating Bio-Material Innovation

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Synthetic biology and precision fermentation are revolutionizing the production of natural products, bioactive compounds, and biopharmaceuticals. By engineering microbial strains, these technologies enable scalable, sustainable, and high-purity manufacturing of materials traditionally limited by extraction challenges or supply instability. This presentation examines how CDMOs (Contract Development and Manufacturing Organizations) leverage synthetic biology tools – such as CRISPR and AI – driven strain design to deliver tailored solutions for bioactive material production. Case studies in natural product alternatives (e.g., plant-derived compounds) and bio-materials demonstrate enhanced efficiency and improved process reliability compared to conventional methods. Global market growth, driven by sustainability demands and regulatory advancements, underscores CDMOs' critical role in bridging R&D and commercialization. Challenges like cost optimization are addressed through circular production models and high-value product pipelines. Aligned with the conference's focus, this talk highlights synergies between academic research and industrial applications, offering actionable insights to advance bio-material discovery and scalable, market-ready solutions.

S2-3

Medicinal plants from Nepal as potential inhibitors of Aβ-aggregation and BACE1

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Medicinal plants and herbs have been used in traditional medicine to treat several human ailments and many of these modern therapeutics agents were derived based on the indigenous knowledge. Owing to its rich source bioactive secondary metabolites, medicinal plants and herbs have drawn the significant scientific attention in recent years to develop the novel therapeutic agents. At the same time, owing to its unique topography and climate, Nepal is known as a hub of floral biodiversity with around 6500 difference species of flowering plants and more than 2300 species were medicinal and aromatic plants. The present study focused on the screening of the medicinal plant extract for inhibition of Aβ aggregation and BACE1 for identification potential inhibitors molecules for Alzheimer's disease (AD) management. In order to identify the potential extract with high inhibition different parts of 33 plant species were evaluated towards Aβ aggregation and BACE1 inhibition. Our results revealed that *Rhus parviflora* Roxb were most potent with IC_{50} values of 7.65±0.58 μg/mL for Aβ aggregation inhibition; whereas *Rheum australe* D. Don showed the highest inhibitory potential, with an IC_{50} value of 0.872±0.006 μg/mL for BACE1 inhibition. Further profiling of the metabolites of *R. australe* D. Don was performed using high-resolution mass spectrometry (HRMS). Results revealed that crude methanol extract of *R. australe* D. Don revealed the presence of aloe-emodin-8-O-β-D-glucoside, rhein-8-O-glucoside, piceatannol-3'-O-β-D-glucoside, emodin-8-glucoside, physcion 8-O-β-D-glucoside, desoxyrhaponticin, chrysophanol-8-O-glucoside, rhapontigenin, rhein, desoxyrhapontigenin, piceatannol, chrysophanol, physcion, and aloe-emodin. *In-silico* docking simulations were performed to identify potent compounds with high binding efficiencies to BACE1. Compound picetannol-3'-O-β-D-glucoside showed the best binding energy (-53.494 kcal/mol) with an IC_{50} value of 1.270±0.130 μM for BACE1. These medicinal plants can be explored to get promising agents for the treatment of AD.

Keywords: Alzheimer's diseases, Medicinal plants, BACE1, Aβ aggregation, HRMS, Nepal medicinal plants

S2-4

Development of medicinal plants for herbal medicine and plant derived drugs from traditional to modern approaches

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Plants have served as tremendous sources for drug discovery for long time. Many drugs in the market have been derived from plants. Development of sciences and technology have contributed to continuously discovery plant derived drugs. The traditional medicines system in the world such as traditional Chinese medicines (TCM), Ayurveda, kampo, unani have been also contributed for human health. Jamu, an Indonesian traditional medicines system has been practised for many centuries in the Indonesian community to maintain good health and to treat diseases. Although modern (conventional) medicine is becoming increasingly important in Indonesia, jamu is still very popular in rural as well as in urban areas. Based on its traditional use jamu is being developed into a rational form of therapy, by herbal practitioners and in the form of phytopharmaceuticals. The production of jamu is also being developed on an industrial scale. The Indonesian government, industry and academia all recognize that to further the development of jamu, extensive research is required to establish the safety and efficacy of the many traditional jamu preparations. The Indonesian government has divided the preparation of medicinal plants into three categories, i.e. jamu, standardized herbal medicines and *fitofarmaka* (phytomedicines). All preparations have to meet basic safety criteria. The therapeutic effects of jamu have to be supported by empirical data. The efficacy of standardized herbal medicines has to be proved in preclinical trials and standardization on active ingredients is required, while for the efficacy of *fitofarmaka*, clinical trials have to be carried out. With the huge numbers of biodiversity in Indonesia. The development of the medicinal plants is a crucial to explore their prospective. Isolation of compounds which are assumed to be responsible for the pharmacological activities is an important. Our groups have isolated more than 500 pure compounds that have been used as markers compounds for quality control of herbal medicines, these compounds belong to a wide range of secondary metabolites such as alkaloid, terpenoid, steroid, flavonoid, lignan, coumarin, tannin, and other phenolic compounds. Few of them have been investigated their pharmacological activities and have shown good results. Secondary metabolites which are responsible for the pharmacological activities of medicinal plants, are normally produced in low level. The low secondary metabolites contents have become a bottleneck for the development of plant-derived drugs as well herbal medicines. Biotechnological approaches, especially plant tissue cultures and genetic engineering have been used as an alternative to produce useful secondary metabolites as medicines from plants. These techniques have been applied in our lab and briefly present in the Symposium

Keywords: Medicinal plants, secondary metabolites, biotechnology, genetic engineering flavonoid, alkaloid, terpenoid, lignan

S2-5

Enzymatic Tailoring and Bioengineering of Aromatic Polyketides

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The biosynthesis of the medically relevant bacterial aromatic polyketide backbones relies on type II polyketide synthases and accessory enzymes, while their structural diversification is mediated by pathway-specific tailoring enzymes. Among the structurally most complex aromatic polyketides are the members of the rubromycin family with antimicrobial and cytotoxic activities that feature a characteristic spiroketal pharmacophore. After studying the key tailoring reactions that give rise to these structures, current efforts focus on exploiting biosynthetic enzymes for the *in vitro* generation of non-natural rubromycin derivatives. In particular, carboxylic acid side chains obtained by ester hydrolysis are modified with amide bond synthetases using various natural and unnatural amine building blocks to improve the compounds' physicochemical properties. In addition, biotinylated rubromycins linked to streptavidin columns are used to identify molecular targets in cell lysates via pull-down assays and proteomic analysis. Eventually, *bona fide* protein targets should be obtained and crystallized in complex with the rubromycin ligands to pave the way for the generation of more selective inhibitors.

S2-6

Elucidating Biochemical Pathway of Neoclerodane Diterpene, Salvinorin A, in *Salvia divinorum*

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Salvia divinorum, a member of the mint family, is a hallucinogenic plant native to Oaxaca, Mexico. Salvinorin A is the active ingredient for the psychoactive effects, and studies of receptor-ligand interactions showed that salvinorin A is a potent and selective κ-opioid receptor agonist. Unlike traditional alkaloidal opioids such as morphine and codeine, salvinorin A is a non-nitrogenous diterpenoid with no affinity for the μ-opioid receptor. A terpene-based opioid that selectively targets the κ-opioid receptor could have therapeutic potential for developing alternative analgesics. Understanding the biosynthesis of salvinorin A would facilitate the bio-manufacturing of semi-synthetic derivatives. However, its biosynthetic pathway remains incompletely understood. Salvinorin A is synthesized and accumulates in trichomes, specialized glandular cells on the leaf surface. To elucidate its biosynthesis, a trichome-enriched transcriptome was generated, yielding approximately 30 million transcript reads. Analysis of these transcriptomes identified several genes encoding diterpene synthases and cytochrome P450 (CYP) enzymes, and these genes were functionally characterized in yeast and tobacco. Notably salvinorin A possesses a distinctive neoclerodane skeleton. One key enzyme, SdCPS2 (clerodane pyrophosphate synthase), was found to efficiently convert geranylgeranyl diphosphate (GGPP) into a neoclerodane hydrocarbon. To further explore oxidation steps in salvinorin A biosynthesis, SdCPS2 was co-expressed with individual CYPs in yeast. This approach revealed that CYP76AH1 catalyzes the formation of a unique dihydrofuran moiety, while CYP728D26 performs three sequential oxidations at the C-18 methyl group, forming a carboxylic acid. The enzymatic activities of these newly identified catalysts provide new insights into neoclerodane diterpene biosynthesis in Salvia species. Further elucidation of salvinorin A biosynthesis will enhance our understanding of neoclerodane chemical diversity and enable the biotechnological production of high-value diterpenoids.

S2-7

Efficient Synthesis of AMF from Biomass-Derived Carbohydrate via Heterogeneous Flow Chemistry

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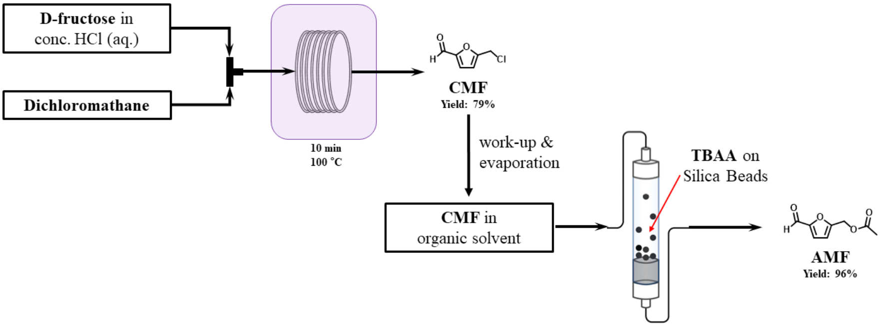
The conversion of renewable biomass into high-value platform chemicals through continuous flow chemistry represents a promising path toward sustainable material production. In this study, we report a two-step flow chemistry process for the synthesis of 5-(acyloxymethyl)furfural (AMF) from carbohydrate-rich biomass sources, including lignocellulose-derived sugars. In the first step, biomass-derived hexoses were selectively converted into 5-chloromethylfurfural (CMF) under acid-catalyzed flow conditions. The resulting CMF was then transformed into AMF via a second acylation reaction, also conducted in a flow system. To enhance efficiency and recyclability, we developed a heterogeneous catalytic system by immobilizing tributylammonium acetate (TBAA) onto silica beads. This solid-supported ionic liquid catalyst enabled high-yield acylation of CMF to AMF with exceptional selectivity, achieving a yield of 96% under optimized flow conditions. Furthermore, the immobilized TBAA-silica beads maintained over 90% yield across four consecutive reuse cycles, demonstrating excellent catalytic stability and sustainability for scaled-up applications. Our study highlights a fully continuous, environmentally benign, and industrially scalable process for producing AMF from renewable carbohydrate feedstocks, offering a viable platform for the future of bio-based polymer precursors.



Symposia

S3-1

When Biorefinery Meets Evolutionary Engineering: Integrated Valorization of Defatted Microalgal Biomass

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The concept of circular biorefinery has been promoted as a sustainable new approach for the nascent microalgae industry. In particular, the solvent extraction of lipid fraction of microalgal biomass is generally performed when aiming to recover marketable compounds from microalgae; the waste residual biomass generated from this process could provide new market opportunities for microalgae in a wide array of commercial sectors. In this work, the heterotrophic cultivation of *Chlorella* sp. HS2 was demonstrated using the hydrolysate recovered following dilute acid hydrolysis of defatted *Chlorella* biomass (DCB). While each of HCl and H_2SO_4 turned out to be an effective catalyst for converting nearly 40% of DCB as fermentable monosugars, the results of microalgal cultivation in diluted hydrolysate indicated high cellular growth without any supplemental nutrients. Notably, the highest microalgal growth was observed when neutralizing HCl- and H_2SO_4-treated hydrolysates with NaOH and $Ca(OH)_2$, respectively, whilst continued lab adaptation of *Chlorella* sp. HS2 further improved its growth in the hydrolysate with distinctive phenotypic shifts as well as genomic structural variations (SVs). Moreover, the fabrication of polymer/residual composite using the residual material obtained after H_2SO_4-catalyzed hydrolysis and $Ca(OH)_2$ neutralization suggested improved tensile performances, seemingly resulted from an improved dispersion of salt precipitates-containing residue in the polymer matrix. Collectively, the results suggest new integrated utilization routes for underutilized byproducts from microalgal industry; further investigations are thus warranted with a special focus on bolstering the economic feasibility and scalability of the postulated microalgal biorefinery.

S3-2

Hydrogen Production and Real Wastewater Treatment in Zero-gap Bipolar Membrane Microbial Electrolysis Cell (BPM-MEC)

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Achieving a carbon-neutral society has become an urgent priority amid growing concerns about climate change and environmental sustainability. Hydrogen is widely recognized as a clean and versatile energy carrier, and biohydrogen, produced from organic waste via biological and electrochemical pathways, offers a sustainable alternative to fossil fuels. Microbial electrolysis cells (MECs) have emerged as a promising technology for high-purity hydrogen production, utilizing electroactive microorganisms at the anode to oxidize organic matter and generate electrons and protons. These electrons travel to the cathode, where they reduce protons to form hydrogen gas. Conventional MECs often suffer from pH imbalances due to the use of cation or anion exchange membranes, which can lead to increased overpotentials and decreased system efficiency. Bipolar membranes (BPMs) offer a solution by enabling internal water dissociation at the membrane interface, generating H^+ and OH^- ions that migrate to their respective electrodes, thereby mitigating pH gradients and enhancing hydrogen evolution. Although BPM-MECs have shown improved performance under controlled conditions, their application to real wastewater treatment remains underexplored. In this study, a novel zero-gap BPM-MEC was designed and tested using three types of real wastewater—brewery wastewater (BW), food wastewater (FW), and livestock wastewater (LW)—as anolytes. To improve cost-efficiency, binderless nickel-based carbon cloth electrodes were used as cathodes, replacing expensive platinum-based materials. Acidified saline conditions were simulated using 0.5 M NaCl as the catholyte to promote hydrogen evolution. Among the tested wastewaters, livestock wastewater showed the highest hydrogen production performance, likely due to its abundance of biodegradable organic acids. The NiCo/CC cathode achieved a current density of 7.6±0.5 A/m^2 and a hydrogen production rate of 21±1 m^3 H_2/m^3·day, with a catalytic efficiency of 90±5% and energy efficiency exceeding 132±9.5%. These results demonstrate the potential of integrating BPMs with cost-effective cathode materials for efficient and scalable biohydrogen production from real wastewater streams.

S3-3

Fe-Mn biochar design for reducing environmental burden of wastewater treatment

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Iron-based technology is one of the most practical approaches to remove toxic metals from industrial wastewater, but faces the problem of low efficiency and requires energy/chemical-demanding steps for safe disposal. Here we develop an efficient material by combining iron and manganese particles with biochar for sustainable decontamination. The formed graphitic biochar layer prevents the embedded zero-valence iron from fast passivation and facilitates the electron transfer, boosting their ability to reduce pollutants and making the iron up to 24 times more efficient than common iron-based materials. Meanwhile, the manganese oxides undergo a 0.02 Å lattice expansion, improving their ability to trap toxic metals. The carbon, iron, and manganese form stable chemical bonds that lock in pollutants, eliminating the need for costly and carbon-intensive stabilization process before landfill disposal. This approach cuts greenhouse gas emissions by 71.8-89.7% compared to conventional treatments and produces only 2.1-3.5% CO2 compared to other iron-based methods. Our strategy can innovate mineral-carbon composite designs and suggest a more sustainable path for wastewater treatment.

S3-4

Environmental Benefits of Microalgal Biotechnology: Bioremediation and Potential Applications

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Microalgae-based biotechnology represents a promising eco-friendly strategy that integrates wastewater treatment with the sustainable production of value-added bioresources. In this study, we explored the functional interactions between microalgae and associated bacterial communities, highlighting how microbial consortia enhance algal growth, nutrient removal efficiency, and resilience to environmental stressors. A multi-phase treatment system utilizing selected microalgal strains was applied to piggery wastewater, resulting in the effective reduction of ammonia, chemical oxygen demand (COD), and phosphorus. Concurrently, the system achieved a marked decrease in pathogenic bacterial populations, underscoring its potential as a bioremediation platform. Importantly, the harvested microalgal biomass exhibited a high lipid content suitable for biodiesel production, thereby demonstrating dual benefits in environmental cleanup and renewable energy generation. Our findings emphasize the ecological and biotechnological importance of algae-bacteria symbiosis, offering insights into the design of robust microbial consortia for next-generation microalgae-based treatment systems.

S4-1

Unveiling Hidden Worlds: Single-Cell Multi-Omics in Environmental Microbiology

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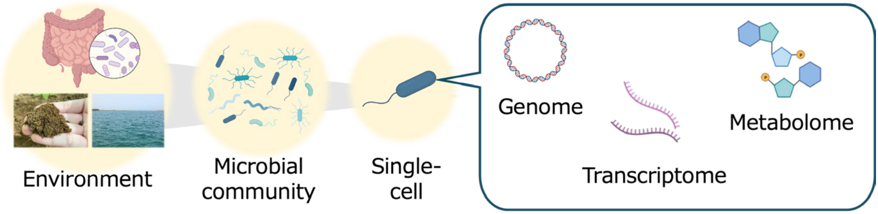
Single-cell analysis is increasingly recognized as a promising strategy for dissecting the detailed characteristics and functions of environmental microbiomes. To enable comprehensive multi-omics investigations, we have developed high-throughput and highly accurate single-cell analysis techniques tailored to environmental microbiomes. In droplet-based genomics, we have carried out large-scale genome sequencing of over 50,000 single-amplified genomes from diverse environmental samples, including seawater, soil, and gut microbiomes [1–3]. We have also developed bioinformatics tools to enhance sequence assembly quality, enabling more precise reconstruction of single-amplified genomes. Currently, these droplet-based single-cell genome analyses are being extended to phages [4], unveiling previously uncharacterized diversity. In Raman microscopy-based metabolomics, we have demonstrated the ability to directly detect intracellular biomolecules, including secondary metabolites, within microbial cells and visualize their subcellular distribution [5–7]. By combining this technology with genome analysis, it becomes possible to gather more detailed information about microorganisms [8]. Furthermore, Raman analysis has been shown to be highly useful for examining microbial colonies to efficiently screen for microorganisms that produce valuable secondary metabolites [9]. In this presentation, we will showcase practical applications of single-cell analysis and discuss future perspectives for single-cell multi-omics approaches.



S4-2

Application of eDNA in Ecological Surveys of Marine Microbiomes

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Coastal zones encompass distinct yet interconnected ecosystems extending from rivers to oceans, significantly influencing global nutrient cycles, including carbon and sulfur fluxes. Typically, oceanic nutrient dynamics are closely linked to river discharge, where seasonal climatic variations and phytoplankton-derived organic matter can modulate riverine carbon and sulfur fluxes. Recent advances in sequencing technology have enabled detailed insights into bacterial roles in degrading phytoplankton-derived dimethylsulfoniopropionate (DMSP), a crucial process within marine microbial food webs. To explore how bacterial biogeography responds to hydrographic changes driven by climate-induced river discharge, this study analyzed bacterial diversity and community composition in Gwangyang Bay (GW), a semi-enclosed estuary at the southern tip of the Korean Peninsula, employing environmental DNA (eDNA) and 16S rRNA gene metabarcoding techniques. Additionally, bacterial involvement in the degradation of phytoplankton-derived DMSP was examined by mapping relevant DMSP degradation genes using shotgun metagenomic databases. Results revealed clear habitat-specific bacterial community patterns aligned with water mass distinctions and transitions from estuarine to coastal environments. Within these communities, the SAR11 clade emerged as the most dominant and widespread operational taxonomic unit (SAR11-OTU). Furthermore, a SAR11 draft genome was successfully assembled from eDNA sequences obtained via shotgun metagenomics, allowing for detailed characterization of its DMSP degradation genes.

S4-3

Prevention of Shiga toxin production in enterohemorrhagic *Escherichia coli*

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Enterohemorrhagic *Escherichia coli* (EHEC) is responsible for the most severe symptoms of *E. coli* infections, including hemorrhagic colitis and hemorrhagic uremic syndrome. Shiga toxin (Stx) plays a critical role as a major virulence factor in the EHEC infection. The genes encoding Stx are located in lambda-like prophage in the EHEC genome. Consequently, Stx is expressed when the phage production is induced via the bacterial SOS response under stress condition. If Stx production is prevented, EHEC pathogenicity will be significantly reduced, and antibiotics may be available to treat the infection without the toxin production. Therefore, we aimed to screen out an inhibitor compound for the Stx production. We conducted two independent screenings to identify the Stx2-production inhibitors for libraries from the RIKEN Natural Product Depository (NPDepo). Niclosamide was identified through the screening from Authentic Library. The compound eliminated Stx production in EHEC under antibiotic treatment. Niclosamide reduced minimum inhibitory concentration (MIC) of ciprofloxacin and showed a synergistic affect to the antibiotic activity. These results suggest that the EHEC cells were killed before express Stx by the combination treatment. Besides, naphthoquinoids were efficiently identified through the two-round of screening of the Pilot and Analog Libraries. Since the structures of these two naphthoquinoids share the 2-amino-3-chloro-1,4-naphthoquinone moiety, quinoclamine which has the shared structure was used for further study. Quinoclamine prevented the cell lysis by phage propagation and dramatically reduced Stx production in EHEC. However, quinoclamine increased MIC for ciprofloxacin and reduced SOS response. It suggests that quinoclamine reduced ciprofloxacin efficacy, as the result, Stx was not induced by the antibiotic treatment. Niclosamide is an FDA approved drug as an intestinal anthelmintic for cestode infections. Repurposing the approved drug can be a shortcut for practical use. The combination of niclosamide and ciprofloxacin will be a potential therapeutic option to treat EHEC infection.

S4-4

Understanding aerosolization of indoor bacterial communities and antibiotic resistomes in swine farms

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Airborne bacteria in swine farms can pose health risks to both pigs and workers. While previous studies have focused on microbial profiles in feces and aerosols, few have examined the stepwise aerosolization process and the influence of antibiotic use in swine farms. This study explored bacterial communities in feces, surfaces, and bioaerosols from six national swine farms categorized by antibiotic use levels (high vs. low, based on the EU's DDDvet). A total of 32 samples were analyzed. Fecal samples exhibited the highest alpha diversity, followed by aerosols and surfaces ($p < 0.05$), with no significant differences by antibiotic use. However, beta diversity revealed distinct microbial compositions between feces and bioaerosols depending on antibiotic usage. Notably, *Staphylococcus, Corynebacterium*, and *Enterococcus* were significantly enriched in bioaerosols from high-antibiotic-use farms ($p < 0.05$), suggesting elevated airborne antibiotic-resistant bacteria. The qPCR results for antibiotic resistance genes indicated high levels of feces, followed by bioaerosols and surfaces. Additionally, a high level of mobile genetic elements, such as intl1, was observed in human nasal samples. Source tracking indicated that over 50% of aerosol bacteria originated from feces and surfaces. Our results showed that different antibiotic uses notably affected indoor bacterial communities and antibiotic resistance during stepwise aerosolization in swine farms.

S5-1

The Content of Nitrosamines in Processed Food and the Health Risk Associated with N-nitrosodimethylamine (NDMA)

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Nitrosamines are compounds formed when nitrites react with secondary or tertiary amines, a process that often occurs during food processing. The International Agency for Research on Cancer (IARC) classifies two nitrosamines N-nitrosodimethylamine (NDMA) and N-nitrosodiethylamine (NDEA) as probably carcinogenic to humans (Group 2A) based on animal studies demonstrating their ability to induce cancers in various organs, including the liver, stomach, esophagus, pancreas, and lungs. In Vietnam, the National Institute for Food Control has carried out risk assessment studies on nitrosamines, focusing on dose-response evaluation, exposure assessment, and risk characterization. The content of six N-Nitrosamines including NDMA, NDEA, N-nitrosopyrrolidine (NPYR), N-nitrosopiperidine (NPIP), N-Nitrosodi-n-butylamine (NDBA) and N-nitrosomorpholine (NMOR) in various food samples were determined using a validated liquid chromatography-tandem mass spectrometry (LC-MS/MS) method, with a detection limit of 0.5 μg/kg. Results indicated that processed meat products exhibited the highest level of nitrosamines of which the NDMA content ranged from 1.2 to 15.0 μg/kg. A chronic toxicological experiment assessing hepatic toxicity via γ-glutamyl transferase (GGT) enzyme activity established that increased serum GGT levels serve as a biomarker for risk associated with NDMA exposure. In addition, a 24-hour dietary recall survey was conducted to estimate daily NDMA intake, yielding lifetime average daily doses (LADD) ranging from 0.0002 to 0.0061 μg/kg body weight/day. Risk characterization based on margin of exposure (MOE) calculations indicated a potential risk for high consumers of processed meat products, evidenced by MOE values below 10,000 for NDMA. These findings provide critical data for risk management and regulatory measures aimed at minimizing nitrosamine exposure and protecting public health.

S5-2

Microplastics in the Environment: Occurrence, Transport, and Ecotoxicological Concerns

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Microplastics (MPs), defined as plastic particles smaller than 5 mm, are increasingly recognized as persistent and pervasive pollutants in terrestrial, atmospheric, and aquatic environments. These particles originate from both primary sources-such as microbeads in cosmetics and synthetic textile fibers-and secondary sources, which result from the fragmentation of larger plastic debris due to environmental weathering processes. As a result of widespread plastic use and inadequate waste management, MPs have now become ubiquitous across global ecosystems, including remote and previously pristine regions. This presentation aims to provide a comprehensive overview of the environmental behavior of microplastics, with a focus on their sources, transport pathways, and ecological effects. MPs have been shown to accumulate in soils, airborne particulate matter, freshwater systems, and marine habitats. Once present in these environments, they can interact with diverse biological systems. A growing body of research indicates that MPs can induce oxidative stress, disrupt physiological functions, inhibit growth, and cause cellular damage in a wide variety of organisms-ranging from invertebrates and vertebrates to plants and microorganisms. In addition to their intrinsic biological effects, MPs are known to possess a high surface-area-to-volume ratio, making them effective carriers of environmental pollutants such as heavy metals, polycyclic aromatic hydrocarbons (PAHs), and endocrine-disrupting chemicals. These adsorbed substances can enhance the toxicity of microplastics and facilitate their movement across environmental boundaries. Although most current research has focused on the environmental accumulation and ecotoxicity of MPs, increasing attention is now being given to their potential migration through food chains. This raises emerging concerns about human exposure through contaminated food and water. Understanding the environmental fate and biological impact of microplastics is therefore essential not only for assessing long-term ecological risks but also for informing regulatory frameworks and mitigation strategies aimed at protecting both environmental and public health.

S5-3

Polystyrene Nanoplastics Promote Premature Cellular Senescence through Skeletal Myoblast Dysfunction in Myoblasts

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Nanoplastics (NPs) are emerging environmental contaminants present in atmospheric, freshwater, and aquatic environments. NPs can rapidly permeate cell membranes and build up in human tissues and organs, causing a potential threat to human health. As the skeletal muscle undergoes aging, myogenesis gradually deteriorates, leading to loss of muscle mass. While previous studies have demonstrated the adverse and toxic effects of polystyrene (PS)-NPs, gaps remain in understanding aging effects and specific mechanisms by PS-NPs in pre-differentiated myoblasts. In this study, we investigated the cellular internalization, aggregation, and senescent effects of PS-NPs using an in vitro model of pre-differentiated C2C12 myoblasts. Pre-differentiated C2C12 myoblasts were exposed to increasing concentrations of PS-NPs and internalization was observed in myoblasts using flow cytometry and transmission electron microscopy. We further investigated whether internalization of these PS-NPs at sublethal cytotoxic concentrations led to an increase in senescence hallmarks, such as increased β-galactosidase activity, increased expression of p16, p21 and senescence-related secretory phenotypes, and cell cycle arrest. In addition, PS-NP treatment caused notable mitochondrial superoxide production and damage, including mitochondrial membrane depolarization, content loss, fragmentation, and decreased ATP production. Rotenone, a mitochondrial function inhibitor, and exacerbated PS-NP-induced cell proliferation inhibition, whereas Mito-TEMPO, a mitochondrial superoxide scavenger, restored the cell proliferation rate and rescued cellular senescence. Therefore, our findings indicate the senescent effects of PS-NPs through mitochondrial superoxide production and dysfunction in pre-differentiated myoblasts.

S5-4

The effects of microplastics on neurodevelopment in mice

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Genetic factors play a significant role in the majority of neurodevelopmental disorders. In recent years, there has been a rapid increase in the number of patients diagnosed with neurodevelopmental disorders. However, this increase cannot be solely attributed to genetic factors. Therefore, the impact of environmental factors on brain development was examined using nanoplastics (NPs) and microplastics (MPs) that are commonly encountered in daily life. NPs and MPs were administered to mice during pregnancy to assess their effects on neurodevelopment. Our study revealed that both NPs and MPs impair neurodevelopment, resulting in abnormal behaviors in treated mice. These findings suggest that perinatal exposure to NPs and MPs disrupts neurodevelopment and behavior in mice.

S6-1

Plant Cell Culture-Driven Breakthroughs in Reverse Aging

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Aging is a complex biological process characterized by cellular senescence, inflammation, and deterioration of skin barrier functions. Recent advances in plant biotechnology and cellular screening platforms have opened new horizons in identifying bioactive compounds that can reverse age-related cellular decline. This study explores a reverse-aging strategy centered on plant cell culture technology, leveraging its potential to generate high-purity bioactives such as plant cell extracts, plant cell-derived polydeoxyribonucleotide (PDRN), and plant cell-derived extracellular vesicles (EVs). By applying a high-throughput skin cell aging model screening platform, we have successfully identified plant-derived actives that restore dermal cell viability, enhance collagen synthesis, and mitigate senescence-associated markers. Our platform specifically screens for anti-inflammatory, antioxidant, and senolytic effects on keratinocytes and fibroblasts under aging conditions. To further enhance efficacy and scalability, we employed BIO-FD&C's proprietary SMART-RC2™ technology—an advanced bio-concentration system that enables efficient extraction and concentration of plant-derived actives while preserving their functional integrity. This process ensures industrial-level yield of high-quality materials suitable for cosmeceutical and dermatological applications. These findings suggest that plant cell culture-derived biomaterials have significant potential as next-generation ingredients in cosmetic and therapeutic formulations targeting skin aging. The integration of plant biotechnology, screening-based selection, and smart bioprocessing technologies may mark a turning point in the development of science-backed, sustainable, and highly efficacious reverse-aging solutions.

Funding: This work was funded by the Ministry of Health & Welfare, Republic of Korea, through the KHIDI under the Korea Health Technology R&D Project (grant number RS-2024-00345193).

S6-2

Antioxidant foods derived from microalgae

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Microalgae is a general term for photosynthetic aquatic single-celled organisms, and is also called phytoplankton. Microalgae have abundant biodiversity, with at least 50,000 species. Since microalgae produce biomass and oxygen by fixing carbon dioxide using light, there have been many studies on their use in the environmental and energy industries. However, since the current technology to produce microalgae biomass through photosynthesis is still expensive, it is not easy to utilize microalgae in low value-added industries, but their use in high value-added industries such as functional materials has great potential. Globally, the market for natural products based on plant extracts continues to grow every year due to consumers' high preference for natural products. The situation is the same in Korea, and it can be said that the development of plant-based natural products is active. However, many natural materials used in the product market depend on imports. This seems to be due to the imbalance between the technology for producing natural materials and the technology for discovering functionality. Since microalgae inhabit various environments, their biodiversity is high, and the variety of materials they produce is also high. Therefore, if their biomass can be produced economically, various natural materials derived from microalgae can be discovered. This presentation will briefly introduce antioxidants produced by photosynthetic microalgae and discuss the potential of utilizing these substances to develop various antioxidant foods.

S6-3

딥테크 창업기업의 성공적인 성장 전략 (초기 기업 중심)

최고

시너지IB투자㈜

■ **기술특례상장 기업에 대한 현황**
- ‘파두 사태’ 이후 기술특례상장 기업의 사업 지속성 및 수익성에 대한 우려 지속 증가
- 2023년말 기준 상장 후 지속적인 적자 누적
- 다수의 기술특례상장 기업이 관리종목 지정 위기
- 클리노믹스(-222억), 지놈앤컴퍼니(-283억), 네오이뮨텍(-3,192만 달러) 등
- 한국거래소는 상장 심사 시 ‘실제 기술 매출 실현력’ 강조 및 공시 기준 강화 발표
- 현재 기술 기반 창업도 수익성과 성장 전략이 명확해야 살아남을 수 있음

■ **딥테크 창업 기업의 현황**
- 딥테크 창업 기업의 경우 기술에 집중되어 사업화 단계에서 PoC 등 B2B 비즈니스 필수
- 시장 설득력 부족, 인프라 구축의 한계로 인해 사업화 어려움과 투자유치 한계
- 설립 초기 B2B 비즈니스로 사업화 성공이 가능한 아이템 선정이 중요함

■ **전문 투자사 펀드 구조의 이해**
- VC 생태계 현황
- 모태펀드 출자 프로세스 및 주목적에 대한 성격 이해

■ **초기 투자유치 및 성장지원 전략**
- 한국 창업 생태계는 정부 주도하에 구축되어 있기 때문에, TIPS와 같은 정부 연계 프로그램 연계 필수
- 투자유치 시기를 놓치지 않도록 지분 및 정관 구조 사전 정비 필요

■ **Scale-Up 성공 사례**
- KIST 연구자 창업 사례 공유

S6-4

New Concept of Aeroponic System

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Hydroponics is an agricultural technology that enables the growth of plants without soil, which can be traced back to ancient civilizations and has developed into its modern form with scientific research in the 20th century. Among these hydroponic methods, aeroponics technology is gaining popularity due to its economy and efficiency. Aeroponics is a method of growing plants by exposing their roots to the air and spraying them with a fine nutrient solution, which improves the speed and quality of growth by increasing the efficiency of oxygen supply and nutrient absorption. It also greatly reduces water and pesticide usage, and is easy to control and automate, making it a promising alternative for the future of agriculture. In this study, we demonstrate and introduce a more utilitarian form of aeroponics cultivation by designing a spraying device that supplies nutrient solution. In particular, by utilizing an ultrasonic part, it is possible to control the amount of spray and secure operational stability through low-energy operation.

S7-1

Fermented aged mountain cultivated ginseng sprout and compound K alleviate allergic asthma and acute lung injury through macrophage polarization modulation

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Macrophage polarization plays a critical role in the pathogenesis of asthma and acute lung injury (ALI), both characterized by inflammation and oxidative stress. However, the effect of fermented aged mountain cultivated ginseng sprout (FAMCGS) and its active component, compound K (CK), on macrophage modulation remains underexplored. FAMCGS, derived from mountain cultivated ginseng sprouts (MCGS) through steaming, aging, and fermentation, is designed to enhance bioactivity and reduce cultivation time. This study investigates the anti-inflammatory and antioxidant effects of FAMCGS and CK in models of allergic asthma and ALI, with a focus on macrophage polarization. Using *in vivo* (ovalbumin-induced asthma and LPS-induced ALI mouse models), *ex vivo*, and *in vitro* (MH-S alveolar macrophages) systems, we assessed their effect through histology, PCR, Western blotting, and ELISA. FAMCGS, particularly in its CK-enriched form, showed superior bioactivity compared to MCGS. In the asthma model, FAMCGS reduced airway hyperresponsiveness, IgE levels, Th2 cytokines, inflammatory cells, goblet cell hyperplasia, mast cell activation, M2 macrophage infiltration, and M2 markers—comparable to dexamethasone. In the ALI model, it suppressed M1 macrophage infiltration, M1 markers, inflammatory cytokines, and NF-κB activation. Both FAMCGS and CK attenuated LPS-induced M1 and IL-4-induced M2 polarization, reduced related markers and MAPK activation in MH-S cells, and lowered reactive oxygen species levels in both lung tissue and macrophages. CK's effects were largely comparable to those of FAMCGS. These findings suggest that FAMCGS and CK exert preventive and therapeutic effects in respiratory inflammatory diseases by alleviating inflammation and oxidative stress through modulation of macrophage polarization.

S7-2

Protective effects of *Lonicerae Flos* against OGD-induced damage in bEnd.3 cells with active ingredient prediction via network pharmacology

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This study aimed to evaluate the neuroprotective effects of *Lonicerae Flos*, a natural herbal resource, against oxygen-glucose deprivation (OGD)-induced damage in mouse microvascular cerebral endothelial cells (bEnd.3), and to predict its active ingredients using a network pharmacology approach. This aligns with the goals of Green Bio by exploring plant-based therapeutics and bioinformatics tools for sustainable healthcare innovation. To simulate ischemic stroke conditions, bEnd.3 cells were exposed to OGD. Cell viability and morphological changes were assessed via MTT assay and microscopy. Protein expression related to HIF-α, MAPK, and NF-κB signaling pathways, as well as apoptotic markers, were analyzed by western blot. Network pharmacology was employed to identify bioactive compounds and potential molecular mechanisms of *Lonicerae Flos*, integrating biological databases and systems biology tools. *Lonicerae Flos* significantly improved cell viability and reduced OGD-induced cellular damage. It inhibited the phosphorylation of ERK, p38, and p65, while enhancing anti-apoptotic Bcl-2 expression and suppressing pro-apoptotic Bax and cleaved caspase-3. Network pharmacology identified 14 key targets and 30 relevant signaling pathways—such as HIF-1α, TNF, and IL-17 pathways—highlighting its potential role in regulating inflammation and hypoxia-related responses in ischemic stroke. These findings underscore the compound's multi-target action, consistent with Green Bio's systems-level approach to therapeutic discovery.

S7-3

Green Bio-Based Integration of Quality Grading and Smart Distribution for Horticultural Products

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The growing demand for sustainable and high-quality horticultural products has prompted the development of innovative postharvest management systems grounded in green bio technology. In this study, we propose a comprehensive framework that integrates physiological traits, omics-based markers, nondestructive sensing technologies, and environmental monitoring data to establish a dynamic quality grading and distribution model suitable for smart agricultural processing center (APC). Samples of key horticultural commodities, including apple, pear, onion, tangerine, and Korean melon were evaluated under controlled storage conditions to identify physiological changes related to freshness degradation. Using MRI, VNIR, and X-ray techniques, we analyzed internal disorders such as water-soaking, core browning, sprouting, and wilting. Correlation analyses with quality indicators such as SSC, firmness, acidity, and weight loss confirmed the potential of these imaging modalities for real-time freshness grading. Additionally, omics profiling (metabolomics and transcriptomics) supported the identification of physiological pathways linked to postharvest deterioration.The study further implemented an IoT-based APC environment to monitor temperature, humidity, and gas concentrations, enabling the creation of predictive models for quality changes during storage and distribution. The integration of digital twins allowed the visualization and simulation of internal quality dynamics, providing a scientific basis for quality classification, shelf-life estimation, and traceability.These findings demonstrate that the convergence of green bio data and digital sensing can lead to the development of standardized, objective grading systems and more efficient smart distribution protocols. The proposed platform supports sustainable supply chains by reducing waste, improving market transparency, and enabling targeted interventions based on physiological and environmental data.

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S7-4

Patent Acquisition and Commercialization Strategy for Biomaterials

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Biomaterials refer to substances derived from living organisms or those that perform biological functions, and they are applicable across a wide range of industries such as pharmaceuticals, food, cosmetics, agriculture, and the environment. The global market size for biomaterials is projected to reach USD 400 billion by 2024, with an annual growth rate of 13-15%. Additionally, patent applications related to biomaterials have increased at an annual rate of 7-10% over the past decade. These trends indicate that biomaterials are rapidly expanding across industries, accompanied by the development of various related technologies. Biomaterials are a key driver in transforming industries into high value-added sectors. Establishing a virtuous cycle—comprising technology development, patent acquisition, technology transfer, commercialization, and revenue generation—is crucial for enhancing both national and corporate competitiveness. This presentation aims to propose strategies for securing strong intellectual property rights for biomaterials and utilizing them to drive commercialization through technology transfer. Based on 13 years of experience at the Korea Agriculture Technology Promotion Agency (KOAT), where the speaker was responsible for patenting various technologies developed by the Rural Development Administration (RDA) and promoting their transfer and commercialization, real-world examples and practical insights from the field will be shared. The reason to focus on the Rural Development Administration (RDA) in terms of biomaterial patenting and commercialization is that the RDA serves as a core institution for fostering the green bioindustry based on biomaterials. It plays a full-cycle role—from research and development, industrialization, technology transfer, to policy integration—leveraging agricultural and biological resources. In particular, RDA achieves outstanding results, including over 500 annual patent applications, more than 1,500 technology transfer contracts, and a practical utilization rate of approximately 46%, positioning it as one of the top-performing institutions in commercialization of R&D outcomes both domestically and internationally. Specifically, this presentation will introduce essential concepts and strategies for researchers and companies to secure strong patents, tailored by research phase and biomaterial type. It will also share the institutional, procedural, and methodological improvements undertaken by the KOAT to enhance success in technology transfer and commercialization of its patents. Lastly, it will present statistical analysis results based on RDA's patent and technology transfer performance data to identify the factors influencing successful technology transfer.

S8-1

The role of Natural Product Cluster in Korea

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Plant-derived natural products (NPs) have been used for disease prevention & health-improvement as raw materials for pharma/nutraceuticals and as starting materials for synthetic therapeutics. The Natural Product Cluster (NPC) aims to provide standardized natural products and high-level information from a single window by establishing standard methods for securing plant resources, standard extract production, phytochemical analysis, and biological activity evaluation. There are two bank of NPs in KRIBB, which was firstly established at 2000 (domestic) and 2006 (overseas), as the largest banks in Korea that provides extracts from domestic/overseas plant resources (domestic, over 1,700 species and overseas ca. 40,000 plants). The two banks have merged to be a Natural Product Central Bank (NPCB) under a project of Natural Product Cluster (NPC) project in cooperation with three other banks (KIST, KIOM, KFRI) and supporting parteners since 2021. NPCB is carrying out the project by operating an unified bank system for domestic and foreign plant extracts, and establishes standard extracts (domestic 1,000 species, overseas 150 species) with information of extract profile, structure of major constituents, screening results) after setting up the standard operation procedure (SOP) of each step. Additionally, it provides standardized data and information for extract production, instrumental analysis and biological evaluation methods in a single portal system. In this presentation, we would like to introduce the role and achievements of NPCB and its future development plans to KSABC members.

Keywords: Natural Prodcut Cluster, Natural Product Central Bank, standardized plant extract, information retrieval system of natural product

S8-2

A Base Bank for Korean Native Plants

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Our purpose of the project is to establish a support system for securing and utilizing Korean Peninsula native plant resources and information to enhance the value of Korean Peninsula native plant resources and build a natural products cluster. We are manufacturing standard extracts of native, securing component data of native plants, evaluating virtual efficacy prediction of native plant-derived compounds, building a database, and jointly utilizing standard extracts through supply and information provision. Firstly, we have established a standardized extract production system for native plants and produced 361 standardized extracts from 117 species of native plants. Secondly, we have built a system for generating qualitative/quantitative analysis data through NMR and HRMS analysis of at least 5 components per species, and we have produced 361 HPLC profile data and 585 component data. Thirdly, we have established a target prediction system for the virtual efficacy prediction of native plant-derived compounds and produced virtual efficacy prediction data for 585 compounds. Lastly, we have established a system for supply and information provision on native plant extracts so that many researchers can utilize them. As a result, it would be possible to lead the bio sector and secure market competitiveness by systematically and efficiently securing, managing, and utilizing domestic native plant resources.

S8-3

Plant-derived natural product resource base bank

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In response to the need for a national-level system to preserve, manage, and utilize plant-derived natural products and associated data, we are operating the Plant-Derived Natural Product Resource Base Bank (Natural Product Cluster). This initiative focuses on producing standard extracts and their analysis data from domestic herbal resource plants for public use. Comprehensive analytical profiling of the extracts has been conducted using techniques such as UHPLC-QTOF-MS, UHPLC-UV-ELSD, and HPLC-UV-ELSD. Structural information, including NMR and HRMS data of major constituents, has also been compiled into a searchable database. In addition, biological activities of the standard extracts have been evaluated. This research is expected to enhance the practical value of domestic medicinal plant resources and lay a foundation for their high value-added industrial application. In this presentation, we will briefly introduce our research progress in relation to these goals.

S8-4

A Base Bank for Plant-derived Food Resources

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This research project aims to establish a plant-derived functional food resource base bank by constructing a database for chemical analysis, efficacy prediction, and material information, along with distribution system for standardized functional food resource extracts. Currently, in the first year of the second phase of study, the preparation and chemical analysis (UPLC-QTOF-MS, UPLC-PDA/ELSD, HPLC-PDA/ELSD) of 103 species and 246 kinds of Korean native food material standard extracts have been completed following the standard operating procedures of the Natural Product Central Bank (NPCB). In this year, approximately 130 species and 330 kinds of food resource will be added to the resource base bank and provided to the central bank of the natural product cluster to contribute to the food material research and industrial development of functional food resource.

S8-5

Establishment of the cooperation center for securing characteristic information of natural compounds to advance Natural Product Cluster and maximize utilization of strategic materials

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The research focuses on expanding the investigation of natural product cluster and strategic materials by obtaining information from natural compounds through the establishment of the cooperation center. Specifically, natural compounds related to strategic materials for the central bank have been secured and provided along with spectroscopic information. Thus far, 101 standard compounds were derived based on molecular networking analysis results using the in-house library. Additionally, 100 compounds were isolated and structurally identified using spectroscopic data acquired from 17 plants. Among the 201 compounds, 170 were submitted to the central bank in physical form. As the next step, an additional 104 compounds are in continuous process of being secured to achieve the final goal of obtaining 231 compounds. Furthermore, an educational training program will be developed to enable users to utilize the natural compounds and characteristic information established through this research project. The results will play a pivotal role in advancing strategic materials sourced from natural products with diverse natural compounds anticipated to be obtained.

S8-6

Advancing natural product data management platform to be more user-friendly by implementing AI-driven efficacy prediction service

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Natural product cluster has been successfully supporting diverse research by operating data management platform supports not only distributing extractions of the natural products but also complex data, including efficacy test results of the extractions, and chromatographic outputs such as Ultra-Performance Liquid Chromatogram(UPLC) generated per extracted parts, collected date, collected location of the original plant. However, how to showcase these diverse datasets and effectively curate the extractions of natural products according to the needs of the users of the data management platform without hindering patentability of the extractions of each plant remains as a challenge. Therefore, we aimed to advance natural product data management platform by implementing AI-driven efficacy prediction service. This case presents the implementation structure and examples of an AI-drivenefficacy prediction service leveraging compound database of Natural product cluster and its chromatographic outputs. Key features include automated efficacy prediction of each identified compound of each natural product extraction that has been uploaded to the data management platform, and user-friendly interfaces for data visualization. In conclusion, by streamlining data workflows to AI-prediction, this case demonstrates effectiveness in showcasing diverse natural product datasets tailored to the needs of the users, leading to improved analytical efficiency and novel bioactive compound identification using the natural product extractions which Natural product cluster provides.

S8-7

Application Strategy of an AI-Based Support Program for Analyzing the Relationships Among Natural Product Components, Diseases, and Targets

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The digitization and automation of natural product analysis is emerging as a major trend in modern drug discovery. In this context, the efficacy analysis of high-value natural products—such as Astragalusextract and goldenseal—as well as the modernization of natural product databases are posing new challenges for researchers. To address these, Fiveworks has developed OMNIMIX-AI, an integrated platform that leverages artificial intelligence and network pharmacology technologies to accelerate natural product research. OMNIMIX-AI is designed to rapidly identify and analyze multidimensional correlations among natural product components, target proteins, and diseases using large-scale bioinformatics data and literature. The platform provides three core modules:

1. O-NetPharm: This module conducts multi-component, multi-target network pharmacology analysis. It visualizes the interaction network of active compounds within a plant material, enabling researchers to intuitively understand complex pharmacological mechanisms. By integrating target gene information across multiple components, it overcomes the limitations of traditional single-target approaches and significantly reduces analysis time using a dataset of over 30 million cases.
2. O-TargetPrediction: Utilizing structural similarity analysis, AlphaFold-based protein structure prediction, and molecular dynamics simulation, this module suggests potential target proteins for new or unexplored natural products. It dramatically shortens the literature review and experimental validation process, providing foundational data for the development of novel functional botanicals and bioactive ingredient certification.
3. O-DtoC (Disease-to-Compound): This reverse search module recommends optimal natural product components based on disease-related target-pathway information. By combining activity prediction algorithms (e.g., IC50 scoring) with molecular docking-based binding affinity analysis, it enhances candidate screening efficiency and improves the reliability of compound selection.

OMNIMIX-AI is continuously evolving toward a more researcher-centric, decision-support platform. As part of this advancement, technologies such as large language models (LLMs) and retrieval-augmented generation (RAG) are being integrated to enable intelligent summarization and analysis of diverse data sources—including academic papers, patents, and public databases. These capabilities aim to further improve prediction precision by incorporating both environmental and biological context. Ultimately, OMNIMIX-AI provides strategic and reliable insights for natural product-based drug discovery, supporting researchers in accelerating the development of next-generation therapeutics.

S8-8

Korea Forest Plant Essential Oil Bank

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The purpose of this project in 2024 is threefold. First, to develop essential oil materials targeting forest plants of the Pinaceae family in the Korean Peninsula and to secure a component data bases. Second, to establish standards as a global bio-material through securing biological activities and safety. Third, to provide public distribution services. This project is composed of a consortium of Hoseo University, Seoul National University, and the National Institute of Forest Science. The achievements for 2024 are as follows.

The development of essential oils from Pinaceae plants and the establishment of their extraction processes have been completed: A total of 13 species of Pinaceae plants were collected by distinguishing leaves, new shoots, fruits, and wood. Using the steam distillation method, 31 types of Pinaceae plant essential oils were developed, and their extraction process was established through yield analysis of the essential oils. The obtained Pinaceae plant essential oils were shared with collaborating research institutions for further studies and stored in the replica repository of the the Korea Forest Plant Essential Oil Bank.

The establishment of sources and specimens for Pinaceae forest plants has been completed: A system for cultivation and management of seven species of Pinaceae plants was set up at Hoseo University's Asan Campus. Based on the standard operating procedure (SOP) for plant collection, the collection, classification, identification, and preparation of plant specimens for target species of Pinaceae forest plants were carried out, and a database of material information by taxonomic group was completed.

The analysis of the basic physiological, physical, and chemical characteristics of Pinaceae plant essential oils has been completed: *In vitro* cell toxicity evaluation, antioxidant activity, whitening activity, anti-inflammatory activity, antibacterial, and antifungal activities were assessed to clarify the basic physiological activities. Based on the chemical composition analysis database of Pinaceae plant essential oils, the safety as a fragrance and flavor, allergen content analysis, and the analysis of harmful substances (heavy metals, pesticides) were completed. The density, acid value, refractive index, freezing point, and aroma characteristics (fragrance notes, persistence) of Pinaceae plant essential oils were measured to analyze the physical and chemical properties, and the optimal storage conditions and period for Pinaceae plant essential oils were established through component profiling under different storage temperature conditions and container conditions.

The comprehensive database and distribution system for Pinaceae plant essential oils have been established: The comprehensive database for basic physiological, physical, and chemical analyses of Pinaceae plant essential oils and their distribution system have been registered in the “Forest Plant Essentials Oil Bank” system, and also plan to be registered and managed on the integrated platform for forest biological resources management. Furthermore, the comprehensive database for Pinaceae plant essential oils has been registered in the National Bio-Resource Information Center (KOBIC) linked to the Natural Product Cluster Central Bank.

Results derived from the research database of Pinaceae plant essential oils: Scientific results were derived, such as publication of SCIE-level papers (1 publication/ 1 in revision), 1 patent application, 9 academic presentations, and 5 registrations in the Korea Cosmetics Ingredients Dictionary. In addition, through the Forest Plant Essential Oil Bank system, distribution of plant essential oils (71 cases), provision of their information, and various promotional/exhibition activities, active research activities were conducted to promote research on forest plant essential oils, including those of the Pinaceae family, and to activate the use of domestic fragrance resources.

In the future, we plan to develop plant essential oils based on forest plants of Cupressaceae forest plants and Lauraceae and four other forest plant species (2026) and study their physiological, physical, and chemical basic properties. Moreover, we will establish a domestic forest plant essential oil distribution system and provide a comprehensive DB information service. In addition, through scientific achievements, we will expand the research and industrial utilization of domestic forest plant essential oils and establish standards of them as global bio-resources, and create their sustainable utilization framework. Through this, we seek to develop domestic forest plant essential oils into bio-materials with international competitiveness.

S9-1

4-Methylthiobutyl isothiocyanate Potentiates the Efficacy of Chemotherapy in Drug-Resistant Breast Cancer Cells

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Breast cancer (BC) remains the most commonly diagnosed malignancy among women and a major cause of cancer-related death. A key obstacle in effective treatment is the development of chemoresistance, which is often associated with overexpression of hypoxia-inducible factor-1 alpha (HIF-1α), a transcription factor that promotes tumor survival and drug resistance under hypoxic conditions. In this study, we evaluated the anticancer potential of 4-methylthiobutyl isothiocyanate (4-Me), a natural compound derived from cruciferous vegetables, in drug-resistant BC. Treatment with 4-Me significantly inhibited the proliferation of MCF-7/drug-resistant (MCF-7/DR) cells in a dose-dependent manner. Moreover, 4-Me enhanced the cytotoxic effect of paclitaxel, a commonly used chemotherapeutic agent, showing a synergistic effect in vitro. In xenograft mouse models bearing MCF-7/DR tumors, combination therapy with 4-Me and paclitaxel led to significantly greater tumor suppression compared to monotherapy. Mechanistically, 4-Me downregulated HIF-1α expression, suggesting its role in sensitizing resistant cells to chemotherapy by targeting ATP-binding cassette (ABC) transporters. These findings highlight the potential of 4-Me as an effective adjuvant agent to improve the efficacy of current chemotherapeutics, particularly in drug resistant tumors. The results underscore the therapeutic value of natural isothiocyanates in overcoming drug resistance in BC.

S9-2

Distinctive ecophysiological Traits of *Nitrosocosmicus* Ammonia-Oxidizing Archaea

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In the global nitrogen cycle, nitrification is driven by ammonia-oxidizing microorganisms, especially ammonia-oxidizing archaea (AOA). Although the abundance and diversity of AOA in various environments are well-studied, the genetic basis for their ecophysiological adaptations is still not clearly understood. Within AOA, high substrate tolerance, low substrate affinity, and large cell size are distinctive physiological traits of *Nitrosocosmicus*. By conducting comparative genomic analysis of 39 cultured AOA, including five strains of *Nitrosocosmicus* we gained a better understanding of the unique physiology of *Nitrosocosmicus*. This study identified that all five *Nitrosocosmicus* strains lack the canonical high-affinity ammonium transporters and typical S-layer structural genes observed in other AOA. Cryo-electron tomography analysis has confirmed the lack of an outermost visible S-layer structure in *Nitrosocosmicus oleophilus* MY3, which suggested *Nitrosocosmicus* strains may possess only a thick periplasmic space, accompanied by a glycoprotein or glycolipid-based glycocalyx covering the outer cell layer. Overall, this study offers profound insights into the niche adaptation mechanisms and the comprehensive ecophysiology of *Nitrosocosmicus* AOA in terrestrial ecosystems.

S9-3

NOX-derived ROS hyperstabilize HIF-1α under normoxia, revealing a target in pulmonary fibrosis

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Idiopathic pulmonary fibrosis (IPF) progresses as excess extracellular matrix accumulates and stiffens lung tissue. Although transforming growth factor-β1 (TGF-β1) is a major profibrotic signal, the oxidative events linking it to matrix deposition are not well defined. Here we show that reactive oxygen species (ROS) generated by NADPH oxidases (NOXs) hyper-stabilize hypoxia-inducible factor-1α (HIF-1α) even in normoxia. Stabilized HIF-1α up-regulates profibrotic genes, drives epithelial-mesenchymal transition, and enhances cell migration, as demonstrated by immunofluorescence, RT-qPCR, western blotting, and wound-healing assays in A549, MRC-5, and BBM cells. Deletion of p22phox—the shared NOX subunit encoded by CYBA—reduced ROS levels and prevented HIF-1α accumulation, pinpointing NOX-derived ROS as the upstream trigger.

Leveraging this insight, we synthesized a small molecule that accelerates HIF-1α degradation. The compound lowered HIF-1α and fibrosis markers in vitro and markedly attenuated bleomycin-induced lung fibrosis in mice, without detectable toxicity. Together, these findings reveal a self-amplifying NOX-ROS/HIF-1α axis that promotes IPF independently of hypoxia and position pharmacologic HIF-1α down-regulation as a promising antifibrotic strategy.

Keywords: pulmonary fibrosis, fibrosis drug candidate, HIF-1α, NOX, ROS

Symposia

S9-4

ACF-1: A Novel Small Molecule for Targeted Inhibition of HIF-1α in Idiopathic Pulmonary Fibrosis

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Idiopathic Pulmonary Fibrosis (IPF) is a progressive, fatal interstitial lung disease marked by aberrant epithelial repair, fibroblast activation, and excessive extracellular matrix (ECM) deposition, leading to impaired gas exchange. A growing body of evidence implicates sustained tissue hypoxia and the consequent stabilization of Hypoxia-Inducible Factor-1α (HIF-1α) as pivotal drivers of IPF pathogenesis. HIF-1α activation orchestrates a profibrotic transcriptional program that promotes epithelial–mesenchymal transition (EMT), myofibroblast differentiation, and ECM remodelling. Targeting HIF-1α degradation thus represents a promising therapeutic strategy. Here, we report the discovery and preclinical evaluation of ACF-1, a novel small molecule rationally developed to promote selective degradation of HIF-1α. ACF-1 was synthesized through a structure-guided approach, incorporating a validated flavonoid scaffold enriched with a catechol moiety to optimize functional activity. Mechanistic studies revealed that ACF-1 enhances transcriptional regulation of HIF-1α hydroxylation, accelerating its proteasomal degradation via the von Hippel-Lindau (pVHL) pathway. ACF-1 treatment led to substantial reduction of HIF-1α protein levels, along with downregulation of NOX4, a transcriptional target of HIF-1α implicated in oxidative stress and fibroblast activation. Consequently, ACF-1 suppressed ECM production and reversed fibroblast-to-myofibroblast transition. In vitro and in vivo models consistently demonstrated potent anti-fibrotic efficacy.

Collectively, these findings establish ACF-1 as a promising candidate for IPF therapy by targeting HIF-1α turnover and disrupting key fibrotic signaling cascades.

Keywords: Idiopathic Pulmonary Fibrosis, Hypoxia-Inducible Factor-1α, ACF-1

S9-5

Toward Optimizing Growth Medium for *Haematococcus lacustris:* Effects of Different Media on Growth and Microbial Dynamics

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Haematococcus lacustris is a valuable microalga widely studied for its high astaxanthin production potential. To improve its cultivation efficiency, we investigated the effects of different culture media on algal growth and associated bacterial communities. *H. lacustris* was cultivated over 12 days, with samples collected at four time points to assess growth performance through cell counts, dry cell weight, and astaxanthin content. Environmental factors, including nutrient concentrations and optical densities related to chlorophyll and astaxanthin, were also measured. Bacterial communities were collected using a single filtration step and analyzed to observe shifts during the cultivation process. Among the tested conditions, the OHM medium consistently supported higher dry cell weight, greater cell diameter, enhanced zoospore production, faster growth rates, and more efficient total nitrogen removal. These findings suggest that OHM provides a more favorable environment for *H. lacustris* growth compared to the other media. The primary goal of this study is to provide insights that will guide the development of an optimized, modified medium to enhance *H. lacustris* biomass and astaxanthin production. The results are expected to contribute to improving large-scale microalgal cultivation strategies.

S9-6

Exploring the Anti-Inflammatory Properties of *Tetragonia tetragonoides* (Pall.) Kuntz in Mouse Macrophages

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Tetragonia tetragonoides (Pall.) Kuntz, commonly known as New Zealand spinach, is a perennial plant of the Aizoaceae family, found in Korea, China, and other parts of Asia. In Korea, it is mainly located along the coast of Jeju Island. Research suggests that the plant has traditionally been used as a herbal remedy to treat and prevent stomach disorders, such as gastritis and peptic ulcers. In addition, *T. tetragonoides* is known to contain various metabolites, including flavonoids, alkaloids, and terpenes. Inflammation occurs as a protective response against bacterial pathogens, irritation, and tissue injury. In this study, we compared the HPLC profiles of *T. tetragonoides* extracts and assessed the expression levels of inflammation markers, including inducible nitric oxide synthase (iNOS) and cyclooxygenase-2 (COX-2), and proinflammatory cytokines such as interleukin-1β, interleukin-6, and tumor necrosis factor-α (TNF-α), by treating LPS-induced J774 macrophages with the extract of *T. tetragonides*. The results showed that LPS strongly induced the expression of proinflammatory cytokine reporters, while the *T. tetragonoides* extract dose-dependently modulated key inflammatory indicators such as IL-1β, IL-6, iNOS, TNF-α, and nitric oxide (NO). We also focused on isolating and identifying biologically active components from *T. tetragonoides*. Through column chromatography, four methoxy kaempferol glucosides (1-4) were isolated from the extract of *T. tetragonoides*. These methoxy kaempferol glucosides are anticipated to serve as antioxidant and anti-inflammatory agents, as their core structure, kaempferol, is known for its antioxidant and anti-inflammatory properties.

Keywords: *Tetraagonia tetragonoides* (Pall.) Kuntz; anti-inflammatory activity; methoxy kaempferol glucosides

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S9-7

p-Coumaric acid prevents hepatic inflammation and fibrosis by suppressing NLRP3 inflammasome activation involved in TLR4 knockout fed a high-fat and high-sucrose diet

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Previously, we demonstrated that p-coumaric acid (PCA) attenuates hepatic NLRP3 inflammasome activation-a central mediator in the pathogenesis of metabolic-associated fatty liver disease (MAFLD) in high-fat/high-sucrose (HFHS) diet-fed mice. Toll-like receptor 4 (TLR4) as the initial "signal" to prime the NLRP3 inflammasome, thereby contributing to liver inflammation and fibrosis. However, the precise role of TLR4 signaling in mediating the hepatoprotective effects of PCA remains unclear. To investigate this, male C57BL/6 wild-type (WT) and TLR4 knockout (TLR4$^{-/-}$) mice were fed either a low-fat diet (LF; 11% kcal fat) or an HFHS diet (60% kcal fat, 0.2% cholesterol, 20% sucrose), with or without PCA treatment (10 mg/kg body weight, orally) for 20 weeks. Chronic HFHS feeding induced obesity, metabolic complications, and elevated fasting glucose levels, which were partially ameliorated by PCA. PCA treatment significantly suppressed hepatic expression of pro-inflammatory cytokines (*Tnfα, Il-1β, Mcp1*), NLRP3 inflammasome genes (*Nlrp3, pro-Il1 β, pro-caspase-1, Asc*), and fibrotic markers (*Col1a1, Timp1, Tgf β*). Notably, TLR4$^{-/-}$ mice treated with PCA exhibited complete reversal of these pathological markers. Furthermore, both WT and TLR4$^{-/-}$ mice treated with PCA showed significant reductions in hepatic steatosis scores, plasma ALT/AST, and hepatic triglyceride and cholesterol levels, alongside suppression of lipogenic genes (*Fas, Pparg, and Lpl*). These findings suggest that PCA ameliorates HFHS-induced hepatic inflammation and fibrosis by suppressing NLRP3 inflammasome activation through TLR4-dependent mechanisms.

S9-8

Investigation of Antioxidant Activities and Chemical Profiles of *Idesia polycarpa* Leaves for Potential Applications

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Idesia polycarpa Maxim. is a deciduous tree of the Flacourtiaceae family, native to China, Japan, Taiwan and Korea. The fruits of *I. polycarpa* are a valuable source of edible oil rich in polyphenols, which are known to regulate inflammation and oxidative stress. Previous studies have found that *I.polycarpa* fruits possess various biological activities including antioxidant, anti-adipogenic and whitening properties. However, the antioxidant and anti-inflammatory effects of *I.polycarpa* leaves have not been investigated. In order to identify the chemical components of the leaves, they were extracted with 70% EtOH and different fractions were prepared. In this study, HPLC-PDA and UHPLC-Q-ToF-MS were used to compare the chemical compositions, while the isolation of compounds was performed using medium pressure liquid chromatography (MPLC). The LC-MS profile showed that extracts from immature fruits and leaves showed different patterns. The main compound isolated from the leaf extract by MPLC is tentatively identified as idescarpin. The antioxidant activity of the extracts was evaluated using several assays, including DPPH radical scavenging activity, ABTS radical scavenging activity, ferric reducing antioxidant power (FRAP), total phenolic content (TPC), and total flavonoid content (TFC). Among the fractions, the methylene chloride fraction showed the strongest antioxidant activities. It also showed the highest DPPH and ABTS radical scavenging activities, with IC_{50} values of 30.98 and 22.94 μg/mL, respectively. This fraction also had the highest TPC and TFC values, indicating a strong correlation between phenolic and flavonoid content and antioxidant activity. The results of our study suggest that the *I. polycarpa* leaf extract has potential antioxidant effects.

Keywords: *Idesia polycarpa* Maxim; antioxidant activity; HPLC-PDA; MPLC; LC-MS; UHPLC-Q-ToF-MS

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S10-1

Introduction and Outcomes of Technical Support for Smart Commercialization of Health Functional Ingredients

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The rapid growth of the global health functional food market highlights the importance of successfully commercializing innovative functional ingredients. However, companies often face challenges such as regulatory complexity, scientific validation, and process standardization. To address these barriers, a comprehensive and inclusive technical support program has been launched since 2022 s a part of a government-funded research project to provide end-to-end consulting, scientific and regulatory guidance, and R&D technical assistance. This program has enabled researchers/companies to accelerate product development, improve regulatory approval rates, and enhance market access. The total of more than 400 technical supports have been conducted to more than 200 researchers/companies for nearly 300 heath functional ingredients. The average number of visits by researchers/companies for technical supports is 1.5, with the most frequent visit being 9. Notably, technical support in the commercialization process increases product success rates and significantly contributes to industrial competitiveness and economic value creation. Case studies show that small and medium-sized enterprises, in particular, benefit from overcoming resource limitations and achieving commercialization milestones. In one case, a total of four consultancies in less than a year dramatically shortened the approval process and time. In conclusion, technical support is vital for fostering innovation and sustainable growth in the health functional ingredient sector. Continued collaboration among academia, industry, and government will contributes to build a sustainable and globally competitive health functional food sector.

S10-2

Organoid-Based Platforms for Functional Food Development: Applications and Future Perspectives

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Organoid-based platforms have emerged as an innovative tool for functional food development, providing human-relevant models that integrate complex metabolic stress and metabolic disease induction processes. Unlike conventional cell or animal models, organoids can recapitulate complex intercellular interactions involved in metabolic stress and chronic tissue injury. This study addresses the need for organoid technology in the analysis of functional food, as conventional in vitro models often fail to capture the complexity of metabolic stress development and chronic liver injury due to interactions between various cells that are difficult to reproduce. In this study, human liver organoids (HLOs), derived from induced pluripotent stem cells and composed of hepatocytes, Kupffer cells, and stellate cells within a physiologically relevant microenvironment, were utilized as a preclinical model to assess the impact of food-derived compounds on human liver function. HLOs exposure to Nε-(carboxymethyl)-lysine (CML), as the dietary advanced glycation end product (AGEs) induced mitochondrial dysfunction and excessive reactive oxygen species (ROS) production, triggering the release of damage-associated molecular patterns (DAMP), Kupffer cell activation with TNF-α and IL-1β secretion, and stellate cell−mediated extracellular matrix deposition. This organoid-based cascade model faithfully replicates the pathogenesis of steatohepatitis and early fibrosis, underscoring the power of liver organoids to model CML-driven liver injury and the critical need to develop targeted therapeutic interventions. Building on this model, Rosa multiflora Thumb. leaf extract (RML) was evaluated in mice, RML lowered circulating CML and liver injury markers; in HLOs, it mitigated mitochondrial stress, suppressed ROS and DAMP release, reduced inflammatory cytokine production, and prevented stellate cell activation and fibrotic marker expression. These results demonstrate the capacity of HLOs to quantitatively evaluate metabolic insults induced by food-derived compounds and the therapeutic benefits of functional food ingredients. Future work will focus on creating integrated gut-liver microphysiological systems by coupling iPSC-derived intestinal and liver organoids in a single microfluidic device. This setup will simulate nutrient absorption, first-pass metabolism, and host-microbial interactions under dynamic flow. Gut-liver organ-on-a-chip platforms allow real-time monitoring of barrier integrity, inflammatory mediators, and metabolic outputs. Physiological flow conditions are essential to accurately capture live bioactive effects. Such integrated systems are expected to significantly improve the predictive power of organoid assays for functional food research.

S10-3

Advancing Natural Product Research with FloraGenesis: Large-Scale Spectral Databases and Deep Learning-Based Functional Analysis

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FloraGenesis is an integrated, AI-powered one-stop service platform designed for the analysis, development, and application of natural products. The platform streamlines the complex workflow of natural product research by combining comprehensive metabolomics data analysis, robust compound identification, and biological activity prediction. First, we developed BMDMS-NP, a large-scale MS/MS spectral database encompassing 288,939 spectra from 2,660 commercially available natural compounds, with a focus on maximizing structural diversity and experimental comprehensiveness. The database was constructed by selecting representative plant metabolites based on principal component analysis and validated using molecular fingerprints, ensuring exhaustive coverage of the chemical space of natural products. Second, we implemented a deep learning-based approach using convolutional neural networks (CNNs) to directly infer structural similarity from MS/MS spectra, overcoming the limitations of conventional spectral matching methods that suffer from experimental inconsistencies. By integrating spectra acquired at multiple collision energies, our method enables more accurate and robust compound identification without the need for manual feature engineering. Third, we introduced an innovative framework that transforms raw LC-MS/MS data into two-dimensional images, allowing CNNs to classify biological activity directly from complex spectral patterns, including signals from unidentified metabolites. Applying this method to antioxidant activity prediction in 545 Glycine soja accessions, our CNN model achieved 84.9% accuracy and up to 89% recall, outperforming traditional methods such as PCA, OPLS-DA, and Random Forests. Collectively, these advances establish FloraGenesis as a next-generation platform that accelerates natural product research by providing efficient, end-to-end solutions for metabolite profiling, identification, and functional prediction, with broad applicability to drug discovery and functional material development.

S10-4

R&D of a Sleep-Promoting Ingredient Derived from Lime Peel for Global Commercialization

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Focusing on the development of globally recognized sleep-promoting ingredients, standardized lime peel supplement (SLPS) has been successfully developed as sleep-promoting ingredient derived from lime peel. It has been approved as a Health Functional Food (HFF) ingredient by the Ministry of Food and Drug Safety (MFDS) of Korea in 2025. Administration of SLPS (100, 200, and 400 mg/kg) resulted in a dose-dependent decrease in sleep latency and increase in sleep duration in the pentobarbital-induced sleep test. The effect of SLPS (400 mg/kg) was comparable to that of zolpidem (10 mg/kg), a well-known hypnotic drug. Administration of SLPS (100, 200, and 400 mg/kg) resulted in a dose-dependent increase in non-rapid eye movement sleep (NREMS). Furthermore, no significant difference was observed between SLPS at 400 mg/kg and zolpidem at 10 mg/kg. SLPS exerts sleep-promoting effects by modulating the GABAA receptors. When active compounds in SLPS binds to the GABA-binding site of the GABAA receptors, it enhances receptor activation, leading to a large influx of Cl- ions into the neuronal cells. This results in hyperpolarization, which inhibits neurotransmission and induces sedative and sleep-promoting effects. SLPS inhibited the binding of [3H]-muscimol, a well-known GABAA receptor agonist, in a dose-dependent manner. SLPS induced GABAA receptor activity and its activity was almost blocked by the GABAA receptor antagonist bicuculline, confirming the specificity of the observed effects on GABAA receptor activity. In the pentobarbital-induced sleep test and sleep structure analysis, the hypnotic effect of SLPS was fully blocked by bicuculline, similar to muscimol, a GABAA receptor agonist. This study aimed to evaluate the effects of SLPS in adults experiencing sleep disturbances. The randomized, double-blind, placebo-controlled clinical trial involved 80 subjects who received either SLPS (300 mg/day) or placebo for a 2-week period. SLPS significantly improved polysomnographic outcomes, including a reduction in sleep latency, wake after sleep onset, and total wake time, and enhancement of sleep efficiency, total sleep time, and stage 2 sleep. Daytime sleepiness, assessed via the Epworth Sleepiness Scale, was also decreased by SLPS. No serious adverse effects or side effects were reported among participants in the SLPS group during the intervention period. Our findings support SLPS as a potential natural sleep aid for improving sleep in adults with sleep disturbance.

Young Scientist Presentation

YS1-1

Type Ⅰ IFN receptor blockade alleviates the liver fibrosis through the macrophages derived STAT3 signaling

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Liver macrophages play a role in the development of liver fibrosis progression via regulation of inflammatory signaling. However, precise mechanisms of macrophages contributing to of liver fibrosis progression remain unclear. Using the preclinical model of CCl4-treated mice, we determined composition of immune cells and alteration of inflammatory gene expression. Our findings revealed a significant increase in liver macrophages, particularly those derived from infiltrated blood monocyte, in fibrotic mice. Moreover, expression levels of type I IFN signature genes such as *IFNα, IFNβ, ISG15, USP18, Ifi44, Ifit1, Ifit2, IRF3,* and *IRF7* were elevated in fibrotic mice. To determine the role of type I IFN signaling in liver fibrosis, we administered the IFNAR-1 antibody to block this pathway for 3 days prior to harvest the liver. Notably, the IFNAR blockade reduced macrophage numbers compared to control mice and alleviated liver fibrosis in mice with increased hepatocytes proliferation and apoptosis. The ratio of P-STAT3/P-STAT1 in monocyte-derived macrophages was increased in the IFNAR-1 blocked group compared to fibrotic mice, and this was related to the appearance of M2 macrophage differentiation. Additionally, single cell RNA seq analysis indicated that IFNAR blockade affected inflammatory pathways involved in hepatocytes regeneration and fibrosis prevention. Taken together, IFNAR-1 blockade alleviates liver fibrosis progression by modulating macrophages inflammatory responses. These results provide insight for developing anti-fibrotic therapies against type I IFN signaling.

Keywords: Liver fibrosis, IFNAR-1, Kupffer cells, STAT3, Tissue repair

YS1-2

TrkB-Mediated Neuritogenic and Synaptogenic Potential of Coriandrum sativum: An Integrated *In Vitro* and Network Pharmacology Study

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Acceleration of neurite outgrowth and halting neurodegeneration are the most critical factors that are negatively regulated in various neurodegenerative diseases or injuries in the central nervous system (CNS). Functional foods or nutrients are considered alternative sources of bioactive components to alleviate various CNS injuries by promoting neuritogenesis and synaptogenesis, while their exact molecular mechanism remains unexplored. Coriandrum sativum L. (CS) is one of the popular herbs in the Apiaceae family. CNS modulating action is a well-documented traditionally but detailed study on memory boosting function yet remains unexplored. Our study evaluated the neurogenic and synaptogenic effects of CS aqueous ethanol extract (CSAE) in primary hippocampal neurons. CSAE treatment (30 µg/mL) significantly promoted early neuronal differentiation, axonal/dendritic arborization, and synaptogenesis, as observed through immunostaining, DiI labeling, and western blot analysis. Network pharmacology and molecular docking revealed that CSAE-induced neurogenesis is likely mediated by TrkB (NTRK2) signaling. Indeed, the observed neurogenic activity of CSAE is markedly reduced upon the co-treatment with a TrkB-specific inhibitor. Among CS metabolites, scoparone exhibited high affinity for the BDNF binding site of TrkB and promoted neuritogenesis, although less effectively than CSAE. TrkB pathway-related proteins (BCL2, CASP3, GSK3, and BDNF) were significantly modulated by scoparone and reversed upon TrkB inhibition. These findings suggest that CSAE enhances neurite outgrowth and synaptogenesis via TrkB-dependent signaling, offering a potential natural therapeutic for memory enhancement and neurodegeneration prevention.

YS1-3

Evolution and diversification of the ACT-like domain associated with plant basic helix–loop–helix transcription factors

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The basic helix–loop–helix (bHLH) proteins represent one of the largest transcription factor (TF) families in eukaryotes. Approximately 30% of bHLH TFs in angiosperms possess an aspartate kinase, chorismate mutase, and TyrA (ACT)-like domain located at varying distances C-terminal to the bHLH domain. Despite its prevalence, the evolutionary origin and functional significance of this bHLH/ACT-like domain association have remained largely unresolved. In this study, we demonstrate that this domain association is unique to the plant kingdom, with a small number of bHLH genes containing ACT-like domains observed in chlorophyte algae. Phylogenetic analyses reveal that bHLH-associated ACT-like domains form a monophyletic clade, suggesting a shared ancestral origin. Our results support the hypothesis that the fusion between ancestral bHLH and ACT-like domains occurred early in the evolution of Plantae, potentially through the recruitment of ACT DOMAIN REPEAT (ACR)-like sequences present in a common ancestor. To investigate the functional relevance of this domain pairing, we show that in *Chlamydomonas reinhardtii*, the ACT-like domain facilitates homodimer formation and attenuates DNA binding by the corresponding bHLH domain. Although the ACT-like domains have evolved more rapidly than their bHLH counterparts, their evolutionary rates exhibit a strong positive correlation, implying that the evolution of the ACT-like domains has been constrained by the structural and functional demands of the bHLH domains. Together, our findings suggest a coevolutionary trajectory for the bHLH and ACT-like domains and reveal their combined influence on plant-specific transcriptional regulation. I will also present recently updated results that expand on these findings.

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YS1-4

Flavonoid profiling of Freshwater Bioresources Culture Collection (FBCC) extracts using LC-MS/MS and their anti-obesity properties by regulating hypothalamic neuropeptides

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The Nakdonggang National Institute of Biological Resources (NNIBR) is a research institute that specializes in freshwater organisms. Established in June 2016 under the Ministry of Environment, NNIBR aims to contribute to the acquisition of sovereignty over freshwater organisms, biodiversity conservation, and sustainable use of biological resources. To this end, NNIBR operates the Freshwater Bioresources Culture Collection (FBCC), which is focused on establishing a genetic resource bank, acquiring culture technologies and extracts of useful resources, and providing personalized support for the bio-industry. Currently, FBCC has collected approximately 1,231 extracts from 319 species, including plants and microorganisms. To discover the future value of freshwater biological resources, we performed flavonoid profiling using UPLC-TQ-MS, which allowed us to identify the types and amounts of flavonoids present in the extracts. Among the extracts, we discovered *Acer pseudosieboldianum* extracts with anti-obesity properties by regulating hypothalamic neuropeptides. *Acer pseudosieboldianum* extracts showed 70% inhibition of appetite-stimulating neurons. In addition, quercetin-3-O-glucoside and quercetin-3-O-α-L-arabinoside were identified as active compounds. These flavonoid glycosides showed almost the same inhibition of appetite-stimulating neurons as liraglutide, an FDA-approved drug for patients with obesity.

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YS1-5

Furanocoumarin enriched *Angelica acutiloba* by metabolite farming based on ethylene and their monoamine oxidase inhibition

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The most important factor in the discovery of nutraceutical substances is the content level of the active ingredient. For this purpose, much effort is being made through molecular breeding and genetic modification-based biotechnology, but there are limits to obtaining satisfactory results. Metabolite farming can be a new technology that dramatically increases the active ingredient of plants in a short period of time and converts general plants into nutraceutical substances. In this study, the content of furanocoumarin(FCs) in *Angelica acutiloba* was significantly increased through metabolite farming. its roots have been used as an ingredient of oriental medicines to treat gynopathic, psychological, and neurogenerative disorders. FCs have various physiological activities such as anti-inflammation, antioxidant, and cognitive function improvement, and is a substance in high demand in nutraceutics and functional food market. FCs content in root part was significantly increased by the treatment of the signaling molecule, ethylene. Newly increased FC derivatives were annotated as xanthotoxin (XAT), psoralen (PSR), isopimpinellin (IPP), and bergapten (BGT). The contents of FCs continued to increase until they reached the level where XAT (54-fold, 64.9 μg/g → 3499 μg/g), PSR (7-fold, 31.9 μg/g → 214 μg/g), IPP (23-fold, 16.2 μg/g → 375 μg/g), and BGT (51-fold, 29.5 μg/g → 1512 μg/g). Hereby, the content of FC derivatives increased selectively, and other metabolites were not affected by ethylene. The metabolite changes were systematically investigated using UPLC-ESI-Q-TOF/MS analysis to obtain a clear difference in the PLS-DA score, S-plot, and heatmap to explain the gradual fluctuation in the metabolite levels over the treatment time (96 h). Meanwhile, monoamine oxidases oxidatively deactivate neurotransmitters such as dopamine, serotonin, norepinephrine, and epinephrine, which lead depression, Parkinson's disease, and Alzheimer's disease. Additionally, FCs enriched roots showed a distinctive inhibitory activity against monoamine oxidase (MAO-A and B) compared to control roots because of the increased FCs content. Target plant with greatly enhanced FCs content is applicable as functional food material for new purposes.

YS1-6

Sustainable extraction of antioxidant and anti-inflammatory compounds from *Polygonum multiflorum* using natural deep eutectic solvents (NADES)

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Polygonum multiflorum (PM) has been traditionally used in East Asian medicine for its various pharmacological effects, such as antioxidant and anti-inflammatory activities, owing to its rich content of bioactive compounds including 2,3,5,4'-tetrahydroxystilbene-2-O-β-D-glucoside (THSG), emodin, and physcion. In this study, deep eutectic solvents (DESs) were explored as sustainable alternatives to conventional extraction methods (hot water and 70% ethanol) for isolating these bioactive compounds. A range of DESs was syn(Pm)thesized and characterized in terms of polarity, viscosity, and stability. Among them, polar and mid-polar DESs demonstrated superior extraction efficiency, with choline chloride-based solvents—particularly malic acid/choline chloride (MAL/CHO)—exhibiting strong potential. Although high viscosity initially limited the extraction performance of MAL/CHO, this was significantly improved through water dilution. Extracts obtained using 90% MAL/CHO exhibited the highest antioxidant activities across multiple assays (DPPH, ABTS, FRAP, ORAC, TBARS), as well as the most effective extraction of polymeric tannins. Additionally, anti-inflammatory activity, assessed via COX-2 enzyme inhibition, was highest in the 90% MAL/CHO extract, followed by the 70% ethanol extract, with the water extract showing the lowest activity. These findings support the application of DESs as green and tunable solvents for the efficient extraction of both antioxidant and anti-inflammatory compounds from *P. multiflorum*. This study highlights the potential of DESs in sustainable herbal medicine processing and functional ingredient development. This work was supported by the Development of Sustainable Application for Standard Herbal Resources (KSN1823320), Development of Innovative Technologies for the Future Value of Herbal Medicine Resources (KSN2511030), Korea Institute of Oriental Medicine through the Ministry of Science and ICT, Republic of Korea. Additionally, it was funded by the Collection, Conservation and Characteristic Assessment of Forest Life Resources (2020-2025), the National Forest Seed and Variety Center under Korea Forest Service.

YS1-7

Anti-Inflammatory Dimeric and Trimeric Flavonoids from the Roots of *Pistacia weinmannifolia*

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Asthma and chronic obstructive pulmonary disease (COPD) have been estimated to be the third leading cause of death globally by 2030. Anti-inflammatory drugs are mainly used to treat asthma and COPD, often together with bronchodilators or as combination therapy. From the successful cases of developing respiratory therapeutics from anti-inflammatory substances, natural products have been extensively explored to find potential anti-inflammatory candidates. As part of an ongoing search for new anti-inflammatory agents from medicinal plants, five new dimeric and trimeric flavonoids (1–5) were isolated from the roots of Pistacia weinmannifolia. The structures of pistachalcone A (1), pistachalcone B (2), pistaflavanone A (3), pistachalcone C (4), and pistachalcone D (5) were elucidated by analysis of spectroscopic data. The known compounds rhuschalcone II (6), rhuschalcone VI (7), and pauferrol B (8) were also isolated and identified. Our in vitro analysis found that compounds isolated from P. weinmannifolia roots extract exert anti-inflammatory effects in phorbol myristate acetate (PMA)-induced NCI-H292 airway epithelial cells by the suppression of expression levels such as interleukin-8 (IL-8) and mucin 5AC (MUC5AC), whichare closely related to thepulmonary inflammatory response in the pathogenesis of COPD. Therefore, these dihydrochalcone derivatives may have value as new starting materials for the development of drug candidates against COPD.

YS2-1

Unlocking Carbon Pathways: Integrating Soil Biochemistry and Physical Structure as the Basis for Carbon Farming

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Carbon Farming is an innovative strategy to reduce greenhouse gases and sequester carbon in agricultural systems. As one of the Nature-based Solution (NbS), it offers a sustainable and promissng approach to mitigate climate change. Although various carbon farming methods have been suggested, the underlying mechanisms remain under active investigation. To develop and efficiently implement these methods, it is essential to understand the intricate processes of carbon cycling in soil. Soil microbial communities are the primary drivers of carbon cycling, where their metabolic processes are critically dependent on the heterogeneous distribution of resources such as oxygen, water, and nutrients. Thus, linking soil microbial activity to the physical structure of the soil can provide insights into carbon cycling and sequestration mechanisms. This talk will present case studies that investigate the mechanisms of greenhouse gas emissions and carbon sequestration in soil. In addition to an introduction of carbon farming, the presentation will delve into new concepts including the roles of soil microbial hotspots and biopores in regulating carbon cycling. The talk will also demonstrate how advanced techniques including X-ray computed tomography and zymography can effectively integrate our understanding of biochemical processes with soil physical structure.

YS2-2

Genomic Insights into the Dissemination of Antibiotic Resistance Genes in *E. coli* from Veterinary Clinics and Animal Farms in South Korea

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Extended-spectrum beta-lactamase (ESBL)-producing Escherichia coli are an increasing threat to public and veterinary health due to their resistance to critical antibiotics, including third-generation cephalosporins. In this study, we performed whole genome sequencing (WGS) on ESBL-producing *E. coli* isolates collected from veterinary clinics and livestock farms across South Korea, aiming to uncover the genomic mechanisms underlying the spread of antibiotic resistance genes (ARGs). By integrating Illumina short-read and Oxford Nanopore long-read sequencing, we generated high-quality genome assemblies and identified ARGs, mobile genetic elements (MGEs), and plasmid types. The dissemination of resistance was analyzed from three genomic perspectives: (1) clonal spread, (2) plasmid conjugation, and (3) associations between ARGs and MGEs such as insertion sequences (IS) and transposons. Clonal spread was frequently observed in veterinary clinics, with certain high-risk sequence types detected across multiple hosts. Plasmid-mediated dissemination appeared more prominent in farms, as conjugative plasmids carrying $bla_{\text{CTX-M}}$ variants were shared between different clonal lineages and environments. Additionally, ARGs were often co-located with MGEs such as IS26 and ISEc9 within close genomic proximity, suggesting potential roles for these elements in ARG mobility and chromosomal integration, though direct mobilization was not experimentally confirmed. Altogether, our findings suggest that multiple genomic factors—including clonal relatedness, plasmid sharing, and MGE associations—may collectively contribute to the dissemination landscape of ARGs in *E. coli*. These results underscore the value of genomic surveillance and highlight the importance of a One Health approach in addressing antimicrobial resistance across human, animal, and environmental interfaces.

YS2-3

Environmental Hazards of Cement Production: Alterations in Soil Microbiomes Due to Heavy Metal Contamination

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The cement industry has been a cornerstone of economic development since the Industrial Revolution. However, cement production also releases heavy metals that can disrupt the balance and function of microbial communities. Despite the potential environmental risks, few studies have examined the impact of cement production on nearby microbiomes. In this study, we collected topsoil from areas surrounding four cement factories in Korea to assess the contamination levels of heavy metals—arsenic, cadmium, lead, nickel, and mercury—and to investigate how the bacterial community responds to these heavy metals. Most of the collected soil samples showed severe heavy metal contamination, raising concerns about environmental hazards and the urgent need for remediation. Heavy metal contamination altered the composition of bacterial communities. Arsenic, cadmium, and nickel were identified as the primary heavy metals responsible for shifts in bacterial community structures. At the genus level, *Ramlibacter, Pseudolabrys, Candidatus* Xiphinematobacter, *Solirubrobacter, Bacillus, Blastococcus, Steroidobacter,* and *Skermanella*, served as biomarkers distinguishing severely contaminated soils from non-contaminated ones. Bacterial communities clustered into modules based on their tolerance to heavy metals. Each heavy metal was associated with a unique set of ASVs in the network. To cope with heavy metal contamination, bacterial communities in heavily polluted soils showed increased enrichment of resistance-related pathways—such as the pentose phosphate pathway and tetrapyrrole biosynthesis—compared to those in non-contaminated soils. Overall, our findings suggest that heavy metal contamination in soils near cement factories is closely associated with distinct bacterial communities that may contribute to bioremediation and promote plant growth.

YS2-4

Navigating the Aquatic Microbial Universe: Absolute Quantification of Microbial Communities through Advanced Metagenomic Approaches

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Microorganisms are present in diverse environments and exhibit various interactions with different organisms. Particularly, freshwater environments serve as reservoirs of terrestrial microbes that can disperse throughout terrestrial ecosystems. These freshwater systems function as critical ecological nexuses, influencing human health, agriculture, and ecosystem stability through microbial transmission pathways. While microbial dynamics have traditionally been investigated using relative profiling approaches, this framework can lead to misinterpretation of ecological patterns by failing to account for variations in absolute microbial biomass. Environmental surveillance specifically requires accurate detection and quantification of microbial biomass. Therefore, we developed a quantitative metagenome-assembled genome profiling (qMAP) framework that enables absolute abundance quantification of microbial communities. Using this framework, we investigated the pathobiome in the Nakdong River over a one-year period and examined the effects of antibiotic residues on freshwater environments using microcosm experiments. qMAP analysis revealed distinctive patterns in the total biomass of antibiotic-resistant bacteria throughout the samples that conventional relative abundance methods could not detect. The application of qMAP provided more accurate assessments of pathogen dynamics in freshwater ecosystems, demonstrating its utility for environmental monitoring purposes. These findings, which would have been obscured by traditional relative abundance analyses, demonstrate the complex dynamics of bacterial communities under antibiotic exposure. Our study provides a robust framework for environmental antibiotic resistance surveillance and highlights the ecological impacts of antibiotics in freshwater ecosystems.

YS2-5

Crosstalk Between Long-Chain Fatty Acids and Taste GPCRs: Distinct Modulatory Effects on Bitter, Sweet, and Umami Signaling Pathways

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Fatty acids, beyond their nutritive roles and contribution to oral texture, are increasingly recognized as modulators of chemosensory signaling. Recent insights into gustatory physiology have established that G protein-coupled receptors (GPCRs), including the TAS1R and TAS2R families, mediate sweet, umami, and bitter taste perception. The sensory effects of fatty acids have conventionally been attributed to mouthfeel or post-ingestive signals. Long-chain fatty acids (LCFAs) have been associated with the fat taste receptor CD36, but the relationships with other taste receptor remain unknown. In this study, we assessed the impact of six LCFAs on receptor-level taste responses relevant to bitter, sweet, and umami perception. Utilizing heterologous HEK293T expression systems and ratiometric calcium imaging, we evaluated how LCFAs modulate receptor activation in response to canonical agonists. Our findings demonstrate that six LCFAs can attenuate bitter taste responses mediated by TAS2R16. In contrast, certain LCFAs were found to either inhibit or enhance sweet and umami signaling depending on their chain length, saturation level, the position of double bonds, and co-stimulation contexts. These results provide insights into lipid-taste receptor interactions and support the role of LCFAs as taste modulators. Understanding such mechanisms offers significant implications for flavor engineering in food design, particularly in the development of healthier, more palatable formulations of functional and plant-based foods.

YS2-6

Saccharomyces cerevisiae GILA induces the alleviation of intestinal inflammation in mouse with colitis

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This study investigates the anti-inflammatory effects of the novel eukaryotic probiotic *Saccharomyces cerevisiae* GILA and its cell wall components in the context of inflammatory bowel disease (IBD). IBD, including Crohn’s disease and ulcerative colitis, is characterized by chronic intestinal inflammation, dysbiosis, and epithelial barrier dysfunction. While bacterial probiotics have been widely studied, eukaryotic probiotics remain relatively uncharacterized. In this study, yeast strains isolated from Korean fermented beverages were evaluated for probiotic properties. *S. cerevisiae* GILA exhibited pronounced auto-aggregation, coaggregation with pathogens, hydrophobicity, antioxidant activity, and low nitric oxide production. In a DSS-induced colitis mouse model, *S. cerevisiae* GILA 118 reduced neutrophil infiltration and TNF-α levels, increased IL-10, and upregulated tight junction protein expression. Furthermore, *S. cerevisiae* GILA118 cell wall polysaccharides and protoplasts, separated via enzymatic and chemical methods, were shown to reduce inflammatory markers (NO, COX-2) and increase PPAR-γ and IL-10 expression in RAW 264.7 cells. *In vivo*, these components modulated immune balance by increasing Treg and decreasing Th17 cells, while also improving gut microbiota composition. These findings suggest that *S. cerevisiae* GILA118 and its derivatives are promising candidates for probiotic-based IBD therapy.

YS2-7

Exploring the Potential of Food By-products in the Prevention of Cardiovascular Disease

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Cardiovascular disease (CVD) remains a leading cause of global mortality, with growing attention on the role of metabolites produced by gut microbiota in disease progression. Among these, trimethylamine (TMA) and its hepatic oxidation product, trimethylamine-N-oxide (TMAO), have been identified as emerging risk factors for CVD. TMA is produced from L-carnitine by the microbial enzymes carnitine monooxygenase (cntA) and reductase (cntB), and is subsequently converted to TMAO in the liver by flavin-containing monooxygenase 3 (FMO3). Accordingly, the inhibition of this pathway offers a promising strategy for CVD prevention. Valencia orange is widely cultivated in Florida for juice production, resulting in the generation of large amounts of by-products each year. Despite its abundance of diverse phytochemicals with various potential health benefits, a significant portion of orange peel is discarded annually. This study investigates the cardiovascular protective potential of the polar (OPP) and non-polar (OPNP) fractions of Valencia orange peel extract, with a particular focus on their inhibitory effects on TMA/TMAO production both in vivo and in vitro. The OPP-fed group significantly reduces TMA and TMAO levels in the plasma and urine of mice without disrupting gut microbiota composition, compared to the OPNP-fed group. Furthermore, OPP treatment markedly inhibits cntA/B enzyme activity in vitro and suppresses FMO3 mRNA expression in hepatocytes. To identify the key bioactive compound, untargeted and targeted metabolomic analyses were conducted. Feruloylputrescine (FP) was confirmed as a major compound in the OPP fraction. FP not only exhibits the strongest inhibitory effect on cntA/B activity and TMA production in vitro but also significantly decreases circulating TMA and TMAO levels in high-fat diet-induced mice. Therefore, these findings demonstrate the potential of orange peel as a valuable source of natural compounds for CVD prevention.

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Graduate Student Presentation

GS1-1

Inhibition of glutamate-induced cell death in HT22 cells by mixed extracts of *Dioscorea batatas* and *Zingiber officinale*

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This study aimed to investigate the neuroprotective properties of mixed extracts of *Dioscorea batatas* and *Zingiber officinale* (DB) against glutamate-induced excitotoxicity in HT-22 cells and to elucidate its underlying molecular mechanisms. Cytotoxicity and neuroprotective effects were assessed using MTT and LDH assays, and morphological changes were evaluated through optical microscopy. DB effectively restored axonal structure that had been compromised due to glutamate exposure. A DCFDA assay demonstrated that DB significantly reduced glutamate-induced reactive oxygen species (ROS) generation in a concentration-dependent manner, highlighting its antioxidant potential. Western blot analysis revealed that DB significantly mitigated glutamate-induced neuronal cell death at concentrations of 0.25 and 0.5 mg/mL. The neuroprotective effects of DB were attributed to the suppression of the MAPK signaling pathway, Caspase-3, and PARP, all of which are involved in apoptotic cell death. Therefore, DB activated the PI3K/AKT/mTOR pathway, thereby promoting cell survival and neuronal resilience. Additionally, DB enhanced antioxidant defense mechanisms by modulating Keap1 and NQO1, contributing to the reduction of oxidative stress and cellular damage. These findings suggest that DB confers neuroprotection by modulating oxidative stress and apoptosis via PI3K/AKT/mTOR signaling. Given its potent antioxidant and anti-apoptotic properties, DB holds promise as a potential therapeutic agent for neurodegenerative diseases. Further investigations are warranted to validate its clinical applicability.

GS1-2

Enhancing Plant Stress Tolerance through Subcellular Targeting of Catalase

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Catalase is a critical antioxidant enzyme that mitigates oxidative damage by decomposing hydrogen peroxide (H_2O_2) into water and oxygen, playing a pivotal role in cellular defense against oxidative stress. Catalase is primarily localized in peroxisomes, where it interacts with PEX proteins through the C-terminal peroxisomal targeting signal (PTS) in plants. This study investigates the functional significance of catalase subcellular localization in Arabidopsis thaliana and its impact on stress. The intact catalase (CAT2-ox) was localized to peroxisomes, while CAT2ΔQKL-ox, which lacked the peroxisome targeting signal, was dispersed across multiple organelles, including the cytosol, chloroplasts, and extracellular spaces. Under extracellular hydrogen peroxide (H_2O_2) treatment, CAT2ΔQKL-ox exhibited relatively higher resistance compared to CAT2-ox, though both constructs showed substantially reduced necrosis relative to wild-type plants. CAT2ΔQKL-ox also exhibited improved salt stress tolerance, indicating that the cytosolic/extracellular localization of catalase selectively neutralizes H_2O_2 in these compartments, thereby enhancing stress adaptation. These results indicate that regulating the subcellular distribution of catalase provides a strategy for enhancing plant resistance to stresses.

GS1-3

Non-secreted peptide OsRALF5 regulate pollen tube growth in *Oryza sativa*

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In angiosperms, pollen tube growth is crucial for double fertilization and directly impacts crop yield. Rapid alkalization factor (RALF) peptides play essential roles in fertilization by interacting with receptor-like kinases in the apoplast, but the function of non-secreted RALFs remains largely unknown. We identified pollen-specific *Oryza sativa* RALF gene, *OsRALF5*, and investigated its role in reproduction. Phylogenetic analysis revealed that OsRALF5 belongs to a distinct clade lacking conserved motifs typical of RALFs. *OsRALF5* was highly expressed in mature anthers and pollen, as shown by qRT-PCR and reporter assays using native promoter-derived GUS and GFP-tagged transgenic lines. Subcellular localization of OsRALF5-GFP revealed that OsRALF5 is localized to both the cytoplasm and plasma membrane in tobacco, whereas in rice it is localized to the cytoplasm, and is not secreted to the apoplast in either system. In both species, OsRALF5 was not detected in the apoplast. Knockout mutants using CRISPR/Cas9 exhibited no defects in pollen viability, but showed significantly reduced pollen germination rates and seed set. Our findings demonstrate that the non-secreted peptide OsRALF5 positively regulates pollen germination and fertilization in rice, representing a unique intracellular mechanism for pollen tube growth among RALF family members.

Graduate Student Presentation

GS1-4

Tongue tissue endoplasmic reticulum stress response in a DSS-induced colitis model from an oral-gut axis perspective

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The tongue and intestine are derived from a common endoderm and are structurally and functionally closely related. Recent studies have suggested that these two organs share a microbiome environment and immune response, and may interact with each other, particularly through the oral-gut axis. In this study, we used an acute inflammatory bowel disease model to examine whether inflammation induced in the intestine is reflected in tongue tissue, focusing on the endoplasmic reticulum stress response. Through this, we aimed to elucidate the molecular biological relationship between the tongue and intestine. Acute colitis was induced by DSS (DextranSulfate Sodium) for two weeks. Colitis severity was assessed using the Disease Activity Index (DAI). Blood analysis showed increased red blood cells in the DSS model, suggesting dehydration. Histological analysis using H&E staining assessed muscle, submucosal, and villus layers in the intestine and mucosal and keratinized layers in the tongue. Immunohistochemistry (IHC) analyzed IRE1and PCNA expression. TUNEL assay and Western blot measured apoptosis and endoplasmic reticulum stress-related proteins IRE1, Bip and PCNA, revealing similar patterns in the tongue and intestine. This study demonstrates that intestinal inflammation in IBD is reflected in the tongue. These findings support the concept of the oral-gut axis and provide a scientific basis for tongue diagnosis (Seoljjin) as a potential tool for assessing gastrointestinal health.

GS1-5

Development of a Method to Discriminate the Geographical Origins of Peanut (*Arachis hypogaea*) Using Physicochemical and Metabolomic Analyses

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Peanuts (*Arachis hypogaea*) are widely consumed around the world and are highly valued for their high fat and protein content in food industry. In Korea, cases of Chinese peanuts being sold as Korean products have raised concerns over food fraud including origin labeling. This study aims to compare the physicochemical properties from Korean and Chinese peanuts. Furthermore, candidate biomarkers were identifed to distinguish the different origin of peanuts. Chinese peanuts showed higher flavonoid content (65.34±30.01 mg QE/L) than Korean peanuts (23.19±17.68 mg QE/L). In contrast, total polyphenol content was higher in Korean peanuts (3,495±809 mg GAE/L) than in chinese peanuts (2,916±703 mg GAE/L). Multivariate statistical analysis were used to evaluate the differences between groups. Free amino acids and fatty acids clearly distinguished between Korean and Chinese peanuts. Espeacially cystine and margaroleic acid were identified as biomarkers through variable importance in projection (VIP) score, fold change, and p-value. This study uses cystine and margaroleic acid to identify the geographical origin of peanuts, which provides a basis for the development of an origin identification system.

Graduate Student Presentation

GS1-6

Integrated CPC–QM–qNMR Platform for Evaluation of Antibacterial Synergy among the Coumarins from *Cnidium monnieri*

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The chemical complexity of natural products demands comprehensive evaluation of their bioactivity for therapeutic development. In this study, an integrated analytical platform combining centrifugal partition chromatography (CPC) and quantum mechanics-based quantitative NMR (QM-qNMR) was established to investigate the antibacterial potential of *Cnidium monnieri* against multi-drug resistant pathogens. Coumarin derivatives in *C. monnieri* were separated into four distinct fractions using CPC with an optimized HEMWat -6 solvent system. They were then quantified as 489.16 mg osthole, 203.64 mg imperatorin, 20.41 mg bergapten, 28.00 mg xanthotoxin, and 23.36 mg isopimpinellin from 3.00 g of total extract using the proposed platform. Subsequently, osthole and imperatorin were selectively separated as six knock-out fractions, which were osthole, imperatorin, mixture of osthole and imperatorin (OI), osthole knock-out, imperatorin knock-out, and both osthole and imperatorin knock-out. Antibacterial assays revealed that both osthole and OI mixture fractions exhibited potent inhibition of drug-resistant pathogen when co-administered as an antibiotic adjuvant. Variable-ratio assessment indicated strong antibacterial activity for OI mixtures, whereas imperatorin alone was inactive. Furthermore, in MIC tests, the synergistic effects of OI were confirmed by FICI values below 0.5. These findings demonstrate the utility of the suggested CPC and QM-qNMR platform for isolation, quantitation, and comprehensive characterization of bioactive constituents in complex natural products, highlighting their synergistic potency.

Keywords: *Cnidium monnieri*, CPC, QM-qNMR, multi-drug resistant pathogen

GS1-7

Development of Quarantine Disinfestation Methods for *Carposina sasakii* in Fresh Apples

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The United States is one of the major importers of apples exported from Korea. *Carposina sasakii*, which uses apples as its primary host, is recognized as a quarantine pests of concern in the U.S. Apples infested by *C. sasakii* are fumigated with methyl bromide (MB). However, MB is highly toxic and classified as an ozone-depleting substance, underscoring the need to develop alternative quarantine disinfestation methods. In this study, the efficacy of phosphine fumigation and cold treatment (1°C) against *C. sasakii* larvae was evaluated. Sorption was examined at 5°C and 23°C under different loading ratios (0%, 10%, and 25%), and phytotoxicity was assessed at a 25% loading ratio under both temperature conditions. As a result of the efficacy tests using *C. sasakii* infested apples, we identified the effective concentration and time of phosphine fumigation and cold treatment required to achieve 100% mortality. Sorption tests showed no significant differences among the different loading ratios. Phytotoxicity was not observed after 2 mg/L phosphine fumigation at 5°C or 23°C followed by 28 days of storage at 1°C, or after cold treatment alone. However, it was observed after 4 mg/L fumigation at 23°C followed by 28 days of storage at 1°C, or after storage at 23°C. These results provide fundamental data for developing effective alternative quarantine disinfestation methods to replace MB in apple exports.

GS1-8

Exploring the molecular mechanism that mediates N-induced stem growth in tomato plants

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Nowadays, in agriculture, lots of nitrogen(N) fertilizers are used for cultivating crops. It is reasonable, as plant cultivation under sufficient nitrogen conditions typically leads to increased yields. However, it is still not clear how N affects various aspects of plant growth and development. Among many physiological changes occurred by N supplementation, we are focused on the molecular mechanisms that mediates N-induced stem elongation. We isolated candidate genes based on their N-responsive expression and co-expression patterns with previously reported genes involved in cell elongation and stem growth. Among the candidates, we found N-responsive transcription factor *SlNRTF550* that modulates internode growth. *SlNRTF550*^{OX} plants show significantly promoted internode elongation without significant change of the node numbers. We found that *SlNRTF550* overexpression led to up-regulation of genes involved in cell elongation and secondary cell wall development. Further biochemical and genetic analysis will clarify the molecular mechanism by which *SlNRTF550* regulates N-mediated stem elongation in plants.

GS1-9

Anti-inflammatory and Antioxidant Activities of *Platycodon grandiflorum* Root Extract Fermented with *Weissella cibaria* HY207

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Platycodon grandiflorum roots have been widely known in Asia for their medicinal properties including anti-inflammatory and anti-microbial. This study evaluated the antioxidant and anti-inflammatory effects of root extracts fermented with *Weissella cibaria* HY207, a lactic acid bacterium isolated from kimchi. The fermented extract showed a 25% increase in DPPH radical scavenging activity in comparison to the non-fermented extract. The cell viability assay for the non-fermented and fermented extract was conducted in RAW 264.7 macrophages. The non-fermented did not show any cellular toxicity at 100 μg/ml, however a higher toxicity was observed in 500 μg/ml. The fermented extract did not show any cytotoxicity at 500 μg/ml. For further anti-inflammatory and antioxidant 100 μg/ml of both extracts were used. In comparison to the non-fermented, the fermented extract at 100 μg/ml significantly reduced LPS-induced nitric oxide (NO) production. It also downregulated the inflammatory markers such as TNF-α, IL-1β, IL-6, iNOS, and COX-2 and upregulated the expression level of antioxidant enzymes (SOD-1, Catalase, HO-1). These findings suggest that fermentation enhances the bioactivity of *P. grandiflorum* extract, supporting its potential as a functional ingredient with antioxidant and anti-inflammatory properties.

GS1-10

Isolation and identification of chemical constituents from aerial part of *Lespedeza cyrtobotrya* Miq.

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Lespedeza cyrtobotrya Miq. (Fabaceae), native to Korea, China, Japan, and eastern Russia, has been traditionally used to treat osteoporosis, lumbago, and joint pain. A 70% aqueous ethanol extract of its aerial parts exhibited significant inhibitory activity against monoamine oxidase A and B (MAO-A and MAO-B). The extract was fractionated via Diaion HP-20 column chromatography using a stepwise methanol gradient (20–100%), and active fractions were analyzed by UPLC-QTOF/MS, revealing flavonoid glycosides as the major constituents. Ten compounds were isolated through repeated preparative HPLC and structurally elucidated as nine flavonol glycosides (**1**–**9**) and one chalcone (**10**) by NMR, ESI/MS, and UV spectroscopy. Among them, 4‴-acetyl-kaempferitrin (**6**) and kaempferin 2″-O-α-L-(3‴-acetyl) rhamnopyranoside (**8**) are identified as new flavonoid glycosides. Additionally, compounds including kaempferitrin (**4**), sutchuenoside A (**5**), 3‴-acetyl-kaempferitrin (**9**), and four others were isolated for the first time from *L. cyrtobotrya*. Major constituents (**4**–**6, 9**) were quantified by UPLC-PDA and UHPLC-TQ/MS, all exceeding 5.0 mg/g. Analytical methods were validated according to KFDA guidelines, demonstrating acceptable linearity, precision, accuracy, and recovery. These results highlight the phytochemical usages of *L. cyrtobotrya* and support its potential as a novel source of bioactive flavonoid glycosides for application in functional foods or herbal medicinal products.

GS1-11

Applying *in vitro* propagation and smart farming for the conservation and sustainable production of *Polygonum multiflorum*

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Polygonum multiflorum (He Shou Wu) is a highly valuable medicinal plant known for its therapeutic properties in traditional medicine. However, the species face significant threats due to overharvesting from wild populations, habitat degradation, inconsistent cultivation methods, and confusion with unidentified species. In response to these challenges, this study explores the integration of *in vitro* propagation techniques with smart farming technologies as a dual strategy for the conservation and sustainable large-scale production of *Polygonum multiflorum*. *In vitro* propagation techniques, such as micropropagation and organogenesis, were employed to produce genetically uniform, disease-free plantlets. Critical parameters such as shoot induction, root formation, and acclimatization were optimized to ensure high survival rates during transfer into smart farm. Simultaneously, smart farming leveraging technologies such as precision irrigation, environmental monitoring, were employed in the smart farm to reduce input use and enable optimized growth conditions, efficient resource use, and real-time data-driven management of plant health. Other parameters that were monitored included soil moisture, light intensity, temperature, and nutrient levels, enabling real-time adjustments to optimize plant health and bioactive compound accumulation. The combined approach significantly increased both biomass volume and overall yield of *P. multiflorum*, maintaining the bioactive compounds while also reducing reliance on wild populations and seasonal constraints, particularly during winter when harvesting is not feasible. This integration supports ecological conservation by alleviating harvesting pressure on natural habitats and ensuring and ensuring year-round production. The findings highlight a scalable, sustainable model for cultivating *P. multiflorum*, delivering both economic and environmental benefits. This research underscores the potential of advanced biotechnology and digital agriculture in shaping the future of medicinal plant conservation and commercial production. Further research will focus on scaling up these methods for broader application across other endangered or economically important herbal species. This research was supported by the Development of Sustainable Application for Standard Herbal Resources (KSN1823320), Development of Innovative Technologies for the Future Value of Herbal Medicine Resources (KSN2511030), Korea Institute of Oriental Medicine through the Ministry of Science and ICT, Republic of Korea. Additionally, it was funded by the Collection, Conservation and Characteristic Assessment of Forest Life Resources (2020-2025), the National Forest Seed and Variety Center under Korea Forest Service.

GS1-12

Schisandrin C Originating from *Schisandra chinensis* Alleviates Depression by Modulating Gut-Brain Axis

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Schisandra chinensis is an herbal medicine that has been reported to exhibit antidepressant activity. Schisandrin C (SCC), a lignan compound isolated from the *S. chinensis*, has been demonstrated to improve the leaky gut conditions. However, the impact of SCC in depression and its molecular mechanisms have never been reported. This study aimed to elucidate the beneficial effect of SCC on intestinal health and its antidepressant effect by modulating the gut-brain axis. Our result indicated that SCC could alleviate the depressive-like behaviors in chronic unpredictable mild stress (CUMS) mice model. Network pharmacology and molecular docking analyses revealed that SCC exhibited antidepressant effects by regulating AKT/CREB/BDNF signaling pathway and inhibiting monoamine oxidase (MAO) activities, which were validated in *in vitro* HT22 cells and CUMS-induced mice. Furthermore, the integration of targeted metabolomics and gut microbiota analyses in CUMS-induced mice model indicated that SCC could modulate the tryptophan metabolism by elevating the serotonin level in the brain and its precursor, 5-hydroxytryptophan, in the serum, which is associated with increased abundance of *Akkermansia* and *Bifidobacterium*. These gut microbiota changes, along with the SCC enhancement of intestinal barrier integrity and reduction of inflammation, support the correlation between depression and the gut-brain axis. In conclusion, these findings highlight SCC as a promising candidate for the treatment of depression through gut-brain axis modulation.

GS1-13

Anti-Inflammatory Effect of Fermented and Aged Mountain-Cultivated Ginseng Sprout and Its Major Component, Compound K, in an LPS-induced Acute Respiratory Distress Syndrome Mouse Model

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Acute Respiratory Distress Syndrome (ARDS) is a life-threatening condition characterized by severe pulmonary inflammation, impaired oxygenation, and extensive apoptosis of lung cells. Fermented and aged mountain-cultivated ginseng sprout (FAMCGS), produced through steaming, aging, and fermentation processes, exhibits enhanced levels of bioactive compounds, particularly compound K (CK). This study investigated the preventive effects of FAMCGS extracts and CK on lipopolysaccharide (LPS)-induced inflammation in a murine ARDS model. Pre-administration of FAMCGS or CK significantly reduced inflammatory cell numbers and pro-inflammatory cytokine productions in bronchoalveolar lavage fluid. Histopathological examination revealed that FAMCGS and CK attenuated LPS-induced lung injuries, including immune cell infiltration, hemorrhage, edema, mucus hypersecretion, and goblet cell hyperplasia (PAS-positive cells). Furthermore, FAMCGS and CK suppressed macrophage infiltration and inflammatory cytokine expressions in lung tissues. Both agents also alleviated LPS-induced apoptosis, as evidenced by reduced TUNEL-positive cells and apoptotic markers. In vitro, FAMCGS pretreatment dose-dependently mitigated morphological changes in RAW 264.7 macrophages exposed to LPS. RT-PCR and Western blot analyses confirmed that FAMCGS and CK downregulated the expression of key pro-inflammatory cytokines and mediators at both transcriptional and translational levels. Mechanistically, FAMCGS inhibited LPS-stimulated phosphorylation of MAPKs (ERK, p38, and JNK) and prevented the nuclear translocation of NF-κB. These findings suggest that FAMCGS and its key component, CK, may serve as promising natural therapeutic agents for the prevention and/or treatment of ARDS.

GS1-14

Development of an Alginate-based Hydrogel Incorporating Alginate Oligomers and Antibacterial Peptides for Wound Healing Applications

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Alginate has been widely employed in wound dressing applications due to its excellent biocompatibility and gel-forming properties. However, conventional calcium-crosslinked alginate hydrogels have been reported to cause cytotoxicity due to the leaching of calcium ions in physiological environments. To address this limitation, we developed a covalently crosslinked alginate hydrogel that excludes calcium ions and investigated the effects of incorporating alginate oligosaccharide (AOS) to improve its functional performance. AOS, a low-molecular-weight polysaccharide, has been reported to exhibit antioxidant, immunomodulatory, and antimicrobial properties. In this study, we tested the hydrogel's hydration behavior and mechanical properties, and potential to support the function of immobilized antimicrobial peptides (AMPs). AMP was conjugated to the hydrogel surface to provide antibacterial activity, and its efficacy was evaluated with the presence of AOS. Water retention, swelling, and reswelling behavior were measured, and cross sectional structure was examined with scanning electron microscope (SEM). Antioxidant activity was analyzed using the DPPH assay, while antimicrobial performance was assessed by contact inhibition method after peptide immobilization. Compression testing was conducted to evaluate mechanical strength, including Young's modulus, stress and strain at fracture. The results suggest that AOS contributes to enhanced hydration and strain at fracture, while AMP retains antibacterial function upon surface conjugation, supporting the potential of this functional hydrogel for wound healing applications.

GS1-15

Optimization of Peanut Sprout Extract for its potential lipid-lowering effects via AMPK activation in murine and canine adipose tissue derived mesenchymal stem cells

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Previously, we demonstrated that peanut sprout extract (PSE), derived from germinated peanuts, exerts anti-obesity effects both in vitro and in vivo models. However, the extraction conditions to maximize its lipid-lowering properties have not yet been fully elucidated. To address this, PSE was prepared using five different extraction methods; water extract at 30℃ or 60℃ with or without 15% of ED (Jeju lava seawater), and 50% of ethanol extract as positive control. Based on screening results, ED15%+60℃ extract showed the most potent lipid-lowering activity in preliminary screenings with elevated levels of bioactive components. Then, validation confirmed that PSE treatment (in ED15%+60℃, 25, 50, and 100 μg/mL) significantly suppressed lipid accumulation in both early and late phase of differentiation by downregulation of mRNA expression, including FAS, FABP4, PPARγ, DGAT2, and SCD1. Strikingly, PSE also attenuated markers related to adipocyte differentiation and lipid storage in both murine and canine white adipose tissue-derived mesenchymal stem cells accompanied by AMPK activation. In conclusion, we identified ED15%+60℃ as the optimal extraction condition and confirmed that PSE exhibits potent anti-obesity adipogenic effects through modulation of lipid metabolism and AMPK activation. These findings support the potential of PSE as a functional natural product for obesity improvement.

Graduate Student Presentation

GS2-1

Perfluorooctanoic Acid Alters Ligand Affinity in Human Serum Albumin Without Structural Unfolding

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Perfluorooctanoic acid (PFOA) is a persistent environmental contaminant widely detected in human serum due to its strong binding affinity for plasma proteins and long biological half-life. Human serum albumin (HSA), the most abundant transport protein in the blood, plays a key role in regulating the pharmacokinetics of numerous drugs and endogenous compounds. This study examines how PFOA affects HSA's ligand-binding properties by using site-specific competitive displacement assays with three standard probes: warfarin for site 1, dansylglycine for site 2, and bilirubin for site 3. The results revealed that PFOA competitively binds to site 3, moderately alters site 2 through allosteric modulation, and has minimal influence at site 1. Interestingly, the binding capacity for dansylglycine increased while its binding affinity decreased, indicating that PFOA induces subtle conformational changes without directly occupying the site. Structural integrity was evaluated through circular dichroism spectroscopy, which confirmed that PFOA binding does not significantly affect the secondary structure of HSA. These findings demonstrate that PFOA can modulate protein–ligand interactions in a functionally disruptive yet structurally silent manner. This mechanism may lead to altered distribution and availability of physiological ligands or pharmaceutical agents in organisms exposed to persistent environmental pollutants. The results highlight the importance of examining both structural and functional responses in protein–chemical interaction studies relevant to environmental toxicology.

GS2-2

Effect of co-digestion and thermal hydrolysis pretreatment on methane production from cow feces and tomato waste

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Organic wastes such as crop residues and livestock feces can directly or indirectly affect the environment. These organic wastes can be used as feedstocks for production of biogas and renewable energy. This study explores the potential to enhance anaerobic digestion efficiency by using co-digestion and thermal hydrolysis pretreatment (THP). Cattle feces (CF) and tomato waste (TW) were selected as substrates and mixed at volatile solid (VS) mass ratios of CF:T = 1:0, 1:1, 2:1, 1:2, and 0:1. The amount of methane produced was measured by conducting a biochemical methane potential (BMP) experiment. Co-digestion alone resulted in increased methane production, and a synergistic effect was observed only at the 1:2 ratio. When combined with THP, all co-digestion ratios showed enhanced methane yields and synergy. These findings suggest that co-digestion when coupled with THP, can significantly improve methane generation from organic wastes. This study offers practical insights for optimizing biogas production using agricultural and livestock residues.

GS2-3

Production of Poultry Manure Biochar and Evaluation of Its Potential as an Organic Fertilizer

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Livestock manure is mostly treated as compost and liquid fertilizer, but these methods face issues like environmental pollution and livestock diseases. This study was evaluated the effect of biochar aplication as an organic fertilizer to improve crop growth. Livestock manure biochar (CMBC) was produced by mixing it with woody biomass at an 80:20 (w/w) ratio, followed by pyrolysis at 400°C for 2 hours. The final product showed an H/C ratio of 0.82, O/C ratio of 0.13, and salinity content of 1.80%. A pot experiment using Kimchi cabbage was conducted in 1/5000a Wagner pots. Treatment conditions divided with control (CN), biochar alone (CMBC3, CMBC5, CMBC7 and CMBC10), and combined treatments of inorganic fertilizer (IF) and CMBC (IF+CMBC3, IF+CMBC5, IF+CMBC7 and IF+CMBC10), respectively. The CMBC5 showed the highest growth, increasing plant height, leaf number, fresh weight, and dry weight by 44.82%, 40.98%, 167.86%, and 86.32%, respectively, compared to CN. The single CMBC treatments were higher than combined treatments. After crop harvesting, soil fertility significantly improved, as indicated by increases in pH, EC, organic matter, available P, total nitrogen, and CEC. These results suggest that manure-based biochar can enhance crop growth and soil fertility without inorganic fertilizers and has strong potential as a sustainable organic resource.

GS2-4

Development of Biochar Treatment Technology for Cyanobacteria Control

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Rising seawater temperatures and nutrient inputs associated with climate change have intensified harmful algal blooms worldwide. In Korea, cyanobacterial densities reached up to 144,375 cells/mL in 2024. Conventional algae control methods, including clay application, ultrasonic treatment, and H2O2 treatment often lack effectiveness and harm ecosystems. Recently, our research team reported the effectiveness of biochar in controlling algal blooms. However, its impact on cyanotoxins and odor compounds produced by cyanobacteria has not yet been reported. In this study, the efficiency of biochar in controlling cyanobacteria was evaluated under monoculture conditions using Anabaena and Oscillatoria. Subsequently, biochar was applied to natural freshwater systems experiencing active cyanobacterial blooms to investigate its effectiveness in reducing associated cyanotoxins and odor compounds. The optimal dosage of biochar for cyanobacterial control was determined to be 4 g/L. Under these optimal conditions, the removal efficiency of chlorophyll-a by biochar was 80% for monocultures of cyanobacteria and 50-90% in freshwater conditions with active cyanobacterial blooms. In freshwater conditions, the efficiency of microcystin removal by biochar was 35-100%, demonstrating a strong dose-response relationship. In freshwater conditions with thriving cyanobacteria, the removal efficiencies of geosmin and 2-MIB by biochar were 40–60% and 20–60%, respectively. Therefore, biochar is deemed effective in controlling harmful cyanobacterial blooms in freshwater ecosystems, particularly in the removal of cyanotoxins and odor compounds.

GS2-5

Can Ammonium Sulfate Reduce Ammonia Volatilization from a Rice Paddy Soil Compared to Urea

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Fertilizer applications improve rice production, yet inappropriate nitrogen (N) fertilization exacerbates ammonia (NH_3) volatilization. Ammonium sulfate (AS) potentially mitigates NH_3 volatilization by reducing floodwater pH compared to urea (U); however, its implication for crop yield and nitrogen losses remains unclear. This study examined the effects of urea (U) and ammonium sulfate (AS) at different N levels (0 [PK, control], 45, 90, and 180 kg N ha^{-1}) on NH_3 volatilization, in a four-year field experiment using the static chamber method. Results showed that NH_3 volatilization increased with N application, stimulated by increasing floodwater pH ($r = 0.32$, $p < 0.001$). For three consecutive years, NH_3 losses were highest in U treatment at 180 kg N ha^{-1} from 15.7 to 18.5 kg NH_3-N ha^{-1} day^{-1} compared to AS at 8.1-10.7 kg NH_3-N ha^{-1} day^{-1}. Specifically, NH_3 volatilization losses under AS were 5.6 times lower than U. Although yield components did not differ statistically between U and AS, AS-treated plots showed higher grain yield, ripening, plant height, and tiller number, likely due to reduced nitrogen loss and greater nitrogen uptake from available N. Despite the statistical significance of the effect of fertilizer on soil pH, the observed pH values were not markedly different across treatments. However, long-term studies are required to evaluate the long-term impact of AS applications on soil acidification and sustainability.

GS2-6

Machine Learning-Based Prediction of Soil Nutrients Levels from Electrical Conductivity

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Real time on-site analysis of soil nutrient levels is essential for the appropriate use of fertilizers and the reduction of environmental pollution. In this study, a machine learning-based nutrient prediction model was developed using soil electrical conductivity (EC) sensing data, which is correlated with soil nutrient content. Two data sets including EC data measured from soil extract and EC data measured using real time sensor and three machine learning algorithms including Random Forest (RF), Support Vector Regression (SVR), and eXtreme Gradient Boosting (XGBoost) were applied to predict the concentrations of nitrate (NO_3^-), available phosphate (Av.P), and potassium ion (K^+), which are the plant-available forms of nitrogen (N), phosphorus (P), and potassium (K). Analysis of EC dataset measured from soil extract revealed coefficient of determination (R2) values for NO_3^- and K^+ of 0.63 and 0.67 using RF, 0.68 and 0.52 using SVR, and 0.24 and 0.57 using XGBoost, respectively. For EC sensing dataset, the results showed that the R^2 values for NO_3^- and K^+ were 0.46 and 0.57 in RF, 0.61 and 0.40 in SVR, and 0.54 and 0.32 in XGBoost, respectively. All models showed low performance in predicting Av.P, indicating that additional research is needed to improve estimation accuracy for P. This study has the potential to serve as a foundational model for implementing precision agriculture in soil nutrient management.

GS2-7

Suppression of Fusarium Wilt of *Cnidium officinale* Using Biocontrol Agents

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Cnidium officinale Makino is a perennial plant of the Apiaceae family widely used for medicinal purposes across various fields. However, stable cultivation is challenged by Fusarium wilt and high sensitivity to climatic conditions. To control Fusarium wilt and improve productivity, four candidate bacterial strains (PT1, ST7, ST8, and SP4) were isolated from the rhizosphere of *C. officinale*. In planta assays showed that treatment with strain PT1 reduced Fusarium wilt damage and enhanced plant growth. Functional characterization revealed that PT1 secretes indole-3-acetic acid (IAA) and solubilizes phosphate. Additionally, PT1 produced siderophores exhibiting antagonistic activity against pathogenic fungi. Transcriptional analysis of siderophore biosynthesis genes by RT-qPCR demonstrated significant upregulation when co-cultured with the pathogen *Fusarium solani*. Comparison of *F. solani* spore formation under varying iron concentrations indicated that spore numbers increased in the control as iron decreased, whereas co-culture with PT1 resulted in a marked reduction in spore production. 16S rRNA–based identification identified PT1 as *Leclercia adecarboxylata*, a species previously reported to exhibit root colonization capacity and antifungal activity. Therefore, PT1 has high potential for enhancing the productivity of *C. officinale*.

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GS2-8

Impact Of Soil Amendments on Soil Microbiota and Plant Defense System: A Study on Beneficial Bacterium and Salicylic Acid in Cucumber Cultivation

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The increasing demand for sustainable agriculture highlights the need for improved biological control agents (BCAs). This study evaluates the co-application of *Bacillus amyloliquefaciens* KACC17029 and salicylic acid (1.0 mM) on cucumber (*Cucumis sativus* L.) performance and rhizosphere microbiota. Combined treatment significantly reduced lesion size (83.8%), enhanced leaf area (101.3 cm^2), and increased shoot biomass (38.2 g). These outcomes correlated with enhanced peroxidase activity (6-fold) and upregulation of defense genes PR1 and LecRK6.1. Amplicon sequencing revealed increases in *Trichoderma*, *Candida*, and *Novierbaspirillum*, with reductions in *Fusarium*, indicating a beneficial microbial shift. In the second phase, encapsulated formulations using perlite–alginate beads maintained high microbial viability and resulted in the highest colonization levels (92.7 copies/µL by Day 15), improving plant traits. Microbiome analysis confirmed higher diversity and treatment-specific clustering (PERMANOVA $p = 0.001$, $R^2 = 0.421$). Integration of amplicon and ddPCR data through Quantitative Microbiome Profiling (QMP) identified dominant genera like *Devosia* and *Streptomyces*. QMP-based co-occurrence networks in perlite-treated soil were more complex, with higher betweenness and eigenvector centrality. LEfSe analysis showed enrichment of *Bryobacter* and *Paenibacillus*. This study provides a framework combining PGPR–elicitor co-inoculation, encapsulation, and QMP to develop effective, field-applicable biofertilizers.

GS2-9

Laccase-producing Bacterium *Pseudomonas palmensis* strain MSK1 isolated from a Plastisphere and its Potential for Decolorization of Synthetic Dyes

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Laccase is a multicopper oxidase that uses oxygen as the final electron acceptor and produces only water as a byproduct. Due to these properties, laccase has attracted attention for the biodegradation of environmental pollutants, particularly synthetic dyes. In this study, laccase-producing bacteria were isolated from agricultural waste plastics, and the decolorization potential was evaluated. Samples were collected from agricultural soils in Taebaek, Gangwon State, South Korea and enriched using guaiacol. Laccase activity was measured using the culture supernatant with 2,6-dimethoxyphenol (2,6-DMP) as a substrate. Whole genome sequencing was conducted to identify the isolate using average nucleotide identity (ANI) and to analyze its laccase gene. Decolorization ability was first screened on agar plates, followed by quantitative analysis using resting cell assays. Among the isolates, strain MSK1 showed extracellular laccase activity (2.93 U/ml) against 2,6-DMP after 24 hours. ANI analysis revealed 99.06% similarity to *Pseudomonas palmensis*. Its laccase gene shared less than 30% identity with previously reported sequences. MSK1 decolorized 0.137 mM of methyl orange, methyl red, malachite green, aniline blue, and methyl blue on agar plate. In resting cell assay, *Pseudomonas palmensis* strain MSK1 achieved 86% decolorization of 0.1 mM malachite green. Taken together, these results suggest that the laccase-producing bacterium *Pseudomonas palmensis* strain MSK1 exhibits broad substrate specificity toward various synthetic dyes, highlighting its potential for biotechnological applications.

GS2-10

Exploration of Nitrogen-fixing and Nitrous oxide-reducing Bacteria from Legume Roots and Soils

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As a task for sustainable agriculture, the development of microbial-based technologies that can reduce dependence on chemical fertilizers and reduce greenhouse gas emissions is attracting attention. In this study, to discover useful microorganisms with nitrogen fixation and nitrous oxide (N_2O) reduction capabilities, we collected domestic agricultural land and natural soil samples and cultivated them for one month. Samples were collected from the root nodules and rhizosphere soil of each plant, inoculated onto Modified Arabinose-Gluconate medium, and cultured. As a result, viscous and white colonies were isolated. The isolated strains were screened for nitrogen fixation capabilities based on color changes in the Bromothymol blue-based nitrogen fixation assay medium. Afterwards, 16SrRNA sequence analysis confirmed that these strains belonged to *Pseudomonas*, *Erwinia*, *Rahnella*, and *Bacillus*, and a phylogenetic tree was created based on this. To evaluate the N_2O reduction ability, PCR analysis of Clade I and Clade II of the N_2O reductase gene (nosZ) was performed for each strain. This study suggests the possibility of securing microbial resources that can contribute to the realization of sustainable agriculture by discovering various genera of soil-derived bacteria that simultaneously have nitrogen fixation and nitrous oxide reduction functions.

GS2-11

Microbial Community Dynamics in Municipal Wastewater and Livestock Manure Treatment Plants

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This study compared changes in microbial community structure and function, as well as the presence of pathogenic microorganisms, throughout treatment processes in livestock manure treatment plants (LMTPs) and municipal wastewater treatment plants (WWTPs) receiving different influent sources. Microbial analyses were conducted using high-throughput 16S rRNA gene sequencing combined with qPCR to quantitatively evaluate microbial community composition and absolute abundances of key potential pathogens. In LMTP influent, anaerobic fermentative and methanogenic microorganisms, including *Candidatus Cloacamonas* and *Methanobrevibacter*, were dominant, with their abundances gradually declining through subsequent treatment stages. In contrast, WWTP influent was primarily characterized by microorganisms of intestinal origin, such as *Faecalibacterium* and *Blautia*. Specific functional groups, notably *Nitrospira* and *Methanothermobacter*, selectively proliferated during sludge treatment and anaerobic digestion stages, respectively. Our results showed that the two treatment plants exhibited distinct initial microbial community compositions reflecting their influent characteristics, and the microbial community structure and function underwent significant reorganization throughout the treatment stages. Although total microbial abundance was markedly reduced in the final effluent, several pathogenic genera, including *Legionella* and A*cinetobacter*, persisted at low levels. These findings highlight the necessity of precise process management, continuous microbiological monitoring, and the integrated application of advanced treatment technologies to effectively control pathogenic microorganisms.

GS2-12

Metabolomic Insights into Korean Red Peppers across Cultivars and Postharvest Conditions

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Red pepper (*Capsicum annuum* L.) is one of the most widely consumed crops in Korea and is primarily processed into dried peppers and red pepper powder. The primary and bioactive secondary metabolites of red peppers are influenced by various factors, including cultivar, maturity stage, drying method, storage conditions, and anatomical part. These factors significantly influence the nutritional quality, sensory characteristics, and functionality of red peppers, necessitating a comprehensive analysis of metabolite variations. To address this, detailed metabolomic profiling was conducted. Primary metabolites were analyzed using gas chromatography–tandem mass spectrometry (GC-MS/MS), while secondary metabolites—including capsaicinoids, capsinoids, phenolic compounds, and carotenoids—were quantified using high-performance liquid chromatography (HPLC) and liquid chromatography–tandem mass spectrometry (LC-MS/MS). Samples representing different cultivars, maturity stages, drying methods, and storage conditions were compared, and metabolite profiles were also examined by tissue type (pericarp vs. seeds). Significant differences were observed in metabolite composition depending on cultivar and maturity. Notably, the contents of secondary metabolites varied markedly between pericarp and seeds. Among the drying methods tested, freeze-drying was most effective in preserving functional compounds. Storage trials revealed gradual metabolic shifts, with elevated temperatures and longer durations causing increased deviations from initial metabolite profiles. These findings may support evidence-based strategies for enhancing quality and establishing processing standards in red pepper products.

GS2-13

Characterization and Immunomodulatory Effects of Alginate and *Sargassum fulvellum* Oligosaccharides Degraded by Crude Enzymes from *Shewanella oneidensis* PKA 1008

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Alginates are poorly bioavailable polysaccharides requiring depolymerization. Enzymatic degradation offers substrate specificity and minimal by-products. *Sargassum fulvellum*, a brown seaweed abundant along Korean coasts, provides a source of bioactive polysaccharides.

In this study, we applied crude enzyme from *Shewanella oneidensis* PKA 1008 to alginate and *S. fulvellum* extract (0–72h), and evaluated their physicochemical profiles and immunomodulatory activities.

Over 72h, at alginate pH and viscosity decreased while reducing sugars and color increased; dimer and trimer appeared. Macrophages showed no cytotoxicity; high doses enhanced NO and TNF-α. *In vitro*, 48h products promoted splenocyte viability and cytokine (IL-2, IFN-γ, TNF-α) release at low-doses. *In vivo* (oral), 12h products maximized proliferation, IL-2 and IL-4; 48h products peaked in IFN-γ and NK-cell activation. For *S. fulvellum*, the 72h treatment yielded the lowest pH and viscosity and highest reducing sugar; dimer and trimer also appeared. Macrophage assay showed no cytotoxicity and a dose-dependent decrease in NO and cytokine release. *In vitro*, splenocytes treated with 48 h products showed the highest IL-2 and IFN-γ; TNF-α peaked at 0 h. *In vivo*, 48h product maximized splenocyte proliferation, IL-2, IFN-γ, and NK-cell activation.

These findings confirm that the PKA1008-derived alginate lyase efficiently produces immunomodulatory oligosaccharides with time-dependent anti-inflammatory effects, supporting their potential as functional agents.

GS2-14

Comprehensive Evaluation and Field Validation of Chlorine Dioxide Washing Technology for Safety and Quality Maintenance in Red Pepper Powder

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This study assessed the effectiveness and field applicability of chlorine dioxide (ClO_2) washing technology for reducing pesticide residues and microbial contamination in red peppers and red pepper powder. Laboratory trials evaluated pesticide removal, microbial inactivation, and quality changes (color, vitamin C, capsaicinoids) under various ClO_2 concentrations and exposure durations. Based on TOPSIS analysis and gas exposure monitoring, 25 mg/L ClO_2 was identified as the optimal concentration balancing efficacy and worker safety. Field validation using red peppers from three farms confirmed that the developed ClO_2 washing device maintained stable concentrations and was practical for farm-level application. Cluster analysis showed that pesticides with higher residual stability were more effectively reduced in red pepper powder, while those with lower stability showed greater reduction in fresh red peppers. These results suggest that, with expanded data, ClO_2 washing guidelines can be refined to better predict and improve pesticide reduction outcomes.

GS2-15

Optimization of Heat-Moisture Treatment for Manufacturing Resistant Starch from Red Bean (*Vigna angularis* var. *nipponensis*)

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Resistant starch (RS) is a nondigestible carbohydrate that reaches the large intestine without being broken down in the small intestine. It helps lower the glycemic index and reduce the risk of metabolic diseases. RS3, one type of RS, is formed through retrogradation of gelatinized starch. RS3, produced through physical processing, has high stability and potential for industrial applications. Red bean (*Vigna angularis* var. *nipponensis*) is a starch-rich legume containing high levels of protein, dietary fiber, and vitamin B_1. In this study, heat-moisture treatment (HMT) was applied to maximize the RS content of red bean flour. A Box-Behnken design of response surface methodology (RSM) was used, with heating temperature (110-130℃), heating time (60-90 min), and moisture content (15-25%) as independent variables, and RS content as the dependent variable. RS content ranged from 10.32 w/w% to 12.47 w/w% depending on treatment conditions. The regression model was statistically significant ($R^2 = 0.939$, Adj-$R^2 = 0.828$, $p < 0.015$). The model showed that the optimal HMT condition for producing RS was 121℃ for 70 min at 22.37% moisture content, with a predicted RS content of 12.26 w/w%. Thus, the RS content increased by 3.47 w/w% from the original 8.79 w/w% in red bean. These results demonstrate that HMT can effectively increase RS content and be optimized through RSM.

K-Inno:Ven
Star Audition

K-1

Upcycling Fish Processing By-Products into Functional pet food for Companion Animals

김욱철, 이윤수, 정서린

MBEL (순천향대학교 의료과학과)

K-2

팽미(米)

정종빈, 장무연, 김다현, 방도윤, 김혜림, 정예림

Space G (경상국립대학교 생명자원과학과)

K-3

식물 조직배양 기반 커피 내 생리활성 물질 생산 연구

김효정, 김지현, 이상민

Cellffee (부산대학교 생명환경화학과)

K-4

망팜 (망을 이용한 수경재배)

김혜민, 차형호, 박나윤

CKP (UST-KIST스쿨 천연물응용과학 전공)

K-5

정유성분/화산석을 활용한 천연항균 수건 건조기

이상윤

혼저 옵서예 (중앙대학교 식물생명공학과)

KSABC
International Symposium 2025

Poster Presentation

Poster Presentation

PBM Biochemistry · Molecular Biology

PBM-1

Neuroprotective of Isoflavone-Enriched Soybean Leaves (Glycine Max) on the Scopolamine-Induced Memory Deficits in C57BL6 Mice via Antioxidative Mechanisms

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This study was aimed to investigate the memory enhancing effect of IESL against scopolamine-induced amnesia in C57BL/6 mice. Soybean leaves are naturally rich in kaempferol glycosides and soyasaponin, but those with enhanced isoflavone content are called isoflavone enriched soybean leaves(IESL). To determine the effect of IESL on the memory and cognitive function, we have injected scopolamine (1 mg/kg, i.p.) and IESL into C57BL/6 mice before behavior tests. We have conducted Morris water-maze, passive avoidance tests to compare learning and memory functions. Scopolamine-induced behavior changes of memory impairment was significantly restored by oral administration of IESL (6.25 mg isoflavones/kg/day (low dose; Low) and 18.8 mg isoflavones/kg/day (high dose; High)). To elucidate the molecular mechanism underlying the memory enhancing effect of IESL. we have examined the antioxidant defense system and neurotrophic factors. IESL treatment attenuated intracellular accumulation of reactive oxygen species and up-regulated expression of antioxidant enzymes activity and western blot analysis, respectively. IESL also increased protein levels of brain-derived neurotrophic factor (BDNF) compared with those in the scopolamine-treated group. Furthermore, as an upstream regulator, the activation of cAMP response element-binding protein (CREB) via phosphorylation was assessed by Western blot analysis. These findings suggest that IESL may have preventive and therapeutic potential in the management of amnesia.

PBM-2

Neuroprotective Effects of Dioscorea bulbifera L. Extract Against Glutamate-Induced Oxidative Stress and Apoptosis in HT22 Hippocampal Cells

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This study examines the neuroprotective properties of a Dioscorea bulbifera L. complex extract against glutamate-induced oxidative stress and neuronal apoptosis in HT22 mouse hippocampal cells. Glutamate exposure is well-documented to induce excitotoxicity, characterized by excessive reactive oxygen species (ROS) generation, mitochondrial dysfunction, and subsequent neuronal death. In this study, co-treatment with the extract significantly enhanced cell viability and mitigated glutamate-induced cytotoxicity in a dose-dependent manner. Morphological assessments demonstrated that the extract effectively reversed glutamate-induced dendritic shrinkage, underscoring its potential to preserve neuronal architecture. Furthermore, the extract markedly reduced intracellular ROS levels and suppressed apoptotic signaling pathways triggered by glutamate exposure. Mechanistic investigations revealed that the extract attenuated the phosphorylation of mitogen-activated protein kinases (MAPKs), specifically ERK, p38, and, most notably, JNK—critical mediators of cellular stress responses. In addition, treatment resulted in a substantial downregulation of key apoptotic markers, including cleaved caspase-3 and poly (ADP-ribose) polymerase (PARP). These findings indicate that the Dioscorea bulbifera L. extract confers neuroprotection by modulating oxidative stress responses, inhibiting pro-apoptotic signaling cascades, and maintaining neuronal integrity. Consequently, this natural extract represents a promising therapeutic candidate for the prevention and treatment of neurodegenerative diseases, including Alzheimer's disease, Parkinson's disease, and other conditions associated with oxidative neuronal damage and glutamate excitotoxicity.

PBM-3

Tissue-Specific Expression and Developmental Regulation of *FAD2* and *FAD3* Genes Involved in Fatty Acid Biosynthesis in Milk Thistle

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Milk thistle (*Silybum marianum*), a diploid member of the *Asteraceae* family, is widely recognized for its medicinal properties, particularly in the treatment of liver disorders. Its seeds are notable for their high lipid content (20–30%) and abundance of silymarin, a potent flavonolignan complex with therapeutic value. The seed oil is rich in unsaturated fatty acids, especially oleic acid (18:1) and linoleic acid (18:2), which are known to support cardiovascular health and prevent age-related diseases, while the content of α-linolenic acid (18:3) is negligible. Fatty acid biosynthesis in milk thistle is mediated by three *FAD2* genes (*FAD2a*, *FAD2b*, and *FAD2c*) that convert oleic acid to linoleic acid, and two *FAD3* genes (*FAD3a* and *FAD3b*) that catalyze the conversion of linoleic acid to α-linolenic acid. All five genes were expressed across various tissues, including leaf, involucre, root, seed, and flower. Notably, *FAD2a* exhibited involucre-specific expression, whereas *FAD2c* was predominantly expressed in seeds. Fatty acid accumulation in seeds was analyzed across five developmental stages, revealing that oil content peaked between stages 2 and 4. This trend corresponded with elevated gene expression levels, as confirmed by RT-qPCR, except for *FAD2a* and *FAD3b*, which showed different expression patterns. These findings enhance our understanding of gene expression dynamics associated with fatty acid accumulation in milk thistle seeds.

PBM-4

Study on the production of foot-and-mouth disease recombinant vaccine candidates using plant expression systems

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Foot-and-mouth disease (FMD) is a highly contagious viral disease that affects cloven-hoofed livestock, including cattle, pigs, and goats. It is clinically characterized by the formation of vesicular lesions on various epithelial tissues such as the hooves, lips, tongue, and teats in females. Due to its high transmissibility, FMD incurs substantial socio-economic losses, and is therefore designated as a Category I notifiable animal disease in Korea. While vaccination remains the primary preventive strategy, all currently available vaccines are imported, underscoring the urgent need for domestically produced alternatives. This study aims to develop a recombinant protein-based virus-like particle (VLP) vaccine against FMD utilizing a plant expression platform. Based on the genomic information of FMD virus, antigenic capsid proteins from the three major serotypes prevalent in Asia (A, O, and Asia1) were selected through thermal stability profiling and evaluated for expression efficiency. Among these, serotype O—most frequently associated with FMD outbreaks in Korea—exhibited the highest expression levels, and was subsequently used for VLP assembly attempts. Although proteolytic cleavage of structural proteins by 3C protease was confirmed, successful assembly of VLPs was not achieve. Consequently, current efforts are focused on optimizing the physicochemical parameters for VLP assembly. Subsequent steps will involve purification of the VLPs and evaluation of their immunogenic potential in animal models.

PBM-5

Generation and validation of a LDL receptor reporter cell line for screening small molecules to treat hypercholesterolemia

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Familial hypercholesterolemia can be caused by mutations in the *LDLR* (LDL receptor), *LDLRAP1* (LDL receptor associated protein 1), *and APOB100* (the limiting apoprotein for LDL formation) genes. Statins, the mainstay drugs have been successful in reducing serum LDL-C to healthy levels, but there are many patients who are statin intolerant due to liver and muscle toxicity or who cannot achieve their treatment goals even by high-intensity statin therapy. Recent studies concerning PCSK9 suggest that increasing LDLR levels may be more efficacious with less side effects than inhibiting cholesterol synthesis. Because PCSK9 is not a druggable target with small molecules and there may be other pathways to upregulate LDLR levels, we have developed an endogenous LDLR reporter U2OS cell line which can be used for screening small molecules to increase LDLR levels. Our reporter cell line has two reporters, luciferase and mRuby3 and has been validated as a drug screening platform for identifying novel cholesterol lowering drugs. Both bioluminescence and fluorescence levels increased significantly in response to treatment with various statins in our reporter cell line. Consequently, absorption of LDL particles into the cells increased. We believe our cell platform can be used with any bioluminometer or fluorometer to screen small molecules in a high-throughput manner.

PBM-6

Immunomodulatory potential of gamma-irradiated macrophage-derived exosomes

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Modulation of macrophage polarization (M1/M2) is a promising immunomodulatory strategy. Despite this, the specific involvement of exosomes in macrophage polarization influenced by ionizing radiation is not well understood. This study investigated alterations in macrophages and exosomes induced by 10 Gy gamma irradiation using the RAW264.7 macrophages, elucidating underlying mechanisms and evaluating irradiated M1 exosomes as potential therapeutics. After exposing M1 macrophages to 10 Gy gamma irradiation, we observed a marked increase in pro-inflammatory cytokine levels, mediated through the NF-κB and NLRP3 inflammasome signaling routes. Exosomes isolated from these irradiated M1 cells (IR-M1 exosomes) displayed characteristics of an enhanced M1 phenotype, indicating their capacity for immunomodulation. This study demonstrates that gamma irradiation can effectively alter the cytokine content of exosomes, presenting a novel strategy for enhancing immune responses. These findings support the development of advanced immunotherapies based on exosomes. Further research is needed to evaluate the applicability of these findings using human macrophages and long-term therapeutic effects in clinical contexts.

PBM-7

Enhancement of Tomato Fruit Sweetness by Targeted ALS1 Gene Editing

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Fruit sweetness is one of the key attributes that influence consumer preference. Tomatoes, being among the most widely consumed fruits and vegetables globally, are evaluated for quality largely based on their sugar content. In this study, the acetolactate synthase (ALS) gene, a key component of the branched-chain amino acid biosynthesis pathway, was edited using CRISPR/Cas9 technology to enhance the sweetness of tomato fruits. Among the two ALS genes in tomatoes, ALS1 and ALS2, a knockout mutant of ALS1 was generated in the Micro-Tom variety. The ALS1 knockout resulted in a notable increase in the Brix index and approximately 1.5-fold higher glucose and fructose levels compared to wild-type plants. Conversely, the levels of branched-chain amino acids valine, leucine, and isoleucine were lower in the mutant. Furthermore, treatment with the ALS-targeting herbicide Imazethapyr also led to elevated sugar content in tomato fruits, with Brix values reaching 9.0%, compared to 6.5% in untreated wild-type plants. These findings suggest that targeting ALS1 can effectively enhance sugar accumulation and sweetness in tomatoes, offering a promising strategy for breeding high-sugar tomato cultivars.

PBM-8

Quantitative analysis of DNA-binding to UidR by fluorescence spectroscopy

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UidR from *Escherichia coli* is a transcriptional regulator that represses the expression of the uid operon by binding to two specific DNA operator sequences. In the presence of glucuronides, UidR is dissociated from the operator sites, thereby allowing transcriptional activation. Previous studies analyzed the binding affinities between UidR and its operator DNA in the presence and absence of glucuronides using isothermal titration calorimetry (ITC). The dissociation constant (K_D) was reported as 0.2 μM in the absence of glucuronides. In this study, we examined these interactions using fluorescence spectroscopy and the binding affinities of UidR to the operator sequences were approximately 100 times higher. In addition, fluorescence spectroscopy enabled the calculation of the stoichiometry of DNA binding to UidR. Discrepancy between previous study and this study may be due to higher sensitivity of fluorescence spectroscopy over ITC.

Poster Presentation

PBM-9

PEP-associated protein 3 is a Key Regulator of Chloroplast Development in Rice

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Chloroplasts, indispensable for photosynthesis, play a central role in plant growth and productivity. Chloroplast development is regulated by the transcription of chloroplast genes, mediated by the plastid-encoded RNA polymerase (PEP). As the transcriptional activity of PEP largely depends on PEP-associated proteins (PAPs), PAPs serve as pivotal determinants of chloroplast development. In this study, we identified and characterized rice *PAP3* (*OsPAP3*) and investigated its role in chloroplast development. The expression of *OsPAP3* was higher in leaves than in roots and was positively regulated by light, similar to the PEP-dependent chloroplast gene *OsRbcL*. Additionally, subcellular localization analysis revealed that OsPAP3 is localized to chloroplast nucleoids, where PEP acts. Loss-of-function *ospap3* mutant plants exhibited an albino phenotype due to impaired chloroplast biogenesis, and transcription levels of PEP-dependent chloroplast genes such as *OsRbcL* and *OsPsbA* were significantly reduced compared with wild-type plants. In contrast, *OsPAP3*-overexpressing plants showed increased chlorophyll content and chloroplast numbers. Moreover, overexpression of *OsPAP3* increased the expression of PEP-dependent genes, indicating that *OsPAP3* is a crucial regulator of PEP-mediated transcription and chloroplast development in rice.

PBM-10

Bacillus velezensis Enhance Drought Tolerance in Rice

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Drought is a major abiotic stress that impedes crop growth and productivity, and its frequency and severity are intensifying under global climate change. Plant growth-promoting rhizobacteria (PGPR), which colonize the rhizosphere, improve plant growth through beneficial interactions with host plants. Recent studies have reported that PGPRs also affect plant tolerance to abiotic stresses, including drought. In this study, we investigated the role of *Bacillus velezensis* GH1-13 in improving drought tolerance in rice. In the Shindongjin cultivar, GH1-13-treated rice exhibited higher chlorophyll content and increased survival under drought stress compared to untreated controls. Similar effects were also observed in another rice cultivar, Saechungmu. Histochemical staining using DAB and NBT revealed that drought stress induced the accumulation of reactive oxygen species (ROS), and GH1-13 treatment markedly reduced the accumulation. Additionally, we found that GH1-13 treatment upregulated the expression of ROS-scavenging genes, suggesting that *Bacillus velezensis* enhances drought tolerance by reducing ROS accumulation in rice.

PBM-11

Tongue tissue endoplasmic reticulum stress response in a DSS-induced colitis model from an oral-gut axis perspective

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The tongue and intestine are derived from a common endoderm and are structurally and functionally closely related. Recent studies have suggested that these two organs share a microbiome environment and immune response, and may interact with each other, particularly through the oral-gut axis. In this study, we used an acute inflammatory bowel disease model to examine whether inflammation induced in the intestine is reflected in tongue tissue, focusing on the endoplasmic reticulum stress response. Through this, we aimed to elucidate the molecular biological relationship between the tongue and intestine. Acute colitis was induced by DSS (Dextran Sulfate Sodium) for two weeks. Colitis severity was assessed using the Disease Activity Index (DAI). Blood analysis showed increased red blood cells in the DSS model, suggesting dehydration. Histological analysis using H&E staining assessed muscle, submucosal, and villus layers in the intestine and mucosal and keratinized layers in the tongue. Immunohistochemistry (IHC) analyzed IRE1and PCNA expression. TUNEL assay and Western blot measured apoptosis and endoplasmic reticulum stress-related proteins IRE1, Bip and PCNA, revealing similar patterns in the tongue and intestine.
This study demonstrates that intestinal inflammation in IBD is reflected in the tongue. These findings support the concept of the oral-gut axis and provide a scientific basis for tongue diagnosis (Seoljjin) as a potential tool for assessing gastrointestinal health.

PBM-12

Interactions of Isocitrate Dehydrogenase with DNA and guanine nucleotides

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Isocitrate dehydrogenase (Icd) is a key enzyme in the tricarboxylic acid (TCA) cycle that catalyzes the oxidative decarboxylation of isocitrate to α-ketoglutarate and CO_2, while concomitantly reducing NADP to NADPH. In this study, we investigated previously uncharacterized interactions between Icd and nucleic acids and signaling guanine nucleotides. Using ModelX, a tool predicting interactions based on structures, we identified potential DNA-binding regions and the sequences of oligonucleotides. Fluorescence spectroscopy showed that the predicted sequence (5′-TAGGACCC-3′) bound to Icd. We further examined the interaction between Icd and ppGpp, a global regulator of the bacterial stringent responses. Fluorescence spectroscopy revealed that ppGpp bound to Icd with approximately 170 μM of the dissociation constant. Enzymatic activity assays showed that DNA inhibited Icd activity, whereas ppGpp enhanced it. These findings provide the first evidence that Icd interacts with both DNA and ppGpp, suggesting a novel mode of regulation for this central metabolic enzyme beyond classical control mechanisms.

Poster Presentation

PBM-13

Effects of Polysaccharide (Polycan) derived from Black Yeast in TNF-α induced Inflammation in the Intestinal Epithelial Cells and Loperamide- induced Constipation Models

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This study was conducted to investigate the anti-inflammatory and laxative effects of Polycan in TNF-α treated HT-29 intestinal epithelial cells and loperamide-induced constipation in vivo models, respectively. Polycan inhibited TNF-α-induced IL-8 expression in dose-dependent manner. Furthermore, Polycan suppressed TNF-α-induced phosphorylation of MAPKs (ERK1/2, p38 and JNK), degradation of Iκ-Bα and nuclear translocation of NF-κB. In an in vivo constipation model, the number of fecal pellets per food intake was significantly increased in rats administered with Polycan, 7 days after loperamide treatment. The water content of fecal pellets was restored in the Polycan groups starting 7 days after loperamide treatment. In addition, Polycan intake significantly enhanced the gastrointestinal transit ratio of a charcoal meal but reduced the number of intestinal fecal pellets. These results suggest that Polycan suppressed TNF-α-induced inflammation by blocking both the MAPK and NF-κB pathways in HT-29 cells. Additionally, in a loperamide-induced constipation model, Polycan showed clear laxative effects by increasing the number of fecal pellets, fecal water content, and intestinal transit ratio of a charcoal meal.

PBM-14

Genetic engineering-driven overexpression of *SlVTE3* resulted in enhanced vitamin E accumulation in tomatoes

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As a pivotal lipid-soluble antioxidant, vitamin E plays a significant role in safeguarding human health by mitigating oxidative stress-induced cellular damage and supporting immune homeostasis. Increasing the vitamin E concentration in edible crops represents a viable strategy for addressing micronutrient deficiencies and enhancing dietary antioxidant intake. In this study, we genetically modified *Solanum lycopersicum* cv. Micro-Tom to enhance tocopherol accumulation by overexpressing key genes in the tocopherol biosynthetic pathway. Specifically, the *SlVTE3* genes—encoding enzymes essential for the methylation step in tocopherol biosynthesis—were introduced into the tomato genome via Agrobacterium tumefaciens-mediated transformation. Putative transgenic lines were molecularly characterized through PCR and quantitative real-time PCR (qRT-PCR). Quantitative colorimetric assays confirmed a statistically significant increase in total tocopherol content in the transgenic lines relative to wild-type controls. Notably, the engineered tomatoes displayed phenotypic characteristics comparable to non-transgenic plants, suggesting no detrimental effects on vegetative or reproductive development and confirming agronomic performance stability. Taken together, these results underscore the potential of metabolic engineering to generate nutritionally enhanced crop varieties. This work establishes a framework for the biofortification of staple crops aimed at improving public health outcomes and mitigating global micronutrient malnutrition. Subsequent studies will focus on agronomic performance under field conditions and consumer perception analyses to facilitate the translational potential of these biofortified tomatoes.

PBM-15

Regulation of Rice Pollen Tube Growth by S1P-mediated Processing of pollen-expressed OsRALF peptides

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Pollen tube growth is essential for double fertilization, directly impacting grain yield in crop plants. Rapid Alkalinization Factor (RALF) peptides act as ligands for signal transduction during fertilization. We previously identified 41 RALF peptides and characterized OsRALF17 and OsRALF19, which are specifically expressed in pollen. Double mutants of OsRALF17 and OsRALF19 exhibited defects in pollen hydration, germination, and elongation, resulting in male sterility. Treatment with mature peptides (OsRALF17M and OsRALF19M) on wild-type pollen showed a dose-dependent regulation of pollen tube length, with high concentrations delaying pollen tube rupture. OsRALF17 and OsRALF19 physically interact with OsMTD2, a member of the CrRLK1L family, to initiate ROS signaling. Additionally, RUPO, another CrRLK1L family member, forms a receptor complex with OsMTD2, OsRALF17, and OsRALF19. For receptor binding, secretion of functional RALF peptides should be occurred, and this processing could be mediated by Site-1 Protease (S1P). Addressing this hypothesis, we identified S1P1, a subtilisin family protein known to process RALF peptides, and confirmed that S1P1 specifically expresses in pollen and physically interacts with OsRALF17 and OsRALF19. The *s1p1* mutant exhibited reduced fertility, increased pollen tube length, and showed reduced sensitivity to exogenous RALF peptide treatment. Further mechanistic studies on RALF peptide processing by S1P are necessary to deepen our understanding of their regulatory roles in rice pollen tube growth and fertilization.

PBM-16

OsRALF4, a RALF peptide conserved in Poaceae species, functions as a key regulator of rice grain development via CrRLK1L signaling

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The coordinated development of the embryo and endosperm is essential for the seed formation in angiosperms. While CrRLK1L receptor kinases are known to regulate plant reproduction, their peptide ligands involved in seed development remain poorly characterized. Here, we identify OsRALF4, a small secreted peptide, as a key regulator of seed development and grain quality in rice (*Oryza sativa*). OsRALF4 is expressed in the early embryonic tissue and endosperm during grain maturation. It localizes to the cell membrane, cytoplasm, and apoplast. Loss of *OsRALF4* function leads to abnormal seed formation and altered grain traits, accompanied by elevated reactive oxygen species, particularly during early embryogenesis. Although *OsRALF4* transcripts were also detected in the pistil prior to fertilization, the absence of pre-fertilization defects in mutants suggests functional redundancy at that stage. In contrast, the strong post-fertilization phenotype indicates that OsRALF4 primarily functions in early zygotic tissues. Co-immunoprecipitation assays revealed that OsRALF4 interacts with six CrRLK1L receptors implicated in seed development, supporting its role in a conserved RALF–CrRLK1L signaling module. OsRALF4 is conserved among Poaceae species, highlighting its potential relevance for cereal crop improvement. Our findings establish OsRALF4 as a secreted peptide acting post-fertilization to regulate seed development and grain quality.

PBM-17

An Albino Seedling-Lethal Mutant Reveals a Key Regulator of Chloroplast Development in *Arabidopsis thaliana*

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Chloroplasts are essential organelles for plant growth and stress resistance, functioning in photosynthesis and the biosynthesis of key phytohormones such as abscisic acid (ABA). In this study, we characterized an *Arabidopsis thaliana* T-DNA insertion mutant, *alb7*, which displays an albino phenotype and seedling lethality. Protoplast-based imaging revealed that the albino phenotype in *alb7* homozygous mutants results from severe defects in chloroplast development. Gene expression analysis showed that knockout of *ALB7* specifically downregulates chloroplast genes transcribed by plastid-encoded RNA polymerase (PEP), while those regulated by nuclear-encoded RNA polymerase (NEP) remain unaffected. These findings demonstrate that *ALB7* is a critical regulator of PEP-dependent gene expression and is required for proper chloroplast biogenesis. In addition, overexpression of *ALB7* was found to enhance drought stress tolerance in plants. This increased tolerance appears to be closely linked to ABA, a major stress hormone synthesized in chloroplasts, further supporting the role of *ALB7* in chloroplast function. Together, our results suggest that *ALB7* coordinates chloroplast development and stress responses by regulating PEP-mediated gene expression and influencing ABA-associated stress signaling in *Arabidopsis thaliana*.

PBM-18

Non-secreted peptide OsRALF5 regulate pollen tube growth in *Oryza sativa*

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In angiosperms, pollen tube growth is crucial for double fertilization and directly impacts crop yield. Rapid alkalization factor (RALF) peptides play essential roles in fertilization by interacting with receptor-like kinases in the apoplast, but the function of non-secreted RALFs remains largely unknown. We identified pollen-specific *Oryza sativa* RALF gene, *OsRALF5*, and investigated its role in reproduction. Phylogenetic analysis revealed that OsRALF5 belongs to a distinct clade lacking conserved motifs typical of RALFs. *OsRALF5* was highly expressed in mature anthers and pollen, as shown by qRT-PCR and reporter assays using native promoter-derived GUS and GFP-tagged transgenic lines. Subcellular localization of OsRALF5-GFP revealed that OsRALF5 is localized to both the cytoplasm and plasma membrane in tobacco, whereas in rice it is localized to the cytoplasm, and is not secreted to the apoplast in either system. Knockout mutants using CRISPR/Cas9 exhibited no defects in pollen viability, but showed significantly reduced pollen germination rates and seed set. Our findings demonstrate that the non-secreted peptide OsRALF5 positively regulates pollen germination and fertilization in rice, representing a unique intracellular mechanism for pollen tube growth among RALF family members.

PBM-19

Enhancing Plant Stress Tolerance through ROS Control and Subcellular Targeting of Catalase

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Catalase is a critical antioxidant enzyme that mitigates oxidative damage by decomposing hydrogen peroxide (H_2O_2) into water and oxygen, playing a pivotal role in cellular defense against oxidative stress. Catalase is primarily localized in peroxisomes, where it interacts with PEX proteins through the C-terminal peroxisomal targeting signal (PTS) in plants. This study investigates the functional significance of catalase subcellular localization in Arabidopsis thaliana and its impact on stress. The intact catalase (CAT2-ox) was localized to peroxisomes, while CAT2ΔQKL-ox, which lacked the peroxisome targeting signal, was dispersed across multiple organelles, including the cytosol, chloroplasts, and extracellular spaces. Under extracellular hydrogen peroxide (H_2O_2) treatment, CAT2ΔQKL-ox exhibited relatively higher resistance compared to CAT2-ox, though both constructs showed substantially reduced necrosis relative to wild-type plants. CAT2ΔQKL-ox also exhibited improved salt stress tolerance, indicating that the cytosolic/extracellular localization of catalase selectively neutralizes H_2O_2 in these compartments, thereby enhancing stress adaptation. These results indicate that regulating the subcellular distribution of catalase provides a strategy for enhancing plant resistance to stresses.

PBM-20

Exploring the molecular mechanism that mediates N-induced stem growth in tomato plants

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Nowadays, in agriculture, lots of nitrogen(N) fertilizers are used for cultivating crops. It is reasonable, as plant cultivation under sufficient nitrogen conditions typically leads to increased yields. However, it is still not clear how N affects various aspects of plant growth and development. Among many physiological changes occurred by N supplementation, we are focused on the molecular mechanisms that mediates N-induced stem elongation. We isolated candidate genes based on their N-responsive expression and co-expression patterns with previously reported genes involved in cell elongation and stem growth. Among the candidates, we found N-responsive transcription factor *SlNRTF550* that modulates internode growth. $SlNRTF550^{OX}$ plants show significantly promoted internode elongation without significant change of the node numbers. We found that *SlNRTF550* overexpression led to up-regulation of genes involved in cell elongation and secondary cell wall development. Further biochemical and genetic analysis will clarify the molecular mechanism by which *SlNRTF550* regulates N-mediated stem elongation in plants.

PBM-21

An *Ehd1*-independent short-day flowering pathway mediated by OsJAZ11 and OsMYC2 in rice

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Rice is a facultative short-day (SD) plant that flowers early under SD conditions through the activation of the florigen genes *Hd3a* and *RFT1*, primarily induced by *Ehd1*. To explore *Ehd1*-independent flowering pathways, we transferred wild-type (WT) and *ehd1* CRISPR/Cas9 knockout mutants from long-day (LD) to SD conditions. WT plants flowered after 40 days of SD, while *ehd1* mutants exhibited a ~16-day delay. In WT, florigen expression increased 8 days after SD treatment, but was delayed to 14 days in *ehd1*. Transcriptome analysis of *ehd1* mutants revealed upregulation of *OsSFL1*, *OsHDAC2*, and *OsHDAC3*, components of the histone deacetylase complex. Consistently, RNA-seq and ChIP-seq showed reduced genome-wide H3 acetylation and lower acetylation at chromatin regions of flowering repressors, such as *OsNF-YC2*, in *ehd1*. Dysfunctional *Ehd1* transcripts were elevated, likely due to diminished acetylation of upstream repressors. In *ossfl1 ehd1* double mutants, *Ehd1* transcript levels and *OsNF-YC2* expression were restored, supporting its role as an upstream repressor. We also identified *OsJAZ11* as upregulated in *ehd1*, and *ehd1 osjaz11* double mutants flowered 4 days later than *ehd1*. Luciferase assays confirmed that *OsMYC2* directly represses *Hd3a* promoter activity, and Co-IP verified its interaction with *OsJAZ11*. These results suggest that *OsJAZ11* promotes flowering independently of *Ehd1* by repressing *OsMYC2*-mediated suppression of *Hd3a* expression.

PBM-22

The Role of the Nitrogen Use Efficiency-Related Gene HNI9 in Regulating Plant Growth under Salt Stress

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Soil salinization is one of the major environmental factors limiting agricultural productivity and is being exacerbated by climate change. Salt stress induces osmotic stress and ion toxicity in plants, leading to the accumulation of reactive oxygen species (ROS), nutrient imbalance, and hormonal disruption. *High Nitrogen Insensitive 9* (*HNI9*) is a gene known to be involved in nitrogen response regulation and has also been implicated in ROS regulation. However, its role under salt stress conditions remains poorly understood. In this study, we investigated the function of HNI9 under salt stress using the Arabidopsis thaliana mutant lines *hni9-1* and *hni9-2*. Plants were grown under 5 mM nitrogen conditions and treated with 150 mM and 175 mM NaCl. Compared to wild-type plants, the hni9 mutants exhibited enhanced tolerance to salt stress, including increased chlorophyll content, altered ROS staining patterns (DAB, NBT), and reduced accumulation of both Na^+ and K^+ ions. These results suggest that HNI9 plays a regulatory role in plant growth under salt stress by contributing to ROS detoxification and maintaining ion homeostasis. Therefore, HNI9 functions not only in nitrogen utilization but also as a key component in plant abiotic stress resistance mechanisms, making it a promising target for developing salt-tolerant crop varieties.

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PBM-23

Comparative leaf metabolomics of soybeans across seed coat colors and developmental stages

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This study analyzed the leaf metabolite profiles of 12 core soybean (*Glycine max L.*) cultivars representing four seed coat colors: yellow, black, brown, and green. Metabolite extraction and analysis were conducted using ultra-high-performance liquid chromatography coupled with quadrupole time-of-flight mass spectrometry (UHPLC-QTOF/MS). Leaf samples were collected at six specific developmental stages, encompassing two vegetative stages (V2 and V4) and four reproductive stages (R1, R3, R5, and R7). A total of 14 metabolites were identified, with clear compositional variation across growth stages, indicating stage-specific metabolic activity. Notably, coumestrol was predominantly accumulated during the late developmental phase, particularly at the R7 stage. Multivariate analysis using partial least squares discriminant analysis (PLS-DA) revealed significant differences in metabolite profiles associated with seed coat color. Black and brown cultivars exhibited similar metabolic patterns, while green cultivars showed greater variation. In contrast, yellow cultivars formed a distinct cluster, suggesting potential metabolic differentiation. Among the key findings, rutin and luteolin were more abundant in black, brown, and green cultivars, whereas kaempferol-3-O-glucoside was predominantly enriched in yellow cultivars. This study provides foundational insights into the dynamic metabolite composition of soybean leaves and highlights their potential for use in functional food and material development.

PBM-24

Physiological and Cytological Responses of Sweet Potato ‘Tongchaeru’ to Irrigation Water Salinity in the Saemangeum Reclaimed Land

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Sweet potato (Ipomoea batatas) is an agronomical important crop known for its vigorous growth and adaptability. Recently, attention has expanded beyond its storage root to include stems and leaves due to their potential uses. However, in salt-affected reclaimed soils, high salinity impairs water uptake and damages cells, limiting plant productivity. This study examined the physiological and cytological responses of the cultivar ‘Tongchaeru’ under different irrigation salinity levels in a rain-sheltered greenhouse in the Saemangeum reclaimed land. From June to October 2024, plants were irrigated twice a week with NaCl solutions at 0% (control), 0.1%, and 0.2%. At harvest, petiole and storage root samples were collected for histological examination, and starch content in storage roots was measured. Salinity temporarily reduced shoot growth during early stages, but growth partially recovered. Sodium accumulation increased in petiole tissues with salinity but remained unchanged in storage roots. Starch content in storage roots decreased as salinity increased. Cytohistological analysis revealed damage to some cell layers due to dehydration during storage in cortical cells of roots from all treatments, but there was no difference between treatments. Suggesting that sweet potato growth can be maintained under irrigation salinity of up to 0.2% NaCl.

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PBM-25

UGT74E2 Negatively Regulates Salt Stress Tolerance in Arabidopsis by Modulating IBA Glycosylation

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Soil salinization, aggravated by irrigation practices, climate change, and excessive groundwater use, threatens sustainable agriculture by reducing crop yields and soil fertility. Salt stress induces oxidative stress, osmotic imbalance, and nutrient deficiencies, which hinder germination, photosynthesis, and productivity. The gene *Uridine diphosphate glycosyltransferase 74E2* (*UGT74E2*), part of the UDP-glycosyltransferase family, is known to glycosylate indole-3-butyric acid (IBA), but its role in salt stress tolerance remains unclear. Since plants typically increase IBA levels under stress, we hypothesized that *UGT74E2* inactivates IBA through glycosylation, thereby reducing stress responses, while loss of *UGT74E2* could enhance stress tolerance by maintaining active IBA levels. To test this, we compared salt stress responses in *ugt74e2* knockout (*ugt74e2ko*) Arabidopsis seedlings and wild-type Col-0. *ugt74e2ko* plants exhibited improved salt tolerance, showing better growth and recovery. After salt treatment, they accumulated fewer reactive oxygen species (ROS) and had higher levels of anthocyanins, proline, and flavanols (kaempferol, quercetin) than Col-0. These results suggest that *UGT74E2* plays a crucial role in regulating plant growth under salt stress by modulating ROS detoxification and maintaining physiological balance. *UGT74E2* may be a promising target for developing salt-tolerant crop varieties

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PBM-26

Neurotrophic Effects of *Foeniculum vulgare* Ethanol Extracts on Hippocampal Neurons: Role of Anethole in Neurite Outgrowth and Synaptic Development

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Foeniculum *vulgare* (fennel) is widely recognized for its medicinal properties, but its neurotrophic potential remains underexplored. This study investigated the neuroprotective and developmental effects of *F. vulgare* ethanol extracts (FVSE) and its major component, anethole, on cultured rat hippocampal neurons. Treatment with 40 µg/mL FVSE and 20 µM anethole significantly enhanced neurite outgrowth and dendritic branching without cytotoxicity. Furthermore, both treatments promoted synaptogenesis, as confirmed by immunocytochemistry. Network pharmacology and in silico pathway analysis revealed that FVSE targets key neurotrophic pathways, including TrkB, PI3K-AKT, GSK3β, and Erk1/2 signaling. Anethole, in particular, showed a strong regulatory effect on these pathways, suggesting its potential as a bioactive lead compound. These findings were supported by experimental data showing increased expression of synaptic markers and enhanced neuronal connectivity. Overall, this study highlights the neurotrophic potential of FVSE and anethole in promoting neuronal maturation and synaptic development, offering a promising direction for therapeutic strategies against neurodevelopmental and neurodegenerative disorders. This work supports the continued investigation of medicinal herbs as sources of bioactive compounds for brain health.

Poster Presentation

PBM-27

Venom gland profiling of three korean *Gloydius* species and recombinant expression of major toxins

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In Korea, the majority of snakebite envenomation cases are caused by three species *Gloydius brevicaudus*, *Gloydius intermedius*, and *Gloydius ussuriensis*. Clinical symptoms following snakebite vary significantly among species, primarily due to interspecific differences in venom composition, which comprises complex mixtures of bioactive peptides. Despite the clinical relevance of snakebite envenomation, Korea lacks an established therapeutic protocol, and molecular studies on indigenous snake venoms are still limited. Therefore, detailed characterization of venom composition is critical for the rational design of species-specific antivenoms. In this study, we performed an integrative omics-based analysis combining two-dimensional gel electrophoresis (2-DE) and RNA sequencing to profile venom gland proteins and transcripts in the three Gloydius species. Proteomic results revealed that *G. brevicaudus* and *G. ussuriensis* venoms are predominantly composed of snake venom metalloproteinases (SVMPs), whereas *G. intermedius* venom shows an abundance of snake venom serine proteases (SVSPs). Phospholipase A2 (PLA_2) was found in all three species, but was more prominently expressed in *G. ussuriensis* and *G. intermedius*. We successfully identified and cloned major toxin-encoding genes including SVMP, SVSP, and PLA_2. These key venom proteins were subsequently expressed and purified in recombinant protein. Our findings provide molecular insights into species-specific venom profiles and offer a valuable foundation for the development of diagnostic tools and effective antivenoms.

PBM-28

Natural variation-driven regulation of temperature- and photoperiod-responsive flowering by FLC and FLC family genes: A potetntial regulatory hub for combating climate change

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Temperature is critical player in determining flowering time, a key adaptive trait in plants. While most natural accessions of Arabidopsis exhibit temperature-responsive flowering, we identified two unique accessions: one that displayed complete insensitivity across a broad range of temperatures (10°C to 27°C), and another that exhibited the opposite phenotype of known accessions, which we termed 'reverse temperature sensitivity. Furthermore, these accessions were also insensitive to photoperiod, exhibiting flowering under both short-days and long-days. Our genetics, genomics, and transcriptomics data revealed that *FLC* and *MAF*s modulate these unusual flowering phenotypes and had natural polymorphisms, resulting in either their downregulation or complete loss of function. Notably, prolonged cold exposure during vernalization, or genetic knockdown of *FLC* ectopically or in the SAM region (*pKNAT*-driven) resulted in the complete loss of temperature sensitivity, leading to uniform flowering regardless of ambient temperature. These data suggest that *FLC* underlines the reverse temperature sensitivity. Our findings highlight the diversity of flowering time regulation in natural populations and introduces *FLC* as a major regulator in ambient temperature-responsive flowering that fine-tunes plant phenology under varying environmental conditions. These insights provide a foundation for further studies on adaptive flowering strategies and could pave ways for devising future breeding programs to combat climate change and ensure global food security.

PBM-29

Development of Recombinase Polymerase Amplification (RPA) method for detection of Herbicide-resistant GM crops

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To minimize the risk of unintentional environmental release of Living Modified Organisms (LMO) and to enhance biosafety management, regular environmental monitoring has been implemented. With the growing use of genetically modified (GM) crops, there is increasing demand for rapid and accurate molecular detection technologies suitable for field application. In this study, we developed and optimized primers and a probe targeting the *EPSPS* gene, which is commonly found in glyphosate-resistant GM crops, using Recombinase Polymerase Amplification (RPA) technology. The assay was designed to enable stable amplification under isothermal conditions and to be compatible with a portable Real-Time PCR device, allowing on-site fluorescence-based detection. The DNA extraction procedure was simplified using a basic buffer method, enabling direct analysis of plant lysates without purification. As a result, the target gene was successfully detected within 25 minutes using an RPA probe system. The RPA using an isothermal PCR device can also be effectively applied to environmental monitoring for GM crop detection.

PBM-30

Mutation of *SlNRTF3* promotes growth under N-limiting conditions through activation of nitrogen assimilation pathway

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Nitrogen (N) is one of the major limiting macronutrient for plant growth and development. To understand molecular mechanisms underlying nitrogen assimilation and utilization pathway, we isolated N-responsive transcription factors based on their inducibility and temporal expression pattern under N limiting conditions. *SlNRTF3* is a gene whose expression is up-regulated by increasing external nitrogen concentration. To address molecular and physiological functions of *SlNRTF3*, we generated *SlNRTF3* overexpressing (*SlNRTF3*^{OX}) and *slnrtf3* mutant plants. Phenotypic analysis under different nitrogen conditions revealed that *slnrtf3* mutant plants exhibited significantly better growth under nitrogen-deficient conditions compared to both the non-transgenic control (NT) and *SlNRTF3*^{OX} plants. Transcriptomic analysis showed that expression of genes related to carbon and nitrogen assimilation is up-regulated in *slnrtf3* mutant plants under low nitrogen compared with non-transgenic control plants. In addition, external N supplement mitigated growth defects observed in *SlNRTF3*^{OX} plants. These results suggest that *SlNRTF3* act as a negative regulator for N-mediated growth promotion in plants potentially through N uptake and assimilation in plants.

Poster Presentation

PBM-31

CRISPR-Cas9 Genome Editing in Tomato Using In Vivo Cas9/tracrRNA Expression and Exogenous crRNA

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CRISPR-Cas9 has emerged as a powerful tool for precise plant genome engineering, yet conventional guide RNA (gRNA) synthesis and in vitro delivery methods impose substantial time and cost burdens, particularly for iterative target validation. To overcome these limitations, we engineered a tomato (Solanum lycopersicum) system in which Cas9 and tracrRNA are constitutively expressed in vivo, enabling simple exogenous delivery of synthetic CRISPR RNA (crRNA) alone. First, we constructed co-expressing Cas9 and tracrRNA tomato via Agrobacterium-mediated transformation. Transgenic lines were confirmed the insertion of T-DNA and expression of Cas9 mRNA. Next, we optimized a protoplast transfection protocol for delivery of crRNA targeting two endogenous loci (ALS2 and SlLCY-E). Our platform has several advantages: (1) Simplification of cloning process for each new target gene, (2) rapid functional screening of several crRNAs in protoplasts, and (3) potential extension to multiplex genome editing by co-transfection of multiple crRNAs. Ongoing work focuses on quantifying editing efficiency across loci, regenerating edited plants from protoplasts. This modular, cost-effective system will accelerate functional genomics and trait engineering in tomato and other Solanaceae crops.

PBM-32

Aureimonas Altamirensis DSM 21988 as a Dual-Function Agent: Promoting Rice Growth and Inducing Systemic Resistance Against Bacterial Blight

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Beneficial microorganisms residing in plants play a crucial role in maintaining plant health and ecological balance. In this study, we identified a specific beneficial bacterium, *Aureimonas altamirensis* DSM 21988 (strain 11704), which is an endophytic bacterium capable of producing a high level of indole-3-acetic acid (IAA). This bacterium is utilized in agrobiotechnology, serving as both a biofertilizer and a biocontrol agent. Among 15 strains isolated from rice genome sequencing, strain 11704 exhibited higher IAA biosynthesis, maintaining stable production over 96 hours and showing a 2.5-fold dose-dependent increase with 2.0 g/L L-tryptophan. The strain demonstrated significant improvements in rice growth: 10% higher germination rates ($p<0.01$), 25% increased shoot length ($p<0.001$), 30–40% greater shoot/root biomass, and enhanced chlorophyll content (35% total, 40% chlorophyll a, 15% chlorophyll b; $p<0.05-0.001$). Molecular analysis indicated the upregulation of auxin-related genes, including a 4-fold increase in *OsSAUR-11* and a 2.5-fold increase in *OsSAUR45*, confirming IAA-mediated growth promotion. Biocontrol assays against *Xoo* demonstrated a 60% reduction in lesion length ($p<0.001$) and a 70% decrease in pathogen populations ($p<0.01$), highlighting robust disease suppression. These findings establish that strain 11704 is a sustainable alternative to chemical fertilizers, simultaneously enhancing rice productivity through auxin pathway modulation and mitigating bacterial leaf blight.

PBM-33

Enhancement of Growth and Bioactive Compound Accumulation in Licorice Sprouts through Symbiotic Association with the Newly Isolated *Mixta theicola* QC88-366

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Seven morphologically distinct microbial strains were isolated, and *Mixta theicola* QC88-366 was selected for its unique colony characteristics and limited prior research. Identification was conducted via 16S rRNA sequencing and phylogenetic analysis. SEM confirmed microbial morphology and colonization, while biochemical assays demonstrated phosphate solubilization and siderophore production, confirming its potential as a plant growth-promoting rhizobacteria. Treatments with *M. theicola* QC88-366 significantly enhanced root length, thickness, and fresh weight of licorice sprouts compared to controls, especially in soil mixture and seed coating groups. Photosynthetic efficiency, chlorophyll content, and stomatal conductance were improved in treated plants. Notably, glycyrrhizic acid and liquiritigenin concentrations increased in both above- and below-ground tissues depending on treatment, correlating with upregulated expression of key biosynthetic genes (CYP72A154, CYP88D6, GuCHS, GuUgat). Hormone (ABA, IAA) and amino acid profiling revealed elevated levels and distinct metabolic patterns among treatments. Sugar-organic acid correlation analysis and mineral profiling indicated enhanced nutrient uptake, particularly phosphorus and potassium, in seed coating groups. Vitamin B and C content was also significantly higher in treated samples. These results suggest that *M. theicola* QC88-366 inoculation can enhance growth, metabolic activity, and bioactive compound accumulation in licorice sprouts, providing a promising strategy for improving crop quality and productivity. This research was supported by Basic Science Research Program through the National Research Foundation of Korea (NRF) funded by the Ministry of Education (RS-2024-00461271)

PBM-34

Determination of Platydin D Content by Cultivation Period of *Platycodon grandiflorum* through Plug Seedling Transplantation

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Platycodon grandiflorum is a natural product widely used as a food material and as a herbal medicine to prevent respiratory diseases. Due to the nature of field cultivation of *Platycodon grandiflorum*, various technical efforts are being made to increase production. Cultivation using plug seedlings is a method used to increase production. Therefore, This study was conducted to analyze the platycodin D content by cultivation period of *Platycodon grandiflorum* through plug seedling transplantation. Analytical samples were collected and analyzed from 1, 2, and 3 years old samples produced through plug seedling formal cultivation. Among platycodin D was extracted with hot water and analyzed by LC-MS/MS. The weights of the *Platycodon grandiflorum* grown for 1, 2, and 3 years were 194.60±45.99 g, 288±76.82 g, and 507.38±358.91 g, respectively. The contents of platycodin D in the 1, 2, and 3-year cultivated samples were 314.45 mg/kg, 179.54 mg/kg, and 199.49 mg/kg, respectively. Compared to seed sowing cultivation based on 1 year old samples, the weight of plug seeding cultivation samples was approximately 4.5 times heavier, and the content of platycodin D was approximately 1.2 times higher. This study is expected to be utilized in the food industry through analysis of platycodin D content and production by the cultivation period of plug seedlings.

Poster Presentation

PBM-35

Cadmium Stress Alleviation in Soybean(*Glycine max* L.) via Chitosan–Melatonin Nanoparticles: Hormonal and Metabolomic Mechanistic Analysis

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Heavy metal contamination in agricultural soils, particularly cadmium (Cd), impairs plant growth, disrupts metabolic processes, and threatens food security. In this study, we investigated the potential of foliar-applied chitosan–melatonin nanoparticles (CSM NPs) to alleviate Cd stress in soybean (*Glycine max* L.) through hormonal and metabolic reprogramming. The synthesized CSM NPs were characterized using SEM, XRD, TGA, and XPS, confirming their nanoscale size, structural stability, and surface composition. Foliar application of CSM NPs under Cd stress significantly altered stress-related phytohormone levels. Abscisic acid (ABA), which was elevated under Cd stress, was reduced upon treatment, while salicylic acid (SA) increased and jasmonic acid (JA) decreased, suggesting stress mitigation via hormonal modulation. Metabolomic profiling using UPLC-Orbitrap-MS identified over 500 metabolites, including amino acids and organic acids, in both shoot and root tissues. Principal component analysis (PCA) and heatmap clustering revealed distinct metabolic separation between Cd-stressed and CSM NP-treated plants. Pathway analysis showed that Cd stress disrupted key metabolic routes such as the TCA cycle, glyoxylate metabolism, and amino acid biosynthesis. Notably, isocitric acid and citric acid levels increased, while fumaric acid decreased. CSM NP application partially reversed these disruptions, restoring central metabolic balance.

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PBM-36

Natural antisense transcript *OsDof2NAT* enhances early heading and drought tolerance by activating *Dof2* expression in rice

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Natural antisense transcripts (NATs) are transcribed in the direction opposite of their target mRNAs and act as key regulators of diverse biological processes in animals and plants. However, despite their widespread presence in plants, their functional roles remain largely unexplored, especially in heading date regulation and abiotic stress responses in rice. In this study, we investigate the functional role of the *OsDof2NAT/OsDof2* module in regulating heading date and drought tolerance in rice. The expression of *OsDof2NAT* and *OsDof2* is regulated by the circadian rhythm and induced under drought stress. *OsDof2NAT* enhances *OsDof2* expression by recruiting OsWDR5a, a component of the MLL complex, which promotes H3K4me3 deposition, whereas its knockdown reduces both *OsDof2* expression and H3K4me3 levels. Furthermore, overexpression of *OsDof2NAT* or *OsDof2* improves drought tolerance and promotes early heading by activating *Ehd1* and *Hd3a*. Our findings elucidate the molecular mechanism by which *OsDof2NAT* regulates *OsDof2* expression through histone modifications, underscoring the functional significance of lncRNAs in plant development and stress responses.

PBM-37

Methyl Jasmonate Preharvest Treatment Activates Plant Defense System and Induces Glucosinolate Production in Wasabi (*Wasabia japonica* Matsum) Leaves

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Wasabi, or Japanese horseradish (*Wasabia japonica* (Miq.) Matsum.), a member of the Brassicaceae family, is cultivated in specific regions; however, wasabi paste is consumed worldwide as a condiment known for its strong pungent flavor. This distinctive flavor results from the enzymatic hydrolysis of glucosinolates—sulfur-containing secondary metabolites, abundantly found in wasabi. To encourage the use of typically discarded plant parts and reduce agricultural waste during wasabi cultivation, our study aimed to enhance glucosinolate content in vegetative leaves and petioles through preharvest treatment with methyl jasmonate (MeJA). MeJA was applied at three concentrations (100, 300, and 500 µM), and samples were collected at two time points: 6 hours and 3 days after treatment (6HAT and 3DAT, respectively). Our results indicated that the chemical composition of leaves was more responsive to MeJA treatment than that of petioles. While MeJA induced only minor changes in flavonoid content, it significantly increased glucosinolate levels in wasabi leaves. Notably, sinigrin content increased by approximately 1.3 to 1.4 times at 3DAT, reaching peak concentrations of 67.576 $\mu mol \cdot g^{-1}$ in mature leaves and 115.583 $\mu mol \cdot g^{-1}$ in young leaves. The formation of allyl isothiocyanate followed a similar pattern to sinigrin accumulation. These findings suggest that MeJA could activate the plant's defense system, and further assessment of myrosinase activity and antioxidant enzymes could provide deeper insights into the underlying mechanisms.

PBM-38

Stage-Specific Effects of Sulfur Fertilization on Glucosinolate Production in *Wasabia japonica* Leaves

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Wasabia japonica is a high-value perennial crop in the Brassicaceae family, known for its pungent flavor derived from the hydrolysis products of glucosinolates (GSLs), especially allyl isothiocyanate. Although previous findings indicated that sulfur fertilization enhances GSL production in Brassicaceae plants, the underlying mechanism relevant to sulfur effects on GSL production in wasabi remained obscure. This study aimed to provide new insights into the effect of sulfur fertilization on wasabi leaves across distinct developmental stages: vegetative (1-year-old) and reproductive (3-year-old). Ammonium sulfate (AS) was applied at a concentration of 40 kg/ha, and leaves were collected two weeks later to analyze biochemical composition and genetic regulation. AS supplementation significantly increased GSL content in vegetative leaves (1.6-fold, $p<0.05$), but slightly decreased (0.94-fold) at the reproductive stage. Sulfur and sulfate levels increased in vegetative leaves, indicating higher sulfur absorption at a younger stage. The sulfur-containing amino acids cystine and methionine increased in both stages, with greater accumulation observed in the reproductive stage. Consistently, *WjSULTR2*.1 and *WjSULTR2*.2 were highly upregulated in vegetative leaves under sulfur treatment. The distinct expression of *WjFLC*, a flowering-related gene, marked two developmental stages of wasabi leaves, and its potential effect on GSL synthetic regulation. These findings suggest developmental stage-specific sulfur responsiveness in *W. japonica*, through coordinating changes in sulfur uptake, amino acid metabolism, GSL biosynthesis, and gene expression.

PBM-39

In rice, Actin-related protein 2/3 complex 2B subunit (ARPC2B) regulates Gibberellin Biosynthesis, and overexpression of *OsARPC2B* gene increases Grain Yield

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Actin-related proteins (ARPs) are also essential for various aspects of plant growth, including cellular elongation and morphological development. Gibberellic acid (GA) plays an important role in regulating plant development and boosting productivity. Despite their importance, the connections between ARPs and the pathways responsible for GA synthesis and signaling remain insufficiently characterized. In this study, we identified the *OsARPC2B* gene in rice (*Oryza sativa*), which encodes a subunit of an ARP complex, through the Ac/Ds transposon knockout system. Plants with an *osarpc2b* knockout (Ko) mutation exhibited stunted growth and reduced height, along with lower GA_3 levels in their shoots. Furthermore, when treated with GA_3, the height of the *osarpc2b* Ko mutant recovered to a level similar to that of wild-type (WT) plants. Unlike *osarpc2b* Ko mutant, overexpression of *OsARPC2B* (Ox) showed enhanced growth and increased grain yield, compare to WT. Transcriptomic analysis of flag leaves from overexpression plants and knockout mutants indicated that *OsARPC2B* gene related to cell development and elongation. These findings point to a regulatory role for *OsARPC2B* in GA homeostasis, which in turn affects rice plant growth and overall productivity.

PBM-40

In rice, microRNA171f regulates expression of *SCL6*, which is involved in drought tolerance and flavonoid biosynthesis

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Plants have developed mechanisms to cope with drought stress. One mechanism that is known to be involved in drought stress responses is the regulation of gene expression by microRNAs (miRNAs). In this study, we identified the role of *osa-miR171f* in *SCARECROW-LIKE6-I* (*SCL6-I*) and *SCL6-II* in rice (*Oryza sativa*) regulation of the drought response, using phenotypic and transcriptome analysis of osa-MIR171f-overexpressing (*osa-MIR171f*-OE) and knockout (K/O) plants generated by Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR)/Cas9. Among *osa-MIR171* family genes (*osa-MIR171a-f*), *osa-MIR171f* was mainly expressed in response to drought stress and ABA plant hormone. In *osa-MIR171f*-OE plants and -knockout (K/O) mutant, the transcript levels of *SCL6-I* and *SCL6-II* were decreased, and the expression of flavonoid biosynthesis genes were regulated. Furthermore, *osa-MIR171f*-OE transgenic plants showed drought tolerance was reduced, compared to non-transgenic (NT) control plants. Consequently, *osa-mir171f* K/O leading to drought tolerance. Our results suggest that association of drought defense system regulatory process with the expression of flavonoid biosynthesis genes and propose a model in which osa-mature-microRNA171a-f (osa-miR171) derived from osa-pre-miR171f regulates flavonoid biosynthesis as a response to drought using its *SCL6-I* and *SCL6-II* targets.

PBM-41

Fumigant Efficacy of Sulfuryl Fluoride Against *Sitophiluls zeamias* and Sorption Characteristics by Origin of Wood Pellets

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Wood pellets are increasingly in global demand as an alternative to fossil fuels and a climate change mitigation strategy. In Korea, exotic pests have been detected in imported wood pellets during quarantine inspections, and the current plant quarantine phytosanitary treatment guidelines recommend treatment with a combination of methyl bromide and phosphine. Methyl bromide is designated as an ozone-depleting substance under the Montreal Protocol and also has been reported to negatively affect the human nervous system, raising the need for alternatives. Phosphine, on the other hand, is facing growing concerns due to the development of resistance among pests, resulting in the need for higher doses and prolonged exposure times. In this study, the fumigant efficacy of sulfuryl fluoride as an alternative fumigant against *Sitophilus zeamais* was assessed, and sorption characteristics of sulfuryl fluoride were compared across wood pellets of different origins to determine significant differences. In the fumigation efficacy evaluation against *S. zeamais*, all developmental stages except the egg stage were effectively controlled at relatively low concentrations of sulfuryl fluoride, while the egg stage required higher concentrations for successful control. The subsequent comparison of sorption characteristics among wood pellets from Russia, Indonesia, and Vietnam showed no statistically significant differences. These findings provide essential data for establishing phytosanitary treatment protocols, contributing to the development of sustainable fumigation strategies for imported wood pellets.

PBM-42

Efficacy of Phosphine Fumigation Against *Ostrinia furnacalis* in Sweet Pumpkin (*Cucurbita maxima*)

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Sweet pumpkins grown in New Zealand are widely imported into South Korea for consumption. Fumigation is frequently applied to secure quarantine compliance and prevent the spread of potential insect pests during postharvest distribution. Although methyl bromide (MB) is commonly used for quarantine treatment of commodities that require rapid disinfestation, it has been classified as an ozone-depleting substance. Thus, this study explored an alternative fumigant for use on imported sweet pumpkin. Laboratory fumigation with phosphine (PH_3) was conducted in the 14-liter desiccators to evaluate the sorption of PH_3 by sweet pumpkin under three different loading ratios and to determine its effect on 2nd instar larvae and eggs of *Ostrinia furnacalis* at 8°C. In addition, potential phytotoxic effects at the maximum loading ratio were evaluated by measuring weight loss rate, firmness, decay, external discoloration, sugar content, external color and through sensory evaluation. As a result, the effects of PH_3 on larvae and eggs were determined, and 100% mortality was observed after 12 hours of exposure. The result also showed no significant differences in PH_3 sorption among loading ratios, nor in phytotoxic effects between the treated sweet pumpkin and control groups after 14 days of storage. Therefore, the results of this study demonstrate that phosphine can serve as an effective alternative to MB for controlling *Ostrinia furnacalis* in sweet pumpkins.

Poster Presentation

PBM-43

Development of Multiplex PCR Assays for Simultaneous Detection of Fungal and Viral Pathogens in *Cymbidium kanran*

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Cymbidium kanran is an endangered orchid native to Jeju Island, Korea, known for its fragrant winter blooms with diverse shapes and colors. This species is susceptible to various pathogens, including four fungal pathogenes, *Colletotrichum gloeosporioides* (Cg), *Pestalotiopsis* sp. (Ps), *Fusarium oxysporum* (Fo), and *F. proliferatum* (Fp), and four viral pathogens, *Odontoglossum ringspot virus* (ORSV), *Orchid fleck virus* (OFV), *Tobacco mosaic virus* (TMV), and *Cymbidium mosaic virus* (CymMV). In this study, we developed two distinct multiplex PCR assays: one for the simultaneous detection of the four fungal pathogens and another for the four viral pathogens. The fungal assay targeted ITS regions, producing specific amplicons for Cg (480 bp), Ps (407 bp), Fo (321 bp), and Fp (279 bp). The viral assay amplified the replicase genes of ORSV (594 bp) and TMV (400 bp), the polymerase gene of OFV (482 bp), and the coat protein gene of CymMV (220 bp). Under optimized conditions, all primer sets produced distinct and non-overlapping amplicons. Both assays reliably detected single and mixed infections of fungal and viral pathogens in symptomatic *C. kanran* leaves. These results demonstrate that the developed multiplex PCR assays offer rapid, reliable, and effective tools for early diagnosis of major fungal and viral pathogens affecting *C. kanran*.

PBM-44

In vitro callus induction of *Psoralea corylifolia* and quantification of bakuchiol under varying plant hormone conditions

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Cullen corylifolium (L.) Medik (also called *Psoralea corylifolia* Linn. and babchi), a medicinal plant known for its antimicrobial and anti-inflammatory properties, is a major natural source of bakuchiol—a meroterpene phenol with high pharmaceutical and cosmetic value. However, overharvesting and limited natural availability have raised concerns about its sustainable production. In this study, we established an in vitro tissue culture system to induce callus formation from different explants (leaf, stem, and root) of *P. corylifolia* by optimizing the type and concentration of cytokinin and auxin hormones. Explants were cultured on Murashige and Skoog (MS) medium supplemented with varying combinations of 6-benzylaminopurine (BAP), kinetin, 2,4-dichlorophenoxyacetic acid (2,4-D), and naphthaleneacetic acid (NAA). Callus induction was observed to be most effective with moderate cytokinin-auxin combinations. To determine bakuchiol production in callus, we extracted metabolites using methanol and analyzed the samples via high-performance liquid chromatography (HPLC) and liquid chromatography–mass spectrometry (LC-MS). We analyzed the presence and concentration of bakuchiol by comparing it with a standard. Our findings provide tissue cultured materials as a promising alternative method for the sustainable and climate-independent production of bakuchiol.

PBM-45

Farnesiferol B and kamolonol as potent BACE1 inhibitors with neuroprotective effects

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β-Site amyloid precursor protein (APP) cleaving enzyme 1 (BACE1) has been targeted for the treatment of Alzheimer's disease (AD). Among the five compounds isolated from Ferula assa-foetida, farnesiferol B (FFB) and kamolonol (KML) showed potent BACE1 inhibitory activity (IC50 values = 8.106 ± 1.800 and 1.631 ± 0.306 µM, respectively), and wered competitive BACE1 inhibitiors. In silico pharmacokinetics predicted FFB had high gastrointestinal absorption and blood-brain barrier permeability. FFB and KML were nontoxic to normal Madin-Darby canine kidney and neuroblastoma SH-SY5Y cells, and showed neuroprotective effects when neurotoxicity was induced to SH-SY5Y cells by Aβ42 treatment. The activities of FFB and KML may be related to their interaction with the flap region and hydrogen bonding with ARG368 as observed in molecular docking simulations. Based on the results, it can be suggested that FFB and KML are potential candidates for the treatment of neurodegenerative disorders including AD with their potent BACE1 inhibitory activity and neuroprotective effects.

PBM-46

Drug Repurposing of D-Cycloserine: A New Approach to Inhibiting Melanogenesis in Cosmetic Science

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Melanogenesis, the process of melanin production catalyzed by tyrosinase, plays a key role in determining skin pigmentation. However, excessive melanin synthesis can lead to hyperpigmentation disorders such as freckles, melasma, age spots, and seborrheic keratosis. Therefore, discovering agents that regulate melanogenesis is critical for developing whitening cosmetics and dermatological treatments. D-Cycloserine, a broad-spectrum antibiotic used as a second-line treatment for drug-resistant tuberculosis, was investigated for its anti-melanogenic properties. In B16F10 melanoma cells, D-Cycloserine significantly inhibited melanin production by downregulating melanogenesis-related proteins including tyrosinase, TRP-1, TRP-2, and the transcription factor MITF. It also suppressed the Akt signaling pathway and modulated GSK-3β activity, contributing to reduced melanin synthesis. Furthermore, it promoted phosphorylation of β-catenin, which decreased its stability and nuclear translocation, thus affecting MITF expression. In human epidermal melanocytes, D-Cycloserine reduced both intracellular melanin content and tyrosinase activity. These findings demonstrate that D-Cycloserine inhibits melanogenesis by targeting multiple pathways, including Akt and Wnt/β-catenin signaling. This study suggests that D-Cycloserine may serve as a promising candidate for repurposing as a functional whitening agent, laying the groundwork for development in cosmetic and therapeutic products aimed at controlling hyperpigmentation.

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PBM-47

Melanogenic Inhibitory and Immunoenhancing Effects of a Novel Lysinibacillus sp. JNUCC 51 Isolated from Baengnokdam, Mt. Halla, Jeju Island

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A novel strain, *Lysinibacillus* sp. JNUCC 51, was isolated from soil collected in the Baengnokdam region of Jeju Island. The strain was cultured in TSB medium and extracted with 80% ethanol. The crude extract was partitioned using ethyl acetate and water to obtain active fractions. HPLC screening and column chromatography purified five compounds, identified by NMR as maculosin, indole-3-carboxaldehyde, diolmycin A2, soraphinol A, and uracil. The biological activities of the extracts and fractions were evaluated for whitening and immunomodulatory effects. Whitening activity was assessed by measuring melanin synthesis in B16F10 melanoma cells, where a significant reduction in melanin production was observed. Immunomodulatory activity was tested using macrophage assays, and the ethyl acetate fraction showed a dose-dependent increase in TNF-α production, suggesting immune-enhancing potential. However, IL-1β and PGE2 levels remained unchanged, indicating selective modulation of early inflammatory responses. These findings demonstrate that *Lysinibacillus* sp. JNUCC 51 produces bioactive compounds with whitening and immunoregulatory properties. This suggests promising potential for their application in the development of cosmetic and functional food products.

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PBM-48

Brevibacillus jejuensis sp. nov., a Novel Species Isolated from Baengnokdam, the Summit Crater Lake of Mt. Halla: Complete Genome Sequencing, Taxonomic Characterization, and Potential Cosmetic Applications

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A novel Gram-positive, endospore-forming, rod-shaped bacterium, designated strain JNUCC 42^T, was isolated from the soil of Baengnokdam Lake, a volcanic crater lake located on Jeju Island, Korea. Phylogenetic analysis based on 16S rRNA gene sequences revealed that strain JNUCC 42^T belongs to the genus Brevibacillus and forms a robust monophyletic clade with Brevibacillus laterosporus DSM 25^T (bootstrap value: 100%). However, a pairwise sequence divergence of 0.0206 and a digital DNA–DNA hybridization (dDDH) value of 52.5% clearly differentiate strain JNUCC 42^T from B. laterosporus and other validly published species, indicating that it represents a novel species. The complete genome sequence of strain JNUCC 42^T comprises 4,925,472 bp with a DNA G+C content of 40.75 mol%. Phenotypic, biochemical, and chemotaxonomic characteristics further support its taxonomic distinctiveness. Moreover, several scientific evidence supporting its potential for cosmetic applications were obtained through preliminary in vitro analyses of its culture extract. Based on the polyphasic evidence, strain JNUCC 42^T represents a novel species for which the name Brevibacillus jejuensis sp. Nov. is proposed.

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PBM-49

Regulation of Flowering Time under Natural Sunlight Conditions by Multiple Florigens in Plants

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The decision of when to flower in plants is crucial, as it influences reproductive success and the survival of progeny. Photoperiod is one of the key factors influencing the timing of flowering, primarily through the regulation of florigen expression, such as *FLOWERING LOCUS T* (*FT*) and its orthologs. In Arabidopsis, *FT* (*AtFT*) expresses high at the end of day under long days. However, we recently identified that expression of *AtFT* under natural sunlight differs from that observed under laboratory conditions. Additionally, some *FT* orthologs in other plant species express high both in the morning and the evening, similar to *AtFT* from plants grown under natural sunlight-mimicking conditions. Besides *FT*, we identified a novel floral activator under natural sunlight-mimicking conditions via cell type-specific transcriptome analyses. FT-producing cells expressed a gene encoding a small protein, FPF1-LIKE PROTEIN 1 (FLP1). FLP1 was required for flowering under sunlight-mimicking conditions, independently of FT, and stem growth. *FLP1*, as *FT*, is also conserved across different plant species. Combined all, our data suggest that multiple florigens function in floral induction and stem elongation in nature, highlighting multilayered regulatory mechanisms for and during floral induction that could be targeted to optimize crop yields.

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PBM-50

Impact of Brassicaceae Biofumigation on Cucurbit Growth and Soil Microbiome

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Biofumigation, a sustainable method of pest and disease control using Brassicaceae plant residues, has emerged as a promising alternative to chemical fumigants. This study evaluated the effects of biofumigation on plant stress responses, growth, and the rhizosphere microbial community in watermelon (*Citrullus lanatus*) and oriental melon (*Cucumis melo* var. *makuwa*). Brassicaceae residues were incorporated into the soil before transplanting. We measured physiological indicators such as hydrogen peroxide (H_2O_2), malondialdehyde (MDA) content, stem diameter, and chlorophyll concentration in both treated and untreated groups. Additionally, 16S rRNA amplicon sequencing was performed to assess the composition of the rhizosphere microbial community. Plants in the biofumigated group showed reduced levels of H_2O_2 and MDA, indicating decreased oxidative stress. They also exhibited increased stem diameter and chlorophyll content, suggesting improved plant vigor and photosynthetic capacity. Microbiome analysis revealed that the microbial community composition differed between the biofumigated and control groups. These results suggest that biofumigation not only improves plant health but also alters the soil microbial environment. The combined physiological and microbial effects highlight the potential of Brassicaceae-based biofumigation as a sustainable strategy for enhancing cucurbit crop performance.

Poster Presentation

PBM-51

Integrative Meta-Transcriptomic and Machine Learning Reveal Key Genes Conferring Resistance to *Magnaporthe oryzae* in Rice

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Rice blast (*Magnaporthe oryzae*) threatens global rice yields, necessitating the need for identification of resistance genes. This study combines meta-transcriptomics and machine learning (ML) to dissect defense mechanisms in susceptible/resistant rice genotypes. We downloaded and analyzed transcriptomic data for 362 rice samples (255 susceptible, 107 resistant) from publicly available databases. We evaluated three ML models (RF, XGBoost, and SVM), with XGBoost demonstrating the best performance (accuracy: 0.91, AUC: 0.98) in classifying the expression profiles. SHAP analysis predicted 500 key genes, including some known positive contributors like *OsSRF3* (*LRR-RLK family protein*), *OsDIR49* (*DIR domain protein 49*), *OsHLH46* (*Helix-loop-helix 46*), *OsEBP2 (AP2/EREBP transcription factor*), and *OsBGL2* (*beta-glucanase*), which possibly target fungal cell walls and degrade their components. Conversely, susceptibility-associated genes like *OsGADD45a2* (*growth arrest and DNA damage-inducible 45a2*), *OsSPL1* (*Sphingosine-1-phosphate lyase*), *APIP4* (*AvrPiz-t Interacting Protein 4*), and *OsLP2* (*leucine-rich receptor kinase*) revealed pathogen exploitation of host translation machinery. Functional enrichment highlighted resistance-linked folate biosynthesis and oxidative phosphorylation (energy for immunity), while susceptibility genes clustered in pantothenate metabolism (fungal cofactor production) and autophagy (nutrient hijacking). Overall, this shows that the integration of ML and multi-omics could resolve multi-layered defense strategies while identifying resistance or susceptibility factors for functional validation, offering a robust pipeline for resistance gene discovery. Finally, this strategy can accelerate the roadmap for developing durably resistant rice varieties through precision breeding.

PBM-52

Genomic insight into Seed Longevity in *Oryza sativa* cultivar. Dharial

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Seed longevity is a critical trait that influences post-harvest management, seed storage, and agricultural productivity in major crops, such as rice. However, the genetic basis of seed longevity remains poorly understood. Here, we investigate the indica rice cultivar Dharial, known for its exceptional seed longevity, retaining high germination rates even after 10 years of storage. Whole-genome sequencing and de novo assembly of cv. Dharial yielded a high-quality genome (~388Mb, N50: ~31 Mb, BUSCO completeness: 99.4%), followed by genome annotation using the MAKER-P pipeline, identifying 41,730 gene models. To explore the genetic basis of the seed longevity trait, we evaluated 240 advanced backcross recombinant inbred lines (AB-RILs) from Dharial × Ilmi crosses, identifying 11 lines with a strong longevity phenotype. QTL mapping revealed two major loci associated with seed longevity on chromosome 5 (21.00–21.75 Mbp; 86 genes) and chromosome 3 (16.00–22.00 Mbp; 445 genes). Transcriptomic analysis of Dharial seeds showed high expression of three glucanase-related genes within these regions. These genes are involved in energy generation and starch degradation, key processes for maintaining seed viability during long-term storage. These genomic and transcriptomic insights provide candidate gene targets for further functional validation and offer a foundation for breeding rice varieties with improved seed longevity and enhanced storage resilience.

PBM-53

PVP-Induced Aggregation of Lysozyme with Minimal Structural Change Leads to Enzymatic Inhibition

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Although lysozyme has been described in various ways, it is generally known as an antimicrobial enzyme abundant in bodily fluids such as tears and saliva. Its interactions with polymeric substances can influence its structure and function. This study investigated the interaction between lysozyme—a major protein in tears—and polyvinylpyrrolidone (PVP), a hydrophilic and water-soluble polymer widely used in artificial tears due to its excellent wetting properties. The molecular weight of PVP was determined by proton nuclear magnetic resonance (^{1}H NMR) to characterize the polymer prior to protein interaction studies. Dynamic light scattering (DLS) analysis showed an increase in particle size when lysozyme was incubated with PVP, indicating the formation of larger aggregates. However, fluorescence quenching analysis revealed only minimal changes in fluorescence intensity, suggesting that the tertiary structure of lysozyme remained largely intact. Enzymatic activity assays confirmed that lysozyme activity was reduced in the presence of PVP. These findings suggest that PVP interacts with lysozyme, inducing aggregation with minimal structural change and subsequently inhibiting its enzymatic activity—possibly due to steric hindrance or reduced substrate accessibility.

PBM-54

Structural Variation Alters Spinosyn A and D Binding Sites on B-Form Bovine Serum Albumin

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Bovine serum albumin (BSA), the most abundant protein in plasma, normally exists in the N-form at physiological pH but converts to the B-form—characterized by increased negative charge and hydrophobicity—under alkaline conditions (≈pH 9.0) or in microenvironments with elevated Ca^{2+} levels, or fatty acids binding. This study evaluated the interactions of B-form BSA (pH 9.0) with Spinosyn A and D, precursors of the insecticide spinosad produced by Saccharopolyspora spinosa. Structurally, Spinosyn A and D are nearly identical macrolides that differ by a single methyl group. Circular Dichroism (CD) spectra revealed a concentration-dependent decrease in ellipticity at 208 nm for both compounds. Spinosyn A also caused a marked reduction at 220 nm, indicating alteration of α-helical structure. Intrinsic fluorescence intensity assays confirmed tertiary structural changes in BSA. Control experiments at pH 7.4, where BSA remains in the N-form, showed minimal spectral changes, suggesting conformation-dependent spinosyn binding. Using site-specific marker ligands identified binding sites: Spinosyn A increased the dissociation constant (K_d) of the BSA–warfarin interaction, whereas Spinosyn D elevated the K_d of the BSA–dansylglycine interaction. These findings reveal that the presence or absence of a single methyl group in Spinosyn A versus D dictates their binding to separate sites on B-form BSA, a surprising demonstration of how minor structural variation profoundly affects protein–ligand interactions.

Poster Presentation

PNB Natural Products · Bioactive Materials · Biomedical Sciences

PNB-1

Modulation of Mitochondrial Apoptosis and Iron Metabolism by 6-Gingerol in Non-Small Cell Lung Cancer Cells

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6-Gingerol, a major phenolic constituent derived from ginger, has attracted attention for its potential anticancer properties. In this study, we investigated the molecular mechanisms underlying the cytotoxic effects of 6-gingerol in non-small cell lung cancer (NSCLC) cells. Treatment with 6-gingerol significantly inhibited cell proliferation and triggered DNA damage, leading to G2/M phase cell cycle arrest and apoptotic cell death. Mechanistic studies using Western blotting, qRT-PCR, and flow cytometry revealed that apoptosis induced by 6-gingerol is mediated through the mitochondrial intrinsic pathway, characterized by increased Bax expression, cytochrome c release, and activation of caspases.

Interestingly, 6-gingerol altered intracellular iron homeostasis, suggesting that dysregulation of iron metabolism contributes to its pro-apoptotic effects. Furthermore, we observed that 6-gingerol upregulated tumor-suppressive microRNAs such as miR-34a and miR-200c, which are known regulators of PD-L1 expression, implying a potential role in enhancing antitumor immune responses. Collectively, our findings highlight the dual action of 6-gingerol in inducing intrinsic apoptosis and modulating iron metabolism, with implications for its use as a potential therapeutic agent in NSCLC and a promising adjuvant in cancer immunotherapy.

PNB-2

Enhanced Antioxidant Activity of Alkylated Protocatechuic Acid Derivatives in Human Dermal Fibroblasts

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Oxidative stress, caused by the accumulation of reactive oxygen species (ROS), plays a central role in the progression of chronic conditions including neurodegenerative diseases, cancers, and dermatological disorders. In particular, excessive ROS production in skin tissues leads to inflammation, pigmentation irregularities, acneiform eruptions, and accelerated aging. As such, developing effective antioxidant agents is critical for both therapeutic and cosmetic applications. In this study, we synthesized a series of protocatechuic acid (PCA) derivatives modified with alkyl ester groups to enhance both antioxidant efficacy and cellular uptake in human dermal fibroblast (HS68) cells. The structural modifications aimed to increase lipophilicity and membrane permeability of the native PCA molecule. In vitro assays demonstrated that these PCA derivatives significantly suppressed intracellular ROS levels and exhibited superior radical scavenging activity compared to unmodified PCA. Our findings suggest that alkylated PCA derivatives are promising candidates for use in cosmetic formulations targeting oxidative stress-related skin aging and disorders. These results offer a valuable strategy for designing functional cosmetic ingredients with enhanced bioavailability and efficacy.

PNB-3

Davallia mariesii Moore Improves Fc ε RI-Mediated Allergic Responses in the Rat Basophilic Leukemia Mast Cell Line RBL-2H3 and Passive Cutaneous Anaphylaxis in Mice

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Davallia mariesii Moore (Drynaria rhizome extract (DRE)) is widely known for its efficacy in treating inflammation, arteriosclerosis, and bone injuries. This study evaluated whether treatment with DRE inhibited FcεRI-mediated allergic responses in the RBL-2H3 mast cells and investigated the early- and late-phase mechanisms by which DRE exerts its antiallergic effects. IgE anti-DNP/DNP-HSA-sensitized RBL-2H3 mast cells were tested for cytotoxicity to DRE, followed by the assessment of β-hexosaminidase release. We measured the amounts of inflammatory mediators (e.g., histamine, PGD2, TNF-α, IL-4, and IL-6) and examined the expression of genes involved in arachidonate and FcεRI signaling pathways. In addition, we confirmed the antiallergic effects of DRE on passive cutaneous anaphylaxis (PCA) in mice. DRE inhibited RBL-2H3 mast cell degranulation and production of allergic mediators in them. In early allergic responses, DRE reduced expression of FcεRI signaling-related genes (e.g., Syk, Lyn, and Fyn) and extracellular signal-regulated kinase phosphorylation in mast cells. In late allergic responses, DRE reduced PGD2 release and COX-2 expression and cPLA2 phosphorylation in FcεRI-mediated mast cells. Lastly, 250-500 mg/kg DRE significantly attenuated the IgE-induced PCA reaction in mice. These findings provide novel information on the molecular mechanisms underlying the antiallergic effects of DRE in FcεRI-mediated allergic responses.

PNB-4

Effect of Black Raspberry on Lipid Metabolism-Related Gene Expression in High-Fat and Fructose-Fed Rats

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High-fat and fructose-rich diets contribute to lipid metabolism dysregulation, leading to obesity, dyslipidemia, and non-alcoholic fatty liver disease. Excessive intake of dietary fat and sugar promotes de novo lipogenesis and disrupts cholesterol homeostasis, resulting in hepatic lipid accumulation and increased cardiovascular risk. Nutritional interventions using natural bioactive compounds have gained attention for their ability to modulate these metabolic disturbances. Black raspberry (BR), rich in polyphenols and anthocyanins, is promising dietary agent with anti-inflammatory and lipid-lowering properties. This study investigated the effects of BR supplementation on hepatic lipid metabolism-related gene expression in Wistar rats. Male Wistar rats were divided into four groups and fed for 16 weeks: control (CON), high-fat/fructose (HFF), HFF with 2.5% BR (HFF+BR2.5%), and HFF with 5% BR (HFF+BR5%). qRT-PCR was performed on liver tissues to analyze lipid metabolism markers, including ACC, FAS, SREBP-1, SREBP-2, CD36, ApoA-1, ApoB100, LDL-R, and SR-A. The HFF group showed significant upregulation of lipid synthesis and transport genes, whereas BR supplementation, particularly at 5%, significantly attenuated these changes. Notably, LDL-R and ApoB100 were downregulated in the HFF+BR5% group, suggesting improved lipid clearance and reduced lipoprotein production. SREBP-2 regulation indicates BR's potential role in cholesterol metabolism. These findings support the potential of BR supplementation to improve lipid metabolism and mitigate high-fat/fructose diet-induced metabolic disorders.

Poster Presentation

PNB-5

Hydroxymethylation of Chlorogenic Acid by Radiolysis with Potent Anti-Inflammatory Agent

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The molecular modification of chlorogenic acid (**1**) by γ-irradiation led to the formation of two novel derivatives, designated as chlorogenosins A (**2**) and B (**3**). The chemical structures of these compounds were elucidated using comprehensive spectroscopic techniques, including one-dimensional and two-dimensional nuclear magnetic resonance (1D/2D NMR), high-resolution electrospray ionization mass spectrometry (HR-ESI-MS). Compared to the parent compound, chlorogenic acid, the newly generated products exhibited significantly enhanced anti-inflammatory activity. Specifically, both chlorogenosins A and B effectively inhibited the production of nitric oxide (NO) and prostaglandin E_2 (PGE_2) in lipopolysaccharide (LPS)-stimulated RAW 264.7 macrophage cells. Furthermore, they suppressed the secretion of key pro-inflammatory cytokines, including tumor necrosis factor-α (TNF-α), interleukin-1β (IL-1β), and IL-6. These results suggest that γ-irradiation-induced structural modifications of chlorogenic acid may contribute to improved anti-inflammatory properties.

PNB-6

The innovated approach from raw materials to final products by co-steam processing: Biological efficacy improvement of KIOM processed *Polygonum multiflorum* as ethnomedicine with enhanced marker compounds

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Polygonum multiflorum has traditionally been processed with black bean juice to reduce its toxicity and enhance therapeutic efficacy. The specific changes in metabolites resulting from the steaming process with black bean juice have not been elucidated. In this study, the metabolite differences between dried KIOM *P. multiflorum* (KIOM D-PM) and black bean juice-steamed KIOM *P. multiflorum* (KIOM P-PM) was statistically analyzed, and the resulting enhancement in efficacy was verified through tyrosinase and elastase inhibition assays. The results revealed significant increases in the levels of key bioactive compounds such as THSG, emodin, and physcion in KIOM P-PM, while the toxic compound 5-hydroxymethylfurfural was notably reduced. The improved enzyme inhibitory effects were attributed to the elevated concentrations of THSG and emodin. This comprehensive study, from raw material to final product, is the first to encompass the development of superior raw materials through tissue culture, processing-induced metabolite changes, and efficacy evaluation, while chemically characterizing *P. multiflorum* root tubers co-steamed with an additive. Given the enhanced levels of major compounds and improved pharmacological activity, KIOM P-PM is expected to offer greater industrial and medicinal value compared to conventional commercial *P. multiflorum* products. This research was supported by (KSN1823320) & (KSN2511030), Korea Institute of Oriental Medicine Additionally, it was funded by the National Forest Seed and Variety Center under Korea Forest Service(2020-2025).

PNB-7

Trichosanthis Radix: Ethnomedicinal Uses, Phytochemistry, Pharmacology, Quality Control, and Toxicology

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Trichosanthis Radix, the dried root of *Trichosanthes kirilowii* Maxim. has been widely used in traditional Chinese medicine for centuries as heat clearing and fire reducing medicine. It is traditionally used to treat a variety of conditions including coughs with thick phlegm, dry throat, lung heat, diabetes, carbuncles, sores, fever, jaundice, boils, mastitis, and abscesses in Asian countries including China, Korea, Japan, North Korea, and Taiwan. In classical formulations, it is employed to clear heat, moisten the lungs, transform phlegm, and toxicity. Phytochemical studies have revealed key bioactive compounds, such as proteins (trichosanthin), terpenoids (cucurbitacins), sterols, saponins, lignans, coumarins, flavonoids, alkaloids, organic acids, nucleotides, and polysaccharides, which contribute to its broad spectrum of biological activities. Pharmacological investigations have demonstrated antitumor, anticancer, antiinflammatory, immunomodulatory, antidiabetic, hypoglycemic, antiviral, abortifacient, antioxidant, and neuroprotective effects supporting its traditional applications. Despite its therapeutic promise, Trichosanthis Radix also poses certain toxicological concerns, particularly related to its protein, trichosanthin which induce adverse effects if not properly dosed or processed. To ensure efficacy and safety, modern quality control methods such as chromatographic fingerprinting and content determination of marker compounds are essential. While traditional knowledge provides a rich foundation for its clinical use, further pharmacological, toxicological and clinical studies are required to substantiate its efficacy and ensure safe integration into modern medical systems. This work was funded by KSN1823320, KSN2511030.

PNB-8

Database of functional activities and flavonoid content of extracts from the Freshwater Bioresources Culture Collection (FBCC)

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The Nakdonggang National Institute of Biological Resources (NNIBR) is a research institute that specializes in freshwater organisms. Established in June 2016 under the Ministry of Environment, NNIBR aims to contribute to the acquisition of sovereignty over freshwater organisms, biodiversity conservation, and sustainable use of biological resources. To this end, NNIBR operates the Freshwater Bioresources Culture Collection (FBCC), which is focused on establishing a genetic resource bank, acquiring culture technologies and extracts of useful resources, and providing personalized support for the bio-industry. Currently, FBCC has collected approximately 1,221 extracts from 307 species, including plants and microorganisms. To discover the future value of freshwater biological resources, we performed flavonoid profiling using UPLC-TQ-MS, which allowed us to identify the types and amounts of flavonoids present in the extracts. In addition, we discovered *Acer pseudosieboldianum* extracts that contain anti-obesity properties through regulation of hypothalamic neuropeptides. *Acer pseudosieboldianum* extracts showed 70% inhibition of appetite-stimulating neurons. Our ultimate goal is to create a database of freshwater biological resources and estimate the active functional compounds by correlating the functional activities with the flavonoid content.

Poster Presentation

PNB-9

Finger Print Analysis for Quality Assurance of Perilla Leaves and Quality Variations in Korean Products

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Abstract: Perilla leaves, derived from Perilla frutescens var. japonica (Hassk.) H. Hara, Melissa maxima Ard. or Perilla avium Dunn, are commonly utilized as food and seeds. This study aimed to establish a simultaneous analytical method for five key components-rosmarinic acid(RMA), caffeic acid(CFA), luteolin-7-o-D-glucoside(L7G), apigenin-7-o-D-glucoside(A7G) and perillaldehyde(PAL)-in Perilla leaves and its extracts using the internal standard method. Paeonol was employed as the internal standard, and HPLC method was developed. The proposed method could be applied to quantify these components in nine domestically available Perilla products. The content of the marker compound, RMA, ranged from 0.126 to 1.652 mg/g based on dried leaf weight, while other components exhibited content variations of up to 30-fold. Further method validation is planned to confirm the method's applicability for quality control of Perilla leaves and its extracts.

PNB-10

Non-targeted metabolomics reveals anorectic compounds from *Acer pseudosieboldianum* extracts

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Korean maple (*Acer pseudosieboldianum*), a native species of Korea, is known for its rich polyphenolic content. To explore its potential in appetite regulation and metabolic modulation, we investigated two 70% ethanol extracts (branch and leaf) provided by the Nakdonggang National Institute of Biological Resources. To evaluate the anorectic response of the extract, the expression levels of hypothalamic neuropeptides (NPY, AgRP, and POMC) involved in appetite and energy balance were assessed. Both extracts significantly modulated gene expression, with approximately 50% downregulation of NPY and AgRP in treated groups. To identify anorectic activity compounds, we performed non-targeted metabolite profiling using UPLC-qTOFMS in both positive and negative ionization modes. The results showed the alignment of 546 metabolite features. Of these, flavonoids were identified 10 flavonols (six quercetin glycosides and four kaempferol glycosides), four phenolic acids, two flavanols (catechins), two flavanones (eriodictyols), and two coumarins. Flavonoid-targeted UPLC-MS/MS analysis was performed to ensure precise identification and quantification of metabolites, with isoquercitrin (Quercetin 3-O-glucoside), guaiaverin (Quercetin 3-O-α-L-arabinoside) and hyperoside (Quercetin 3-O-galactoside) was highly enriched in both extracts. Further gene expression experiments showed that isoquercitrin and guaiaverin downregulated NPY and AgRP. Thus, these metabolites proved to be major bioactive flavonoids. These findings highlight the utility of non-targeted metabolomics in the discovery of functional phytochemicals and support the potential of *Acer pseudosieboldianum* as a source of anti-obesity compounds.

PNB-11

Development of an Alginate-based Hydrogel Incorporating Alginate Oligomers and Antibacterial Peptides for Wound Healing Applications

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Alginate has been widely utilized in wound dressing applications owing to its excellent biocompatibility and gel-forming ability. However, conventional calcium-crosslinked alginate hydrogels have been reported to exhibit cytotoxicity due to the leaching of calcium ions under physiological conditions. To overcome this limitation, we developed a covalently crosslinked alginate hydrogel that excludes calcium ions and investigated the functional effects of incorporating alginate oligosaccharide (AOS). In this study, we evaluated the hydration capacity, water retention, and mechanical performance of the hydrogel through compression testing, focusing on Young's modulus, hysteresis, and fracture stress and strain. Additionally, an antimicrobial peptide (AMP) was conjugated to the hydrogel surface to confer antibacterial activity, which was assessed using a contact inhibition assay. The cross-sectional morphology of the hydrogel was analyzed by scanning electron microscopy (SEM). The results demonstrated that AOS improved hydration and increased fracture strain without affecting elastic modulus, while the AMP retained antibacterial efficacy after conjugation, supporting the potential of this functional hydrogel for wound healing applications.

PNB-12

Physiological Effects of a Cannabidiol-Encapsulated Nanoemulsion for Therapeutic and Nutraceutical Applications

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Oral administration of cannabidiol (CBD) is hindered by its poor aqueous solubility and limited bioavailability, thereby constraining its therapeutic efficacy. In this study, we developed an oil-in-water nanoemulsion encapsulating CBD, utilizing octenyl succinic anhydride (OSA)-modified starch as an emulsifier, to overcome these limitations. The resulting CBD-loaded nanoemulsion (CBD-NE) exhibited a uniform particle size (39.18±0.15 nm), high encapsulation efficiency (99.80±0.13%), and sustained colloidal stability over a 28-day storage period. Simulated gastrointestinal digestion revealed significantly greater bioaccessibility of CBD in the nanoemulsion compared to unformulated CBD. Additionally, in vitro assays using RAW264.7 macrophages demonstrated that CBD-NE significantly ($p<0.05$) inhibited lipopolysaccharide-induced secretion of pro-inflammatory cytokines, including interleukin-6 and tumor necrosis factor-α. Collectively, these findings suggest that CBD-NE enhances the oral bioavailability and anti-inflammatory efficacy of CBD, underscoring its promise for therapeutic and nutraceutical applications.

PNB-13

Immunomodulatory Effects of Ethanol-Extracted Ginseng Sprouts via the HO-1/NF-κB Pathway in an LPS-Induced Macrophage Model: Potential for Cytokine Storm Mitigation

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The COVID-19 pandemic that emerged in 2020 highlighted the pathological relevance of cytokine storm, a hyperinflammatory response contributing to systemic inflammation and tissue damage. This underscores the urgent need for effective immune-regulatory strategies to control dysregulated immune activation. While immunomodulatory agents such as dexamethasone and IL-6 inhibitors (e.g., Tocilizumab) have shown therapeutic potential, their clinical use is limited by adverse effects including hepatotoxicity, leukopenia, and drug interactions with NSAIDs. This study evaluated ethanol-extracted ginseng sprouts (Panax ginseng C.A. Meyer) as a potential natural immunomodulator. Ethanol extraction was employed to enhance the concentrations of bioactive ginsenosides, specifically Ginsenoside Rd and Ginsenoside Re. These compounds significantly suppressed cytokine production in an LPS-induced RAW264.7 macrophage inflammation model. Mechanistically, this effect was associated with modulation of the HO-1/NF-κB signaling pathway. These findings suggest that ginseng sprouts may offer therapeutic potential for managing cytokine storm-associated inflammatory conditions.

PNB-14

Structure-Based Discovery of Anticancer Peptides from Channa argus: A Traditional Bio-Source Applied to In Silico Screening

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Anticancer peptides(ACPs) are an emerging class of therapeutic agents with low toxicity and minimal drug resistance compared to conventional chemotherapeutics. Despite their potential, few ACPs have been translated into clinical use. Recently, in silico approaches have enabled rapid construction and screening of peptide libraries, accelerating ACP discovery. In this study, we explored the anticancer potential of peptides derived from the viscera of Channa argus(snakehead fish), historically known for women's health benefits in traditional Korean medicine. Initial screening against breast cancer cell line MDA-MB-231 revealed anticancer activity. To identify bioactive components, SDS-PAGE was performed and a trypsin-sensitive protein band was extracted and subjected to LC-MS analysis for sequence identification. A peptide library was generated based on this sequence, and structural modeling and target binding were evaluated using AlphaFold and in silico docking. Among the candidates, two peptides were selected for synthesis based on high binding affinity. Further studies are underway to verify whether the computational predictions are recapitulated in vitro and in vivo.

PNB-15

Anticancer effect of peptide W-0094 derived from Anoplophoa glabripennis

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Cancer remains one of the most difficult diseases to treat, with pancreatic cancer in particular exhibiting an extremely high mortality rate. Pancreatic cancer is known for its strong resistance to conventional chemotherapeutic agents, making effective treatment especially challenging. To address this issue, we investigated W-0094, an anticancer peptide that exhibits low resistance and selectively binds to the membranes of cancer cells. This peptide was extracted from beetles and possesses a stable alpha-helical structure with a well-balanced composition of cationic and hydrophobic amino acids, enabling preferential interaction with the negatively charged surface of cancer cells. The peptide was applied to the human pancreatic cancer cell line PANC-1 in various concentrations, and cell viability was measured using a WST-1 assay. In the results, cell viability decreased in a dose-dependent manner, indicating that W-0094 effectively induces cell death. These findings suggest that W-0094 has strong potential as a novel therapeutic agent for pancreatic cancer treatment.

PNB-16

Validation of analytical methods for *Rosa rugosa*'s flower buds water extracts for standardization as functional ingredients

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This study was perfomed to establish a simple and reliable HPLC/UV analytical method to determine ellagic acid contents for the standardization of water extracts of *Rosa rugosa*'s flower buds as functional health food ingredients. The quantitative HPLC method was optimized using a reversed-phase C18 column with a gredient elution of water (0.1% fomic acid) and acetonitrile (0.1% formic acid) at 35°C and flow rate of 0.5 ml/min. The eluate was detected at 254 nm. For validation, the specificity, linearity, accuracy, precision, limit of detection (LOD) and limit of quantification (LOQ) of ellagic acid were measured. The calibration curve for the detection of robinin had high linearity (R^2=0.999) with LOD and LOQ values of 1.11 and 3.78 μg/ml, respectively. Recovery of the quantified compound ranged from 96.26 to 104.02 %. The relative standard deviation values of the intra-day and inter-day precision were confirmed to be 0.763%~2.288% and 3.721%, repectively. The established method gave the suitable ranges to qunatitate ellagic acid from the hot-water extract of *R. rugosa*'s flower buds.

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PNB-17

Evaluation of modified benzaldehyde derivatives as dual α-glucosidase and α-amylase inhibitors: a viable alternative to acarbose

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The inhibitory effects of the active constituent isolated from *Periploca sepium* barks and its derivatives against α-glucosidase and α-amylase were studied. The active constituent was identified as 4-methoxy-2-hydroxybenzaldehyde by various spectral analyses. 4-Methoxy-2-hydroxybenzaldehyde was 5.44 times more effective at blocking α-amylase than acarbose, but it reduced its blocking ability against α-glucosidase by 0.57 times. The K_m values for α-glucosidase and α-amylase did not change with different amounts of 4-methoxy-2-hydroxybenzaldehyde, which is typical of non-competitive inhibition. To ascertain the structure-activity relationships, 3,4-dihydroxybenzaldehyde and 3,5-dihydroxybenzaldehyde demonstrated inhibitory activities against α-glucosidase. With regard to α-amylase, 2,4,5-trihydroxybenzaldehyde exhibited the most efficacious inhibitory effect, followed by 2,3,4-trihydroxybenzaldehyde, 2,4,6-trihydroxybenzaldehyde, and 3,4,5-trihydroxybenzaldehyde. The combination of benzaldehyde with hydroxyl, methyl, or methoxy groups suggests the potential for benzaldehyde to serve as a parent compound for the development of selective inhibitors. The results indicate that 3,4-dihydroxybenzaldehyde, 3,5-dihydroxybenzaldehyde, 2,5-dihydroxybenzaldehyde, 2,4,5-trihydroxybenzaldehyde, and 2,3,4-trihydroxybenzaldehyde may prove beneficial in alleviating diabetic pathological conditions.

PNB-18

Comparative Analysis of Allithiamine Content in Garlic-Based Grain Mixtures

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Allium sativum L. is high in sulfur compounds with varied biological activities, and grains act as natural forms of thiamine. The lipophilic thiamine derivative allithiamine is generated through the reaction between allicin from garlic and thiamine from grains, promoting intestinal absorption and bioavailability. Regional variation in the composition of the matrix in garlic and grains was studied for its impact on allithiamine formation. From the garlic varieties sampled from all the major regions in South Korea, Jeju garlic contained the highest allicin level and, hence, is a desirable source for functional formulations. While the raw grains in general contained very low thiamine, fortification with thiamine and subsequent blending with the extract from garlic produced allithiamine in different yields based on the grain type. The allithiamine in the garlic *Avena sativa* mixture was the most prominent, emphasizing matrix dependent physical and chemical characteristics taking precedence over the initial thiamine concentrations. The findings strongly point to the need for the optimization of the selection of the garlic cultivar as well as the grain matrix composition for the best formation of the bioavailable thiamine derivatives. The paper provides the basic information for the development of advanced functional foods having potential in the prevention and treatment of conditions related to metabolism.

PNB-19

Optimization of Quadrupole Type Mass Spectrometer Conditions for the Quantitative Analysis of Platycosides in Divalent Form

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Platycosides, the primary saponins found in Platycodon grandiflorum, have gained considerable attention due to their diverse pharmacological properties. However, because of its high molecular weight and structural complexity, most were analyzed in monovalent ion form using high-performance LC-QTOF-MS, or LC-ELSD and DAD, which have relatively low sensitivity, were analyzed in other states. In this study, we optimized liquid chromatography-tandem mass spectrometry (LC-MS/MS) conditions for the quantitative analysis of nine platycosides, including platycodin D and platycoside C, by promoting the formation of divalent ions. This MS condition detecting divalent ion showed stable signal and improved sensitivity at LC-MS/MS with m/z scan range below 1200. The optimized conditions yielded clear and reproducible fragmentation patterns, facilitating accurate quantification of these platycosides in complex plant extracts. This approach offers a reliable analytical method for the quality control and pharmacokinetic studies of platycoside-enriched formulations, potentially contributing to more accurate quality assessment and a better understanding of their in vivo behavior.

PNB-20

Elucidating the Mode of Action of Sorgoleone Analogs via Metabolomics

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Metabolomics tracks fluctuations in small-molecule profiles to uncover shifts in cellular pathways. This approach clarifies metabolic responses to xenobiotics and reveals mechanisms of action for new compounds. When coupled with targeted in vitro assays, it becomes a powerful platform for characterizing pesticides whose targets are unknown.

Here, we applied GC-MS/MS–based metabolite profiling to investigate the herbicidal mechanism of sorgoleone analogs. Sorgoleone, a natural allelochemical, served as the scaffold for synthesizing structural variants. Two derivatives—2-Hydroxy-5-methoxy-3-octadecyl-1,4-benzoquinone (1g) and 2-Hydroxy-5-methoxy-3-(2-Phenylethyl)-1,4-benzoquinone (1h)—showed potent inhibition of *Lactuca sativa* growth. Prior studies attribute sorgoleone's bioactivity to reactive oxygen species (ROS) production through inhibition of photosystem II and suppression of 4-hydroxyphenylpyruvate dioxygenase (HPPD). Our metabolic profiling revealed significant disturbances in ascorbate and glutathione metabolism, glyoxylate and dicarboxylate pathways, vitamin B_6 turnover, and tyrosine catabolism. These results support a dual mechanism for sorgoleone analogs: induction of oxidative stress and disruption of aromatic amino acid metabolism. This study demonstrates how metabolomics can provide foundational insights into the mode of action for promising herbicidal compounds.

Poster Presentation

PNB-21

Structural Effects of Ginsenosides on Inhibiting α-Amylase and α-Glucosidases for Regulating the Postprandial Glycemic Response

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In this study, three structurally unique ginsenosides, Rb1, Rg1, and Rg3, were screened as biomarkers of ginseng to systematically investigate the structural requirements of ginsenosides as natural inhibitors of the endo-acting α-amylase and exo-acting α-glucosidase to control the postprandial glycemic response. The distinct inhibition properties of these three ginsenosides against the enzymes were verified through various analytical techniques: an in vitro assay for inhibition rate, intrinsic fluorescence quenching for binding affinity, kinetic studies for inhibition mechanisms, ANS fluorescence quenching for protein tertiary structural changes, and molecular modeling for binding modes. Considering the distinct chemical structures of ginsenosides, it was confirmed that the hydroxyl group at C3 and glucose conjugation at C6 of ginsenoside were critical for inhibiting α-amylase and α-glucosidase, respectively, due to the differences in the catalytic active site structures. Therefore, our findings provide insights into applying ginsenosides to inhibit α-glucosidase and improve physiological responses.

PNB-22

The standardization of the RNA content test and the encapsulation percentage test for mRNA vaccine

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The SARS-CoV-2 Pandemic, which began in Wuhan, China, in 2019, accelerated the development of novel vaccine technologies, including the world's first mRNA-based vaccines by Pfizer-BioNTech and Moderna. these vaccines showed high efficacy and enabled the further development of mRNA vaccine platforms against other infectious diseases such as RSV, influenza, and multivalent targets, many of which are now in clinical trials or under regulatory review. Vaccines differ from therapeutic drugs in that they are administered to healthy individuals, including vulnerable populations. therefore, ensuring their quality and safety through rigorous national lot release testing by each country's National Control Laboratory(NCL) is critical. During the COVID-19 Pandemic, Due to the urgency and novelty of the mRNA Platform, authorities had to rely on manufacturer-provided testing methods. even Today, standardized mRNA vaccine test methods are not included in major pharmacopoeias like the USP or EP. mRNA vaccines use lipid nanoparticles (LNPs) to protect the intrinsically unstable mRNA. Thus, testing RNA content and encapsulation efficiency is essential for determining vaccine quality and ensuring consistent dosing. This study aims to compare and standardize test methods for these two key parameters across different manufacturers and evaluate their applicability to national lot release systems. The outcomes are expected to contribute to the regulatory science field and serve as a guideline for future mRNA vaccine development and quality control.

PNB-23

Ameliorative Effects of a Phenolic Glycoside from *Castanopsis echinocarpa* on Sensorineural Hearing Loss and Its Mechanistic Insights via Molecular Docking Analysis

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Sensorineural hearing loss is caused by damage to the auditory nerve or inner ear, and its global prevalence is steadily increasing. *Castanopsis echinocarpa*, an evergreen tree belonging to the Fagaceae family, is native to tropical regions such as Southeast Asia. Molecular networking analysis of the MeOH extract of *C. echinocarpa* revealed distinct clusters of phenolic glycosides. From the BuOH fraction, ten phenolic glycosides were isolated. In a zebrafish model of neomycin-induced ototoxicity, treatment with isolated phenolic glycosides significantly increased the number of hair cells, in compounds **1**, **5**, and **6**. To elucidate the mechanism of bioactivity, we utilized the KEGG database to identify potential protein targets involved in GABA metabolism, a pathway known to contribute to hearing restoration. Six target proteins—HDAC1, Daxx, GAT1, GAT3, GABA-T, and BGT1—were selected for molecular docking simulations. Docking analysis revealed strong binding affinities between **1** and HDAC1/GAT1, **5** and Daxx/GABA-T, and **6** and Daxx/GAT1. These results suggest that the active compounds may improve hearing by either enhancing intracellular GABA synthesis, inhibiting degradation, and suppressing extracellular transport. This study provides mechanistic insight into the potential of phenolic glycosides from *C. echinocarpa* to ameliorate hearing loss and lays the groundwork for future mechanistic and therapeutic research.

PNB-24

Photosensitizer Candidates from Marine *Streptomyces* sp. ME-0223

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Marine actinomycetes are rich sources of novel drug-like secondary metabolites. The marine strain *Streptomyces* sp. ME-0223 produces two major compounds, resistomycin and resistoflavin, both featuring an unusual pentacyclic core structure distinct from typical aromatic polyketides. Similar to hypericin, a well-known photosensitizer from *Hypericum perforatum*, these compounds possess highly conjugated π-systems that enable efficient light absorption and facilitate energy transfer to molecular oxygen, thereby generating singlet oxygen ($^1O_2$). We therefore assayed $^1O_2$ generation by the ME-0223 crude extract, its MeOH fraction, and its acetone fraction. At 440 nm, the optical densities of the MeOH and acetone fractions closely matched that of 5.55 μM Rose Bengal used as positive control, confirming comparable light absorption and $^1O_2$ production. Guided by this activity, we optimized the culture medium to enhance metabolite yields. Cultivating ME-0223 in starch-casein broth with soybean meal (SCB-soy) instead of marine broth (MB) increased crude-extract yield from 52.5 to 94 mg L^{-1}. LC-MS analysis (320 nm) of 1 mg mL^{-1} extracts showed the resistomycin peak area rising from 134 (MB) to 1,293.7 (SCB-soy), whereas resistoflavin remained essentially unchanged. We are currently planning further evaluations of antimicrobial and anticancer photosensitizing activities of these metabolites.

PNB-25

Evaluation of Natural Red Argan Oil-Based Complex on Skin Barrier Recovery and Elasticity Enhancement

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This study investigates the functional efficacy of the argan oil-based natural complex, on skin barrier modulation and dermal elasticity via in vitro gene expression profiling. The naturally red-tinted oil was obtained by extracting 11 botanical ingredients into argan oil, using a low-temperature infusion process to maximize active compound retention. The argan oil-based natural complex was applied at 1% concentration to HaCaT (keratinocyte) and Hs68 (fibroblast) cell lines. In inflammatory conditions induced by Poly I:C and IL-4, TNF-α mRNA levels ($p<0.001$) were significantly suppressed, indicating skin recovery potential. Gene expression analysis further showed upregulation of ECM-related genes, COL1A1 and ELN, in Hs68 cells following 24-hour treatment ($p<0.01$), suggesting enhanced dermal elasticity. Additionally, the red argan oil-based natural complex treatment modulated key genes involved in skin barrier function, although moisturizing and regenerative effects were not statistically significant in the tested conditions. All assays were conducted using quantitative RT-PCR, with dexamethasone and TGF-β as positive controls for anti-inflammatory and elasticity assays, respectively. These findings support that the natural argan oil-based complex has significant potential as a multifunctional cosmetic ingredient capable of improving skin barrier resilience and elasticity through modulation of structural gene networks.

PNB-26

Identification of molecular targets and therapeutic potential of ginsenosides through proteome-wide profiling

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Identifying the precise molecular targets of natural products (NPs) is essential for elucidating their mechanisms of action (MoA). This knowledge not only aids in interpreting clinical observations related to drug metabolism but also facilitates the exploration of mechanisms in related basic research fields. However, due to the unknown molecular targets of most NPs identified through phenotypic assays, it remains challenging to determine their exact MoA. In this study, we predicted the molecular targets of NPs using proteome-wide target interaction profiling and discussed their therapeutic potential and MoA. For this study, ginsenosides were selected as a representative class of NPs to investigate proteome-wide target interaction profiles, owing to their high structural diversity, well-characterized biological activities, and significance in natural product research. The resulting target profiling enabled the identification of distinct target interactions for ginsenosides. Based on these interaction patterns, we classified functionally similar ginsenosides and inferred their MoA and therapeutic potential. These results could provide a valuable resource for understanding the biological activities of NPs, especially ginsenosides, and for advancing the identification of novel therapeutic applications.

PNB-27

An undescribed anti-inflammatory meroterpenoid from the brown alga *Sargassum macrocarpum*

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Sargassum macrocarpum has been reported to possess various structures for biological activities. The aim of this study was to determine the isolation, structures and anti-inflammatory activity from *S. macrocarpum*. An undescribed meroterpenoid (**1**), and four known compounds (**2-5**) were isolated from the MeOH extract of *S. macrocarpum*. Their structures were determined using nuclear magnetic resonance (NMR) and high resolution electrospray ionization-mass (HR-ESI-MS) spectroscopic data. The compounds (**1-5**) were evaluated for their anti-inflammatory activities by assessing their effect on the production of nitric oxide (NO) and prostagradin E_2 (PGE_2). In particular, the compounds **1** and **3** evaluated by assessing their ability to inhibit NO and PGE_2 production induced by LPS treated RAW264.7 cells.

PNB-28

In vitro Screening of Adipogenesis Inhibitory Effect of Halophyte Plant Extracts for Potential Anti-obesity Treatment

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In order to find new anti-obesity treatments in present study, we investigated 26 halophyte extracts (HEs) for adipogenesis inhibitory effect in 3T3-L1 preadipocytes. Lipid accumulation as a major marker of adipogenesis was quantified at the end of differentiation period (Day 8) by Oil Red O staining. Among the 26 HEs, *Rosa rugosa*, *Suaeda maritima*, *Salsola komarovii*, and *Asparagus oligoclonos* extract evidenced potent adipogenesis inhibitory effect, and its reduced intracellular triglyceride levels. Therefore, to observe the inhibitory effect of 4 HEs on expression of adipogenic-specific transcription factors such a peroxisome proliferator-activated receptor-γ (PPARγ), CCAAT/enhancer-binding proteins α (C/EBPα), and sterol regulatory element-binding protein 1 (SREBP-1), 3T3-L1 preadipocytes were incubated in medium in the presence of 4 HEs, and expression levels of adipogenic-specific transcription factors were determined. Based on western blot analysis, 4 HEs significantly decreased protein expression levels of PPARγ, C/EBPα, and SREBP-1 in a dose-dependent manner. In addition, lipid metabolism factor such as fatty acid binding protein 4 (FABP4) was down-regulated by 4 HEs during adipocyte differentiation in a dose-dependent manner compared with those in adipocytes without 4 HEs treatment. These results demonstrated that 4 HEs could be used as an ingredient for potential anti-obesity agents.

Poster Presentation

PNB-29

Effects of Fermented Polygonum cuspidatum on the Skeletal Muscle Functions

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Plant extract fermentation is widely employed to enhance the nutritional and pharmaceutical value of functional foods. Polygonum cuspidatum (Pc) contains flavonoids, anthraquinones, and stilbenes, imparting protective effects against inflammation, cancer, diabetes, and cardiovascular diseases. However, the effects of fermented Pc on skeletal muscle strength remain unexplored. In this study, we generated fermented Pc using a complex of microorganisms containing Lactobacillus spp. (McPc) and assessed its effects on muscle strength and motor function in mice. Compared to un-fermented Pc water extract, elevated levels of emodin and resveratrol were noted in McPc. This was identified and quantified using UPLC-QTOF/MS and HPLC techniques. Gene expression profiling through RNA-seq and quantitative RT-PCR revealed that McPc administration upregulated the expression of genes associated with antioxidants, glycolysis, oxidative phosphorylation, fatty acid oxidation, and mitochondrial biogenesis in cultured C2C12 myotubes and the gastrocnemius muscle in mice. McPc significantly improved skeletal muscle strength, motor cordination, and traction force in mice subjected to sciatic neurectomy and high-fat diet (HFD). McPc administration exhibited more pronounced improvement of obesity, hyperglycemia, fatty liver, and hyperlipidemia in HFD mice compared to control group. These findings support the notion that emodin and resveratrol-enriched McPc may offer health benefits for addressing skeletal muscle weakness.

PNB-30

Comparative Analysis of Chlorogenic Acid and Eleutheroside E in the Stems of *Eleutherococcus sessiliflorus* from Wild and Cultivated Environments

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Eleutherococcus sessiliflorus (Rupr. & Maxim.) S.Y.Hu (Araliaceae) is a medicinal plant traditionally used in East Asia and is known for its diverse pharmacological properties. Recent studies have reported various biological activities, including anti-inflammatory, anti-aging, and anticancer effects, many of which are attributed to its bioactive constituents. Among these, the phenolic compound chlorogenic acid and the lignan eleutheroside E are particularly notable. In this study, 114 stem samples were collected from 26 cultivated and 12 wild sites across South Korea, with triplicate sampling per site. Samples (500 mg) were extracted using 100% methanol (10 mL) by ultrasonic extraction at 30°C for 1 hour. The extracts were analyzed by UPLC using an ACQUITY HSS T3 column with a gradient of 0.1% formic acid in water and acetonitrile, and detection was performed at 220 and 254 nm. The analytical method was validated in accordance with ICH guidelines. In cultivated sites, the average contents of chlorogenic acid and eleutheroside E were 238.49±9.12 μg/g and 65.78±3.37 μg/g, respectively, totaling 304.27±10.76 μg/g. In contrast, the corresponding values for wild habitats were 129.04±16.60 μg/g and 14.89±2.33 μg/g, totaling 143.94±18.34 μg/g. Independent t-tests confirmed that all three contents were significantly higher in cultivated samples than in wild ones ($p < 0.0001$ for all comparisons).

PNB-31

Isatin derivatives as promising inhibitors of SARS-CoV-2 Main Protease (Mpro)

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The SARS-CoV-2 pandemic, which emerged in late 2019, has profoundly impacted global health and economic stability. Consequently, antiviral drug discovery has become a leading priority for researchers and the pharmaceutical industry. Considering the established antiviral activity of isatin derivatives, we synthesized and evaluated a novel series of isatin-based compounds as potential inhibitors of the SARS-CoV-2 Main Protease (M^{pro}). Initially, a FRET-based enzymatic assay was used to screen all synthesized compounds at 100 μM for inhibitory activity against M^{pro}. Subsequently, IC_{50} values were determined for the three most active inhibitors (**Compound I-1, Compound I-2, and Compound I-3**). Additionally, their cytotoxicity was assessed in normal cells (IMR90) to establish preliminary safety profiles. Enzyme kinetics analysis via Michaelis-Menten models at various inhibitor concentrations clarified the inhibition mechanisms of these promising compounds. Furthermore, molecular modeling studies were conducted to predict and characterize binding interactions between these compounds and the active site residues of SARS-CoV-2 M^{pro}. Overall, these findings suggest that the newly developed isatin derivatives are promising scaffolds for further optimization into effective antiviral agents against SARS-CoV-2.

PNB-32

Integrated Genomics and Metabolomics for Isoflavone-Enriched Soybean Resource Discovery and Functional Characterization

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To discover and commercialize high-value bioactive soybean materials, we conducted an integrative analysis using publicly available genomic and metabolomic datasets from a Korean soybean core collection. Genomic data for 430 soybean genotypes were retrieved from the NCBI Sequence Read Archive (SRA) and used for SNP-based analyses, while metabolomic profiles for 393 matched accessions—focusing on the key isoflavone glycosides daidzin and genistin—were obtained from previous LC-MS/MS analyses conducted by the National Institute of Crop Science. Genome-wide association study (GWAS) identified significant SNPs associated with isoflavone accumulation, including a highly significant locus on chromosome 1 ($P=8.47\times10-9$), and additional signals on chromosomes 4, 17, and 18. Genomic selection (GS) was also applied to predict high-isoflavone accessions based on genotype data. To prioritize candidate genes, we performed linkage disequilibrium (LD) block analysis and retrieved genes located near lead SNPs. Functional enrichment analysis using Gene Ontology (GO) and KEGG pathways revealed significant terms related to glycosylation, primary metabolism, hormone regulation, and plant defense—consistent with the known roles of isoflavones. This study establishes a robust genomics–metabolomics integration framework for identifying functional soybean resources. The LD-based candidate gene identification and functional annotation underscore the biological relevance of selected loci, providing a foundation for future functional validation, molecular breeding, and the development of export-oriented soybean products enriched in health-beneficial compounds.

Poster Presentation

PNB-33

Anti-Inflammatory Effect of Fermented and Aged Mountain-Cultivated Ginseng Sprout and Its Major Component, Compound K, in an LPS-induced Acute Respiratory Distress Syndrome Mouse Model

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Acute Respiratory Distress Syndrome (ARDS) is a life-threatening condition characterized by severe pulmonary inflammation, impaired oxygenation, and extensive apoptosis of lung cells. Fermented and aged mountain-cultivated ginseng sprout (FAMCGS), produced through steaming, aging, and fermentation processes, exhibits enhanced levels of bioactive compounds, particularly compound K (CK). This study investigated the preventive effects of FAMCGS extracts and CK on lipopolysaccharide (LPS)-induced inflammation in a murine ARDS model. Pre-administration of FAMCGS or CK significantly reduced inflammatory cell numbers and pro-inflammatory cytokine productions in bronchoalveolar lavage fluid. Histopathological examination revealed that FAMCGS and CK attenuated LPS-induced lung injuries, including immune cell infiltration, hemorrhage, edema, mucus hypersecretion, and goblet cell hyperplasia (PAS-positive cells). Furthermore, FAMCGS and CK suppressed macrophage infiltration and inflammatory cytokine expressions in lung tissues. Both agents also alleviated LPS-induced apoptosis, as evidenced by reduced TUNEL-positive cells and apoptotic markers. In vitro, FAMCGS pretreatment dose-dependently mitigated morphological changes in RAW 264.7 macrophages exposed to LPS. RT-PCR and Western blot analyses confirmed that FAMCGS and CK downregulated the expression of key pro-inflammatory cytokines and mediators at both transcriptional and translational levels. Mechanistically, FAMCGS inhibited LPS-stimulated phosphorylation of MAPKs (ERK, p38, and JNK) and prevented the nuclear translocation of NF-κB. These findings suggest that FAMCGS and its key component, CK, may serve as promising natural therapeutic agents for the prevention and/or treatment of ARDS.

PNB-34

Mitigation of Salinity Stress via Improving Growth and Nutrient Uptake in *Raphanus sativus* L. with Biochar

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Salt stress is a major environmental constraint that significantly impairs plant growth, yield, and quality worldwide. Radish (*Raphanus sativus* L.), an economically important root vegetable, is particularly sensitive to high salinity, which hampers its cultivation in affected regions. Biochar (BC) has emerged as a promising soil amendment with the potential to alleviate salt-induced damage by improving soil properties and plant physiological responses. This study investigated the ameliorative potential of BC applied at different rates (0.5, 1.0, and 1.5 t/10a) in combination with NPK under 200 mM NaCl stress on radish cultivation. Soil analysis revealed that BC incorporation improved key physicochemical properties including pH, EC, and exchangeable cations, with the 0.5 t/10a BC treatment notably increasing soil P_2O_5 and available K levels. Enhanced nutrient availability was mirrored in the plant nutrient profile, with increased Fe and Zn concentrations observed, particularly under the 0.5 t/10a treatment. This treatment also yielded the highest radish biomass (1830.0 g), suggesting a synergistic effect between moderate BC input and saline stress tolerance. These findings suggest that BC mediates a novel soil–plant interaction module that contributes to salt stress resilience in radish.

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PNB-35

Sex-Specific Behavioral and Sleep Architecture Alterations Induced by Sleep Deprivation in Mice

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Sleep deprivation (SD), characterized by reduced sleep quantity or quality, disrupts neuroendocrine balance and increases susceptibility to psychiatric disorders including anxiety and depression. To investigate sex-specific effects of SD, seven-week-old male and female C57BL/6 mice were subjected to sleep deprivation using the Modified Multiple Platform Method. Behavioral tests included the Open Field Test, Elevated Plus Maze, Forced Swimming Test, Tail Suspension Test, and Passive Avoidance Test. Sleep–wake cycles were assessed using the PiezoSleep system and analyzed with SleepStats software. Sex-specific behavioral and sleep changes were observed. Male SD mice exhibited reduced locomotion, increased immobility in FST and TST, and greater latency in PAT—markers of depressive-like behavior. Female SD mice showed milder behavioral alterations. Sleep patterns also varied: male SD mice had increased total sleep with fewer bouts, while female SD mice showed decreased total sleep and higher fragmentation, particularly during the dark phase. SD mice of both sexes experienced shifts toward shorter sleep bouts compared to controls. These results highlight higher male vulnerability to behavioral disruptions and female susceptibility to sleep fragmentation under SD. This model offers valuable insights into sex-specific mechanisms underlying sleep deprivation and can aid the development of targeted therapies for sleep-related mood disorders.

PNB-36

Anti-inflammatory Effects of Plasma-Induced Phloridzin Derivatives in LPS-stimulated RAW 264.7 Macrophages

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Phloridzin (**1**), a natural dihydrochalcone, is well known for its antioxidant and anti-diabetic properties. In this study, we examined the anti-inflammatory effects of three plasma-induced phloridzin derivatives, deglucosyl-methylene-bis-phloridzin (**2**), methylene-bis-phloridzin (**3**), and phloretin (**4**), using LPS-stimulated RAW 264.7 macrophage cells. Cells were treated with various concentrations (12.5, 25, 50, and 100 μM) of compounds **1**–**4**. Among them, compound **2** exhibited the most potent inhibitory effect on nitric oxide (NO) production without cytotoxicity. Compound **2** also inhibited LPS-induced intracellular reactive oxygen species (ROS) production in a dose-dependent manner as measured by DCFDA fluorescence assay, and free radical scavenging activity was confirmed using the DPPH assay. Moreover, compound **2** markedly downregulated the expression of inducible nitric oxide synthase (iNOS) and cyclooxygenase-2 (COX-2) as confirmed by western blot assay. In addition, compound **2** led to a decrease in the secretion of pro-inflammatory cytokines, including tumor necrosis factor-alpha (TNF-α) and interleukin-6 (IL-6). These findings suggest that deglucosyl-methylene-bis-phloridzin (**2**), a plasma-induced phloridzin derivative with anti-inflammatory and antioxidant activities, may serve as promising natural agent for the prevention and treatment of inflammatory diseases.

PNB-37

Metabolomic profiling evaluation of drought-tolerant transgenic rice

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Transgenic rice plants overexpressing the *CaMsrB2* gene have been shown to exhibit reduced oxidative stress and enhanced drought tolerance. Since high soil salinity induces osmotic stress and ion toxicity, it often leads to secondary metabolic disturbances. In this study, we performed a comparative metabolomic analysis of two *CaMsrB2*-expressing rice lines and the parental Ilmi cultivar under salt stress conditions. A total of 63 hydrophilic and lipophilic metabolites were identified using gas chromatography – time-of-flight mass spectrometry (GC-TOF-MS), followed by multivariate statistical analyses. After 7 days of treatment (0 mM vs. 225 mM NaCl), the transgenic lines exhibited smaller changes in proline and GABA levels, suggesting reduced salt-induced damage. Methionine content was also altered, possibly due to *CaMsrB2* expression. Higher levels of soluble sugars were observed in the transgenic lines, potentially contributing to improved reactive oxygen species (ROS) scavenging and suppression of excessive ROS accumulation. Additionally, amino acids involved in nitrogen metabolism and osmotic regulation — such as asparagine, aspartate, glutamine, and glutamate — showed distinct accumulation patterns compared to Ilmi. These results indicate that *CaMsrB2* may enhance salt stress tolerance through metabolic adjustments involving osmolyte accumulation, redox balance, and nitrogen metabolism.

PNB-38

Correlation Analysis between Metabolites and Ginsenosides of Wild-Simulated Ginseng with Different Harvest Times

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The biosynthesis of ginsenosides of wild-simulated ginseng (WSG, *Panax ginseng* C.A. Meyer) depends on growth stage and metabolic characteristics. This study aimed to determine the metabolic changes in WSG according to harvest time by analyzing metabolites and ginsenosides in WSG collected monthly from May to September. Fifteen metabolites were profiled by using GC-MS analysis. Significant differences in metabolite levels were observed between aerial and root parts. In particular, sugars (fructose, glucose, sucrose, xylose) were highly accumulated in aerial part in May, but they decreased during the summer months, whereas sucrose levels increased in the root part over the same period. Twenty-two different ginsenosides were analyzed using LC-MS/MS. In the aerial part, ginsenosides Rd, Rg3(S), Re, F1, F3, F4, and F5 were identified as major components, while ginsenosides Rc, Rb1, Rb2, Rb3, mRb1, and Ro were identified as major components in the root part. In the analysis of correlations between primary metabolites and ginsenoside contents in WSG, sucrose exhibited significant positive correlations with ginsenoside Ro ($r = 0.861$), Rb3 ($r = 0.849$), Rc ($r = 0.848$), while it showed negative correlations with ginsenosides F4 ($r = -0.882$) and F2 ($r = -0.785$). This study is expected to provide fundamental data for understanding the metabolic changes and accumulation of active components in WSG according to its growth stages and harvest times.

PNB-39

Chemical Profiling of Flavonoid Glycosides in *Quercus mongolica* Pollen Using LC-MS/MS-Based Molecular Networking

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Bee pollen is a nutrient-rich natural product essential for the development of bee larvae and adults and is known to exhibit antibacterial, anti-inflammatory, and antioxidant activities. Among its bioactive constituents, polyphenols, especially flavonoids, contribute significantly to its potent antioxidant activity. Flavonoids represent the primary chemical constituents of plant pollen and predominantly occur in the form of flavonoid glycosides. These compounds exhibit remarkable structural complexity and diversity due to variations in glycosylation sites, linkage types, and sugar moieties. In this study, we conducted a untargeted profiling of flavonoid glycosides present in *Quercus mongolica* pollen using LC-MS/MS-based molecular networking in negative ion mode. In the molecular network, two major clusters were identified as flavonoid glycosides and polyamines. A total of 86 flavonoid glycosides were tentatively annotated based on GNPS spectral library matching, reference compounds, and previous literature data. Among them, two major compounds from *Q. mongolica* pollen, isorhamnetin 3-*O*-*β*-D-xylopyranosyl(1→6)-*β*-D-glucopyranoside and isorhamnetin 3-*O*-neohesperidoside, were confirmed through comparison with authentic reference compounds. Based on their characteristic fragmentation patterns, kaempferol, quercetin, and isorhamnetin were identified as the major aglycone backbones, with *Q.mongolica* pollen found to be particularly rich in isorhamnetin derivatives. This study provides fundamental insights into the diverse flavonoid composition of *Q. mongolica* pollen and contributes to a broader understanding of its secondary metabolite profile.

PNB-40

Effects of Irrigation Water Salinity on Growth and Bioactive Compound Activity of Sweet Potato (*Ipomoea batatas*) in the Saemangeum Reclaimed Land

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Sweet potato (*Ipomoea batatas*) is an alkaline food rich in proteins, dietary fiber, minerals, and vitamins, and is widely utilized for both direct consumption and processed food products. In addition to the storage roots, other aerial parts such as leaves, stems, and petioles are also utilized. Notably, the aerial parts are known to contain bioactive compounds with strong antioxidant activities and potential benefits for the prevention of ocular diseases, thereby increasing the value of sweet potato for industrial processing. This study aimed to evaluate the growth and bioactive compound activity of sweet potato cultivated under different salinity levels of irrigation water (0%, 0.2%, and 0.4%) in reclaimed land conditions in the Saemangeum region. Plant growth was initially delayed at a 0.4% salinity level by 30 days after transplanting, but gradually recovered, resulting in normal development by the harvest stage (120 days after transplanting). The aerial biomass yield was highest in cultivars Sodammi, Gogeonmi, and Tongchaeru, whereas the highest underground yield was observed in Hopungmi. The total polyphenol content in the aerial parts was greater in Gogeonmi and Tongchaeru, with levels increasing in response to higher irrigation salinity. The total flavonoid content was highest in Gogeonmi, and lutein content was particularly high in Tongchaeru and Jinhongmi, especially at 0.2% and 0.4% salinity levels.

PNB-41

Multifunctional Skin Benefits of Hot Water Extract from the Improved Cultivar of *Camellia japonica* 'Double-Flowered Camellia'

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Camellia japonica has traditionally been cultivated as an ornamental plant; however, increasing interest in its bioactive constituents has recently highlighted its potential as a natural ingredient for skin health applications. This study aimed to comprehensively evaluate the antioxidant, whitening, anti-wrinkle, and moisturizing effects of a hot water extract derived from the flowers of the improved cultivar of *C. japonica*. The antioxidant capacity was assessed via intracellular reactive oxygen species (ROS) scavenging assays, revealing potent free radical elimination activity. Whitening effects were demonstrated using B16F10 melanoma cells, where the extract significantly inhibited intracellular tyrosinase activity and reduced melanin synthesis, suggesting potential for mitigating hyperpigmentation. Anti-wrinkle effects were confirmed through the suppression of MMP-1 expression in human dermal fibroblasts, indicating a potential role in maintaining skin elasticity. Moisturizing activity was evaluated using a hyaluronic acid ELISA, which showed a significant increase in hyaluronic acid production following treatment with the extract. Moreover, phytochemical profiling using LC-MS/MS analysis revealed the presence of diverse bioactive compounds, which are presumed to act synergistically to elicit the observed skin benefits. Collectively, these findings suggest that the hot water extract of 'double-flowered Camellia' possesses multifunctional dermatological effects—antioxidant, whitening, anti-wrinkle, and moisturizing—and may serve as a promising natural ingredient for applications in the functional cosmetics industry.

PNB-42

Luteolin-mediated GDH1 inhibition suppresses colon cancer progression via autophagy and angiogenesis pathways

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Glutamate dehydrogenase 1 (GDH1) is a key metabolic enzyme implicated in colon cancer progression, with our previous studies demonstrating its upregulation in tumor tissues and cell lines. In this study, we investigated luteolin, a natural flavonoid, as a potential GDH1 inhibitor. Fluorometric and enzymatic assays revealed that luteolin effectively inhibits GDH1 activity in a dose-dependent manner. Computational molecular docking further supported its high-affinity binding to GDH1, suggesting a strong inhibitory interaction. To assess the broader functional impact of GDH1 modulation, we analyzed key autophagy (LC3, p62) and angiogenesis (VEGF, HIF-1α) markers following luteolin treatment. Our results indicate that GDH1 inhibition by luteolin correlates with altered autophagic flux and reduced angiogenic signaling, implicating its role in metabolic reprogramming of colon cancer cells. These findings position luteolin as a promising therapeutic agent targeting GDH1, with potential dual effects on autophagy and angiogenesis. Further mechanistic studies will explore the precise pathways linking GDH1 suppression to these anticancer effects.

PNB-43

Kaempferol induces apoptosis and suppresses proliferation and migration in colon cancer via hypoxia-mediated inhibition of HIF-1α/VEGF and Wnt/β-Catenin signalling

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Kaempferol, a bioactive flavonoid with demonstrated anticancer properties, exerts multi-targeted effects against hypoxic colon cancer progression. Our study reveals" that kaempferol has multi-faceted anti-tumor effects in hypoxic colon cancer cells, HCT-15 and HCT-116, by inhibiting HIF-1α/VEGF angiogenesis, Wnt/β-catenin signalling, and epithelial-mesenchymal transition (EMT) progression. In conditions of hypoxia, kaempferol inhibited the stabilization of HIF-1α and its downstream targets (VEGF, ANG1, VEGFR2), while also obstructing Wnt/β-catenin activation by decreasing β-catenin and modifying the expression of pathway components (c-Myc, Cyclin-D1, LEF1, APC, and Axin-2). Kaempferol mitigated hypoxia-induced EMT by reinstating E-cadherin and inhibiting N-cadherin, Vimentin, and MMP-2/9, which corresponded with diminished migration in transwell and wound-healing assay. Mechanistic investigations demonstrated dual regulation of HIF-1α transcriptional activity (HRE luciferase) and MAPK signalling (p-ERK/p-38), in conjunction with ROS-induced DNA damage and intrinsic apoptosis (cleaved caspase-3/9 and Bcl-2 protein expression). The impact on angiogenesis, EMT, and survival pathways significantly diminished the proliferation, invasion, and metastatic capacity of hypoxic colon cancer cells, which identifies kaempferol as an innovative multi-pathway inhibitor, thereby offering a strong justification for its advancement as a therapeutic agent for advanced colorectal cancer.

PNB-44

Comparison of Inflammatory Cytokine Levels in Blood from Patients with Pancreatic Cancer Before and After Surgery/Chemotherapy

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Levels of inflammatory cytokines in blood samples from 3 patients with pancreatic cancer who were treated with surgery or chemotherapy were compared. Patients were enrolled for the joint research project between KIST and GangNeung Asan Hospital. Blood samples were obtained after biopsy, before surgery, and after the surgery (just before the first chemotherapy). Human inflammation antibody array kits were used to detect the levels of cytokines in the blood using chemiluminescence. The densitometric data was extracted using an image processing software and further analyzed with a graphing and statistics software. Of the 40 cytokines detected with the kits, 11 were chosen based on their marked difference in levels before and after surgery/chemotherapy. Levels of RANTES (regulated on activation, normal T-cell expressed and secreted; CCL5), PDGF-BB (platelet-derived growth factor), and MIG (monokine induced by gamma interferon; CXCL9) cytokines increased, whereas the level of IL-6 sR cytokine decreased for all 3 patients. Other cytokines such as MIP-1-beta (macrophage inflammatory protein; CCL4), MIP-1-delta and TIMP-2 (tissue inhibitor of metalloproteinases) showed mixed trends for each patient. Further studies of cytokine levels which exhibit high fluctuation in levels before and after surgery/chemotherapy may assist in more effective treatments for patients with pancreatic cancer.

Poster Presentation

PNB-45

Isolation and Characterization of Megastigmane Derivatives from *Ardisia humilis* Val Leaves Extract

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*Ardisia humil*is Val. (AHV) is a flowering plant belonging to the Ardisia genus, which is known for its wide distribution across the tropical rainforests of Southeast Asia. This species is particularly abundant on the Indonesian islands of Sumatra, Java, and Sulawesi, where it has traditionally been used in various forms of herbal medicine. Previous phytochemical screenings have revealed that AHV contains a diverse array of secondary metabolites, including carotenoids, flavonoids, triterpenoids, and alkylbenzoquinone derivatives. These bioactive compounds have been associated with a broad spectrum of pharmacological activities, such as thrombolytic (beneficial in stroke prevention), antioxidant, antidiabetic, antitubercular, immunostimulant, anticancer, anti-HIV, and anti-inflammatory properties. Despite these promising findings, the complete chemical profile of AHV remains poorly characterized, and comprehensive studies focusing on the identification and structural elucidation of its phytoconstituents are still limited. In the present study, we successfully isolated and identified four megastigmane-type compounds from the leaves of AHV using a combination of chromatographic techniques. These findings contribute valuable insights into the phytochemical composition of AHV and serve as a foundation for future research aimed at exploring its therapeutic potential and mechanisms of action at the molecular level.

PNB-46

Identification and quantification of trans-anethole in *Foeniculum vulgare* Mill. (Fennel) grown in Korea

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Foeniculum vulgare Mill. (Umbelliferae family) consists of dried, ripe fruits. The plant has also been used as a traditional herbal medicine in Korea. It is widely used in traditional medicinal systems in China, Japan, Europe, and the United States. *Foeniculum vulgare* is renowned for its ability to aid digestion, relieve gas and combat colic. The fruits of *Foeniculum vulgare* and its main component, trans-anethole, were identified using high-performance thin-layer chromatography (HPTLC). In this study, the fruits of *Foeniculum vulgare*, harvested in Korea, were extracted using hexane. HPTLC analysis of the sample was performed on an HPTLC Silica Gel 60 F254 plate using a hexane/ethyl acetate mobile phase (20:1, v/v). The sample was then identified and subjected to quantitative tests using HPTLC. For the methanol extraction, the sample was quantified using HPLC. HPLC analysis was performed using a water/acetonitrile mobile phase at 220 nm. Pressed, dried specimens were prepared and stored in herbariums (KHR) for future reference. This study provides an overview of the HPTLC and HPLC techniques that can be used to standardise *Foeniculum vulgare*.

PNB-47

Cognitive-enhancing effects of subtropical natural resource extracts

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In this study, ethanolic extracts of 50 subtropical plants and 10 cruciferous vegetables were initially evaluated for their acetylcholinesterase (AChE) inhibitory activity as part of the development of natural product-derived functional materials to help improve cognitive function. Among them, six extracts (Ampelopsis brevipedunculata(Maxim.) Trautv., Albizia kalkoraPrain, Alnus firmaSiebold & Zucc., Robinia pseudoacaciaL., Persicaria filiformis(Thunb.) Nakai ex T. Mori, Sinomenium acutum(Thunb.) Rehder & E. H. Wilson) with the best AChE inhibitory activity were selected, and the protective effects of scopolamine-induced cholinergic dysfunction in SH-SY5Y neurons and neuronal protection against oxidative stress were investigated. Active ingredient research is also being conducted on six extracts that have been shown to improve cognitive function. These results are expected to enable the exploration of safe and effective candidate substances that can effectively improve memory impairment and cognitive function.

PNB-48

Efficient Separation of Spinach-Derived Saponins Using Twin-Column N-Rich Technique

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Among the most critical needs of natural product chemistry is a complete library of pure reference substances. Some spinach-derived saponins of pharmacological importance are either still lacking reference substances or references are only available in limited amounts. To address this need, a twin-column cyclical enrichment process (N-Rich technique) strategy was adopted to improve the saponins separation efficiency from Spinach (*Spinacia oleracea* L.). Among the most critical needs of natural product chemistry is a complete library of pure reference substances. Some spinach-derived saponins of pharmacological importance are either still lacking reference substances or references are only available in limited amounts. To address this need, a twin-column cyclical enrichment process (N-Rich technique) strategy was adopted to improve the saponins separation efficiency from Spinach (*Spinacia oleracea* L.). Under the optimal isolation conditions, we obtained pure substances, particularly oleanane-type saponins. Isolated compounds attained purities greater than 95% as determined by ultra-performance liquid chromatography-charged aerosol detector (UPLC-CAD). Two major ones (Compounds **1** and **2**) were selected as representative targets to evaluate efficiency of the N-Rich system. Compared to conventional prep-LC, the N-Rich system improved recovery by 8 – 10 times and reduced purification time by ~50%. The proposed methods of N-Rich obtained the same amount of product as conventional systems while being simple, increasing efficiency and reducing cost.

PNB-49

Stage-Specific Anti-Cancer Metabolites from *Paulownia tomentosa* Fruit Identified by UPLC-QTOF/MS

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Paulownia tomentosa is a traditional medicinal plant that has long been used in Asia to treat various diseases, including tonsillitis, bronchitis, asthma, enteritis, and dysentery. In particular, the fruit of *P. tomentosa* fruits has been reported to possess a wide range of biological activities. It is especially known to contain dihydroflavonols and prenylated flavanones, which have demonstrated anti-cancer properties. In this study, multivariate statistical analysis based on ultra-performance liquid chromatography coupled with quadrupole time-of-flight mass spectrometry (UPLC-QTOF/MS) was conducted to analyze the key metabolites in *P. tomentosa* fruit at different growth stages and to investigate their potential anti-cancer properties. Major metabolites identified at each stage were isolated and structural elucidation, followed by evaluation of their cytotoxic effects on human lung cancer (A549) and liver cancer (HepG2) cell lines. As a result, most of the key stage-specific metabolite was found to improve cytotoxic effects compared to the reported controls. These findings suggest that the bioactive metabolites exhibiting efficacy in *P. tomentosa* fruit are stage-specific marker metabolites with anti-cancer potential, highlighting their promise as lead compounds.

PNB-50

Inhibitions of monoamine oxidase A and B by new bioactive flavonoid glycosides isolation from aerial part of *Lespedeza cyrtobotrya* Miq.

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Lespedeza cyrtobotrya Miq. (Fabaceae), native to Korea, China, Japan, and eastern Russia, has been traditionally used to treat osteoporosis, lumbago, and joint pain. A 70% aqueous ethanol extract of its aerial parts exhibited significant inhibitory activity against monoamine oxidase A and B (MAO-A and MAO-B) compared to another *Lespedeza* species. The extract was fractionated via Diaion HP-20 column chromatography using a stepwise methanol gradient (20 – 100%), and active fractions were analyzed by UPLC-QTOF/MS, revealing flavonoid glycosides as the major constituents. Nine compounds were isolated through repeated preparative HPLC and structurally elucidated as nine flavonol glycosides (**1 – 9**) by NMR, ESI/MS, and UV spectroscopy. Among them, 4'''-acetyl-kaempferitrin (**6**) and kaempferin 2''-*O*-α-L-(3'''-acetyl) rhamnopyranoside (**8**) are identified as new flavonoid glycosides. Additionally, compounds including kaempferitrin (**4**), sutchuenoside A (**5**), 3'''-acetyl-kaempferitrin (**9**), and four others were isolated for the first time from *L. cyrtobotrya*. Isolated compounds **4 – 6** and **9** exhibited significantly inhibition effects against MAO-A and MAO-B enzymes. Major active constituents (**4 – 6, 9**) were quantified by UPLC-PDA and UHPLC-TQ/MS, all exceeding 5.0 mg/g. Analytical methods were validated according to KFDA guidelines, demonstrating acceptable linearity, precision, accuracy, and recovery. These results highlight the phytochemical usages of *L. cyrtobotrya* and support its potential as a novel source of bioactive flavonoid glycosides for application in functional foods or herbal medicinal products.

PNB-51

Discrimination of *Oenothera* Species using UPLC-QTOF/MS-Based Metabolomics

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Metabolomics aims to investigate the diverse characteristics of metabolites within biological systems. In particular, plant metabolomics is well-suited for distinguishing differences based on plant parts, harvest times, and species. Previous studies have shown that evening primrose (*Oenothera spp*.), including its young shoots and seeds, can be used as food materials. Traditionally, these plants have been used to treat various ailments such as colds, fever, sore throat, nephritis, and hypertension. They are rich in bioactive compounds such as flavonoids, phenolic acids, tannins, and sterols. In the standardization of raw materials, efficacy equivalence is closely linked to the content of distinguishable marker metabolites and is regarded as one of the most critical aspects of the standardization process. This study aimed to identify key metabolites that differentiate various *Oenothera* species using multivariate statistical analysis based on ultra-performance liquid chromatography coupled with quadrupole time-of-flight mass spectrometry (UPLC-QTOF/MS). In addition, quantitative analysis and validation were performed to compare different *Oenothera* species and to establish marker compounds to prevent the unintentional mixing of raw materials.

PNB-52

Application of a Validated UPLC-CAD Method to Evaluate Saponin Content Variation in Spinach across Cultivars and Seasons

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Spinach (*Spinacia oleracea* L.) is a widely cultivated leafy vegetable exhibiting significant varietal and seasonal diversity. The content and composition of phytochemicals, particularly saponins, vary depending on genotype, environment, and harvest season. Although saponins are increasingly recognized for their bioactivity, their structural diversity and distribution in spinach cultivars remain underexplored. In this study, six major saponins (spinasaponin A – E and celosin I) were quantified across 15 commercial cultivars grown in Namhae, Korea, during spring, fall, and winter seasons. Samples were freeze-dried and extracted three times with 30% prethanol at 40°C. Quantification was performed using a validated UPLC-CAD method (BEH C_{18} column, I-Class system, Waters) in accordance with ICH guidelines. The method demonstrated excellent linearity ($R^2 \geq 1.000$), accuracy (90.2 – 106.2%), and precision (RSD < 2%), with LOD and LOQ ranging from 0.201 – 0.966 μg/mL and 0.609 – 2.927 μg/mL, respectively. Among the tested cultivars, Luckyyou and Shinwoldong showed consistently high saponin contents, with Luckyyou exhibiting the highest concentrations across multiple compounds. Seasonal comparison revealed that several cultivars harvested in spring contained elevated saponin contents, indicating optimal conditions for industrial application. These results demonstrate the practical applicability of UPLC-CAD for accurate saponin quantification and provide foundational data for selecting spinach cultivars with high saponin content and highlight their potential for development as functional food ingredients.

PNB-53

Comparative Analysis of the Morphological and Chemical Characteristics of *Carthamus tinctorius* L. from Different Countries

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Carthamus tinctorius L., commonly known as safflower and belonging to the Compositae family, is widely cultivated in several countries, including Korea, China, and Japan. In recent years, safflower seed oil has gained prominence in the cosmetic and pharmaceutical industries due to its diverse bioactive properties. In this study aimed to compare the morphological and chemical characteristics of safflower seeds collected from seven countries: Korea, Japan, China, The United States, The United Kingdom, Italy, and Australia, in order to establish basic data for cultivar classification and standardization. Chemical profiling was performed using High-Performance Thin-Layer Chromatography (HPTLC) and High-Performance Liquid Chromatography (HPLC). Through these analyses, key components were quantified, with a particular focus on the marker compound tracheloside. Differences in tracheloside content were identified among the different accessions. Morphological analysis revealed variations in leaf characteristics and growth dynamics. The consistent detection of tracheloside in both HPTLC and HPLC analyses, consistent detection of tracheloside supported its utility as a chemotaxonomic marker. Overall, the combined data suggest that both morphological and chemical traits vary according to geographical origin. These findings provide valuable basic data for the future development of classification systems and standardization of *Carthamus tinctorius* L. cultivars.

PNB-54

Glut-1 Inhibitor Enhanced the Therapeutic Efficacy of ^{64}Cu-DOTA-Trastuzumab in Osteosarcoma Cells

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Introduction: Osteosarcoma exhibits poor outcomes, with limited trastuzumab efficacy linked to HER2 heterogeneity. GLUT-1 overexpression sustains tumor glycolysis and survival. This study investigates the potential of GLUT-1 inhibition to enhance the targeted therapeutic efficacy of ^{64}Cu-DOTA-Trastuzumab in osteosarcoma cells.
Methods: SJSA-1 cell lines were treated with BAY-876 and WZB-117 for 48 hours followed by 3-hour incubation with ^{64}Cu-DOTA-Trastuzumab 1 μCi/well and 5 μCi/well. Post treatment, the media was removed and fresh media was added. Cell viability was measured after 24-hour recovery using Ez-Cytox assays.
Results: Combination treatment with ^{64}Cu-DOTA-Trastuzumab (5 μCi) and BAY-876 (500 nM) significantly reduced the viability of SJSA-1 cells (28.42±3.5%) ($p<0.0022$) compared to alone BAY-876 (500 nM) (37.75±4.38%). Similarly, combination treatment with ^{64}Cu-DOTA-Trastuzumab (5 μCi) and WZB-117 (10 μM) showed significantly reduced viability of SJSA-1 cells (16.03±1.33%) ($p<0.0022$) compared to WZB-117 (28.78±2.09 %) alone.
Conclusion: GLUT-1 inhibition enhanced the therapeutic effect of ^{64}Cu-DOTA-trastuzumab, supporting its potential in combination therapy for HER2 expressing osteosarcoma cells.

PNB-55

GLUT-1 inhibition enhanced therapeutic efficacy of radiolabeled PSMA in prostate cancer cells

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Background: This study investigates the potential of GLUT-1 inhibition to enhance the therapeutic effects of ^{64}Cu- and ^{177}Lu with PSMA I&T in prostate cancer.
Methods: Radiolabelling of ^{64}Cu- and ^{177}Lu with PSMA I&T was done and then used for In vitro cytotoxicity assays, clonogenic assays in 22Rv1, LNCaP, and PC3 cell lines in combination with different concentrations of BAY-876(GLUT-1 inhibitor). Also, cell uptake test was performed with [^{64}Cu] Cu-PSMA-I&T for 22RV1, and LNCaP to compare PSMA membrane expression.
Results: Combination treatment with [^{64}Cu] Cu-PSMA-I&T and BAY-876 significantly reduced 22Rv1 cell viability (16.9±3.1%) compared to BAY-876(1 μM) alone (44.0±2.4%) or [^{64}Cu] Cu-PSMA-I&T alone (33.2±7.0%) ($p<0.0001$). Similarly, combined treatment with [^{177}Lu] Lu-PSMA-I&T and BAY-876 decreased viability to 34.5±2.1%, compared to BAY-876 alone (52.6±4.4%) or [^{177}Lu] Lu-PSMA-I&T alone (51.7±8.1%) ($p<0.001$). Notably, LNCaP showed the better response, even with lower concentration of BAY-876 (0.1 μM) (24.3±4.4%) ($p<0.0001$), attributed to its co-expression of PSMA and GLUT-1 and making it more susceptible to both therapeutic targets.
Conclusion: The combination of GLUT-1 inhibition and PSMA-targeted radionuclide therapy results in enhanced therapeutic efficacy in PSMA- and GLUT-1–expressing prostate cancer cells.

PNB-56

Therapeutic potential of *Staphylea bumalda* leaf extract for obesity and sarcopenia

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Obesity and sarcopenia are the major metabolic disorders characterized by excessive fat accumulation and progressive loss of skeletal muscle mass, respectively. Both diseases are closely associated with impaired metabolic function and increased risks of chronic diseases, leading to the reduction of physical performance and negative impact on the quality of life. With increasing prevalence and the side effects of current synthetic treatments, there is a growing need for safe and effective multifunctional agents to manage these diseases. Many studies have focused on natural phenolic compounds to improve various metabolic disorders such as diabetes, hypertension, obesity, and muscle atrophy. Therefore, our study aimed to explore the effects of extract from *Staphylea bumalda* leaf (SBE) on obesity and sarcopenia *in vitro*. We observed that SBE effectively regulated lipogenic pathway and reduced fat accumulation in 3T3-L1 cells. Moreover, SBE significantly alleviated dexamethasone (DEXA)-induced muscle atrophy by regulating mTOR/Akt signaling pathway and ubiquitin proteasome system in C2C12 myotube. Hence, this study suggests the potential of SBE as a multifunctional agent to improve metabolic disorders such as obesity and sarcopenia.

PNB-57

Extraction and Purification of Sulfated Polysaccharides with Anticoagulant Activity from *Sticopus japonicus*

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Natural products have attracted increasing attention as promising sources for pharmaceuticals and functional foods due to their low toxicity and reduced risk of inducing resistance. Heparin, a widely used antithrombotic agent, can cause side effects such as bleeding, heparin-induced thrombocytopenia, and osteoporosis, especially with long-term use, thereby highlighting the need for safer alternatives. Sulfated polysaccharides, in particular, exhibit a variety of biological activities, including anticoagulant, antioxidant, immunomodulatory, and antimicrobial effects. However, due to limitations in extraction and purification techniques, most studies have been limited to crude polysaccharide extracts. In this study, sulfated polysaccharides were extracted from *Stichopus japonicus*, a sea cucumber native to Korean coastal waters. A multi-step extraction protocol was employed, including enzymatic deproteinization, selective polysaccharide isolation using cetylpyridinium chloride, and ethanol precipitation to enhance purity. This process yielded polysaccharides with over 95% purity. Subsequently, purification was performed using ion-exchange chromatography with a salt gradient, and two distinct sulfated polysaccharide fractions were separated and confirmed by the DMMB assay. The optimized extraction and purification protocols provide a foundation for future studies on these polysaccharides. Further structural analyses using NMR, GC-MS, and LC-MS will elucidate their monosaccharide composition, glycosidic linkages, sulfation patterns, and molecular weight characteristics.

PNB-58

Chamaecyparis pisifera Essential Oil: Chemical Composition Analysis and Evaluation of Antioxidant and Skin Whitening Potentia

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Chamaecyparis pisifera (Siebold & Zucc.) Endl. (*C.* pisifera; family Cupressaceae) is native to Japan and has been widely cultivated in Korea have increased since the 1970s. We here investigated the effects of *C. pisifera* essential oil on the biological activities of the skin, particularly, its antioxidant properties and skin whitening effects. The fresh *C. pisifera* was obtained from the Hoseo University Forest Plant Essential Oil Bank Plantation. *C. pisifera* essential oil (CPEO) was extracted by steam distillation (yield of 0.67% v/w) and its components were analyzed by GC-MS. Twenty-eight components were identified in CPEO and the major components of CPEO were (-)-bornyl acetate (26.72%), α-phelllandrene (21.33%), and myrcene (17.51%). CPEO exhibited a dose-dependent antioxidant activity, scavenging ABTS radicals. In B16BL6 cells, CPEO reduced serum-induced proliferation. CPEO also inhibited α-MSH-stimulated increases in melanin synthesis and tyrosinase activity in B16BL6 cells. This effect was mediated by regulating melanogenesis-related proteins (MITF, tyrosinase, TRP-1 and -2) and melanosome transport-related proteins (Rab27a, Melanophilin, Myosin Va) through the MAPKs (p38, ERK1/2, and JNK) signaling pathway. Additionally, when B16BL6 cells were exposed to conditioned medium from UVA-irradiated HaCaT cells with CPEO, a reduction in melanin production and tyrosinase activity was observed. These results suggest that CPEO may have potential as a natural material for the development of agents for skin protection and whitening.

PNB-59

A Study on the Analytical Method for Measuring *l*-Menthol in Three Domestically Cultivated *Mentha arvensis* L. Species

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Mentha arvensis L.(Mentha), a perennial herbaceous plant belonging to the family Lamiaceae, is traditionally used as a medicinal herb in Korea, China, Japan, and Europe. Due to its high commercial value, it is extensively applied in the food, Pharmaceutical, cosmetic, and healthcare industries. However, Mentha species includes approximately 30 taxa comprising numerous interspecific hybrids and variants. Due to frequent interspecific hybridization and vegetative propagation through spontaneous mutations, there is a significant risk of misidentification and unintentional admixture. In this study, DNA barcoding using universal primers was employed to characterize the genetic profiles of three domestically cultivated Mentha species. *Mentha arvensis* and its major constituent, *l*-menthol, were initially identified using high-performance thin-layer chromatography(HPTLC). Petroleum ether extracts of the powdered *Mentha arvensis* materials were fingerprinted in a cyclohexane:ethyl acetate(3:1) solvent system and visualized under UV using 2% sulfuric acid/1% vanillin in methanol as a derivatization reagent. Quantitative analysis of *l*-menthol was subsequently performed using gas chromatography coupled with mass spectrometry (GC-MS). The results suggest that *l*-menthol is a reliable marker compound for the quality control and authentication of *Mentha arvensis* herbal resources.

PNB-60

Anti-Melanogenic Potential of Exosomes Derived from *Hordeum vulgare* L in B16F10 Melanoma Cells and Zebrafish Model

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Plant-derived exosomes are gaining attention as novel bioactives for dermatological and cosmetic use. This study evaluated the anti-melanogenic activity of exosomes obtained from *Hordeum vulgare* L (barley sprouts) in B16F10 melanoma cells and zebrafish models. The barley-derived exosomes (HvEXOs) were successfully isolated and characterized through nanoparticle tracking analysis and transmission electron microscopy. In vitro analysis revealed that HvEXOs effectively suppressed melanin accumulation and tyrosinase enzymatic activity induced by α-MSH in a dose-dependent fashion. Furthermore, HvEXOs significantly reduced the expression of melanogenesis-associated genes such as TYR, TRP-1, and MITF. In vivo zebrafish assays further corroborated the depigmenting potential of HvEXOs, with no signs of developmental toxicity observed. Collectively, these results indicate that exosomes from Hordeum vulgare possess notable melanin-inhibitory effects and may serve as a promising natural whitening ingredient in functional cosmetic applications.

Poster Presentation

PNB-61

Comparison of metabolite accumulation and antioxidant activity in metabolite-enhanced mung bean leaves by ethylene treatments

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This study aimed to evaluate changes in secondary metabolites and antioxidant activity in metabolite-enhanced mungbean leaves (MEML) by optimizing ethylene treatment conditions. Plants were divided into four groups, seed (SD), germination (GM), control leaves (CTL), and ethylene-treated leaves (ETL), and analyzed for metabolite profiles and biological activities. NMR analysis identified two previously uncharacterized compounds, determining the structures of 2′-hydroxydaidzin (2HDAI) and 2′-hydroxydaidzein. HPLC quantification revealed a dramatic accumulation of key isoflavones in ETL, particularly 2HDAI (from 273.24 μg/g in to 21,159.88 μg/g) and daidzin (from 429.67 μg/g to 31,845.13 μg/g). In terms of bioactivity, ETL exhibited the highest radical scavenging activities (DPPH and ABTS assays) and the strongest inhibition of lipase and α-glucosidase. Notably, the ETL extract also demonstrated DNA-protective effects, confirming its antioxidant functionality. These findings indicate that ethylene-mediated metabolomic modulation effectively enhances both the accumulation of functional secondary metabolites and the biological activity of mungbean leaves. Furthermore, the properties conferred by ethylene treatment support the use of MEMLs in the high-value bioresource industry.

PNB-62

Inhibition of Melanin Synthesis in Melanoma Cells and α-MSH Expression in UVA-irradiated Keratinocytes by *Vitex rotundifolia* L.f. cone Essential Oil

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Vitex rotundifolia L.f. (VRL), a plant belonging to the Verbenaceae family, is native to Korea and other parts of Asia. In Korea, VRL has been traditionally used for its antipyretic, analgesic, and anti-inflammatory properties. However, there is limited research on the whitening effects of essential oil extracted from the cone of *Vitex rotundifolia*. In this study, we obtained the essential oil of VRL cone (VRLCEO) through steam distillation and aimed to investigate its effects on melanin synthesis and underlying mechanisms. Gas chromatography-mass spectrometry analysis identified 13 components, including eucalyptol (32.23%), α-terpineol (22.13%), and β-pinene (20.32%). VRLCEO inhibited the generation and secretion of α-MSH in keratinocytes exposed to UVA (10J). It also suppressed the activity of tyrosinase and melanin synthesis in B16BL6 mouse melanoma cells induced by exogenous α-MSH. Furthermore, VRLCEO dose-dependently reduced the expression of tyrosinase, MITF, and TRP-2 involved in melanogenesis, as well as Rab27a and melanophilin involved in melanosome transport. However, it did not affect the expression of TRP-1 protein.

The results of this study suggest that VRLCEO may serve as a potential whitening agent by inhibiting α-MSH induction in keratinocytes and suppressing melanogenesis and melanosome transport in melanoma cells. Future expansion of research on VRLCEO may provide potential applications as a bioactive material not only in whitening functional cosmetics but also in food and pharmaceuticals.

PNB-63

Study on the Improvement of Atopic Dermatitis through SNARE Protein Expression Inhibition by *Paulownia coreana* Uyeki flower absolute

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Atopic dermatitis (AD) is a chronic inflammatory skin disorder influenced by immunological and environmental factors. Its global prevalence has spurred significant research into effective treatments. *Paulownia coreana* Uyeki (PCU), a plant from the bignoniaceae family, is known to have therapeutic effects on respiratory diseases and its anti-inflammatory and antimicrobial properties. Its bark has been used for treating bruises and aiding wound healing, but research on PCU flowers in treating AD is limited. This study explored the effects and mechanisms of PCU flower absolute (PCUFAb) on AD-related responses. PCUFAb was extracted from PCU flowers using an organic solvent, and its composition was analyzed by gas chromatography-mass spectrometry. Cytotoxicity testing using the WST assay on rat basophilic leukemia cells, RBL-2H3, showed a survival rate of less than 70% at 200 μg/mL. PCUFAb reduced mast cell degranulation and the release of β-hexosaminidase and histamine induced by anti-DNP IgE and DNP-BSA in RBL-2H3 cells. Additionally, it suppressed the expression of v-SNARE proteins (VAMP7 and VAMP8) involved in degranulation, but did not affect t-SNARE proteins. These findings suggest that PCUFAb inhibits histamine release through regulation of v-SNARE proteins, offering potential therapeutic effects for AD. PCUFAb could be a promising bioactive material for cosmetics, food, and drug applications.

PNB-64

Inhibitory effects of *Lonicera japonica* Thunb. Absolute on neointimal formation-related activities of rat vascular smooth muscle cells

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Lonicera japonica Thunb. (LJ) is a traditional herbal plant known for its anti-oxidant, anti-microbial, and anti-inflammatory properties. However, its effects on atherosclerosis remain underexplored. Atherosclerosis, a chronic inflammatory disease, is aggravated by the abnormal proliferation and migration of vascular smooth muscle cells. This study investigates the anti-atherosclerotic effects and underlying mechanisms of LJ flower absolute (LJFAb) using rat aortic smooth muscle cells (RASMCs) from Sprague-Dawley rats. LJFAb was extracted using organic solvents and analyzed via GC/MS, identifying 11 components including methyl linoleic acid (46.08%) and methyl hexadecanoate (15.21%). Cytotoxicity was assessed with a WST assay, showing no cytotoxicity at concentrations up to 50 μg/mL. Proliferation analysis using WST and direct cell counting assays demonstrated significant inhibition of platelet-derived growth factor-BB (PDGF-BB; 10 ng/mL)-induced RASMCs proliferation. LJFAb also significantly reduced PDGF-BB-induced RASMCs migration, as determined by a Boyden chamber assay. *Ex vivo* aortic ring assays showed that LJFAb significantly suppressed PDGF-BB-stimulated RASMCs sprout outgrowth. Additionally, LJFAb inhibited the phosphorylation of platelet-derived growth factor receptor-β (PDGFR-β), spleen tyrosine kinase (Syk), and p38 mitogen-activated protein kinase (p38 MAPK) in PDGF-BB-stimulated RASMCs. These findings suggest that LJFAb suppresses the proliferation and migration of RASMCs by modulating the PDGFR-β/Syk and/or p38 MAPK signaling pathways. Collectively, our results indicate that LJFAb has potential as a natural therapeutic for vascular diseases associated with neointimal hyperplasia and atherosclerosis.

Poster Presentation

PNB-65

Lindera obtusiloba Blume wood essential oil suppresses UVA-induced α-MSH production and melanogenesis: Potential for natural skin-whitening applications

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Lindera obtusiloba Blume wood has been shown to possess various bioactive properties, including anti-photoaging, neuroinflammation-attenuation, anti-bacterial, and anti-inflammatory properties. However, its potential for skin whitening has not been explored. In this study, *Lindera obtusiloba* Blume wood essential oil (LOWEO) was obtained by steam distillation and analyzed by GC/MS, identifying 28 components, with major constituents being limonene (24.62%), 2-ethyl-m-xylene (10.90%), and β-pinene (8.50%). The cytotoxicity of LOWEO was assessed on B16BL6 melanoma cells using a WST assay, revealing no cytotoxicity at concentrations up to 50 μg/mL. LOWEO significantly inhibited 2%-fetal bovine serum-induced cell proliferation in a BrdU incorporation assay and reduced UVA-induced secretion of α-melanocyte-stimulating hormone (α-MSH) in HaCaT keratinocytes. It also inhibited α-MSH-induced tyrosinase activity and melanin synthesis in B16BL6 cells. Immuno-blotting analysis showed that LOWEO downregulated melanogenesis-related proteins (MITF, tyrosinase, TRP-1) and melanosome transport proteins (melanophilin, Rab27a) in B16BL6 cells exposed to α-MSH. These results suggest that LOWEO suppresses α-MSH secretion from keratinocytes and reduces melanin synthesis by downregulating melanogenic signaling pathways. Moreover, by targeting the early signaling events of melanin synthesis initiated by UV-stimulated keratinocytes, LOWEO demonstrates potential as a dual-functional bioactive agent for UV protection and skin whitening. Collectively, this study indicates LOWEO as a promising candidate for cosmetic applications aimed at mitigating UV-induced pigmentation.

PNB-66

Modulation of lipid metabolism by ethanol extract of shiitake mushroom in high-fat diet-induced mice

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In this study, shiitake mushrooms (*Lentinus edodes*) were fermented with lactic acid bacteria, and their lipid metabolism-modulating effects were evaluated using high-fat diet (HFD)-fed mouse models. Mice were administered a HFD supplemented with fermented shiitake mushroom extracts for 12 weeks. Throughout the experimental period, body weight, food intake, and water consumption were monitored. In addition, serum levels of total cholesterol, triglycerides, HDL-cholesterol, and LDL-cholesterol were measured. HFD consumption resulted in increased body weight, as well as elevated levels of total cholesterol, LDL-cholesterol, and triglycerides, compared to the normal control group. However, supplementation with lactic acid bacteria-fermented shiitake mushroom extracts attenuated weight gain and significantly reduced serum levels of total cholesterol, triglycerides, and LDL-cholesterol, without altering HDL-cholesterol levels. Notably, fermented extracts derived from dried shiitake mushrooms exhibited greater efficacy in improving lipid metabolism than those obtained from fresh shiitake mushrooms. These findings suggest that fermented shiitake mushroom extracts may hold potential as functional food ingredients for improving serum lipid profiles and regulating lipid metabolism in HFD-induced obesity.

PNB-67

Enhancement of metabolites and biological activities in mung bean roots cultivated under a vertical farming system

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The trace and unstable nature of metabolite accumulation in plants poses significant challenges for large-scale industrial utilization. To address this issue, we applied metabolite farming under controlled conditions using ethylene, a key plant senescence hormone, to enhance the bioactivity and biomass of mung bean (*Vigna radiata*) roots. Plants were classified into four groups: seed (SD), germinated (GM), untreated control (CTL), and ethylene-treated (ETL) roots. NMR analysis identified 14 metabolites, including two novel compounds—2′-Hydroxydaidzein-4′,7-*O*-diglucoside and daidzein-4′,7-*O*-diglucoside—specifically detected in the roots. HPLC analysis revealed that key isoflavones and flavones were significantly elevated in the ETL group, particularly 2HDAEDG and VTX (2HDAEDG: CTL 13,863.01 μg/g → ETL 19,261.68 μg/g; VTX: CTL 6,830.54 μg/g → ETL 15,786.75 μg/g). The ETL group exhibited the highest radical scavenging activities (DPPH, ABTS) and inhibitory effects on digestive enzymes (lipase, α-glucosidase). Furthermore, DNA protective effects—indicated by the presence of open circular (OC) and supercoiled (SC) forms—were observed exclusively in the ETL group. These results demonstrate that ethylene-induced metabolomic regulation can significantly enhance the accumulation of functional secondary metabolites in mung bean roots, highlighting their potential as high-value materials for nutraceutical and bioresource industries.

PNB-68

Elucidation of the protective effect of schisandrin C originating from *Schisandra chinensis* against indomethacin-induced intestinal injury

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Nonsteroidal anti-inflammatory drugs (NSAIDs), especially indomethacin, have severe adverse effects on the gastrointestinal system. Here, we hypothesized that *Schisandra chinensis*, an herbal medicine used for the treatment of several gastrointestinal diseases, might effectively reduce indomethacin side effects. Therefore, we aimed to investigate the main bioactive compounds from *S. chinensis* and their molecular mechanism for protecting against indomethacin-induced intestinal barrier dysfunction. Schisandrin C (Sch C) could be a candidate compound potentially responsible for the protective activity of *S. chinensis*, as it reverses the intestinal cell death and inflammation induced by indomethacin. Sch C was also demonstrated to reverse apoptotic cell death in indomethacin-stimulated Caco-2 cells. In addition, Sch C ameliorated indomethacin-induced intestinal permeability dysfunction by increasing transepithelial electrical resistance (TEER) and decreasing the permeability of FITC-dextran in indomethacin-injured Caco-2 cell monolayers. Moreover, Sch C restored the indomethacin-induced decrease in tight junction (TJ) and adherens junction (AJ) protein expression. *In vitro* cell experiments also confirmed that Sch C can ameliorate intestinal permeability dysfunction by modulating the Akt/GSK-3β and NF-κB/MLCK/MLC signaling pathway. In addition, Sch C could improve the intestinal atrophy induced by indomethacin and increase the intestinal lysosome level in the *C. elegans* model. In summary, Sch C could be a potential candidate for developing a protective agent that reverses the side effects of indomethacin on the gastrointestinal tract.

Poster Presentation

PNB-69

Comparative study on the bioactivities and marker compound contents of *Citrus reticulata* and Jeju-native *Citrus sunki* peels

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The peel of Citrus has traditionally been used as a herbal medicine known as Chenpi, with *Citrus reticulata* officially listed in the Korean Pharmacopoeia for its antioxidant, anti-inflammatory, and digestive benefits. However, much of the Chenpi used in Korea is imported from China, and current pharmacopoeial standards include only *C. reticulata* and *C. unshiu*, limiting the use of native Korean citrus varieties. This study aimed to evaluate the potential of *Citrus sunki*, a native citrus species from Jeju Island, for inclusion in the Korean Pharmacopoeia, based on the Swingle and Tanaka classification systems. The Swingle system, which classifies *C. sunki* as *C. reticulata*, was used as a basis to provide scientific evidence for its inclusion through a comparison of their biological activities. DNA sequencing identified the Jeju-native variety Jingyul as *C. sunki*, while commercial Chenpi products and other Jeju citrus peels were identified as *C. reticulata*. HPLC analysis showed that *C. sunki* contained hesperidin levels comparable to or higher than those of *C. reticulata*. Furthermore, *C. sunki* demonstrated equivalent or superior antioxidant, skin-whitening, anti-wrinkle, and anti-inflammatory activities. These findings suggest that *C. sunki* has comparable therapeutic potential to Chenpi, supporting its inclusion in the Korean Pharmacopoeia. The study also underscores the importance of an integrative classification approach considering pharmacological efficacy in evaluating herbal medicines.

PNB-70

Potential biological activities of *Citrus trifoliata* Flower Essential Oil as a Natural Antioxidant and Skin Whitening Agent

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Citrus trifoliata L. (CTL; family Rutaceae) is commonly used in traditional herbal medicine for both edible and therapeutic purposes, known for its antibacterial, anti-inflammatory, and anticancer properties. However, its antioxidant and skin-whitening effects has not been clearly elucidated. This study investigated whether CTL flower essential oil (CTLFAb) have the antioxidant and skin whitening activities. CTLFAb was obtained as an absolute type using a solvent extraction method and its components were analyzed using gas chromatography/mass spectrometry analysis. Antioxidant activity was analyzed using ABTs. Other biological activies were examined in B16BL6 cells or HaCaT cells. Ten components were identified in CTLFAb. CTLFAb showed a concentration-dependent ABTs free radical scavenging activity. CTLFAb inhibited the 2% FBS-induced B16BL6 cell proliferation. CTLFAb also reduced α-MSH-stimulated increases in melanin synthesis and tyrosinase activity in B16BL6 cells by regulating melanogenesis-related proteins (MITF, tyrosinase and TRP-1) and melanosome transport-related proteins (Rab27a, Melanophilin, Myosin Va) through the MAPK(p38, ERK1/2, and JNK) signaling pathway. In addition, UVA irradiation induced α-MSH production in HaCaT cells, but this induction was effectively suppressed by the CTLFAb. Treatment of B16BL6 cells with conditioned medium from UVA-irradiated HaCaT cells in the presence of CPEO led to a reduction in both melanin synthesis and tyrosinase activity. These results suggest that CTLFAb may serve as a useful natural biomaterial for skin protection and skin-whitening applications.

PNB-71

Protective effect of Polysaccharides from *Halocynthia roretzi* Tunic on Particulate Matter-Induced Skin Damage and its Anti-Melanogenesis Effect *in vivo* and *in vitro* model

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Many studies have reported that external factors such as fine dust and ultraviolet (UV) radiation can cause skin damage. Accordingly, numerous efforts have been made to develop protective strategies against these harmful stimuli. Natural products have been extensively studied, and among them, *Halocynthia roretzi* tunic extract (HTVE) has shown various biological activities, including antioxidant and anti-obesity effects. However, the anti-melanogenic and protective effects of crude polysaccharides derived from HTVE against particulate matter (PM)-induced skin damage have not yet been reported in skin cells or zebrafish models. HTVE inhibited tyrosinase activity and suppressed melanogenesis through molecular mechanisms in α-MSH-stimulated B16F10 cells. In HaCaT cells, HTVE treatment reduced reactive oxygen species (ROS) levels and downregulated the expression of pro-inflammatory cytokines and inflammatory proteins via modulation of the MAPK signaling pathway. Additionally, HTVE enhanced the expression of skin barrier-related proteins. Furthermore, in vivo zebrafish models, HTVE alleviated α-MSH- and PM-induced oxidative stress in a dose-dependent manner. These findings suggest that HTVE effectively inhibits melanogenesis and oxidative stress, highlighting its potential as a natural therapeutic agent for protecting the skin from environmental pollutants.

PNB-72

Comparative analysis of bioactive compounds and the anti-inflammatory and wound-healing properties of *Centella asiatica*

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Centella asiatica and its compounds, such as asiaticoside, madecassoside, madecassic acid, and asiatic acid, have been used in pharmaceutical and cosmetic products due to their anti-inflammatory and skin-regenerating effects. This study assessed the potential of Jeju-grown *Centella asiatica* as a substitute for imported varieties by analyzing bioactive compound content and evaluating anti-inflammatory and wound-healing effects. Samples collected from three Jeju regions were analyzed monthly using HPLC for triterpenoids (asiaticoside, madecassoside, asiatic acid, and madecassic acid). The triterpenoid content in *Centella asiatica* from Sangmo-ri remained consistently high throughout the collection period, with maximum concentrations in May and a subsequent increase observed in August and September. Anti-inflammatory activity, evaluated in lipopolysaccharide-stimulated RAW 264.7 macrophages and HaCaT keratinocytes, showed that Jeju extracts effectively suppressed NO production and inflammatory cytokines (iNOS, COX-2, IL-1β, and IL-6), comparable to or better than Vietnamese and French imports. Wound-healing assays in HaCaT cells revealed that Jeju extracts promoted faster wound closure, particularly from June to August. Overall, Jeju *Centella asiatica* demonstrates strong potential as a domestic alternative to imported sources, with consistent anti-inflammatory and wound-healing effects and high bioactive compound content, particularly in samples collected from June to September.

PNB-73

Enhancement of Skin Regeneration by Sargassum pallidum-Derived Polysaccharides through Modulation of Wnt/β-Catenin Pathway

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Seaweeds are rich in bioactive compounds, with polysaccharides particularly noted for their excellent biocompatibility and low toxicity. These polysaccharides exhibit antioxidant, anti-inflammatory, and skin-regenerative effects, including enhanced cell proliferation, wound healing, and extracellular matrix (ECM) production. This study evaluated the skin regenerative potential of crude polysaccharides extracted from *Sargassum pallidum* using Viscozyme-assisted hydrolysis and ethanol precipitation (SVCP). To assess its bioactivity, a series of in vitro and in vivo assays were conducted. In human dermal fibroblasts (HDFs), SVCP showed no cytotoxicity and significantly enhanced cell proliferation and migration, as measured by MTT and scratch assays. Western blot analysis revealed upregulation of Wnt/β-catenin signaling proteins (β-catenin, PCNA). ELISA results confirmed elevated levels of VEGF, IGF-1, EGF, and type I collagen. In zebrafish embryos, SVCP exhibited no developmental toxicity and also increased β-catenin and PCNA expression. Taken together, these findings highlight the strong skin-regenerative potential of SVCP and support its potential use in functional cosmetics or therapeutic applications.

PNB-74

Metabolomic Profiling of Ginger (*Zingiber officinale*) from Diverse Geographical Origins and Analytical Validation of Marker Compounds via UPLC

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Ginger (*Zingiber officinale* Roscoe) is widely used as a spice and traditional remedy, known for its distinctive aroma and diverse pharmacological properties, including antioxidant and anti-inflammatory activities. These bioactivities are primarily influenced by its chemical composition, which can vary depending on environmental and cultivation conditions. However, as most medicinal plants are distributed in processed forms, identifying origin-based chemical differences remains challenging. This study aimed to develop a comprehensive analytical strategy to distinguish ginger from three different geographical origins. Nuclear magnetic resonance (NMR) spectroscopy and ultra-performance liquid chromatography coupled with quadrupole time-of-flight mass spectrometry (UPLC-QTOF/MS)-based metabolomics were employed to profile primary and secondary metabolites, respectively. Multivariate statistical analyses were used to identify discriminant markers associated with geographic origin. Subsequently, an UPLC method was developed and validated by assessing linearity, precision, accuracy, limit of detection (LOD), and limit of quantification (LOQ). The results demonstrate that a metabolomics-based approach is effective in differentiating ginger based on its origin. Furthermore, the validated UPLC method enables rapid and simultaneous quantification of marker compounds, offering a reliable tool for both origin authentication and quality control of ginger products.

PNB-75

Metabolomics-Based Differentiation of Korean ginseng(*Panax ginseng*) and American ginseng(*Panax quinquefolius*) with Molecular Networking, and Method Validation for Marker Compounds of Korean Ginseng

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Ginseng is widely consumed as both a health supplement and medicinal ingredient worldwide. Among the species of the *Panax* genus, *P. ginseng* and *P. quinquefolius* are the most extensively studied and commercially utilized. *P. ginseng*, predominantly cultivated in Korea, is characterized by distinct seasonal growth dynamics that are thought to contribute to its enhanced functional properties. However, once processed into powder or extract form, it becomes practically impossible to distinguish the two species based on morphology. Therefore, metabolomics-based analytical methods are necessary for accurate species identification and quality assurance. In this study, ginsenosides in two species were profiled using UPLC-QTOF/MS. To elucidate compositional differences among ginsenosides, molecular networking analysis was conducted using the GNPS platform. The result of molecular networking demonstrated the utility of ginsenoside Rf and pseudoginsenoside F11 as biomarkers for distinguishing two species. In addition to the conventional marker compounds ginsenoside Rg1 and Rb1 of *P. ginseng*, the validity of ginsenoside Rf as an additional marker compound was confirmed. An HPLC method was developed and validated to simultaneously quantify ginsenoside Rg1, Rf, and Rb1, with average contents of 7.03, 3.35, and 26.58 mg/g, respectively. These findings highlight the utility of selected ginsenosides as marker compounds for the discrimination of *Panax* species, especially in commercial contexts where species admixture may occur.

PNB-76

Comparative analysis of secondary metabolites and antioxidant activities in white and red radish (*Raphanus sativus*) hairy roots

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Hairy root cultures can be expected to stably produce plant-derived bioactive compounds and induce rapid and abundant accumulation. In this study, we investigated the metabolite composition and antioxidant properties of white and red *Raphanus sativus* L. hairy roots to evaluate their potential as natural sources of functional ingredients. We revealed distinct patterns in the accumulation of secondary metabolites. Red radish hairy roots accumulated a higher content of anthocyanin, which correlated with their pigment and physiological activity, as well as a greater variety of glucosinolates, phenolics, and flavonoids, which correlated with their defense systems and bioactivities. In addition, antioxidant activities, such as radical scavenging activities of DPPH and ABTS and reducing power, were stronger in red radish than in white radish hairy roots. These findings support the application of red radish hairy roots as promising bioactive resources in the development of natural product-based therapeutics and functional food ingredients, particularly in contexts related to oxidative stress modulation and health promotion. This work was supported by the Korea Institute of Planning and Evaluation for Technology in Food, Agriculture, and Forestry (IPET) through Cutting-edge Precision Breeding Development Program, funded by Ministry of Agriculture, Food and Rural Affairs (MAFRA) (RS-2025-02303365), Republic of Korea.

PNB-77

Neuroprotective Potential of a New Phenolic Compound from *Scrophularia buergeriana* Roots Revealed by Network Pharmacology

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Scrophularia buergeriana, a perennial herb in the Scrophulariaceae family, is traditionally used in East Asia to treat various ailments, including high fever, inflammation, and arthritis. It contains a diverse range of bioactive constituents, such as iridoid glycosides, phenylethanoids, terpenoids, and flavonoids. Previous studies have demonstrated that these compounds possess hepatoprotective effects and reduce cytotoxicity associated with oxidative stress. Furthermore, extracts of *S. buergeriana* have been shown to inhibit the expression of pro-inflammatory cytokines—TNF-α, IL-1β, and IL-6—in immune cells. The present study focuses on the isolation and identification of phenolic compounds from the roots of *S. buergeriana*, with particular emphasis on their anti-neuroinflammatory properties in BV2 microglial cells. Interestingly, a previously unreported phenolic compound was isolated and structurally characterized using spectroscopic techniques. To further elucidate its mechanism of action, network pharmacology analysis was conducted using open-source target prediction platforms and databases. This analysis revealed that the novel compound modulates key signaling pathways involved in neuroinflammation and oxidative stress responses, including NF-κB, MAPK, and Nrf2 pathways. By exploring both the pharmacological effects and molecular targets of this new compound, the study provides insights into its potential therapeutic role in the management of neurodegenerative disorders. These findings lay the groundwork for future pharmacological development and application of *S. buergeriana*-derived compounds as neuroprotective agents.

PNB-78

Antioxidant and Anti-Aging Effects of Panax Ginseng Root Extract and Its Major Compounds in Human Dermal Fibroblast

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Panax ginseng (Korean ginseng) is renowned for its health-promoting properties, attributed to its bioactive compounds, including saponins, polyphenols, and polysaccharides, which possess both antioxidant and anti-aging activities. This study investigated the anti-aging and anti-inflammatory effects of compounds isolated from the hot water extract of fresh *P. ginseng* roots, evaluating their resistance to TNF-α/IFN-γ-induced skin cell damage. Among 14 compounds, ginsenoside Rf (compound **2**) showed significant multi-target effects. In NHDFs, ginsenoside Rf and others effectively reduced intracellular ROS, demonstrating strong antioxidant properties. Additionally, they inhibited MMP-1 expression, a key enzyme in collagen degradation, and promoted pro-collagen Type I synthesis, countering the negative effects of TNF-α and supporting skin health. Further analysis showed that ginsenoside Rf reduced the secretion of inflammatory cytokines like IL-1β and IL-6, exhibiting anti-inflammatory effects. It also promoted the expression of crucial skin barrier proteins, including LOR, AQP3, FLG, and KRT1 in TNF-α/IFN-γ-stimulated NHEKs, enhancing skin hydration and structural integrity. These results suggest that compounds from *P. ginseng* roots, especially ginsenoside Rf, hold promise as skincare agents targeting skin aging and inflammation. Future research should further explore their mechanisms and optimize their applications in dermatological treatments.

PNB-79

The effect of the season and region on the yield and quality of Torreya nucifera essential oil in South Korea

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Torreya nucifera, a coniferous tree, produces essential oil rich in bioactive compounds. This study examined seasonal and regional variations in leaf oil yield and composition using samples collected in spring, summer, and autumn (2023–2024) from Jeju, Jinju, and Hwasoon, South Korea. While seasonal oil yields remained relatively stable (0.94±0.19–1.63±0.32% DW), regional differences were significant ($p<0.05$). Autumn yields from Hwasoon (1.43±0.26%) were over 30% higher than those from Jeju. This consistency across seasons may reflect the tree's perennial, evergreen nature. The essential oils primarily contained D-limonene and 3-carene (48.47–72.56%). Chemical composition varied by season and region. 3-carene levels were significantly influenced by region ($p<0.0001$), with Jeju showing higher levels. D-limonene was significantly affected by season, region, and their interaction ($p<0.001$), peaking in Hwasoon during summer and autumn (up to 70.63%). Oils from Hwasoon in autumn are considered premium due to high D-limonene and 3-carene content. These results underscore the role of environmental factors in oil quality and support optimized production strategies for *T. nucifera* essential oils.

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PNB-80

Anti-Obesity Effects of Citrus unshiu Leaf Extract in 3T3-L1 Adipocytes and High-Fat Diet-Induced Obese Mice

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Lipid accumulation in adipocytes is driven by factors including overnutrition, reduced physical activity, and genetic predisposition, contributing to obesity. Although citrus unshiu leaves are generally regarded as agricultural by-products and often discarded. In this study, the anti-obesity effects of Citrus unshiu leaf extract (CLE) were evaluated in differentiated 3T3-L1 cells and high-fat diet (HFD)-induced obese mice. CLE treatment significantly reduced intracellular lipid accumulation, as confirmed by histological analysis, and improved serum levels of hepatic enzymes (ALT, AST, GGT) and lipid profiles. Furthermore, CLE downregulated the expression of genes related to adipogenesis and lipogenesis while upregulating markers associated with energy metabolism. These findings suggest that CLE ameliorates obesity by regulating intracellular lipid metabolism and enhancing energy expenditure in adipose tissue.

Poster Presentation

PNB-81

Anti-inflammatory and anti-atopic effects of *Elaeocarpus sylvestris* leaf extract in LPS-stimulated HaCaT cells and DNCB-induced BALB/c mice

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The skin acts as a crucial immunological and physical barrier against environmental factors. Disruption of skin barrier triggers inflammation mediated by pro-inflammatory cytokines and signaling molecules. Atopic dermatitis (AD) is a chronic inflammatory skin disorder characterized by erythema, edema, and disrupted epidermal homeostasis. Corticosteroids and calcineurin inhibitors are standard treatments for AD, but long-term safety concerns highlight the need for safer alternatives. *Elaeocarpus sylvestris*, native to Jeju Island, has been reported to anti-inflammatory properties, yet its effects on AD remain underexplored. Therefore, the anti-inflammatory and anti-atopic effects of *E. sylvestris* leaf ethanol extract (ESLE) were examined using LPS-stimulated HaCaT keratinocytes and DNCB-induced BALB/c mouse model. HPLC analysis identified geraniin (254.8±0.4 mg/g) as the major compound. Moreover, ESLE effectively decreased inflammatory mediators NO and PGE_2 by suppressing their enzymes iNOS and COX-2, and it reduced pro-inflammatory cytokines TNF-α, IL-6, and IL-1β. ESLE also suppressed IRAK4 expression and inhibited phosphorylation of multiple downstream effectors within the MAPK, NF-κB, and JAK/STAT signaling pathways. Furthermore, ESLE mitigated dermatitis severity and decreased transepidermal water loss, while significantly reducing ear and epidermal thickness, mast cell infiltration, serum IgE levels, as well as spleen and lymph node hypertrophy. These results suggest ESLE as a promising candidate for AD treatment through modulation of inflammatory responses.

PNB-82

Comparison of Anti-inflammatory Activities and Chemical Composition of Essential Oils Extracted from Cupressaceae Family

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The Cupressaceae family is distributed in various geographical locations and is used in ethnomedicine. Essential oils can be used in a variety of ways, thereby increasing the added value of forest resources. This study compared the anti-inflammatory activity and composition of essential oils extracted from the Cupressaceae family to discover new usefulness. The study used essential oils of *Chamaecyparis obtusa*, *Chamaecyparis pisifera*, *Cryptomeria japonica*, *Juniperus chinensis* L., *Juniperus chinensis* var. *sargentii* A. Henry, *Juniperus rigida*, *Thuja koraiensis*, and *Thuja orientalis*. The essential oils were extracted by hydrodistillation, and the composition of the essential oils was analyzed using GC-MS. Anti-inflammatory effects were assessed by analyzing the effects of essential oils on the expression of genes(IL-4, IL-5, IL-6, IL-13, TNF-α, COX-2) involved in inflammatory responses. The results showed that the essential oils were effective in the following order; *J. chinensis* var. *sargentii* A. Henry, *C. japonica*, J. *rigida*, *C. pisfera*, *J. chinensis* L., *T. koraiensis*, *T. orientalis*, and *C. obtusa*. All essential oils significantly reduced IL-6 gene expression. *J. chinensis* var. *sargentii* A. Henry significantly inhibited the expression of all genes except IL-4. GC-MS analysis of J. chinensis var. sargentii A. Henry confirmed that the main components were sabinene(22.2%), elemol(21.1%), terpinen-4-ol(8.4%), and γ-terpinene(4.6%). These results indicate that *J. chinensis* var. *sargentii* A. Henry is more suitable for use as an anti-inflammatory agent.

PNB-83

Novel Cucurbitane-type Terpenoid and Anti-obesity Effects from Chrysosplenium flagelliferum

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Chrysosplenium flagelliferum, a Korean forest medicinal plant, was extracted with 70% ethanol, resulting in the isolation of a novel compound (**1**) and several known compounds (**2**–**12**). The structure of the new compound (**1**) was elucidated by spectroscopic methods, including 1D and 2D NMR, and HRESIMS analyses. The absolute configuration of the compound was further determined by quantum mechanical calculations of NMR chemical shifts and electronic circular dichroism (ECD) spectra. To assess the anti-obesity potential of the isolated compounds, 3T3-L1 preadipocytes were treated with these compounds and lipid accumulation was evaluated by Oil Red O staining. The results showed that cirsimaritin (**6**) significantly reduced lipid accumulation in a concentration-dependent manner, with a 33.6% reduction observed at 20 μM. Compound **6** inhibited the expression of PPARγ, CEBPα, and FABP4, which are key regulators of adipocyte differentiation, as well as the expression of Perilipin-1, a protein involved in lipid accumulation.

PNB-84

Assessment of Herbicidal Activity of Natural Triketone Compound from Manuka Oil

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As interest in natural-product-based herbicides continues to grow, studies on the herbicidal activity of various groups of natural compounds have also increased. Manuka oil is known to contain a high proportion of triketones, including leptospermone, grandiflorone, and flavesone. These compounds share structural similarity with mesotrione, a synthetic 4-Hydroxyphenylpyruvate dioxygenase(HPPD) inhibiting herbicide, therefore these are presumed to possess herbicidal potential. In this study, triketones were extracted from commercial manuka oil to obtain an enriched fraction, which was found to contain over 80% leptospermone. Considering molecular docking predicted that grandiflorone would exhibit stronger activity than leptospermone, both compounds were individually synthesized and applied at the same concentration to lettuce seeds to validate the prediction. During five days, bleaching symptoms appeared at 5 μg/ml for leptospermone, while grandiflorone induced strong bleaching at 1 μg/ml. These results indicate that manuka oil-derived compounds can show herbicidal activity at low concentrations. This study suggests that triketones from manuka oil, particularly grandiflorone, could serve as lead compounds for developing natural herbicides.

Poster Presentation

PNB-85

Preclinical Evaluation of the Therapeutic Effect of Bee Venom on Rheumatoid Arthritis Based on TNF-α Inhibition

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Bee venom (BV), a natural therapeutic agent traditionally used in treating inflammatory diseases, contains key bioactive components such as melittin, apamin, phospholipase A2, and hyaluronidase, which exert anti-inflammatory, immunomodulatory, and analgesic effects. This study aimed to evaluate the therapeutic potential of a purified bee venom-loaded microneedle patch (MNP) in a collagen-induced arthritis (CIA) model using DBA/1J mice. Over a 4−5 weeks treatment period, the efficacy of MNP was compared with that of purified bee venom (PBV) and methotrexate (MTX). Outcome measures included paw scoring, micro-CT imaging for bone density, histological analyses (H&E and Safranin-O staining), and serum levels of inflammatory cytokines (TNF-α and IL-1β). The MNP group demonstrated similar or superior effects compared to MTX in reducing joint swelling, preserving bone and cartilage integrity, and suppressing cytokine expression. Moreover, the minimally invasive and low-pain nature of the microneedle patch supports its potential as a patient-friendly delivery system. These findings suggest that BV-based microneedle patches represent a promising and safe therapeutic alternative for the treatment of rheumatoid arthritis.

PNB-86

Effects of Bee Venom and Its Derived Peptides Against Dexamethasone and Hydrogen Peroxide-Induced Stress in C2C12 Skeletal Muscle Cells

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Bee venom has been studied for its various pharmacological effects, but its impact on skeletal muscle cells under stress conditions remains unclear. The aim of this study was to evaluate the stress-protective effect of bee venom (PBV) and its derived peptides (PPA, PPN, PPP) on myotube differentiation in C2C12 myotube cells exposed to dexamethasone (DEX) and oxidative stress. C2C12 myoblasts were differentiated for 6 days to form myotubes, followed by treatment with Dex (10 μM) or hydrogen peroxide (H_2O_2, 1 mM) for 24 hours. PBV and its peptides were co-treated. Morphological changes were observed via phase-contrast microscopy, and the expression of myogenic markers MyoD, MyoG, and MyHC were analyzed using qPCR and western blot. Dex and H_2O_2 treatments significantly reduced the expression of MyoD, MyoG, and MyHC, indicating impaired myogenic differentiation. Treatment with PBV or peptides preserved myotube morphology and significantly restored the expression levels of these differentiation markers. Bee venom and its derived peptides counteract stress-induced suppression of muscle differentiation by maintaining the expression of key myogenic markers. These findings suggest their potential therapeutic application in preventing or treating muscle atrophy and oxidative muscle damage. However, further studies are needed to elucidate the underlying molecular mechanisms and to validate these effects *in vivo* models.

PNB-87

Inhibition of TNF-α-Induced Collagen Degradation and Oxidative Damage by *Centipeda minima* and Brevilin A in Human Dermal Fibroblasts

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Skin aging and inflammatory skin lesions are exacerbated by reactive oxygen species (ROS) generated in the mitochondria of human dermal fibroblasts (HDFs). These oxidative stressors degrade the extracellular matrix (ECM), promote inflammation, and accelerate skin aging. Antioxidants that suppress reactive oxygen species (ROS) production play a crucial role in mitigating these effects. This study investigated the protective effects of *Centipeda minima* (CMX) and its active constituent, brevilin A, against tumor necrosis factor-alpha (TNF-α)-induced oxidative stress and ECM degradation in normal human dermal fibroblasts (NHDFs). Both CMX and brevilin A significantly inhibited TNF-α-induced elevations in ROS, nitric oxide (NO), and prostaglandin E_2 (PGE_2) levels, thereby reducing oxidative stress and inflammatory responses. Additionally, they effectively suppressed matrix metalloproteinase-1 (MMP-1) expression and restored the procollagen I α1 (COLIA1) levels, indicating their potential to preserve ECM integrity. Mechanistically, brevilin A selectively inhibited ERK phosphorylation in the mitogen-activated protein kinase (MAPK) pathway, suggesting its role in regulating collagen degradation and inflammation. These findings highlight that CMX and brevilin A are promising natural agents for protection against skin aging and inflammation. However, further in vivo studies are necessary to validate their efficacy and explore their potential applications in dermatological formulations.

PNB-88

Potential Natural Modulators of *Schisandra chinensis* and *Citrus unshiu* Extracts on Prostate and Gut Health

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As of December 2024, South Korea has become an “ultra-aged society” with over 20% of its population aged 65 or older. Consequently, prostate diseases and gut health issues are emerging as significant factors that diminish the quality of life for seniors, thus increasing interest in preventative and ameliorative strategies. *Schisandra chinensis* (SC) is well-known for containing lignans, a prominent class of bioactive compounds recognized for their antioxidant and anti-inflammatory properties. Similarly, *Citrus unshiu* (CU) is rich in flavonoids, reported to improve digestive function and exert anti-inflammatory effects. This study evaluated the impact of SC and CU extracts on prostate cancer cells (LNCaP) and human colon cells (HT29). Our findings indicate that both SC and CU extracts reduced Androgen Receptor (AR) protein levels, a key factor in benign prostatic hyperplasia. Notably, SC extract significantly decreased prostate-specific antigen (PSA), a crucial biomarker for prostate disease. Furthermore, CU extract significantly increased cell viability and mucin production in HT29 cells. These results suggest that SC and CU extracts are effective natural materials for maintaining prostate health and promoting gut function. This study provides scientific evidence for the beneficial effects of SC and CU on prostate and gut health. These findings are expected to inform the future development of health functional foods and therapeutic agents.

Poster Presentation

PNB-89

Organ-Specific Dynamics of Bioactive Compounds and Antioxidant Activity in *Wasabi Japonica* Across Developmental Stages

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Wasabi (*Wasabia japonica*) is a perennial plant in the Brassicaceae family, and research has traditionally focused on its commercially valuable rhizome. However, recent studies have also explored other parts of the plant, with particular attention given to the leaves as promising raw materials for functional foods. This study analyzed bioactive compounds and antioxidant activity in various organs of one- to two-year-old wasabi across growth stages to assess their functional traits. In results, each glucosinolate exhibited different accumulation patterns according to growth stage and organ. The most abundant glucosinolate, sinigrin markedly increased from vegetative to reproductive stages and, with its hydrolysis product allyl isothiocyanate, peaked in roots during flowering. Glucoibervirin and neoglucobrassicin were also detected at relatively high levels. Phenolic compounds were abundant in the leaves at the early growth stage, with isosaponarin being the most prevalent among the flavonoid derivatives, followed by isoorientin and isovitexin. These compounds tended to decrease as growth progressed. Antioxidant activity was highest in the leaves and flowers compared to other organs, and its pattern closely resembled the distribution of phenolic compounds, suggesting that these compounds contribute significantly to the antioxidant effects. This study provides fundamental data that can be applied to optimize harvest timing and manage quality based on bioactive components, and is expected to support the expanded utilization of wasabi.

PNB-90

Quantitative Analysis Using High-Performance Liquid Chromatography (HPLC) for the Stability Evaluation of Ginseng Radix

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Panax ginseng C.A. Meyer (Ginseng Radix), a member of the Araliaceae family, is widely used in functional foods, pharmaceuticals, and cosmetics, and is available in various processed forms. Given its broad range of applications, it is essential to assess the stability of its main active constituents in order to establish reliable quality control standards. In this study, we evaluated the stability of the key ginsenosides Rg_1 and Rb_1 under accelerated stress conditions, in accordance with the guidelines of the Korean Pharmacopoeia (KP). Both medicinal plant reference materials and chemical reference standards were exposed to high temperatures ($\geq$50 °C) and high humidity ($\geq$75% RH) to simulate conditions that may occur during storage and distribution. The identity of the reference materials was confirmed through high-performance thin-layer chromatography (HPTLC), and quantitative analysis was conducted using high-performance liquid chromatography (HPLC). The results revealed significant differences in the stability of ginsenosides between the plant reference materials and the chemical reference standards under the tested conditions. These findings underscore the importance of considering the type of reference material used in quality control protocols and provide valuable data for the development of improved storage and distribution strategies for herbal medicinal products.

PNB-91

Stability assessment of Reference Medicinal Plant Material and Analytical Marker for *Scutellaria baicalensis*(Scutellaria root) under stressed conditions

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Scutellaria baicalensis(Scutellaria root) is a medicinal plant belonging to the Lamiaceae family. The establishment of reference medicinal plant material is essential for the scientific quality control of herbal medicinal products facilitating quantitative and qualitative analyses of active constituents, specification setting and stability assessments. In this study, the contents of analytical marker including baicalin, baicalein and wogonin in *Scutellaria baicalensis* were quantified according to the official methods stipulated in the Korean Pharmacopoeia. Furthermore, stability assessments under stressed conditions (elevated temperature and humidity) were conducted using HPLC and HPTLC to provide fundamental data for the future distribution of reference materials and quality standardization. The results enabled quantitative comparison of the stability differences between the reference medicinal plant material and the analytical marker under stressed conditions with the reference material demonstrating notably higher stability. This study provides foundational data expected to support the standardization and quality control systems for herbal medicinal resources.

PNB-92

Uncaria Rhynchophylla and hirsuteine as TRPV1 agonists inducing channel desensitization

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Uncaria rhynchophylla (UR), an herb traditionally used in Eastern medicine, is recognized for its therapeutic applications in treating hypertension and inflammation. However, the specific molecular mechanisms how UR and its bioactive constituents modulate inflammatory pathways remain unknown. Here, we discovered that UR extract activated Transient receptor potential vanilloid 1 (TRPV1) in HEK293T cell. Notably, consecutive application of UR extract on TRPV1 exhibited inhibitory action through channel desensitization. Further analysis led to the isolation of hirsuteine (HST), a compound within UR extract that robustly activates and subsequently desensitizes TRPV1 in HEK293T cells. The molecular docking simulation revealed that the residues S501, F507, Y511, L515, and E570 in TRPV1 were associated with the binding of HST. Additionally, applying HST on TRPV1-positive sensory neurons showed significantly reduced electrical activity compared to capsaicin. Our findings collectively suggest that UR and HST possess distinct agonistic and desensitizing effects on TRPV1.

PNB-93

Stable Carbon Isotope Based Honey Protein Analysis Used in Geographic Origin Discrimination of Robinia Honey

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Robinia honey is widely consumed for its distinctive aroma and taste. It was produced in many countries, making it difficult to distinguish its geographic origin, and cases of imported honey being falsely labeled as domestic have been reported. Traditional stable carbon isotope ratio($\delta^{13}C$) analysis of whole honey has limitations in distinguishing between honeys from different countries, especially when the primary sugar source derives from C3 plants. In this study, we aim to newly analyze $\delta^{13}C$ values of proteins in Robinia honey, hypothesizing that protein fractions better reflect both bee metabolism and regional ecological characteristics. As a result, its values of whole honey and protein fractions did not show statistically significant differences among samples from three countries. However, multivariate statistical analysis using PLS-DA revealed distinct separation among samples of different geographic origins. Importantly, Component 1 explained 74.2% of the total variance, while Component 2 accounted for 25.8%, allowing clear differentiation between samples of domestic and foreign origin. These findings suggest that $\delta^{13}C$ values in honey proteins may serve as a more precise and biologically meaningful marker for identifying the origin of honey. Serving as a preliminary reference for geographic origin identification, this dataset highlights the need for future studies to include a greater number and more diverse sampling to enhance the robustness and applicability of the authentication technique.

PNB-94

Improves skin barrier and anti-inflammatory effect of exosomes derived *Fructobacillus fructosus* subsp. NSH-1 strain isolated from *Campsis grandiflora* Flower

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Inflammation is a defense mechanism of the body in response to harmful stimuli such as ultraviolet (UV) radiation and oxidative stress. However, persistent or excessive inflammation is closely associated with the development of various chronic diseases, including cancer, underscoring the importance of controlling inflammatory responses. In this study, we investigated the anti-inflammatory and skin barrier-enhancing effects of exosomes derived from *Fructobacillus fructosus* subsp. NSH-1, a lactic acid bacterium isolated from the flowers of *Campsis grandiflora*. To assess anti-inflammatory activity, RAW 264.7 macrophage cells stimulated with lipopolysaccharide (LPS) were treated with NSH-1-derived exosomes at concentrations of 5.0×10^{7}, 1.0×10^{8}, and 2.0×10^{8} particles/mL. The exosomes showed no cytotoxicity and significantly inhibited the production of inflammatory mediators such as nitric oxide (NO) and prostaglandin E2 (PGE2). Additionally, treatment of HaCaT keratinocytes stimulated with TNF-α and IFN-γ resulted in a dose-dependent upregulation of skin barrier-related proteins, including involucrin, filaggrin, and loricrin. These findings indicate that NSH-1-derived exosomes possess dual functions in reducing inflammation and enhancing the skin barrier, suggesting their potential as a functional ingredient for improving skin inflammation and barrier function.

PNB-95

Development of a reliable UPLC analytical protocol for purified Apitoxin

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The aim of this study was to develop and validate an analytical method for the simultaneous quantification of the major components Apamin, Phospholipase A2 (PLA2), and Melittin in purified bee venom using ultra-performance liquid chromatography (UPLC). An ES-C18 peptide column (2.1×100 mm, 2.0 µm) was employed under gradient elution with acetonitrile and water containing 0.2% trifluoroacetic acid (TFA). Detection was performed at 220 nm. The method demonstrated excellent linearity for all three compounds with correlation coefficients (R^2) above 0.99 within the tested concentration ranges (Apamin: 25–400 µg/mL, PLA2: 50–1000 µg/mL, Melittin: 50–1000 µg/mL). Limits of detection (LOD) and quantification (LOQ) ranged from 0.49–3.49 µg/mL and 1.28–8.76 µg/mL, respectively. Intra-day and inter-day precision showed relative standard deviations (RSD) below 4%, confirming high reproducibility. Accuracy, evaluated via recovery tests, ranged between 95.2% and 101.4%. Application of the method to 15 purified bee venom samples revealed average contents of Apamin (3.6%), PLA2 (20.1%), and Melittin (55.3%). These findings suggest that the developed UPLC method is a reliable tool for simultaneous determination of bee venom constituents, offering superior resolution and shorter run times compared to conventional HPLC techniques.

PNB-96

Anti-Inflammatory effect of exosomes derived from lactic acid bacteria isolated from the flower of *Aster koraiensis* in LPS-stimulated RAW 264.7 Macrophage cells

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Chronic inflammation is a critical contributing factor to the development and progression of a wide range of diseases, including metabolic syndromes, cardiovascular diseases, and cancer. Therefore, identifying safe and effective agents capable of modulating inflammatory responses is of significant interest.This study investigated the anti-inflammatory activity of exosomes (BK-5) derived from a lactic acid bacterium isolated from *Aster koraiensis*, using LPS-stimulated RAW 264.7 macrophage cells as an in vitro model. BK-5 exhibited no cytotoxicity at concentrations below 6.75E+07 particles/mL and significantly reduced nitric oxide (NO) production in a dose-dependent manner. Furthermore, BK-5 treatment downregulated the expression of key pro-inflammatory enzymes, including inducible nitric oxide synthase (iNOS) and cyclooxygenase-2 (COX-2), and inhibited the secretion of major inflammatory mediators such as prostaglandin E_2 (PGE_2), interleukin-6 (IL-6), and interleukin-1β (IL-1β). Western blot analysis demonstrated that BK-5 suppressed the activation of the NF-κB signaling pathway by stabilizing IκBα, thereby preventing the nuclear translocation of NF-κB p65. In addition, BK-5 modulated mitogen-activated protein kinase (MAPK) signaling, suggesting a broader regulatory effect on inflammation-related pathways. Taken together, these findings indicate that BK-5 possesses strong anti-inflammatory activity through the modulation of multiple signaling pathways. Our results support the potential application of BK-5 as a functional probiotic strain for the development of natural, microbiota-based anti-inflammatory therapeutics.

Poster Presentation

PNB-97

Inhibition activity of inflammation of *Borassus flabellifer* fruit extract

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Chronic inflammation, often triggered by factors such as oxidative stress, infection, and environmental stimuli, plays a critical role in the pathogenesis of various diseases, including cancer, cardiovascular disorders, and metabolic syndromes. As a result, the search for natural compounds with anti-inflammatory properties has garnered increasing attention. In this study, we investigated the antioxidant and anti-inflammatory activities of *Borassus flabellifer* fruit extract (BF) in lipopolysaccharide (LPS)-stimulated RAW 264.7 macrophage cells. BF was administered at concentrations of 50, 100, and 200 μg/mL in combination with LPS (1 μg/mL), and it exhibited no cytotoxic effects. BF significantly suppressed nitric oxide (NO) production in a dose-dependent manner. Furthermore, treatment with BF markedly reduced the levels of pro-inflammatory cytokines, including interleukin-1β (IL-1β), interleukin-6 (IL-6), tumor necrosis factor-α (TNF-α), and prostaglandin E2 (PGE2). Western blot analysis revealed a concentration-dependent downregulation of inflammation-associated proteins, inducible nitric oxide synthase (iNOS) and cyclooxygenase-2 (COX-2), with the most substantial effects observed at 100 and 200 μg/mL. These findings suggest that BF possesses strong antioxidant and anti-inflammatory properties and may serve as a promising natural agent for the prevention and management of inflammation-related diseases.

PNB-98

Exploring the potential blood pressure regulatory and vasodilatory effects of enzyme-assisted hydrolysate and purified peptides from olive flounder

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Aquacultured fish are a rich natural source of protein. However, overproduced biomass is often discarded due to production imbalance, resulting in significant losses to the fishery industry. Therefore, it is necessary to utilize surplus fish and add value to overproduced biomass. We conducted complex enzyme-assisted hydrolysis to investigate the correlation between its physical characteristics and antihypertensive activity in vitro and in vivo using an SHR model. The Protamex–Pepsin-assisted hydrolysate from Paralichthys olivaceus (POppH) contained low-molecular-weight peptides and amino acids with antihypertensive potential. POppH regulated blood pressure, serum angiotensin II, and ACE levels, and histological and ultrasound analyses revealed significantly reduced carotid aorta thickness and diameter in the POppH-administered SHR group. Additionally, histological images of myocardial and renal tissues indicated that oral POppH administration remarkably alleviated hypertension-induced tissue damage. To elucidate the vasodilatory effects and mechanisms of peptides (IE; Leu-Glu, IER; Leu-Glu-Arg, IDD; Leu-Asp-Asp) derived from POppH, we assessed nitric oxide (NO) and hydrogen sulfide (H_2S) production and analyzed vasodilation-related protein expression, such as PI3K/Akt/eNOS, in EA.hy926 cells. Peptide treatment significantly enhanced NO and H_2S release. Furthermore, POppH-derived peptides significantly increased NO levels by modulating PI3K/Akt/ERK signaling in EA.hy926 cells. These findings suggest that the antihypertensive effects and functional properties of POppH and its peptides can help reduce food waste and support their use in functional foods or therapeutic applications.

PNB-99

Effect of *Microbacterium esteraromaticum* Extract on anti-inflammation response of LPS-induced RAW 264.7 cells

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A Gram-positive, rod-shaped bacterium, *Microbacterium esteraromaticum*, was isolated from international waters in the Northwest Pacific Ocean and belongs to the genus *Microbacterium*. Although this strain is primarily known to inhabit soil—particularly plastic-contaminated environments—it exhibits the metabolic versatility to degrade and synthesize various compounds. In this study, the cytotoxicity and anti-inflammatory activity of *M. esteraromaticum* extract (MEE) were investigated in RAW 264.7 cells stimulated with 1 μg/mL of LPS and treated with 50, 100, and 200 μg/mL of *M. esteraromaticum* extract. Evaluation of nitric oxide (NO) production revealed a concentration-dependent inhibition, with NO levels reduced by 23.5%, 42.9%, and 52.8%, respectively. Nitric oxide (NO) production was significantly suppressed in a dose-dependent manner. Furthermore, the production of prostaglandin E2 (PGE2) and pro-inflammatory cytokines including IL-6, IL-1β, and TNF-α also decreased dose-dependently. Western blot analysis revealed that the expression levels of inflammatory mediators such as iNOS and COX-2 were reduced in a concentration-dependent fashion. In addition, the phosphorylation of p38 (p-p38) was significantly decreased depending on the extract concentration, indicating that the sample effectively inhibited the upstream p38 MAPK signaling pathway involved in inflammation. Therefore, this study suggested that *M. esteraromaticum* cell extract can be used as a potential source of natural anti-inflammatory agents without toxicity.

PNB-100

Anti-Inflammatory effects of exosomes derived from *Lactococcus* spp. isolated from *Clematis terniflora* flowers in LPS-stimulated RAW 264.7 Macrophage cells

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Exosomes, which reflect the characteristics of their originating cells, play crucial roles in intercellular communication and the transmission of physiological and pathological signals. Recently, they have garnered increasing attention in bioactivity research and the development of functional biomaterials. In this study, exosomes (designated Uari ae-1) were isolated and purified via tangential flow filtration (TFF) from *Lactococcus* strains obtained from *Clematis terniflora* flowers. The anti-inflammatory activity of Uari ae-1 exosomes was evaluated in lipopolysaccharide (LPS)-stimulated RAW 264.7 macrophages by assessing nitric oxide (NO) production. Uari ae-1 exosomes significantly inhibited NO production in a dose-dependent manner without inducing cytotoxicity. Western blot analysis further demonstrated reduced expression of key inflammation-related proteins, including inducible nitric oxide synthase (iNOS) and cyclooxygenase-2 (COX-2), in response to exosome treatment. Additionally, decreased levels of pro-inflammatory cytokines further supported the anti-inflammatory effects of Uari ae-1. These findings suggest that Uari ae-1 exosomes possess potent anti-inflammatory properties and may serve as a promising candidate for use in functional health products targeting inflammation-related conditions.

Poster Presentation

PNB-101

Hair growth-promoting properties of Bacillus/Esculetin ferment filtrate(BEFF) derived through biorenovation

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In this study, Bacillus/Esculetin Ferment Filtrate (BEFF) was produced by applying biorenovation to Esculetin (ES), and its hair growth-promoting activity was investigated using human dermal papilla cells (HDPCs). Cell viability was assessed by MTT assay after treating HDPCs with BEFF, ES, and the positive control minoxidil (MXD) at concentrations of 1, 10, and 25 μg/mL. MXD-treated cells exhibited viabilities of 120.2%, 122.9%, and 110.8%, respectively, while ES-treated cells showed 100.9%, 107.7%, and 108.5%. In contrast, BEFF-treated cells demonstrated significantly increased viability of 136.8%, 134.3%, and 126.3%, surpassing MXD at the same concentrations. Additionally, the effects of BEFF on the growth of micro-patterned 3D hair follicle organoids were examined. After treating the organoids with BEFF and MXD at 1, 5, and 10 ppm for 5 days, BEFF resulted in growth rates of 109.81%, 123.70%, and 114.19%, respectively, with the 5 ppm dose showing higher growth than MXD (119.94%). Furthermore, to evaluate the anti-inflammatory effects related to hair loss, the inhibition of nitric oxide (NO) production was tested in Propionibacterium acnes-stimulated RAW264.7 cells. BEFF treatment effectively inhibited NO production and reduced the generation of pro-inflammatory cytokines such as IL-6, IL-1β, and PGE2. The results suggest that BEFF demonstrates both hair growth-promoting and anti-inflammatory effects, indicating its potential as an active ingredient in hair care products aimed at improving scalp and hair health.

PNB-102

Anti-Inflammatory Activity of *Peziza vesiculosa* Culture Filtrate Extract in LPS-Stimulated RAW 264.7 Cells

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Chronic inflammation contributes to the progression of various diseases, including cancer, diabetes, cardiovascular, and autoimmune disorders. Although synthetic anti-inflammatory agents are widely used, their long-term application often causes adverse effects, emphasizing the need for safer alternatives. Natural products, particularly those derived from fungi, are promising sources of bioactive compounds. *Peziza vesiculosa*, an ascomycetous fungus, has been underexplored despite its potential as a functional bioresource. In this study, the anti-inflammatory effects of *P. vesiculosa* culture filtrate extract (PVCE) were evaluated using LPS-stimulated RAW 264.7 macrophages. The extract, applied at 12.5, 25, and 50 ppm, showed no cytotoxicity. At all tested concentrations, it significantly suppressed the production of inflammatory mediators, including nitric oxide, IL-6, IL-1β, TNF-α, and PGE2, by more than 50%. Western blot analysis confirmed the downregulation of COX-2 and iNOS protein expression, indicating that the extract exerts anti-inflammatory effects through the inhibition of key inflammatory signaling pathways. These findings suggest that PVCE has strong anti-inflammatory activity and may serve as a valuable natural resource for the development of safe and effective anti-inflammatory agents.

PNB-103

Protective Effects of *Trametes hirsuta* mycelia culture Filtrate on H_2O_2-induced oxidative stress in C2C12 myoblast

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This study was conducted to investigate the effect of *Trametes hirsuta* mycelia culture Filtrate (TS_MY) on sarcopenia, and the cytoprotective effect of TS_MY was evaluated in C2C12 myoblasts in which apoptosis was induced by hydrogen peroxide (H_2O_2). As a result, cell viability was decreased to 54.7% in the group treated with H_2O_2 alone. On the other hand, when TS_MY was administered, cell viability was significantly increased to 65.6% at 25 µg/mL, 72.6% at 50 µg/mL, and 92.7% at 100 µg/mL. In addition, Bcl-2 expression was dose-dependently increased and Bax expression was decreased by TS_MY, as determined by Western blot analysis, leading to the inhibition of apoptosis induced by oxidative stress. Moreover, nitric oxide production was strongly inhibited by TS_MY at non-toxic concentrations in RAW264.7 cells, the NF-κB signaling pathway was blocked, and the expression of interleukin (IL)-1β, IL-6, and tumor necrosis factor-α was down-regulated. These results suggest that muscle loss induced by oxidative stress and inflammation can be effectively suppressed by TS_MY, indicating its potential to be used as a therapeutic and preventive agent for sarcopenia.

PNB-104

Alleviate Drought Stress on Cereals Using Extracts of *Psidium guajava*, *Aloe vera*, *Allium sativum* and *Medicago sativa* plantAlleviate Drought Stress on Cereals Using Extracts of *Psidium guajava*, *Aloe vera*, *Allium sativum* and *Medicago sativa* plants

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Drought and chemical application adversely affect plant productivity. This study evaluates extracts from Psidium guajava, Aloe vera, Allium sativum, and Medicago sativa in mitigating drought stress in cereals under greenhouse conditions. Following 4 hours of water immersion, plants were dehydrated 7 days to create drought stress. Two days after drought treatment, seedlings were saturated with 0.05%, 0.1%, 0.5%, and 1% extracts. In maize, barley, and rice, stress alone decreased plant height by 31%, 22%, and 23%, and decreased shoot fresh weight by 60%, 59%, and 46%. Drought-stressed plant extracts reduced plant height of maize, barley, and rice by 14–25%, 5–15%, and 9–15%, and decreased shoot fresh weight by 37–62%, 24–46%, and 29–40% compared to control. Compared to drought stress, extracts enhanced plant height of maize, barley, and rice by 6–17%, 7–17%, and 5–11%, and raised shoot fresh weight by 2–23%, 13–35%, and 6–17%. Specifically, 0.1% extracts of P. guajava, A. sativum, and M. sativa in maize and rice, as well as A. vera in barley, safeguard drought-stressed plants. Extracts of P. guajava, A. vera, A. sativum, and M. sativa promoted plant growth and mitigated drought stress, making them appropriate for sustainable grain production.

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Poster Presentation

PNB-105

BF Root Extract Suppresses Stress-induced Cancer Metastasis by Targeting Src Kinase

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BF root has long been utilized in traditional medicine to manage stress-related somatic and emotional disturbances by soothing the liver and relieving *qi* stagnation. This study investigated the anti-metastatic properties of an ethanolic extract of BF root (EBF) in the context of metastasis exacerbated by chronic psychological stress and explored the underlying molecular mechanisms. Cancer cell motility was evaluated via Transwell migration and invasion assays. A mouse lung metastasis model mimicking chronic stress conditions was established through repeated exposure of mice to unpredictable stressors. Public bioinformatics databases were employed to identify potential molecular targets of BF, followed by enrichment and interaction analyses. EBF effectively reduced catecholamine-induced motility in both MDA-MB-231 breast cancer and Hep3B hepatocellular carcinoma (HCC) cells. *In vivo*, EBF significantly inhibited stress-induced pulmonary metastasis of 4T1 breast cancer cells. Src kinase was identified as a key hub target through network pharmacology analysis, and its reduced phosphorylation following EBF treatment was confirmed by Western blotting. Among the saikosaponins, compounds A and D demonstrated notable inhibitory activity against adrenergic agonist-induced cancer cell migration. These findings suggest that EBF mitigates stress-driven cancer progression by targeting Src, supporting its therapeutic potential in metastatic disease contexts.

PNB-106

Deoxypodophyllotoxin Exerts Anticancer Effects via Inhibition of the Glucocorticoid Receptor in NSCLC Cells

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Deoxypodophyllotoxin (DPT) is a natural compound with notable anticancer properties. This study explored its molecular mechanism in non-small cell lung cancer (NSCLC) cells. DPT inhibited NSCLC cell proliferation and colony formation, and induced apoptosis, as evidenced by an increase in sub-G1 DNA content, annexin V-positive cells, and cleavage of PARP and caspase-3. Target prediction, molecular docking, and gene ontology analyses identified the glucocorticoid receptor (GR) as a potential target. DPT showed strong binding to the GR ligand-binding domain and suppressed dexamethasone-induced proliferation and TSC22D3 expression, a GR-regulated gene. TSC22D3 overexpression partially rescued viability, and GR inhibition by mifepristone mimicked the effects of DPT. Eight genes commonly linked to DPT, GR, and NSCLC were associated with negative regulation of steroid hormone receptor signaling. Public dataset analysis revealed that high GR expression correlated with poorer survival across multiple cancers. These findings suggest that DPT exerts anticancer effects by disrupting the GR/TSC22D3 axis, highlighting its therapeutic potential for GR-associated cancers.

PNB-107

Dual Anti-Angiogenic Action of PP Root Extract in Endothelial and Gefitinib-Resistant Lung Cancer Cells

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PP root is a traditional medicinal herb used in Korea to relieve respiratory symptoms. This study examined the anti-angiogenic effects of its ethanolic extract (EPP). EPP significantly inhibited the migration and tube formation of human umbilical vein endothelial cells (HUVECs), accompanied by reduced phosphorylation of VEGFR2 and its downstream effectors AKT and ERK, indicating suppression of angiogenic signaling. Gefitinib-resistant PC9 cells (PC9/GR) displayed enhanced angiogenic activity compared to parental PC9 cells. Conditioned media (CM) from PC9/GR cells (GR con CM) promoted HUVEC migration and tube formation more than CM from PC9 cells. Among angiogenic factors, angiopoietin-1 (ANG-1), fibroblast growth factor 2 (FGF2), and transforming growth factor-β (TGF-β) were significantly upregulated in PC9/GR cells. Notably, CM from EPP-pretreated PC9/GR cells (GR EPP CM) suppressed the pro-angiogenic effects of GR con CM. EPP treatment selectively downregulated ANG-1 expression in a dose-dependent manner, while FGF2 and TGF-β were unaffected. Supplementation with recombinant ANG-1 (rhANG-1) fully restored HUVEC migration suppressed by GR EPP CM, indicating ANG-1 as a key mediator. Praeruptorin A (PA) and praeruptorin B (PB), constituents of EPP, exhibited anti-angiogenic activity comparable to EPP. These findings suggest that EPP inhibits angiogenesis by acting directly on endothelial cells and suppressing ANG-1 in gefitinib-resistant lung cancer cells, supporting its therapeutic potential.

PNB-108

Extract of *Lindera aggregata* Root Tuber Suppresses Catecholamine-Induced Metastatic Potential in Cancer Cells

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The root tuber of *Lindera aggregata* (LA) has long been used in traditional Korean medicine for enhancing qi circulation and relieving pain. This study examined the anti-metastatic potential of an ethanolic extract of LA (ELA) and investigated its molecular mechanisms of action. Transwell migration and invasion assays were employed to assess the inhibitory effects of ELA on cancer cell motility stimulated by catechoamines, including epinephrine (E) and norepinephrine (NE). Western blot analysis was performed to assess Src phosphorylation in response to E or NE, with or without ELA treatment. Network pharmacology approaches—including KEGG and Gene Ontology enrichment, protein–protein interaction analysis, and disease relevance mapping—were applied to identify key molecular targets of LA. Adrenergic agonists markedly promoted the migration and invasion of MDA-MB-231 breast cancer and Hep3B liver cancer cells, which were significantly suppressed by ELA in a dose-dependent manner. ELA also blocked E- and NE-induced Src phosphorylation, implicating Src as a key mediator. Computational analysis supported this result by identifying Src as a central hub in predicted target network of ELA. Collectively, these findings suggest that ELA suppresses catecholamine-driven metastatic behavior in breast and liver cancer cells by inactivating Src signaling, highlighting its therapeutic potential as a Src-targeting anti-metastatic agent, particularly in the context of chronic psychological stress.

Poster Presentation

PNB-109

Extract of *Scutellaria baicalensis* Root Inhibits Macrophage Migration and M2 Polarization

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The root of *Scutellaria baicalensis* (SB) has demonstrated diverse pharmacological properties, including antitumor activity. This study investigated the effects of an ethanolic extract of SB root (ESB) on tumor-associated macrophages (TAMs). A transwell migration assay was conducted to assess macrophage motility in response to conditioned medium (CM) derived from lung cancer cells. M2-like polarization was evaluated by quantifying the IL-4- or IL-6-induced expression of M2 markers, including CD206, arginase-1, and IL-10, using qRT-PCR. STAT3 activation was analyzed by Western blotting. To assess the functional impact of macrophage modulation, CM from ESB-treated RAW 264.7 cells was applied to lung cancer cells in a transwell migration assay. ESB treatment significantly suppressed the migration of both RAW 264.7 and THP-1 macrophages. It also attenuated IL-4- and IL-6-induced expression of M2 markers and inhibited STAT3 phosphorylation, indicating impaired M2 macrophage polarization. Furthermore, CM from IL-6-induced M2-like macrophages enhanced Lewis lung carcinoma (LLC) cell migration, whereas CM from macrophages co-treated with ESB and IL-6 reversed this effect. Taken together, these findings suggest that ESB may inhibit tumor progression by limiting macrophage migration toward tumor sites and blocking polarization toward the M2 phenotype, supporting its potential as a TAM-targeted therapeutic agent.

PNB-110

Induction of Apoptosis by a Marine-Derived SM Extract in Lung Cancer Cells

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SM, a brown macroalga widely distributed along the Korean coastline, exhibits diverse pharmacological properties, including anti-inflammatory, antioxidant, and anticancer effects. Although its inhibitory effects on the migration and invasion of head and neck cancer cells have been previously reported, its cytotoxic potential against lung cancer cells remains largely unexplored. This study aimed to evaluate the anticancer effects of an ethanolic extract of SM (ESM) in lung cancer cells, with a particular focus on apoptosis induction. Our results demonstrated that ESM treatment reduced the viability of H1299, PC9, and H1975 human lung cancer cells in both a dose- and time-dependent manner. ESM treatment also led to a concentration-dependent increase in the sub-G1 cell population and the proportion of annexin V-positive cells. Furthermore, ESM consistently upregulated the expression levels of cleaved PARP and cleaved caspase-3 across all tested cell lines. Collectively, these findings suggest that ESM exerts anticancer effects by inducing caspase-dependent apoptosis in lung cancer cells. Thus, ESM may serve as a promising natural resource for the development of novel therapeutic agents against lung cancer.

PNB-111

A Brown Macroalga SR Extract Triggers Apoptosis in Lung Cancer Cells

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SR is a marine brown macroalga widely distributed in temperate to subtropical coastal waters, characterized by its thread-like fronds and distinctive cellular structure. It has been reported to exhibit antioxidant, anti-aging, and potential anti-inflammatory activities. However, its anticancer properties have not yet been investigated. In this study, we evaluated the anticancer effects of an ethanolic extract of SR (ESR) in human lung cancer cells, with particular emphasis on the induction of apoptosis. Our results showed that ESR treatment led to a significant decrease in the viability and proliferation of H1299, PC9, and H1975 lung cancer cells. This anti-proliferative effect was attributed to apoptosis, as evidenced by a concentration-dependent increase in the sub-G1 DNA content and annexin V-positive populations. In addition, condensed and fragmented nuclei were observed, indicating apoptotic morphological changes. Consistently, ESR treatment upregulated the expression of cleaved PARP and cleaved caspase-3 in all three cell lines. Taken together, our data indicate that ESR induces apoptosis via a caspase-dependent mechanism, thereby contributing to its anticancer activity in lung cancer cells. These results highlight the potential of ESR as a bioactive marine-derived candidate for lung cancer therapy.

PNB-112

Discovery of α-Glucosidase Inhibitors from Paenibacillus sp. JNUCC 31 via Genome Mining, Metabolite Profiling, and In Silico Analysis

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With the increasing demand for safer antidiabetic agents, this study explored α-glucosidase inhibitory metabolites from Paenibacillus sp. JNUCC 31. Whole-genome sequencing revealed diverse biosynthetic gene clusters, suggesting its potential for secondary metabolite production. GC-MS analysis identified anteiso-C15:0 as the dominant fatty acid. Among extracts screened, the ethyl acetate fraction exhibited the strongest α-glucosidase inhibition (52.4±0.7%). Bioassay-guided isolation yielded five known compounds, including adenosine, uridine, and dibutyl phthalate (DBP), all known for α-glucosidase inhibition. Kinetic assays showed uridine as a competitive inhibitor, while adenosine and DBP displayed mixed-type inhibition. Molecular docking and dynamics simulations confirmed stable binding of these compounds to human MGAM and microbial isomaltase. DBP showed the strongest affinity, with binding energies of −31.00 kcal/mol (MGAM) and −27.74 kcal/mol (isomaltase). Fatty acids bound more weakly. Key interacting residues included Trp406 in MGAM and Tyr158/Gln279 in isomaltase, forming stable hydrogen bonds and aromatic interactions. These findings highlight Paenibacillus JNUCC 31 as a promising source of α-glucosidase inhibitors, with implications for functional food and pharmaceutical applications.

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Poster Presentation

PNB-113

Ginsenoside MC Modulates Neuroinflammation via the TLR4/MD2 and Nrf2/ARE Pathways in BV2 Microglial Cells

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The neuroprotective effects of ginsenoside Mc (G-MC), a protopanaxadiol-type ginsenoside metabolite known for its anticancer and anti-photoaging properties, remain unexplored. Therefore, we aimed to investigate G-MC's potential as a neuroprotective agent. To this end, inflammation was induced in BV2 microglial cells using lipopolysaccharide and treated with G-MC. Cell viability, nitric oxide (NO) production, and protein expression of key inflammatory markers, including inducible nitric oxide synthase (iNOS), cyclooxygenase-2 (COX-2), and cytokines, were analyzed. The Nrf2/antioxidant response element (ARE) pathway activation was examined, and molecular docking studies were performed to assess the interaction of G-MC with the TLR4/MD2 complex. G-MC reduced NO production, suppressed iNOS, COX-2, and pro-inflammatory cytokine expression, and activated the Nrf2/ARE pathway. Molecular docking revealed strong G-MC binding affinity to TLR4, suggesting an inflammation-modulating role. G-MC demonstrates anti-inflammatory and neuroprotective effects in vitro. These findings highlight its potential as a therapeutic candidate for neuroinflammatory diseases.

PNB-114

β-sitosterol induces ferroptosis in triple-negative breast cancer cells by modulating the ROR1/YAP/TAZ signaling pathway

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Radioresistance presents a challenge for the treatment of triple-negative breast cancer (TNBC), and its underlying mechanisms remain unclear. While β-sitosterol has shown promise in addressing chemoresistance, its impact on radiosensitivity remains unexplored. This study aimed to investigate the mechanisms underlying radioresistance in MDA-MB-231/radioresistant (RR) cells, a radioresistant TNBC cell line, and the potential of β-sitosterol to enhance radiosensitivity in TNBC treatment. We found that MDA-MB-231/RR cells exhibit ferroptosis resistance, with enhanced expression of solute carrier family 7 member 11 (SLC7A11) and glutathione peroxidase 4 (GPX4), and also showed upregulated expression of ROR1, YAP, and TAZ. Inhibiting ROR1 reduced SLC7A11 and GPX4 levels, suggesting that ROR1 is crucial for regulating ferroptosis resistance. β-sitosterol treatment suppressed the ROR1/YAP/TAZ pathway and induced ferroptosis and radiosensitivity in MDA-MB-231/RR cells. Moreover, β-sitosterol treatment inhibited the ROR1/YAP/TAZ pathway and impeded subcutaneous tumor formation in a xenograft mouse model without significantly affecting body weight. Our results indicate that targeting the ROR1/YAP/TAZ pathway is a promising therapeutic approach to overcome TNBC radioresistance and that β-sitosterol is a potential anticancer agent that induces ferroptosis.

PNB-115

Acute treatments of *Myristica fragrans* Houtt. essential oil improved depression-like behaviors enhancing GABAB signaling and stress resilience

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Background: Current antidepressants based on monoamine modulation show limited efficacy and delayed onset. While GABAergic dysfunction is increasingly recognized in depression pathophysiology, therapeutic approaches targeting this system remain underexplored.

Purpose: This study investigated whether intranasal administration of Myristica fragrans essential oil (MFEO) could provide rapid antidepressant effects through GABAergic modulation.

Methods: Using network pharmacology and GC/MS analysis, we identified key MFEO constituents and their molecular targets. We evaluated MFEO's therapeutic potential through three paradigms: stress resilience in social defeat stress (SDS), acute antidepressant response, and chronic efficacy in restraint stress, with comprehensive behavioral and molecular analyses.

Results: Acute intranasal administration produced rapid antidepressant effects within 30 minutes, associated with enhanced GABABR1 signaling and elevated BDNF levels. Mechanistically, MFEO's effects were primarily mediated through GABAB receptor-dependent neuroplasticity, with eugenol identified as a key rapid-acting component.

Conclusion: This study establishes intranasal MFEO as a novel rapid-acting antidepressant strategy that enhances stress resilience through GABAB receptor modulation, offering a promising alternative to current delayed-onset treatments.

PNB-116

Characterization and Discrimination of *Panax ginseng* Based on Multi-Platform Metabolomics Combined Molecular Networking Analysis

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Panax ginseng is widely cultivated in East Asia, including Korea, China, and Japan, and is well known for its health-promoting properties, which are attributed to its diverse pharmacological effects. It contains various metabolites, particularly ginsenosides, whose composition can vary depending on environmental factors such as cultivation region and climate conditions. This study aimed to compare the metabolic profiles of *P. ginseng* grown in Korea, China, and Japan to investigate metabolic variations influenced by environmental conditions. Primary and secondary metabolites were comprehensively analyzed, with primary metabolites identified using gas chromatography-time-of-flight mass spectrometry (GC-TOF/MS) and nuclear magnetic resonance (NMR), covering sugars, amino acids, and organic acids. Secondary metabolites, including ginsenosides, were characterized using ultra-performance liquid chromatography-quadrupole time-of-flight mass spectrometry (UPLC-Q-TOF/MS). Multivariate statistical analysis (PCA, PLS-DA) was applied to identify region-specific metabolic markers, and their bio-synthetic pathways were explored to elucidate the impact of environmental factors on metabolite composition. Regional metabolic characteristics were clearly distinguished, enabling origin discrimination. Furthermore, molecular networking visualized the chemical diversity and structural relationships among metabolites, effectively distinguishing ginsenosides and their derivatives while highlighting region-specific clusters. The resulting integrated metabolite database provides a valuable reference for origin authentication, quality control, and pharmacological research, offering insights into the environmental influence on ginseng metabolites and establishing a foundation for the standardization and functional evaluation of ginseng products.

Poster Presentation

PNB-117

Integrated Metabolomics and Biological Functional Assessment of *Platycodon grandiflorum* Extract in Alcohol-Related Liver Disease

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Platycodon grandiflorum has been traditionally used in East Asia to treat respiratory and hepatic disorders. Although its hepatoprotective properties are well recognized, the metabolic mechanisms underlying its protective effects against alcohol-induced liver damage (AILD) remain incompletely understood. This study employed both in vivo and in vitro approaches to assess the hepatoprotective activity of *P. grandiflorum* extract (PGE), using nuclear magnetic resonance (NMR)-based metabolomic analysis to characterize its metabolic profile. Alcoholic liver injury was induced in mice by oral administration of 25% ethanol (5 g/kg) for three weeks. PGE was administered at doses of 50, 100, and 200 mg/kg. Ethanol exposure significantly elevated serum levels of aspartate aminotransferase (AST) and alanine aminotransferase (ALT), which were significantly reduced by PGE treatment. In addition, PGE restored hepatic antioxidant enzyme activities, including superoxide dismutase (SOD) and catalase (CAT). These biochemical findings were supported by histopathological analyses. In ethanol-stimulated HepG2 cells, PGE inhibited nitric oxide (NO) production and downregulated the expression of COX-2, iNOS, and IL-6, while upregulating the cytoprotective enzyme HO-1. NMR-based metabolomic profiling, followed by multivariate statistical analysis, identified key metabolites potentially responsible for the hepatoprotective effects of PGE. Collectively, these findings demonstrate that PGE mitigates AILD through coordinated functional and metabolic modulation, underscoring its potential as a therapeutic candidate for the prevention and treatment of alcohol-related liver disease.

PNB-118

Neuroprotective Effects of Coumarin derivatives Isolated from *Peucedanum japonicum*

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Peucedanum japonicum Thunberg, a perennial herbaceous plant belonging to the Apiaceae family, has been traditionally used in East Asia including Korea, China, and Japan for the treatment of various ailments such as colds, inflammation, and asthma. This plant contains a range of bioactive compounds, including coumarins, phenolic acids, and chromones, which have been reported to possess anti-inflammatory, antioxidant, and cytoprotective properties. Previous studies have shown that extracts of *P. japonicum* suppress nitric oxide (NO) production in macrophages, thereby mitigating inflammatory responses. In this study, coumarin derivatives were isolated from the aerial parts of *P. japonicum* using chromatographic techniques such as open column chromatography and medium-pressure liquid chromatography (MPLC). Structural elucidation of the isolated compounds was performed using nuclear magnetic resonance (NMR) spectroscopy and ultra-performance liquid chromatography coupled with quadrupole time-of-flight mass spectrometry (UPLC-Q-TOF/MS). Furthermore, the anti-neuroinflammatory activities of these compounds will be evaluated in BV2 microglial cells. By elucidating the underlying mechanisms of action, this study aims to advance the understanding of therapeutic strategies targeting oxidative stress and inflammation in neurodegenerative diseases and to provide a scientific basis for future pharmacological applications.

PNB-119

Isolation and Characterization of Bioactive Compounds from *Phedimus aizoon* for Sleep Quality Improvement

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Phedimus aizoon, a perennial herb of the Crassulaceae family, has traditionally been used in East Asia to treat various ailments, including fever, inflammation, and bleeding. This plant is known to contain bioactive constituents such as phenolic compounds, terpenoids, and flavonoids. Deterioration in sleep quality can result from several factors, including reduced melatonin levels, alterations in neurotransmitters and their receptors, elevated stress, aging, and disrupted sleep patterns. These changes may contribute to sleep disorders such as insomnia, sleep-related breathing disorders, and central hypersomnia. Recent studies have demonstrated that *P. aizoon* extract exerts sedative and sleep-promoting effects, including reduced spontaneous activity, prolonged sleep duration, and increased sleep incidence. In particular, in vivo experiments using male Kunming mice showed that *P. aizoon* extract significantly suppressed autonomic activity and enhanced both the duration and frequency of sleep, supporting its potential as a sedative and hypnotic agent. This study aimed to isolate and identify phenolic compounds from *P. aizoon*. Active constituents were separated using chromatographic methods, including open column chromatography and medium-pressure liquid chromatography (MPLC). The chemical structures of the isolated compounds were elucidated by nuclear magnetic resonance (NMR) spectroscopy. This approach aims to explore potential therapeutic strategies for improving sleep quality and to establish a foundation for the application of *P. aizoon* extract as a functional health food ingredient and for pharmacological use.

PNB-120

Evaluation of the Antioxidant and Antiaging Effects of the Native Plant Genus *Schisandra* Extracts and Application in Cosmetics

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Schisandra sphenanthera is the vine plant belong to the *Schisandra* genus and grows naturally in East Asia and southern Korea. This plant is known to have liver-protecting and antioxidant effects in traditional medicine. Belong to the same genus *Schisandra* chinensis contains various bioactive ingredients and has been reported as a natural product with an antioxidant activity and skin protection effects. Plants belonging to the genus *Schisandra* are reported to have lignans and polyphenol derivatives. These ingredients are known to inhibit skin cell damages and reduce skin aging by removing reactive oxygen species (ROS). In this study, the native plants *Schisandra sphenanthera* and *Schisandra chinensis* are used together, they showed improved antioxidant and collagen systhesis effects compared to using alone. And liposome technology was applied to complement the skin absorption rate of the active ingredients from these extracts. These results support this combination has potential as a functional cosmetic ingredient.

PNB-121

Inhibitory Effect of *Citrus unshiu* on the Spread of Antibiotic Resistance Genes

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Antibiotic resistance is a major global health concern, often driven by horizontal gene transfer (HGT) among bacteria. Conjugation, a key HGT mechanism involving plasmid transfer, plays a significant role in spreading antibiotic resistance genes (ARGs). Recent studies suggest that reducing reactive oxygen species (ROS) can inhibit conjugation and ARG dissemination. This study investigates the potential of *Citrus unshiu* extract, known for its antioxidant properties, to suppress the transfer of ARGs. Conjugation experiments were conducted using E. coli DH5α (donor, carrying RP4 plasmid with gentamicin resistance) and E. coli EC500 (recipient, rifampicin-resistant). The frequency of conjugation was measured with and without *Citrus unshiu* extract. Intracellular ROS levels were assessed using the DCFH-DA assay, and the expression of conjugation-related and oxidative stress-response genes was analyzed via qPCR. Results showed that green tangerine extract significantly decreased ROS levels and downregulated genes involved in the conjugation process, leading to a reduced frequency of ARG transfer. These findings suggest that Citrus unshiu can serve as a natural inhibitor of ARG dissemination. This study provides a scientific basis for using natural antioxidants to control antibiotic resistance and highlights the potential application of *Citrus unshiu* in food and environmental fields to curb resistance spread.

PNB-122

Generation of Chrysoeriol-Producing Transgenic Lettuce as a Flavonoid Production Platform

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Natural compounds derived from plants have been used in traditional medicine and folk remedies for centuries. Chrysoeriol has pharmacological effects such as anticancer, anti-inflammatory, antioxidant, antidiabetic, and rheumatoid arthritis treatments. We generated transgenic lettuce heterologously producing chrysoeriol. A multigene expression cassette containing *AtPAL*, *OsCHS*, *OsFNS*, *OsF3’H*, and *CrOMT2* in the chryseriol biosynthetic pathway was assembled in a binary vector referred to as *PCFFO*. The constructs were introduced into Lactuca sativa Ninja cv. using Agrobacterium-mediated transformation. A total of 91 transgenic lettuce plants were regenerated. Among them, 43 plants were selected for analysis. From the T1 stage, we screened transgenic plants. And flavonoids were extracted from the leaves. The analyzed using LC-MS MRM, resulting in the highest chrysoeriol production with 29.2 μg/g DW and 27.2 μg/g FW. Among the T1 generation, six plant lines with the highest compound content were selected for analysis in the T2 generation. Flavonoids were extracted and analyzed via LC-MS following a 10-fold concentration procedure. As a result, chrysoeriol was detected in all 66 samples at concentrations ranging from 3.32 to 255.30 ng/g (FW). The extraction yield was comparable to that of the previous generation, suggesting conserved genetic traits and sustained metabolite production capacity.

This study demonstrates that transgenic lettuce can serve as a stable production platform for chrysoeriol, with potential applications in pharmaceuticals and industry.

PNB-123

Investigation of Zinc Finger Proteins (LsZNFPs) in Laticifer Differentiation for Enhanced Rubber Accumulation in Lettuce

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Natural rubber, primarily *cis*-1,4-polyisoprene, is a valuable industrial material traditionally sourced from *Hevea brasiliensis*. However, the slow growth rate of *H. brasiliensis* has driven research into alternative rubber-producing plants such as *Taraxacum kok-saghyz*, *Ficus carica*, *Solidago levenworthii* and *Lactuca sativa*. These species produce latex, a milky white emulsion accumulated specialized rubber-producing cells called laticifers, which are strategically located within the phloem vascular system. Latex serves crucial purposes in plant defense, including wound sealing and protection against pests and diseases. Despite their importance, little is known about the molecular mechanisms underlying laticifer differentiation and development. In this study, we examined the potential role of zinc finger proteins, known as regulators of phloem development, in laticifer formation in *Lactuca sativa*. We identified five homologous zinc finger proteins, designated several LsZNFPs We employed CRISPR/Cas9-mediated targeted mutagenesis to generate gene knockouts by specifically targeting the functional domains of *LsZNFPs*. Furthermore, to elucidate their mechanisms, we are developing overexpression lines and conducting complementation studies in heterologous plant systems, including *Arabidopsis thaliana* and *Solanum nigrum*. By analysing the transgenic plants, we aim to clarify whether phloem development could affect the laticifer differentiation and latex biosynthesis in lettuce.

PNB-124

Phytochemical Constituents of *Glehnia littoralis* Leaves and Their Chemotaxonomic Significance

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A phytochemical investigation of the leaves of *Glehnia littoralis* led to the isolation of 27 secondary metabolites. The isolated compounds comprised twelve coumarins, four benzofuran glucosides, two phenolic constituents, one lignan, three alkaloids, two chromone glycosides, and three caffeoylquinic acid derivatives. Regarding published data, their structures were identified using NMR spectroscopy, mass spectrometry, and optical rotation. Among these, compounds **16**, **19** to **21**, and **26** have not been previously reported from the Apiaceae family. Additionally, compounds **12** to **15**, **18**, **23** to **25**, and **27** were obtained from the genus *Glehnia* for the first time. Notably, the three alkaloids, indole-3-carbaldehyde, deoxyhyrtiosine A, and naphthisoxazol A appear to be characteristic of *G. littoralis*, and may serve as chemotaxonomic markers that distinguish it from other Apiaceae species.

Poster Presentation

PNB-125

Cytotoxic effects of C17 polyacetylenes isolated from the roots of *Glehnia littoralis* against drug resistant colorectal and lung cancer cells

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Preliminary studies revealed that falcarinol and falcarindiol, C_{17} polyacetylenes isolated from the roots of *Glehnia littoralis* F. Schmidt ex Miq (Umbelliferae), exhibited notable cytotoxic effects against both oxaliplatin-sensitive/resistant colorectal cancer (CRC) and gefitinib-sensitive/resistant non-small cell lung cancer (NSCLC) cells. In the present study, 13 polyacetylenes, including a new compound, (3*R*,11*R*)-11-hydroxy-isofalcarinolone (**1**), were isolated from *G. littoralis*, and the chemical structures were characterized by NMR, HRMS, optical rotation, and DP4+ computational analysis. Among the isolates, (3*S*,8*S*)-oplodiol (**5**) demonstrated cytotoxic activity against oxaliplatin-sensitive and -resistant CRC (HCT116 and HCT116-OxR) cells. Unexpectedly, newly purified (3*R*,8*S*)-falcarindiol (**3**) and (3*S*)-falcarinol (**12**) did not show cytotoxic activities, in contrast to prior results. Subsequent analysis confirmed that both falcarinol and falcarindiol, previously evaluated, were decomposed, which seems to be the cause of inconsistent biological results. These findings indicated that C_{17} polyacetylene could be a good starting compound for the development of anticancer leads against drug-resistant CRC and NSCLC cells, however, the stability of C_{17} polyacetylens should be considered for further studies.

PNB-126

Metabolite Profiling and Antimicrobial Activities of *Brassica rapa* ssp. *narinosa* (Tatsoi), *B. rapa* var. *narinosa* × *chinensis* (Dacheongchae), and *B. rapa* ssp. *chinensis* (Pakchoi)

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Pakchoi and Tatsoi are agriculturally and commercially important subspecies of *Brassica rapa*. Dacheongchae is a new crop generated via the hybridization of Tatsoi and Pakchoi. *Brassica* plants are recommended for human health due to their nutritional benefits. While metabolic profiles of Pakchoi and Tatsoi have been studied individually, research comparing the metabolites and their antimicrobial effects across these *Brassica* cultivars, including Dacheongchae, remains scarce. Furthermore, to date, no studies have explored the correlation between bioactive compounds and their pharmacological effects in these *Brassica* vegetables. This study aimed to compare the metabolites in the three *Brassica* cultivars, and investigate the relationship between the identified metabolites and their biological activities. Metabolite profiles of carbohydrates, sugar alcohols, amines, amino acids, carotenoids, phenolics, organic acids, and glucosinolates were analyzed in the three *B. rapa* cultivars. The majority of amino acids were higher in Dacheongchae than in Pakchoi and Tatsoi. In addition to the amino acid content, Dacheongchae contained higher levels of phenolic compounds and carotenoids. Notably, glucosinolates were higher in both Dacheongchae and Pakchoi than in Tatsoi. Furthermore, Dacheongchae exhibited stronger antimicrobial activity against *Candida albicans* and methicillin-resistant *Pseudomonas aeruginosa* compared to other subspecies, and only Dacheongchae showed inhibitory activity against *Salmonella paratyphi*. These results suggest synergistic antimicrobial properties derived from the higher amounts of bioactive compounds in Dacheongchae.

PNB-127

Validation of an Analytical Method for Caffeoylquinic Acid Derivatives Content Enhanced in *Aster × chusanensis* by UV Irradiation

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A. chusanensis at the bud stage was subjected to controlled exposure to UV-A and UV-B radiation in a growth chamber with specialized lighting systems. The metabolites from the aerial parts of UV-irradiated and control *A. chusanensis* were identified by UPLC-Q-TOF/MS such as 3-O-caffeoylquinic acid (1), rutin (2), 3,4-di-O-caffeoylquinic acid (3), 3,5-di-O-caffeoylquinic acid (4), biorobin (5), luteolin-7-O-β-glucoside (6), 4,5-di-O-caffeoylquinic acid (7), and luteolin (8). As a result, UV-A irradiated aerial *A. chusanensis* selectively improved the contents of four CQA derivatives. Thus, the increased four CQA derivatives were used for the comprehensive analysis to establish and validate analytical methods for their quantification using HPLC-DAD.

PNB-128

Neotenone from *Pachyrhizus erosus* with Whitening Effects on Tyrosinase Inhibition and Anti-pigmentation Activity

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In this study, neotenone were isolated from the seeds of *Pachyrhizus erosus*. The chemical structure was completely identified through spectroscopic data, including UV and NMR. Neotenone exhibited the inhibitory effects on tyrosinase with IC_{50} at 11.1 μM, dose-dependently. Neotenone also regulated the catalytic effects to combine with enzyme-substrate (ES) complex. A double reciprocal showed a decrease in V_{max} (the maximal velocity) while a constant K_m, it was indicated the typical noncompetitive inhibition mode. Moreover, the melanin formation examined for their ability to suppress pigment formation in B16 melanoma cells, which was stimulated through melanin production by α-melanocyte-stimulating hormone (α-MSH). The inhibitor concentrations were adjusted to be non-toxic to B16 melanoma cells. Neotenone showed a significant reduction of melanin content dose-dependently from 10 to 30 μM concentrations.

Poster Presentation

PNB-129

Neutrophil Elastase Inhibitory Furanocoumarins from *Angelica dahurica* Roots

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Angelica dahurica root traditionally has used for its analgesic and as an ingredient in health functional food, traditional herbal medicines. In this study, six furanocoumarins (**1-6**) were isolated from *Angelica dahurica* root. The isolated compounds were identified the chemical structure using 1D, 2D-NMR analyses. All of the isolated compounds (**1-6**) showed significant inhibition of HNE with the IC_{50} at less than 10 μM, respectively. In the enzyme kinetic study, the compounds having a substituent at C-5 showed mixed inhibition type, while the compounds having a substituent at C-8 displayed noncompetitive inhibition type. Furthermore, the relative distribution of HNE inhibitory furanocoumarins **(1-6)** in *A. dahurica* extract was evaluated using LC-Q-TOF/MS analysis.

PNB-130

Whitening Effect of lignan derivatives from Anise hyssop (*Agastache foeniculum*)

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Tyrosinase (EC 1.14.18.1) belonging oxidoreductase catalyzes two distinct reactions: the hydroxylation of monophenols and the oxidation of o-diphenols to the corresponding o-quinones. Tyrosinase inhibitory lignan derivatives (**1** and **2**) were isolated from Anise hyssop seed. The powdered Anise hyssop seeds were extracted with methanol for weeks on room temperature. The evaporated extract was separated with organic solvent of *n*-hexane and methanol to remove the oil layer from the seeds. The isolation targeted methanol layer was chromatographed on a silica-gel column to yield two lignan derivatives (**1** and **2**). All the isolated compounds were identified through the spectroscopic data including NMR, UV, and HRESIMS data. Two lignan derivatives (**1** and **2**) showed tyrosinase inhibitory effects with IC_{50} values about 40 μM, respectively. Furthermore, the inhibition kinetics established for active compounds against tyrosinase.

PES Environmental Sciences

PES-1

Characterisitics of Variation of Organic Pollutants in Agricultural Water in Gyeongbuk Province(2023~2024)

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Residual pesticides in soil can migrate to surface or groundwater, affecting risks to the environment and agricultural product safety. Accordingly, continuous monitoring is essential for effective risk management. This study aimed to investigate the occurrence and distribution characteristics of residual pesticides in agricultural water in Gyeongbuk Province. Water samples were collected from 12 surface water sites and 11 groundwater sites in 2023 and 2024. A total of 327 compounds were analyzed in 2023 and 463 compounds in 2024. Surface water samples were collected three times a year(April, July and October), while groundwater samples were collected twice a year(April and July). The collected samples were pretreated using liquid-liquid extraction and analyzed using LC-MS/MS and GC-MS/MS. In 2023, 13 pesticides were detected in surface water in April, 26 in July, and 12 in October. In groundwater, 12 and 14 pesticides were detected in April and July, respectively. In 2024, 20, 30, and 5 pesticides were detected in surface water in April, July, and October, respectively, while 15 and 17 pesticides were detected in groundwater in April and July, respectively. Dinotefuran and azoxystrobin were most frequently detected in 2023, while ortho-phenyl phenol most frequent in 2024. These results provide baseline data for the safe and effective management of pesticide use in agricultural environments.

PES-2

Predictive modeling of pesticide half-life in soil using machine learning

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Predicting the concentration changes of residual pesticides in soil is a critical task in pesticide safety management. This study optimized the soil half-life (DT50), a key variable for modeling dissipation, using artificial intelligence (AI) learning models. Time-series concentration data for nine pesticides obtained from soil column experiments were used to train AI models. To select the best-performing DT50 prediction model, three machine learning algorithms—Support Vector Machine (SVM), Random Forest (RF), and Light Gradient Boosting Machine (LightGBM)—were compared based on the coefficient of determination (R^2) and root mean square error (RMSE). RF outperformed others with the highest accuracy ($R^2 = 0.805$) and the lowest error (RMSE = 28.20). Compared to the original DT50 values from the Pesticide Properties Database (PPDB) ($R^2 = -0.175$, RMSE = 0.302), the AI-predicted values significantly improved prediction performance. To validate the improvement, a paired t-test was conducted using Butachlor as a case study. The original DT50 was overestimated by 0.288 days on average ($t = -14.08$, $p < .001$, Cohen's $d = -3.07$), whereas the RF-adjusted value reduced this difference to 0.177 days ($t = -13.70$, $p < .001$, Cohen's $d = -2.99$). These results confirm that RF-based correction significantly enhanced prediction accuracy. This approach highlights the potential of AI as a powerful tool for improving pesticide safety management in the environment.

PES-3

Effects of Biochar Type, Application Rate, and Frequency on Soil Carbon Content in the Saemangeum Reclaimed Land

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The Saemangeum reclaimed land, with an area of 9,400 ha, has significantly lower soil carbon content compared to typical agricultural land, creating unfavorable conditions for crop cultivation. However, from a carbon storage perspective, its low initial carbon level offers high potential as a carbon sink. Biochar, produced through pyrolysis of organic materials, is rich in carbon and highly resistant to decomposition, making it a promising amendment for soil carbon sequestration. This study, conducted in the second year of a multi-year experiment, evaluated changes in soil carbon content according to biochar type, application rate, and frequency in the Saemangeum area. Biochars derived from wood, rice husk, and coconut were applied at 1, 2, and 3 t ha^{-1} (coconut biochar at 3 t ha^{-1} only) with three replications. Annual and biennial application intervals were compared. Soybean (Glycine max (L.) Merr.) was cultivated to assess plant growth response. After two years of annual application, soil carbon content increased from the baseline (0.28%) to 0.33–0.48% across treatments. Increases by application rate were 0.35, 0.43, and 0.42% for 1, 2, and 3 t ha^{-1}, respectively. Carbon content differences by application frequency were minimal.

Keywords: Saemangeum reclaimed land, Biochar, Soil Carbon, Soybean

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PES-4

Leachability characteristics of heavy metals in contaminated forest soils

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Forest soils around the abandoned metallic mine were heavily contaminated with toxic metals like As, Cd, Pb, Zn. However, research works on leachability characteristics along with ecological and health risks assessment of heavy metal-contaminated forest soils. Leachability characteristics of heavy metals in 21 forest soils, collected from abandoned mine, using various leaching procedures(toxicity characteristic leaching procedure, synthetics precipitation leaching procedure and simple bioavailability extraction test and sequential extraction method). Results showed that studied soils were heavily contaminated with heavy metals like As, Cd, Pb, Zn. The total contents of studied metals in almost samples exceeded tolerable levels. Especially, the total content of As ranged from 26 to 3,179 mg kg-1. For identification of metal fraction, most of the metals were found to be associated with residual fraction like silicates and organic matters except for lead, which were mainly bound to the Fe-Mn oxide fraction. For TCLP test, the heavy metals did not exceed TCLP regulatory level. The concentrations of metals extracted by SBET were higher than others. There were some correlations in the concentrations of heavy metals in leaching procedure, extraction test and individual fraction of heavy metals.

PES-5

Impact of Soil Amendments on Soil Microbiota and Plant Defense System: A Study on Beneficial Bacterium and Salicylic Acid in Cucumber Cultivation

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The increasing demand for sustainable agriculture highlights the need for improved biological control agents (BCAs). This study evaluates the co-application of *Bacillus amyloliquefaciens* KACC17029 and salicylic acid (1.0 mM) on cucumber (*Cucumis sativus* L.) performance and rhizosphere microbiota. Combined treatment significantly reduced lesion size (83.8%), enhanced leaf area (101.3 cm^2), and increased shoot biomass (38.2 g). These outcomes correlated with enhanced peroxidase activity (6-fold) and upregulation of defense genes *PR1* and *LecRK6.1*. Amplicon sequencing revealed increases in *Trichoderma*, *Candida*, and *Novierbaspirillum*, with reductions in *Fusarium*, indicating a beneficial microbial shift. In the second phase, encapsulated formulations using perlite–alginate beads maintained high microbial viability and resulted in the highest colonization levels (92.7 copies/μL by Day 15), improving plant traits. Microbiome analysis confirmed higher diversity and treatment-specific clustering (PERMANOVA $p=0.001$, $R^2=0.421$). Integration of amplicon and ddPCR data through Quantitative Microbiome Profiling (QMP) identified dominant genera like *Devosia* and *Streptomyces*. QMP-based co-occurrence networks in perlite-treated soil were more complex, with higher betweenness and eigenvector centrality. LEfSe analysis showed enrichment of *Bryobacter* and *Paenibacillus*. This study provides a framework combining PGPR–elicitor co-inoculation, encapsulation, and QMP to develop effective, field-applicable biofertilizers.

PES-6

Distribution of Soil Microbial Communities in Greenhouse Soils of Gyeongbuk Province

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Greenhouses provide enclosed environments that influence the structure and function of soil microbial communities, which are vital to crop productivity and soil health. This study analyzed bacterial and fungal communities in greenhouse soils from Gyeongbuk Province using 16S rRNA and ITS sequencing. Community composition was evaluated through alpha diversity indices, including richness (Chao1, Ace), diversity (Shannon, Inverse Simpson), and evenness (Shannon Evenness, Simpson Evenness). Microbial diversity in Gyeongbuk greenhouses was slightly lower than the national average for both bacteria (Chao1: 3,018; Shannon: 5.83) and fungi (Chao1: 527; Shannon: 3.22). Fungal evenness was also reduced (Shannon Evenness: 0.543 vs. 0.574), suggesting the potential dominance of specific taxa in certain samples. PCA analysis revealed that the microbial community structure in Gyeongbuk was more clustered and less dispersed compared to national samples, indicating that community diversity may be sensitive to differences in cultivation practices, soil conditions, and management factors. The dominant bacterial phyla were *Firmicutes* (31%), *Proteobacteria* (22%), and *Actinobacteriota* (16%), while *Ascomycota* (49%), *Mortierellomycota* (18%), and *Basidiomycota* (11%) dominated the fungal communities. These findings contribute baseline data for developing biological indicators to evaluate soil quality, particularly when combined with physical and chemical soil analyses in future research.

Poster Presentation

PES-7

Effects of Zerovalent Iron Nanoparticles on the Growth and Photosynthesis of *Arabidopsis thaliana* under Elevated CO_2 Concentrations

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Engineered zero-valent iron nanoparticles (nZVI) are used for environmental remediation due to their high surface area and reductive capacity; however, rising atmospheric CO_2 may alter plant physiology, and nZVI effects under elevated CO_2 remain underexplored. This study evaluates how soil-applied nZVI influences growth and photosynthetic performance of *Arabidopsis thaliana* under ambient (400 ppm) and elevated (800 ppm) CO_2. Responses to soil treatments with 0, 500, and 1000 mg nZVI kg^{-1} were assessed via biomass, leaf chlorophyll content, fluorescence imaging, and leaf spectral reflectance. The results confirmed that under ambient CO_2, nZVI at 500 and 1000 mg kg^{-1} increased dry biomass by 21% and 2%, whereas under elevated CO_2 the same doses boosted biomass by 54 % and 35%. At 800 ppm CO_2, nZVI reduced plant water content by 1.5% (500 mg kg^{-1}) and 1.3% (1000 mg kg^{-1}), reflecting greater dry-mass allocation through enhanced photosynthetic carbon assimilation. Comparing ambient versus elevated CO_2, dry biomass rose by 4%, 33%, and 38% at 0, 500, and 1000 mg kg^{-1}, demonstrating that nZVI dosage exerts a stronger influence on growth than CO_2 concentration. Our findings indicate that nZVI induces a larger growth boost in *Arabidopsis thaliana* under elevated CO_2 than ambient conditions, driven primarily by early-stage enhancements in photosynthetic efficiency and pigment accumulation.

PES-8

A Study on Biochar Production for Recycling of Spent Growing Media

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With the expansion of greenhouse horticulture in Korea, the generation of by-products and spent growing media from controlled environment agriculture, including smart farms, has increased. This study was conducted to assess the feasibility of utilizing biochar derived from spent growing media through pyrolysis as an organic fertilizer for crop production. The spent growing media were completely dried and then pyrolyzed at 400℃ for 2 hours. The biochar had a pH of 10.18, total nitrogen (T-N) content of 1.24%, and total phosphorus (T-P) content of 0.33%. The lettuce (Lactuca sativa) was cultivated in five treatments: IF (inorganic fertilizer, N-P-K = 200-59-128 kg/ha), BC5(spent growing media biochar at 5 t/ha), BC10(10 t/ha), IF+BC5, and IF+BC10, respectively. The fresh weight of lettuce in BC5, BC10, IF+BC5 and IF+BC10 was increased by 53.6%, 29.82%, 106.5%, 98.31% than IF treatment. Also, the plant height of lettuce in BC5, BC10, IF+BC5 and IF+BC10 was increased by 19.34%, 20.9%, 31.43% and 30.4% than IF treatment. After harvesting, the pH and CEC of soil were improved in the biochar treatments compared to the IF treatment. In conclusion, biochar from spent growing media promotes plant growth and enhances soil properties. Further research is needed to optimize biochar application and assess its performance across various crops and environment.

PES-9

Crop-Specific Metabolic Differences and Risk Assessment of Sulfoxaflor in Thistle and Olive

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Sulfoxaflor is a sulfoximine-based insecticide targeting nicotinic acetylcholine receptors (nAChRs). Recent reports of its potential systemic toxicity have raised concerns about its presence in food crops and highlighted the need for monitoring pesticide residues. This study evaluated the dissipation behavior, metabolic fate, and dietary risk of sulfoxaflor in two minor crops, following foliar application. The differences in application volume were normalized by dividing the residue levels by the amount of active ingredient applied. Initial normalized residues were 14.23 mg/kg/g in thistle and 2.54 mg/kg/g in olive, likely reflecting differences in plant morphology. The metabolite X11719474 was identified exclusively in thistle, suggesting species-specific metabolic pathways. The estimated half-lives were 4.1 days in thistle and 14.7 days in olive. For thistle, consumption data were unavailable, intake data of green tea (when consumed as tea) and spinach (when consumed as a vegetable) were used as substitutes due to their similar consumption patterns. When thistle was harvested on the day of application, the hazard index (HI) for tea consumption exceeded the safety threshold (HI = 1.203), but fell below 0.5 after three days. In olive, HI values remained consistently low across all sampling points, indicating negligible risk. These findings provide baseline data for understanding sulfoxaflor residue behavior in minor crops and support the establishment of maximum residue limits (MRLs) for thistle and olive.

PES-10

Correlation Analysis Between Leaf Chlorosis and Flooding-Responsive Metabolites Under Waterlogging Stress During Early Growth of Maize

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Waterlogging during early maize growth severely impairs plant development and physiological responses. This study investigated the correlation between leaf chlorosis and metabolite changes under waterlogging to identify genotypes with potential stress tolerance. Eight maize genotypes were grown under control and waterlogged conditions. Growth parameters (plant height, fresh and dry weight) and leaf chlorosis scores were recorded. Principal component analysis and correlation analysis revealed significant negative correlations between chlorosis and both plant height and biomass under waterlogged conditions. Three genotypes (M01, M02, M05) were selected based on differential chlorosis levels with minimal differences in growth traits. GC-MS-based metabolomic analysis was conducted on shoot and root tissues of these selected genotypes. A total of 44 shoot and 70 root metabolites showed significant changes due to waterlogging. Several metabolites, including glucose, fructose, malic acid, and shikimic acid, were strongly correlated with chlorosis, showing either positive or negative trends. Notably, many of these metabolites exhibited correlation coefficients $r > 0.5$ and determination coefficients $R^2 > 0.5$, indicating strong predictive relationships. Additionally, metabolite profiles varied across genotypes.These results suggest that chlorosis-associated metabolites can serve as biochemical markers for selecting maize genotypes with tolerance to early-stage waterlogging, offering valuable insights for future breeding strategies

Poster Presentation

PES-11

Synthesis and Characterization of Nutrient-Enriched, Mineral-Like Particles from Wastewater-Activated Sludge

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Wastewater sludge disposal poses environmental risks, yet its nutrient-rich composition makes it a promising sustainable resource for fertilizer production. This work presents an approach to utilize wastewater-derived activated sludge and convert it into mineral-like particles through combined heat and acid treatment. During this process, essential elements (e.g., P, K, Ca, N, and Fe) and fragmented organic compounds derived from the sludge are solubilized. The treatment is subsequently followed by alkaline precipitation, forming mineral-like particles high in nutrients and phenolic compounds. Compositional analysis of these particles confirms the successful incorporation of essential nutrients and phenolic polymers. While structural analysis gave insight into the formation of amorphous and poorly crystallized regions in these particles, it also showed compacted clusters with heterogeneous textures. This analysis confirmed the successful conversion of wastewater sludge into functional particles, establishing a foundation for producing slow-release smart fertilizer.

PES-12

Synthesis and Characterization of Nutrient-Enriched, Mineral-Like Particles from Wastewater-Activated Sludge

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Wastewater sludge disposal poses environmental risks, yet its nutrient-rich composition makes it a promising sustainable resource for fertilizer production. This work presents an approach to utilize wastewater-derived activated sludge and convert it into mineral-like particles through combined heat and acid treatment. During this process, essential elements (e.g., P, K, Ca, N, and Fe) and fragmented organic compounds derived from the sludge are solubilized. The treatment is subsequently followed by alkaline precipitation, forming mineral-like particles high in nutrients and phenolic compounds. Compositional analysis of these particles confirms the successful incorporation of essential nutrients and phenolic polymers. While structural analysis gave insight into the formation of amorphous and poorly crystallized regions in these particles, it also showed compacted clusters with heterogeneous textures. This analysis confirmed the successful conversion of wastewater sludge into functional particles, establishing a foundation for producing slow-release smart fertilizer.

PES-13

Adsorption characteristic of chlorantraniliprole on biochar

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Residual pesticides degrade slowly in the environment and can negatively affect ecosystems by spreading to other media through adsorption, dispersion, or volatilization. Chlorantraniliprole (CAP), a diamide insecticide increasingly used as a substitute for organophosphorus and carbamate insecticides due to its higher selectivity and efficacy, tends to persist in soil and crops because of its low water solubility and volatility, and thus requires careful management under maximum residue limit regulations. Biochar is a solid, eco-friendly material produced by pyrolysis of organic matter, and can adsorb organic compounds and heavy metals. This study investigated the aqueous adsorption behavior of CAP (2−0.125 mg/L) using biochar derived from pepper stems (PSB), a widely generated agricultural byproduct. After 48 hours of the sorption experiment, the residual concentration of CAP in the aqueous phase was analyzed using LC-MS/MS. The equilibrium adsorption capacity increased as the concentration of CAP increased, and the Freundlich isotherm ($R^2=0.8611$) model was more suitable than the Langmuir isotherm ($R^2=0.7781$) model for describing the adsorption characteristics. This suggests the occurrence of multilayer adsorption and indicates that PSB has potential as an effective adsorbent in environments with complex pollutants at varying concentrations, such as in water treatment or industrial wastewater processes. However, further research is needed to evaluate the adsorption potential under various environmental conditions and to optimize the overall adsorption efficiency.

PES-14

Applicability of *Festuca ovina* var. *coreana* for Amendment-Assisted Phytoremediation of Arsenic-Contaminated Soil

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Arsenic (As) contamination is a serious problem in mine-affected soils because As is carcinogen. Therefore, it is essential to prevent As from leaching and runoff of into agricultural soils. The purpose of this study was to evaluate the potential of using native plants, *F. ovina var. coreana*, for phytoremediation of As contaminated soil near an abandoned mine and to assess the feasibility of converting the harvested biomass into biochar as a sustainable strategy for the treatment of phytoremediation residues. The experiment was conducted in abandoned coal mine site with 285 mg/kg As in soil. Four amendments including biochar, compost, lime, and urea were applied. The highest dry weight was observed in the control and amendments did not significantly enhance the growth of *F. ovina var. coreana* indicating that the indigenous plant managed to grow without soil amendments due to the inherent tolerance and phytoextraction capacity. The As concentration in the plants reached up to 4.02 mg/kg. The phytoremediation residue of *F. ovina var. coreana* was pyrolyzed. Total As content in biochar was 13.38 mg/kg, while the bioavailable As was only 0.45 mg/kg, indicating that most of As in biochar was immobile. *F. ovina var. coreana* was promising for As phytoremediation, converting the contaminated biomass to biochar effectively reduced volume and immobilized As, thereby lowering the environmental risks associated with its disposal.

Poster Presentation

PES-15

Machine Learning-Based Prediction of Soil Nutrients Levels from Electrical Conductivity

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Real time on-site analysis of soil nutrient levels is essential for the appropriate use of fertilizers and the reduction of environmental pollution. In this study, a machine learning-based nutrient prediction model was developed using soil electrical conductivity (EC) sensing data, which is correlated with soil nutrient content. Two data sets including EC data measured from soil extract and EC data measured using real time sensor and three machine learning algorithms including Random Forest (RF), Support Vector Regression (SVR), and eXtreme Gradient Boosting (XGBoost) were applied to predict the concentrations of nitrate (NO_3^-), available phosphate (Av.P), and potassium ion (K^+), which are the plant-available forms of nitrogen (N), phosphorus (P), and potassium (K). Analysis of EC dataset measured from soil extract revealed coefficient of determination (R^2) values for NO_3^- and K^+ of 0.63 and 0.67 using RF, 0.68 and 0.52 using SVR, and 0.24 and 0.57 using XGBoost, respectively. For EC sensing dataset, the results showed that the R^2 values for NO_3^- and K^+ were 0.46 and 0.57 in RF, 0.61 and 0.40 in SVR, and 0.54 and 0.32 in XGBoost, respectively. All models showed low performance in predicting Av.P, indicating that additional research is needed to improve estimation accuracy for P. This study has the potential to serve as a foundational model for implementing precision agriculture in soil nutrient management.

PES-16

Deep Soil Contributes to More Reliable Soil Property Estimation

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Deep soil physicochemical properties, such as organic carbon, inorganic carbon, soil texture, and exchangeable ions, differ from those of shallow soil. Therefore, estimating whole-profile soil properties based solely on shallow soil data is unreliable. Diffuse Reflectance Fourier-Transform Mid-infrared (DRIFT-MIR) has been widely used to estimate soil properties. However, most DRFIT-MIR research on soil property estimation has focused on shallow soil. Here, we collected 476 soil samples at 0-240 cm and developed three DRIFT-MIR models to estimate soil properties: all-sample model, shallow-sample model, and deep-sample model. The all-sample model showed reliable accuracy ($R^2_{CV} > 0.8$) in estimating organic carbon, inorganic carbon, nitrogen, pH, exchangeable magnesium, exchangeable calcium, and sand, silt, and clay contents at 0−240 cm. For deep soil property estimation, the deep-sample model outperformed the other models, while the shallow-sample model exhibited limited accuracy compared to both the all-sample and deep-sample models. These findings highlight that developing DRIFT-MIR soil property estimation models using only shallow soil is insufficient for reliable monitoring across both shallow and deep soil.

PES-17

Soil Heterotrophic Respiration Is More Sensitive to Seasonal Changes in Temperature and Water Content than Autotrophic Respiration in a Monsoon Continental Climate

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Soil respiration (R_S) comprises the second-largest terrestrial carbon flux. However, uncertainties in seasonal variations of R_S and spatial biases in existing datasets make it difficult to predict future R_S. Here, we partitioned R_S into heterotrophic (R_H) and autotrophic respiration (R_A) under a monsoon continental climate to understand how R_H, R_A, and R_S respond to changes in temperature and water content. We also compared our R_H:R_S ratio with vales from the global Soil Respiration Database (SRDB) and domestic forest data (published in Korean, so not included in the SRDB) to assess the generalizability of our results and provide region-specific data from a relatively less-studied climate zone. In field, mean R_H:R_S ratio was relatively high during monsoon (1.09±0.04), but decreased during non-monsoon (0.54±0.08). The temperature sensitivity of R_H (2.67) was higher than that of R_S (2.29), indicating that R_H is more sensitive to temperature than estimated R_A. The mean R_H:R_S ratio excluding the monsoon season was similar to values reported in the SRDB and other Korean studies. This study demonstrates that R_H is more sensitive to seasonal variation in soil temperature and water content than R_A, and that the mean R_H:R_S ratio may be globally comparable when extreme precipitation during the monsoon season is excluded.

PES-18

Effect of Biochar Derived from Agricultural Residues and Livestock Manure on Crop Productivity and Soil Properties

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Biochar, a carbon-rich material produced by pyrolyzing biomass, has gained attention for its potential to mitigate global warming through carbon sequestration and improve soil quality. In Korea, biochar has been incorporated into national Fertilizer Standards, highlighting the need to determine optimal application rates for different biochar types. This study assessed the impact of biochar derived from agricultural residues and livestock manure on crop productivity and soil chemical properties. Treatments included a control (no amendment), NPK fertilizer (32.0-7.8-19.8 kg/10a), and biochar from two sources applied at 100 kg/10a and 300 kg/10a. Results showed that crop yields in biochar treatments were comparable to those with NPK fertilizer, with no significant differences between biochar types or rates. However, increasing biochar rates led to higher soil pH, EC, total carbon, and exchangeable cations. Soil carbon stocks were higher with agricultural residue biochar (47.2~67.3 ton C/ha) than with livestock manure biochar (32.2~38.0 ton C/ha), and increased with application rate. These findings indicate that biochar type influences carbon sequestration more than crop productivity. Long-term studies are needed to evaluate the cumulative effects of repeated biochar applications on soil health and carbon storage.

Poster Presentation

PES-19

Distribution of Microbial Extracellular Enzymes in Soil

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Microbial extracellular enzymes (EE) play a pivotal role in organic matter decomposition and nutrient cycling in soil. However, their spatial distribution within the soil remains unclear. This study aimed to quantify EE activities at three locations: mineral-bound, cell-bound, and free. We sampled topsoil from a pine forest (0-10 cm) at the Seoul National University Faculty Club and a rice paddy (0-25 cm) at the Seoul National University Research Farm. We chose three hydrolytic EE (β-glucosidase, N-acetyl-β-glucosaminidase, and acid phosphatase) and one oxidative EE (peroxidase), and assessed their activities saturating substrate concentrations (800 μM for hydrolytic and 3000 μM for oxidative EE). To measure EE activities at three locations, we prepared three types of soil slurries: (1) total EE slurry containing mineral-bound, cell-bound, and free EE, (2) slurry containing cell-bound and free EE, and (3) slurry containing only free EE. Mineral-bound EE activities were calculated by subtracting the activity in (2) from (1), and cell-bound EE activities by subtracting the activity in (3) from (2). Our results showed that over 70% of EE activity was mineral-bound regardless of EE types, suggesting potential stabilization of EE on mineral surfaces.

PES-20

Optimizing the Application of Organic Fertilizers Mixed with Pyrogenic Carbon Materials for Enhanced Crop Growth and Soil Carbon Sequestration

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To mitigate climate change, many countries have declared carbon neutrality goals. Korea has set a target of reducing 18 million tons of CO_2-equivalent emissions from the agriculture sector by 2030. One promising strategy is the application of pyrogenic carbon materials, such as biochar, to sequester carbon in soils. This study evaluated the effects of mixing organic fertilizers with carbonized materials on crop growth and soil chemical properties. Treatments included: control (no input), NPK fertilizer (32.0-7.8-19.8 kg/10a), organic fertilizer (full or basal application), and organic fertilizer combined with carbonized material at 100 kg/10a and 300 kg/10a. Results showed that crop growth and yield increased by 1.3~1.4 times in treatments with carbonized material compared to NPK or organic fertilizer alone. Nitrogen use efficiency was also improved. Importantly, basal-only organic fertilizer combined with carbonized material achieved yields similar to full-dose treatments. Soil analysis after harvest indicated a trend of increasing total carbon with higher application rates of carbonized material, though other chemical properties showed no significant change. These findings suggest that co-application of organic fertilizers and carbonized materials can reduce fertilizer input while enhancing carbon sequestration, offering a practical approach for sustainable and climate-resilient agriculture.

PES-21

Evaluation of Fertilizer Usage and Type in Facility Crops Cultivation

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South Korea is one of countries that have high application rate of inorganic fertilizer and is known to cause significant environmental issues. The inorganic fertilizer to the soil has led to a nutrient supply that exceeds the nutrient requirements of crops, resulting in an excess of nutrients in agricultural soil. Hence, many agricultural policies have been legislated to reduce the fertilizer application rate since the 1990s. This study aims to investigate total fertilization rates by nutrients and facility crops in 9 provinces of Korea. In results, the average of total fertilizer inputs (N-P2O5-K2O) was 40.3-31.6-35.7 kg 10a-1. Based on N, the total fertilizer usage of pumpkin was higher than other crops. Moreover, except for oriental melon, all facility crops exceeded the recommended levels of fertilizer usage. The order of contribution to total fertilizer use was inorganic fertilizer > compost > organic fertilizer. As a result, main concern of excess and use of fertilizers were focused on inorganic fertilizer. However, because of the high nutrient content of compost, the application rate of compost should be monitored and controlled. Therefore, the proper training and monitoring is required to reserve environmental sustainability and understand nutrient characteristics of fertilizer in facility crop cultivation.

PES-22

Evaluation of Fertilizer Usage and Nutrient Management Practices in Korean Rice Cultivation

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For sustainable agriculture and soil conservation, evaluation changes in soil nutrients due to fertilizer use in crop fields is essential. The amount of fertilizer applied can be inferred from the soil analysis, but the basic data on the actual amount of fertilizer used are insufficient. This study investigated the actual usage and nutrient contents of chemical fertilizers, organic fertilizers, and composts at 320 rice cultivation sites across 8 regions in Korea (Gyeonggi, Gangwon, Chungbuk, Chungnam, Jeonbuk, Jeonnam, Gyeongbuk, and Gyeongnam), and compared them with recommended fertilizer application rates derived from soil analysis to construct foundational data. The average nutrient application rates ($N-P_2O_5-K_2O$) for chemical fertilizers, organic fertilizers, and composts were 9.3-3.0-4.5, 1.2-0.5-0.3, and 98.0-7.5-9.2 kg 10a-1, respectively. The average nutrient contents of organic fertilizers and composts were 5.2-2.3-1.5 and 21.7-20.8-24.8 kg 10a-1, respectively. Compared to the recommended fertilizer application rates, the overall average usage of chemical and organic fertilizers was 0.4 kg 10a-1 lower for N, 0.5 kg 10a-1 lower for P_2O_5, and 0.9 kg 10a-1 higher for K_2O. However, there were significant differences in fertilizer usage among the regions. Compost usage also showed large variability among farms due to differences in products and farmer discretion. These findings provide fondametal data for understanding fertilizer usage in rice cultivation.

PES-23

Extracellular Enzyme Products Drive a Pulse of Microbial Respiration upon Rewetting of Dry Soil

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Rewetting of dry soil prompts a pulse of microbial respiration. Given its rapid onset, this pulse is likely fueled by readily available low-molecular-weight compounds. We propose that extracellular enzymes contribute to the accumulation of these labile substrates in soil prior to rewetting. To test this, we measured three extracellular enzyme activities, their products, microbial respiration, biomass C and water-extractable organic carbon (WEOC) at multiple time points over three weeks of a drying-rewetting cycle in forest soil. Drying suppressed microbial respiration and significantly reduced microbial biomass C compared to moist controls, while enhancing WEOC accumulation. Despite overall 45-56% reduced activities of extracellular enzymes, their persistence coupled with near-zero microbial activity led to significantly higher concentrations of glucose and N-acetyl-glucosamine in dry soils than controls. Once the dry soils were rewet, these accumulated products were immediately depleted, and microbial biomass C increased to control levels. Contrary to glucose and N-acetyl-glucosamine, orthophosphate concentrations did not significantly differ between treatments. By simultaneously assessing soil enzyme activities and their products, this study provides the first evidence that persistent enzyme activities even in dry conditions drive a pulse of microbial respiration upon rewetting. These findings highlight a complementary mechanism to previously proposed pathways for respiratory pulses upon rewetting (e.g., microbial cell lysis and aggregate disruption), and advance our understanding of carbon losses under changing precipitation.

PES-24

Influence of Growing Environment on Major Compounds and Growth Characteristics of Wild *Cudrania tricuspidata* Fruit

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Cudrania tricuspidata is a traditional medicinal herb in East Asia. However, fewer studies have been done on the correlation between growth characteristics and compounds in *C. tricuspidata* fruit in its habitat. So, we aimed to investigate their relationship. Fruit samples of *C. tricuspidata* and soil samples were collected in 18 habitats in September 2022. Six growth characteristics and three active compounds (6,8-diprenylorobol, 6,8-diprenylgenistein, and 4′-*O*-methylalpinumisoflavone) were investigated. We developed and validated an optimized method for quantifying active compounds using ultra-performance liquid chromatography (UPLC), and performed correlation analysis of growth characteristics and contents of active compounds. The UPLC-UV method for determining active compounds was validated by measuring the linearity, limit of detection, limit of quantification, precision, and accuracy using UPLC. Fruit growth was more affected by weather, and sugar content tended to decrease as the temperature rose. The active compounds were negatively correlated with the size of the fruit, especially the fresh weight and number of seeds. The results of this study can be used as basic data for the standard cultural practices and quality control of *C. tricuspidata* fruits.

PES-25

Adsorption characteristics of imidacloprid by two types of microplastics and biochar

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In agricultural environments, microplastics (MPs) present in soil can adsorb pollutants and act as vectors for their transport to other environmental media. Biochar (BC), a high-carbonaceous material produced through the pyrolysis of biomass at elevated temperatures, has a high specific surface area and porous structures, making it an effective adsorbent for contaminants. This study investigated the adsorption behavior of imidacloprid (IMD), a widely used and persistent pesticide, on two types of MPs (polyethylene (PE), polyvinyl chloride (PVC)) and on rice straw-derived biochar (RBC). Isothermal adsorption experiments were conducted using IMD solutions with MPs (<125 μm) and RBC (<250 μm), both individually and in combination. The adsorption data were best described by the Freundlich isotherm model, suggesting that multilayer adsorption mechanisms predominated. After adsorption, the residual concentration of IMD was most significantly reduced in the IMD+RBC treatment. In contrast, both the IMD+MP and IMD+MP+RBC treatments showed similarly lower reductions, regardless of MP type. This suggests that MPs may interfere with IMD adsorption onto RBC, possibly through competitive adsorption or other complex interactions. Further studies are needed to clarify why the presence of MPs leads to higher residual IMD concentrations compared to the RBC only treatment. This study confirms that both MPs and BC have the potential to adsorb residual pesticides, highlighting the need for further research into their adsorption potential for various environmental contaminants.

PES-26

A Subsoil-Inclusive Framework for National-Scale Soil Health Assessment

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Soil health is the capacity of soil to sustain essential functions such as food production, nutrient cycling, water purification, climate mitigation, and biodiversity conservation. Yet, most national soil health frameworks focus on topsoil ($<$ 15 cm), disregarding depth variability in soil properties and limiting comprehensiveness of soil health assessment. Here, we present a national-scale soil health assessment framework that incorporates both topsoil and subsoil, offering management recommendations to enhance soil health. We set assessment priorities based on soil functions linked to the UN Sustainable Development Goals, which are represented by physical (bulk density, porosity, available water capacity, water-stable aggregates), chemical (pH, exchangeable K, Ca, Mg, and cation exchange capacity), and biological (soil organic carbon) indicators. We adopted the cumulative normal distribution method to standardize indicator values. Scoring parameters used in this method were derived from the Korean soil series dataset, which includes 405 representative profiles from the national soil survey. This method allows indicators to be evaluated in the context of nationwide soil variability. We applied the framework to a cropland under different agricultural practices to assess its applicability. Results showed that the framework diagnoses soil health differences in response to the practices. However, the framework includes one biological indicator, due to limited nationwide data. This limitation highlights the need for future studies to validate and refine the indicators.

Poster Presentation

PES-27

Effects of Biochar Application on Soil Enzyme Activities under Lettuce Cultivation

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Biochar, a carbon-rich byproduct of biomass pyrolysis, is increasingly applied in agriculture for its capacity to reduce contaminant mobility, enhance microbial diversity, and stimulate soil biochemical processes. This study investigated the short-term effects of pine bark biochar (PB) and oak mushroom biochar (OM) on soil enzyme activities under lettuce cultivation. Both biochars were applied to soil at 0%, 1%, and 5%, and enzyme activities – alkaline phosphatase (ALK), β-glucosidase (BGL), and dehydrogenase (DHA) – were monitored over a 30-day period. ALK activity showed a significant increase in the PB 1% treatment on days 20 and 30, while OM treatments exhibited no statistically significant differences, though both biochars demonstrated time-dependent trends. BGL activity was not significantly influenced by biochar type, concentration, or plant presence. Notably, DHA activity remained stable in PB treatments but was significantly enhanced in the OM 5% treatment on days 10 and 20. These results aligned with previous findings from non-vegetated soil conditions, suggesting limited influence of lettuce on enzyme responses. Overall, the results show the potential of biochar to positively influence soil enzyme activities in the short term. Further research is required to explore long-term effects of biochar application.

PES-28

Effects of Transition Metals on the Digestibility in Rumen System

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In 2020, greenhouse gas (GHG) emissions from domestic ruminants accounted for 22.2% of agricultural and 48.5% of livestock-related GHG emissions in Korea. To access methane emissions from ruminants, many studies have been performed in the use feed additives based on plant and seaweeds. Among these, seaweeds contain various transition metals such as Fe, Mn, Rb, Zn and Co. These transition metals would catalyze the hydrogenation in rumen, and these are expected to reduce methane emission. This study investigated to evaluate the effects of minerals on methane reduction and digestibility in ruminants.

PES-29

Establishment of analytical methods for nicotine, propylene glycol and glycerol content in aerosol of heated tobacco products using GC-FID

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Heated tobacco products(HTPs) are new type of tobacco products using an electronic device that heats an inserted dedicated stick. Each stick contains tobacco leaves and additives such as flavoring ingredients and humectants, to inhale the exhaust. The stick contains nicotine, which causes addiction and dependence, and highly viscous substances such as propylene glycol(PG) or glycerol, which are used as humectants. These substances have been known to be harmful to the human body when inhaled. It was necessary to establish an analytical method of nicotine, PG and glycerol content in aerosol of HTPs to control and regulation. In this study, we optimized an analytical method to determine nicotine, PG and glycerol content in aerosol of HTPs by using gas chromatograph-flame ionization detector(GC-FID) for effective management of compounds in HTPs. And also we validated the method as verifying linearity, limits of detection, limits of quantification, precision, accuracy and recovery. The established method would be suitable for the determination of nicotine, PG and glycerol content in aerosol of HTPs.

PES-30

Size-Dependent Toxicity of Polyethylene Nano- and Microplastics on the Growth of *Arabidopsis thaliana*

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Polyethylene microplastics (PE-MPs), derived from the chemical degradation of agricultural mulching films, have emerged as significant pollutants in soil ecosystems. These particles exhibit increased toxicity to organisms as their size decreases to the nanoscale. However, compared to other plastics types, the environmental fate and phytotoxic effects of PE-MPs remain understudied. This study assessed the physiological and toxicological responses of *Arabidopsis thaliana* to polyethylene nano- and microplastics exposure by measuring biomass, germination index (GI), chlorophyll fluorescence imaging parameters (Fv/Fm_Lss, Rfd_Lss), leaf spectral reflectance indices (NDVI, MCARI1), and chlorophyll content. In concentration-dependent experiments (0, 500, 1000 mg/kg) using MS solid medium, no significant changes were observed in Fv/Fm_Lss, Rfd_Lss, indicating that PE-MPs did not directly affect photosynthetic performance or biomass accumulation. In contrast, soil-based experiments with different particle sizes (0.3, 10, 100, 1000 μm) revealed significant decreases in chlorophyll-related indices (NDVI, MCARI1), with the 100 μm treatment group showing a 31% reduction in dry weight compared to the 0.3 μm group. These results suggest that indirect factors — such as alternation in soil physicochemical properties mediated by soil–plastic interactions — can influence plant growth. Our findings provide experimental evidence of PE-MP impacts on plant growth under realistic soil conditions and offer baseline data for ecological risk assessment of residual PE-MPs in agricultural soil.

PES-31

Investigation of Pesticide Residues in Soil from Facility Cultivation Areas in Gyeongsangnam-do

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Pesticides are major agricultural materials used to improve farm productivity through pest control during crop cultivation. Pesticides used in agricultural environments can leak into non-sprayed areas due to natural factors such as scattering and rainfall and artificial factors such as drainage, thereby contaminating the surrounding environment. Pesticides remaining in soil in the surrounding environment can cause unintentional contamination by remaining in crops through absorption and transfer processes. Therefore, soil safety management are necessary through investigation of pesticide residues in farmland and surrounding environments. This study investigated the residues in facility cultivation areas at 71 locations in Gyeongsangnam-do and investigated pesticides used during cultivation. The soil samples were analyzed using the QuEChERS EN method, and the dried soil was moistened, extracted with acetonitrile, filtered, and then analyzed by instrumental LC-MS/MS. The analysis results showed that 141 pesticides, including acetamiprid, were detected. The main crops were strawberries, watermelons, peppers, and lettuce. Organophosphates, benzoylureas, and neonicotinoids were mainly investigated as insecticides, and Triazoles, Pyrazole-4-carboxamides, and Imidazoles were frequently detected as fungicides.

PES-32

Residue Characteristics of Dinotefuran and Methoxyfenozide in Mulberry

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This study was conducted to investigate the residue characteristics of the insecticides dinotefuran and methoxyfenozide in mulberry fruit and to provide fundamental data for establishing pre-harvest residue limits (PHRL). In a field trial, both pesticides were applied twice at 7-day intervals according to the recommended safe use guidelines. Mulberry samples were collected at 0 (within 2 hours), 1, 2, 3, 5, 7, 10, and 14 days after the final application. The collected samples were analyzed using the QuEChERS method followed by LC-MS/MS. The limit of quantitaion (LOQ) for both dinotefuran and methoxyfenozide in mulberry was 0.01 mg/kg. The recovery rates of dinotefuran were 93.0-102.7% at the LOQ (0.01 mg/kg), 82.6-88.8% at 10×LOQ (0.1mg/kg), and 103.4-106.7% at the MRL (1.0 mg/kg). For methoxyfenozide, recoveries were 86.7-90.7%, 91.0-94.3%, and 70.7-72.4% at the LOQ, 10×LOQ, and MRL (1.5 mg/kg), respectively, confirming the reliability of the analytical method. The dissipation half-lives in mulberry were 8.8-11.3 days for dinotefuran and 6.3-7.2 days for methoxyfenozide. Residue levels at 10days before harvest (PHRL 10) were all below 2.29 mg/kg. These results provide scientific evidence for pesticide safety management and the establishment of PHRL in mulberry production.

PES-33

Monitoring of Pesticide Residue on Greenhouse Soil in Jeonnam Province

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Pesticides are one of the important agricultural materials indispensable to modern agriculture because they prevent yield reduction through pest control and have a great effect on reducing labor and production costs. Pesticides treated in agricultural ecosystems are adsorbed, desorbed, and decomposed by soil organic matter, clay minerals, rainfall, and microorganisms, but their residual properties differ greatly depending on their chemical structure, composition, and physicochemical properties. In particular, when crops are grown in a closed greenhouse, the decomposition caused by light or rainfall is slower than that of often field cultivation, so management is important to prevent unintentional contamination of pesticides remaining in the greenhouse soil. Therefore, continuous environmental monitoring of pesticides in greenhouse soil is necessary for the production of safe agricultural products through the management of pesticides remaining in the agricultural environment. The collected samples were shaded to prevent photolysis, and the shaded samples were moistened with distilled water, extracted using acetonitrile, and then subjected to liquid chromatography mass spectrometry(LC/MS/MS) and gas chromatography mass spectrometry(GC/MS/MS) was used for quantitative and qualitative analysis. As a result of the analysis, the most frequently detected pesticides in greenhouse soil in 2020 were chlorantraniliprole(57 smaples) > boscalid(45) > flubendiamide(37) > imidacloprid(33) > tetraconazole(31), and in 2024 were In-EQW78(62) > chlorantraniliprole(58) > flubendiamide(52) > MNG(45) > boscalid(40).

PES-34

Optimization of Shrimp Shell-Derived Biochar Production for Agricultural Utilization

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Over the past decade, approximately 1.09 million tons of fishery by-products have been generated annually in South Korea, but only about 19.5% are recycled. Fishery by-products have low recycling rates due to their high salt and moisture content. Among them, shrimp shells are rich in valuable components such as chitin, nitrogen, phosphorus, and calcium, suggesting that shrimp shell-derived biochar may have high agricultural value. This study aimed to establish a production method for shrimp shell-derived biochar and evaluate its agricultural potential. The pyrolysis conditions for producing shrimp shell-derived biochar were set at 350, 400, 450, 550, and 650°C for 2 hours. As the pyrolysis temperature increased during the production of shrimp shell-derived biochar, the specific surface area and the contents of phosphorus and calcium increased, while the contents of carbon, hydrogen, nitrogen, and oxygen decreased. Shrimp shell-derived biochar produced at higher temperatures had a decreased H/C ratio, which improved carbon stability. However, at pyrolysis temperatures above 450°C, carbon loss increased, reducing the carbon sequestration effect of the biochar. In a cabbage cultivation test, application of shrimp shell-derived biochar increased yield by 77% compared to conventional treatment. Based on these results, the optimal pyrolysis condition was identified as 400°C for 2 hours. Shrimp shell-derived biochar has strong potential for agricultural utilization due to improving crop yield and its carbon sequestration effect.

PES-35

Screening of Endophytic Bacteria Isolated from Wheat to Control Streptomycin-Resistant phytopathogens

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The emergence of antibiotic-resistant phytopathogens is largely attributed to the repeated applications of antibiotics. In Korea, streptomycin has been extensively used to control bacterial pathogens in citrus orchards and Kimchi cabbage fields, resulting in the emergence of streptomycin-resistant phytopathogens such as *Xanthomonas citri* subsp. *citri* (Xcc) and *Pectobacterium carotovorum* subsp. *carotovorum* (Pcc), which cause citrus canker and bacterial soft rot, respectively. Citrus canker significantly reduces fruit quality and yield and poses a serious risk to citrus exports due to strict international quarantine regulations. Bacterial soft rot is a major issue in Kimchi cabbage production during the summer in Korea, and its severity is increasing, particularly with the onset of high temperatures and humid conditions in early summer. In our laboratory, we are actively isolating endophytic bacteria from wheat ears obtained from Korea's wheat core collections and evaluating their antibacterial activity against Xcc and Pcc. Among various antagonistic endophytic strains, we are specifically screening those with the potential to control streptomycin-resistant Xcc and Pcc. Previously isolated endophytes from our lab, such as *Bacillus subtilis*, *B. velezensis*, and *Streptomyces* sp., have shown promise, and we expect that these newly isolated strains will also serve as valuable resources for controlling streptomycin-resistant pathogens. These beneficial endophytes can be utilized directly in organic agriculture or used for the development of bioactive compounds to combat phytopathogens effectively.

PES-36

Biochar production using ecosystem-disrupting plants and its heavy metal adsorption

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This study produced biochar (GRB) using Giant ragweed (***Ambrosia trifida* L.**), a plant known as an ecosystem-disrupting plant, and evaluated its heavy metal adsorption characteristics. The pH and EC of GRB tended to increase as the pyrolysis temperature increased, and the carbon content increased in a temperature-dominant manner. On the other hand, the contents of sulfur, nitrogen, oxygen, and hydrogen in GRB tended to decrease as the pyrolysis temperature increased due to the loss of moisture and volatile organic components. The adsorption amount of Pb by GRB according to the pyrolysis temperature was investigated, and the highest adsorption amount was observed at GRB650, and these results were well described by the Langmuir isotherm and second order kinetic models. In addition, the adsorption characteristics of Pb by GRB showed significant differences depending on environmental changes (pH, dose, temperature). The adsorption of Pb by GRB is judged to be mostly due to adsorption by the outer boundary of the surface and some internal diffusion, and it is considered that this adsorption is mainly dominated by the cations and functional groups present on the surface. In conclusion, it is expected that the use of maple leaf ragweed, an ecosystem-disrupting plant, to manufacture biochar is an effective method for environmental conservation and waste resource recycling.

PES-37

Adsorption characteristics of methylene blue by rice husk extracted Si

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This study was conducted to extract silica using NaOH for efficient resource utilization of rice husk, and to evaluate the adsorption characteristics of methylene blue (MB) using the remaining residue (Si-RH). To establish the optimal conditions for extracting Si from rice husk, experiments were conducted under different conditions of rice husk particle size, NaOH concentration, mixing ratio of rice husk and NaOH, reaction time (w/v), and reaction temperature. As a result, the optimal conditions for extracting silica from rice husk were mixing 0.6 M NaOH (1:10 ratio) with rice husk (> 2 mm) and reacting at 70℃ for 2 h. The adsorption characteristics of MB by RH and Si-RH were better in accordance with the Langmuir and Pseudo-second orders, indicating that the adsorption of MB by Si-RH is a chemical adsorption. The maximum adsorption amounts of MB by RH and Si-RH derived from the Langmuir model were 34.36 and 99.01 mg/g, respectively, indicating that the adsorption efficiency of MB by Si-RH was about three times higher than that of RH. It was found that the adsorption of MB by Si-RH was greatly affected by environmental changes such as reaction time, pH, and dosage. Therefore, it is believed that when applying Si-RH to actual wastewater, the properties and environmental changes in the wastewater should be given priority.

PES-38

Agro-Environmental role of biochar derived from spent coffee ground in pepper cultivation

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This study produced biochar (SCGB) using a pyrolysis method (350-650℃) for efficient resource utilization of spent coffee grounds (SCG) and evaluated their physicochemical properties and agricultural environmental applicability. The carbon content in SCGB increased depending on the pyrolysis temperature, whereas hydrogen and oxygen tended to decrease. In this study, the stability of carbon was performed through various physicochemical methods (water, H_2O_2 and TGA), and although there were slight differences depending on each method, SCGBs produced at high temperatures generally showed high carbon stability. The carbon content and stability in SCGB were higher than those in other previously reported biomass-based biochars, which is believed to be because volatile and water-soluble carbon were preferentially removed during the roasting and extraction processes. Through various functional evaluations, the optimal thermal decomposition temperature for agricultural utilization of SCGB was selected as 350℃, and different levels were applied to pepper cultivation soil. Application of SCGB350 enhanced crop growth and reduced CO_2 emissions compared to the untreated control. Furthermore, when co-applied with NPK fertilizer, SCGB350 not only further improved crop growth compared to NPK alone, but also contributed to reductions in NH_3-N and CO_2 emissions. In conclusion, the application of SCGB to agricultural land is considered an effective treatment technology that can sequester carbon, reduce greenhouse gas emissions, and improve soil properties while contributing to environmental control.

Poster Presentation

PES-39

Early Multi-Omics Insights into *Fusarium proliferatum*-Induced Dysbiosis in Soybean: Microbiome and Metabolome Rewiring Under Pathogen Stress

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Soybean (*Glycine max*) productivity is severely compromised by the fungal pathogen *Fusarium proliferatum*, causing considerable agricultural losses globally. This study aims to elucidate the alterations induced by *F. proliferatum* infection on soybean phytobiome structure and metabolomic profiles. Soybean plants inoculated with the pathogen are being systematically analyzed at early time points (3 and 7 days post-inoculation) using high-throughput amplicon sequencing (16S and ITS) and targeted metabolomics (LC-MS/MS). Preliminary observations suggest pathogen-induced dysbiosis in microbial communities across rhizosphere, phyllosphere, and endosphere compartments. Concurrently, early shifts in metabolomic profiles indicate altered pathways associated with plant defense and stress responses. Key biomarkers indicative of infection-driven microbiome disruption are being identified, supporting the hypothesis of induced systemic resistance (ISR) activation. This ongoing multi-omics investigation aims to advance our understanding of host-pathogen interactions in soybean and provide a foundation for future biocontrol strategies.

PES-40

Effects of Planting Density on Head Rice Yield under Delayed Transplanting in the Central Plain Region of Korea

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In the Central Plain region, the transplanting period has shifted to early–late June, approximately 10–21 days later than previous guidelines. This study aimed to identify the optimal planting density that can compensate for the shortened growth duration caused by delayed transplanting and maximize head rice yield. Rice yield showed a slight decrease under the delayed transplanting date. However, the head rice ratio significantly increased to 92.8%, compared to 80.9% under the conventional date ($p < 0.05$), resulting in no significant difference in head rice yield between the two schedules. In 2023, the highest rice yield and head rice yield were observed at a spacing of 30×14 cm (80 hills per 3.3 m^2) with 5 seedlings per hill ($p < 0.001$). In 2024, the highest rice yield occurred at 30×12 cm (90 hills) with 3 seedlings, while the head rice ratio was higher at 30×18 cm (60 hills) with 3–5 seedlings. A negative correlation was found between rice yield and head rice ratio. In 2024, under high-temperature conditions, the head rice ratio slightly declined (88.0–89.1%) at the densest spacing. Dense planting may therefore be unsuitable for producing high-quality rice under heat stress. Further multi-year studies are required to validate these results.

PES-41

Effect of Phosphogypsum Derived Byproduct Hydrated Lime compost on Crop Safety and Soil Properties

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This study evaluated the crop safety and soil chemical properties of compost formulated by incorporating BHL into manure compost (referred to as byproduct hydrated lime compost; BHLC). A pot experiment was conducted with lettuce (*Lactuca sativa* L.) under five treatments: no fertilization (NF), inorganic fertilizer only (NPK; $N-P_2O_5-K_2O=7.0-3.0-3.6$ kg $10a^{-1}$), inorganic fertilizer + manure compost (MC), inorganic fertilizer + phosphogypsum compost (PGC), and inorganic fertilizer + BHLC(BHLC). Lettuce growth and yield were significantly improved in all compost treatments (MC, PGC, BHLC) compared to NF and NPK, with the BHLC treatment showing the highest fresh weight (148 g $plant^{-1}$) and yield (4,878 kg $10a^{-1}$). Soil analysis revealed that BHLC notably increased soil pH, organic matter, and exchangeable cations (Ca and Mg) compared to other treatments. These results demonstrate that BHLC can effectively supply calcium essential for crop growth and enhance soil quality, suggesting its potential as an eco-friendly alternative to limestone. Furthermore, recycling industrial byproducts such as phosphogypsum may contribute to resource-circulating agriculture and greenhouse gas mitigation. Further studies are warranted under diverse crop species and cultivation conditions.

PES-42

Soil Texture Prediction Using Mid-Infrared Spectroscopy: Model Development and Evaluation

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Soil texture affects crop growth and nutrient mobility, but conventional methods for its measurement are time-consuming, require skilled labor, and are also expensive. Therefore, the study objective was to develop and evaluate a rapid and efficient model for predicting soil texture (sand, silt, and clay) using Mid-infrared spectroscopy (MIRS) assisted cutting-edge technology. For this study, 1,167 topsoil samples were collected from various regions across South Korea. Reference texture data were obtained using the standard hydrometer method, and MIR spectra were acquired for the same samples within the range of 4000-600 cm-1. Spectral data were pre-processed using baseline correction, first derivatives, and standard normal variate (SNV) transformation. Predictive models were developed using partial least squares regression (PLSR), random forest, Cubist, and memory-based learning (MLB) algorithms, and evaluated through 15-fold cross-validation using R^2, RMSE, and concordance metrics.Among the tested models, the MLB-based model for clay prediction achieved relatively high accuracy, with $R^2 = 0.66$, RMSE = 3.8, and concordance = 0.81. Models for silt and sand also showed promising results, each with an R^2 of 0.73. In contrast, the random forest-assisted model exhibited lower accuracy with R^2 values of 0.66 (sand), 0.60 (silt), and 0.56 (clay), respectively. This study demonstrates that MIR spectroscopy has the potential to serve as a rapid and scalable alternative to conventional methods for analyzing soil texture.

PES-43

Chemical and Heavy Metal Variability in Greenhouse Soils of Jeonnam Province

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Since 2000, a periodic soil monitoring survey has been conducted every four years to assess the chemical properties of greenhousse soils. In 2024, the soil pH of greenhouse soils was 6.4, which is within the recommended optimal ragne. The organic matter content in the topsoil was 39 g kg-1, which is higher than the recommended range. However, 18.3% of the surveyed sites had levels below the optimal range, while 52.8% exceeded it, indicating a large disparity between dificient and excessive levels. Soil pH showed a strong positive correlation with exchangeable calcium, magnesium, and nitrate nitrogen. Electrical conductivity (EC) was negatively correlated with pH, but positively correlated with exchangeable cations and nitrate nitrogen. Soil heavy metals such as cadmium, copper, and zinc showed strong correlations with soil organic matter, available phosphorus, potassium, and calcium. Copper and zinc, which have been pointed out as potential issues in some livestock manure composts, were analyzed at 30.8 mg kg-1 and 127.2 mg kg-1, respectively. Although these levels do not exceed the soil contamination concern standards, they are relatively higher than the heavy metal contents typically found in paddy fields, upland soils, and orchards. Therefore, for greenhouse cultivation areas, it tis deemed necessary to implement management policies to ensure safety-such as promoting the use of high-quality compost-for the health maintenance of soil.

PES-44

Establishment of Pre-Harvest Residue Limits (PHRLs) of Novaluron in *Amaranthus mangostanus* L.

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This study aimed to investigate the residue characteristics of the insecticide Novaluron in amaranth (Amaranthus lividus) by monitoring the residue dissipation patterns after the final pesticide application and to calculate the biological half-life, providing essential data for establishing Pre-Harvest Residue Limits (PHRLs). Field trials were conducted at three separate greenhouse locations: Yangpyeong-gun, Gyeonggi-do (Field 1 and Field 2), and Chilgok-gun, Gyeongsangbuk-do (Field 3). Novaluron was applied twice at 7-day intervals following standard pesticide safety guidelines. Samples were collected on days 0, 1, 2, 3, 5, 7, and 10 after the final application. Residue analysis of Novaluron in amaranth was performed using the multi-residue method (Method 2) established by the Ministry of Food and Drug Safety. The method limit of quantification (MLOQ) was 0.01 mg/kg. Recovery tests were conducted at MLOQ, 10×MLOQ, and maximum residue limit (MRL) levels, and recovery rates ranged from 81.7 – 90.8%, 87.1 – 97.3%, and 70.9 – 94.6%, respectively. The biological half-lives of Novaluron in amaranth were calculated as 6.6 days (Field 1), 8.4 days (Field 2), and 6.1 days (Field 3). These results provide a scientific basis for setting appropriate PHRLs and can contribute to improving the safety management of pesticide residues in leafy vegetables like amaranth.

PES-45

Differential Phytotoxicity of PPO-Inhibiting Herbicides in Monocotyledonous and Dicotyledonous Plants

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Herbicide application is essential for weed control and maintaining agricultural productivity. Among various herbicidal modes of action, inhibition of protoporphyrinogen oxidase (PPO) is widely used due to its rapid phytotoxic effects and broad-spectrum activity. This study investigated the morphological responses of representative monocot and dicot plants to four widely used PPO-inhibiting herbicides: sulfentrazone, oxyfluorfen, oxadiazon, and flumioxazin. Each herbicide was individually applied to both monocot and dicot plant groups under controlled environmental conditions. The experiment was conducted in triplicate, with 15 individual plants per replicate. Plants were grown under a photoperiod of 12 hours light and 12 hours dark to simulate standard growth conditions. Visible symptoms, including necrosis and growth inhibition were recorded and compared across treatments. The results revealed distinct differences in herbicidal injury between monocots and dicots, suggesting species-dependent sensitivity and potential for selective application.

PES-46

Sustainable Soil Management Strategy to Enhance Net Ecosystem Carbon Budget and Sequestration by Optimal Woody Biochar Application in Red Pepper Cropping Systems: Three-year Field Experiment

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Woody biochar (WB), as a low carbon (C)-emitting organic matter, plays a crucial role in enhancing soil C sequestration. However, there is a lack of research on optimal WB application levels to improve the net ecosystem C budget (NECB) and soil C sequestration at different soil depth, particularly in red pepper cropping systems. Therefore, this study was focused on suggesting a reasonable WB application level based on the NECB and C sequestration at three different soil depth under the different WB application levels (0, 2.5, 5, and 10 Mg d.w ha^{-1}) for 3 years. Our results showed that C input and C output from respired C losses (CO_2 and CH_4) increased with increasing WB application levels. As a result, the highest NECB was observed in the WB10, followed by WB5, WB2.5, and WB0. To maintain a positive NECB, the optimal WB application level was estimated to be 7.2-11.4 Mg d.w ha^{-1}. At three soil depth, the annual C sequestration increased with WB application level, following the order WB10 (5.08 Mg C ha^{-1}) > WB5 (3.42) > WB2.5 (2.29). The C sequestration at the optimal WB application levels based on NECB was estimated approximately 4.3-5.2 Mg C ha^{-1} year^{-1}. Conclusively, WB application could be a sustainable strategy to mitigate climate change by increasing C sequestration and improving NECB.

Poster Presentation

PES-47

Regional and strain-level distribution of nitrogen-fixing and N_2O-reducing Bradyrhizobium in South Korea

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Agricultural activities significantly contribute to atmospheric nitrous oxide (N_2O), a potent greenhouse gas. This study examined the strain-level diversity and regional distribution of soybean-associated *Bradyrhizobium* species that carry the *nosZ* gene, which encodes nitrous oxide reductase —a key enzyme in N_2O reduction. Among 227 native *Bradyrhizobium* strains isolated from soybean nodules across South Korea, 162 possessed the *nosZ* gene, indicating potential for mitigating N_2O emissions in agricultural soils. *Bradyrhizobium diazoefficiens*, the most prevalent species, exhibited a high proportion of *nosZ*-positive strains, suggesting a widespread denitrification capacity. In contrast, *Bradyrhizobium elkanii*, mainly found in the southwest, largely lacked the gene, indicating possible regional N_2O emission hotspots. Notably, the *nosZ* gene varied even within species, highlighting the importance of strain-level identification. These findings underscore the potential for developing targeted microbial inoculants to enhance nitrogen fixation while reducing greenhouse gas emissions.

PES-48

Insecticide resistance of *Myzus persicae* (Hemiptera: Aphididae) populations collected from kimchi cabbage fields in South Korea

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Myzus persicae (Hemiptera: Aphididae) is one of the most significant agricultural pests worldwide. In this study, we assessed the resistance of *M. persicae* to eight insecticides using aphid populations collected from kimchi cabbage fields in 15 different regions of South Korea between 2022 and 2024. A laboratory-reared population was used as a susceptible reference to estimate the relative resistance levels of the field populations. Insecticide resistance was evaluated using a standard leaf-dip bioassay, assessing lethality at the recommended application rate and calculating the resistance ratio (RR) (Lethal concentration 50 (LC_{50}) of the field population / LC_{50} of the laboratory population). Overall, deltamethrin was the least effective insecticide, with lethality below 35% across all field populations. In contrast, sulfoxaflor, spirotetramat, and thiacloprid exhibited high efficacy, with mean lethality exceeding 80%. However, sulfoxaflor also yielded a mean RR of 7.7, with four field populations exhibiting RRs greater than 10, indicating a concerning level of resistance development. Despite their high efficacy, the elevated resistance levels observed for sulfoxaflor underscore the need for cautious and judicious application. Additionally, imidacloprid and flonicamid demonstrated the greatest variability in field efficacy, with more than a 50% difference in lethality observed among populations, highlighting the importance of extensive, area-wide monitoring of insecticide resistance in *M. persicae*. Our study provides baseline information for developing an effective aphid management program.

PES-49

Effect of Liquid Fertilizer from Rendered Livestock Carcass Residues on Tomato Growth and Productivity

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Due to climate change, the global average temperature has been rising, and the increasing frequency and duration of heatwaves and tropical nights have led to higher mortality rates in the livestock industry. Currently, rendering disposal is being proposed as a animal carcass disposal method that causes relatively less environmental harm. The residues generated from rendering processes are high in protein content and were hydrolyzed into amino acids using protease to develop an amino acid-based liquid fertilizer. This study was conducted to evaluate the effectiveness of the developed amino acid liquid fertilizer on improving tomato growth and fruit sugar content. The experimental treatments included a control group with no treatment (CN), inorganic fertilizer (IF), commercial amino acid liquid fertilizer (CMLF), and amino acid liquid fertilizer derived from rendering residue (RLF). As a result, the fresh weights of tomato plant parts ranged from 31.1 ~ 57.1, 116 ~ 204, and 158 ~ 172 g plant^{-1} for leaves, stems, fruits. respectively. Fruit perimeter and sugar content ranged from 22.1 ~ 25.1 cm plant-1 and 6.45 ~ 7.37 ˚Brix, respectively. In conclusion, the amino acid liquid fertilizer produced from rendered residues demonstrated positive effects on tomato growth and sugar content. Based on its foundation in resource recycling and biological processing, it shows strong potential as an eco-friendly organic input for sustainable agriculture.

PES-50

Development of a Microalgae-Based Carbon Capture System for Cement Industry Flue Gas Mitigation

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Despite its key role in modern civilization, the cement industry is a major source of air pollution and greenhouse gas (GHG) emissions. Thus, various physical, chemical, and biological approaches are being explored to control flue gas emissions. Microalgae represent one of the most productive biological models for converting light and CO_2 into chemical energy and are used for capturing inorganic carbon into biomass. In this study, four microalgal strains, *Chlamydomonas* (CH), *Chlorella sorokiniana* (CS), *Chlorella vulgaris* (CV), and *Desmodesmous multivariabilis* (DM) were used. A bioconversion process was performed in a photobioreactor (PBR) designed to increase CO_2 retention time. This bioconversion study is based on the algal carbon capture (CC) system by calculating the mass balance between CO_2 and algal biomass in the PBR. Final biomass concentrations were 2.53 g/L (DM), 2.4 g/L (CH), 1.85 g/L (CV), and 1.36 g/L (CS). The CO_2 reduction efficiencies related to the supplied volume were 69% for CH, 53% for CV, 52% for CS, and 46% for DM and specific CO_2 reduction per unit of algal biomass was 0.0075 g/g for CS, 0.0056 g/g for CV, 0.00056 g/g for CH, and 0.00036 g/g for DM. CS exhibited the highest conversion efficiency. An algal mixture composed of four strains at different ratios, determined by their individual CO_2 consumption rate, was adopted for advanced CCUS applications.

Poster Presentation

PES-51

Organic Matter Recycling Enhances Soil Carbon Sequestration: A Comparative Analysis of Paddy and Upland Agroecosystems

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Winter cover crops are widely promoted for enhancing soil organic carbon (SOC) storage, yet their effectiveness can differ by field conditions. This study investigated how recycling winter cover crops affects SOC dynamics in a rice paddy and an adjacent upland maize field in South Korea. Two fertilization regimes, chemical inputs and organic amendments from barley and hairy vetch, were applied in both fields. Cover crops were grown during the winter fallow period and incorporated into the soil before planting the main summer crop. Despite similar grain yields across treatments, organic amendments led to increased biomass production in both systems. In paddy fields, anaerobic conditions suppressed decomposition, supporting SOC accumulation. Conversely, in upland fields, the same practice stimulated microbial respiration, reducing the net carbon gain. SOC stocks increased in paddy fields with organic amendments but declined in upland fields, even with substantial organic inputs. These contrasting outcomes underscore the importance of field-specific carbon cycling processes. Our results suggest that winter cover crop recycling is effective for SOC sequestration in anaerobic paddy systems. However, in aerobic upland systems, cover crop incorporation alone may be insufficient, and complementary strategies, such as maize stover retention, may be necessary to achieve a positive carbon balance and support long-term soil sustainability.

PES-52

Yields and Film Properties of Biodegradable Mulching Films in Onion, Pepper, and Soybean Cultivation across Different Region

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This study evaluated the applicability of biodegradable (BD) mulching films (F, H, E) in onion, pepper, and soybean cultivation across Seocheon, Yeongam, and Suncheon. Crop yields showed no significant difference between BD and polyethylene (PE) films, regardless of location or crop. However, yields were lower in the no-mulching (NM) treatment. Thus, BD films did not negatively impact crop growth and are considered suitable for use. In onion fields in Seocheon and Yeongam, only the F film showed light transmittance similar to PE film; H and E films had significantly higher transmittance. In Suncheon, no significant differences were observed. In pepper fields, F and H (except E in Seocheon) had higher transmittance than PE, and all BD films in Yeongam showed higher values. In soybean fields, BD films consistently had higher transmittance than PE. Degradation scores for BD films were significantly higher than for PE, especially in pepper and soybean fields. Decomposition rates were also significantly higher in BD films for pepper and soybean (up to 33.4%), while differences were less clear in onion fields. These results suggest BD films are highly applicable for pepper and soybean cultivation.

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PES-53

Interactions between polyethylene microplastics and imidacloprid in soil

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Microplastics (MPs) and residual pesticides commonly coexist in agricultural ecosystems. However, research on their interactive effects remains limited. In this study, soil column experiments were conducted to investigate the effects of interactions between MPs and a pesticide on their mobility and persistence in soil. For the column experiments, polyethylene MPs (<125 μm) and imidacloprid (IMD) were applied to soil, and leachate was collected using water as the eluent at predetermined times. The concentration of IMD in the leachate was measured by HPLC analysis, and the weight of MPs was determined using a density gradient separation method. The presence of MPs reduced the concentration of IMD in the leachate (19.8 μg/g) compared to IMD-only treatments (30.4 μg/g). The weight of MPs in the IMD+MP treatment column leachate was 1.1 mg, which is higher than the 0.9 mg in the MP-only treatment column. This indicates complex interactions such as changes in soil pore structure and adsorption caused by the presence of MPs. This study quantitatively confirmed the influence of soil interactions between pesticides and MPs on the environmental behavior of each pollutant, showing that MPs can alter the transport characteristics of pesticides in soil, potentially changing their environmental impact. Therefore, further research on the interactions between MPs and pesticides in environments where both coexist is necessary.

PES-54

Planting Density Effects on Yield Components of Rice Varieties with Contrasting Nitrogen Response

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This study evaluated the impact of reduced nitrogen fertilization and varying planting densities on rice (Oryza sativa L.) yield and quality using two cultivars, Saeilmi and Saenuri. Saeilmi maintains stable yield under low nitrogen, while Saenuri is more sensitive. Saeilmi has a smaller grain size and panicle-oriented yield structure, whereas Saenuri shows a grain weight–oriented structure, suggesting differing responses to planting density. Field trials were conducted under standard (NPK = 9-4.5-5.7 kg/10a) and reduced (NPK = 7-3-3 kg/10a) fertilization. Under the reduced regime, combinations of planting densities (70, 80, 90 hills/3.3 m^2) and seedling numbers (3, 5, 7 per hill) were tested, with 80 hills and 5 seedlings as control. Dense planting (90 hills) increased panicle number and filled grains, especially in Saenuri, improving yield without affecting grain quality traits such as head rice ratio and protein content. These results suggest that increased planting density under reduced nitrogen input can compensate for yield loss and sustain rice quality, particularly in cultivars with larger grain size and grain weight–driven yield traits.

Poster Presentation

PES-55

Interactions Between Aggregate-Associated Carbon Storage and Soil Biological and Chemical Properties in Organic Upland Fields

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Soil organic carbon (SOC) stored within aggregates plays a key role in maintaining soil health, especially under organic farming practices where synthetic inputs are restricted. This study aimed to assess carbon storage across aggregate size classes and its interactions with soil biological and chemical indicators in organic upland fields. Soils from 25 organic fields in Jeonnam were analyzed for bulk properties including pH, total carbon, bulk density, and carbon stocks. Aggregate were fractionated into large macroaggregates (>2 mm), small macroaggregates (250–2000 μm), microaggregates (53–250 μm), and silt + clay (<53 μm) using the wet sieving method. Carbon content was measured for each fraction, with Intra-POM and IntramM-POM showing the highest carbon storage. Regression analyses revealed strong positive correlations between carbon in IntramM-POM and bulk soil C stocks ($R^2 = 0.71$), WHC ($R^2 = 0.09$), microbial biomass carbon ($R^2 = 0.18$), and respiration. These findings indicate that aggregate-associated carbon, particularly that stored within microaggregates, plays a crucial role in soil function. This form of carbon was strongly positively correlated with key chemical and biological indicators. This study provides empirical evidence for the role of intra-aggregate carbon as a key determinant of soil chemical and biological quality, thereby contributing to improved strategies for soil carbon sequestration and health assessment in organic agriculture.

PES-56

Effect of Long-term Fertilization on Intra- and Inter- Particular Carbon in Upland Soils

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Soil organic carbon (SOC) stock changes by agricultural practice of fertilization under intensive crop cultivation which affects on soil productivity and nutrient cycling in maintaining soil quality. This study was to evaluate the effect of long-term fertilization on carbon stock associated with aggregate size. We selected 4 treatment(control, NPK, Compost, NPK+Compost) in long-term fertilized experimental field after corn harvest. Aggregate size were fractionated into large macroaggregates (>2 mm), small macroaggregates (250–2000 μm), microaggregates (53–250 μm), and silt + clay (<53 μm) using the wet sieving method. Expecially, Carbon stock associated with aggregate size compared the Intra-mM POM and Inter-POM between long-term fertilized treatments. Continuous application of soil compost and mixture of NPK increased soil organic carbon, which was mean weight diameter(MWD) improved in upland soil with corn cultivation. Macro-and micro-aggregate size was higher at the upland soil applied with compost or NPK plus compost than NPK application. Inter-and intra-particular C stock in micro-and micro-aggregate was highest at upland soil applied with compost, which ranged from 1.40-1.77 times compared with NPK. However, NPK plus compost application was lower 8.3-27.6% than sole compost application. These aggregate formation with continously compost application could contribute the SOC stock by storing carbon associated with intra-and inter-aggregate, which maight improve for sustainable cultivation and soil quality development in uplands.

PES-57

Optimization of Soil-Based QuEChERS Extraction and Comparative Assessment of Analytical Efficiency by Physicochemical Characteristics of Pesticides

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This study aimed to optimize the QuEChERS (Quick, Easy, Cheap, Effective, Rugged, and Safe) extraction method specifically tailored for pesticide residue analysis in soil samples and to establish standardized soil sample criteria for enhanced analytical reliability. Initially, twelve QuEChERS extraction reagent combinations were evaluated using TOPSIS (Technique for Order of Preference by Similarity to Ideal Solution) analysis, resulting in the selection of an optimal condition ($MgSO_4$ 6 g + calcium acetate 1.5 g) that effectively minimized soil particle interference and improved purification efficiency. The analytical performance under varying soil physicochemical conditions (pH, organic matter, clay content) was systematically assessed, revealing significant impacts primarily in soils with high organic matter (≥3%) and clay content (~30%). Consequently, these challenging conditions were established as representative worst-case scenarios for method validation. Method validation conducted across three laboratories demonstrated high accuracy and reproducibility, with recovery rates within acceptable limits (70–120%) for 98% of 489 pesticides tested and relative standard deviations (RSD) below 20% for 95% of compounds.

PES-58

Risk Assessment and Management of Soil Pesticides Using Physicochemical Properties and Statistical Analysis

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Pesticides have greatly improved agricultural productivity but pose environmental risks due to their toxicity, particularly in soils where safety management is lacking. This study aimed to enhance pesticide management at national and regional levels using the physicochemical properties of selected pesticides, field monitoring data, and statistical tools. Using the Pesticide Properties Database (PPDB), data on 10 properties for 116 pesticides were collected. Principal Component Analysis (PCA) was used to identify high-risk pesticides, while Cluster Analysis (CA) grouped pesticide concentrations from 300 soil samples by similarity. The Risk Quotient (RQ)—calculated as the ratio of detected concentration to the predicted no-effect concentration—was used to recommend lower-risk alternatives. PCA explained 78.2% of variance using three principal components, identifying Boscalid, Difenoconazole, Fluquinconazole, and Tebuconazole as high-risk pesticides. CA categorized the sites into five levels of environmental concern: very high (3 sites), high (11), intermediate (47), low (78), and very low (161). Replacing Fluquinconazole with Azoxystrobin at a high-risk site (Site 27) led to a 42% drop in RQ over five years. Despite generally low pesticide levels, apple and pear farms showed higher residues. This study underscores the value of identifying and replacing high-risk pesticides to reduce environmental risks while maintaining productivity, offering a practical system for pesticide monitoring and soil safety management.

PES-59

Analytical Method for Dichlobenil and 2,6-Dichlorobenzamide Residues in Beef, Milk, and Fat Using GC-MS/MS

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Dichlobenil is a broad-spectrum herbicide used to control unwanted weeds in garden beds, orchards, and berry fields. It is considered one of the more toxic substances, with significant toxicity reported in animals. Additionally, dichlobenil is not easily degraded in soil and has a long half-life, making it important for monitoring its persistence in the environment. Here, we present a fast and simple analytical method using the QuEChERS technique combined with gas chromatography–tandem mass spectrometry (GC-MS/MS) for the analysis of dichlobenil and its major metabolite, 2,6-dichlorobenzamide. The multiple reaction monitoring (MRM) transitions and GC oven program were carefully optimized to achieve the best peak sensitivity. To ensure the robustness and efficiency of the analytical method, various clean-up procedures using dispersive solid-phase extraction were compared following acetonitrile extraction. Matrix effects were evaluated across different sample types, and the potential of analyte protectants (APs) as an alternative to matrix-matched calibration for compensating matrix effects in GC analysis was assessed. Results from recovery tests at three fortification levels demonstrated that the optimized method is suitable for the determination of dichlobenil and its metabolite in livestock-derived samples.

PES-60

Development of a Sweetness Booster for Fruits with Antimicrobial Function

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“Sugar Pump,” a fast-acting sweetness booster with functional sugar as its main ingredient, was launched in 2024 as a new plant biostimulant for foliar spray and has shown excellent effects in increasing the sugar content of various crops such as strawberries, grapes, and plums. However, when applied to strawberries or grapes several times in a raw, it was often observed that the sweetness boosting effect was not as expected. One of the causes was thought to be the loss of sugar due to the rapid proliferation of microorganisms living on the leaves. This study was conducted to develop a sweetness booster that can suppress the growth of microorganisms living on the leaf surface when SugarPump is continuously applied. Three species of microorganisms, including *Sphingomonas zeae*, and 3 species of microorganisms, including *Monosporozyma servazzi*, were identified as dominant microorganisms in strawberry leaves and grape leaves, respectively. By screening antimicrobial materials using the paper disc diffusion method targeting this strain, transition metal salts and cationic surfactants were selected as additive candidates for antimicrobial agent. Among them, the component showing the highest inhibitory activity was added to SugarPump and treated on strawberry leaves. The amount of sugar residue on the leaf surface was higher than that of the control group, suggesting the possibility of developing a sweetness booster with antimicrobial function.

PES-61

Temporal Analysis of Soil Physical Properties in Greenhouse Cultivation Areas of Jeollanam-do, South Korea (2016–2024)

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Scientific monitoring of soil conditions is essential for stable crop yields and sustainable agriculture. Among soil quality indicators, physical properties are key, as they influence water retention, nutrient supply, and fertility. This study investigated temporal trends in soil physical properties across 40 greenhouse cultivation sites in Jeollanam-do, South Korea, based on monitoring data collected in 2016, 2020, and 2024. The findings serve as baseline information for the sustainable management of protected agricultural systems. Key parameters assessed were topsoil depth, bulk density, porosity, soil hardness, and organic matter content. Topsoil depth increased steadily from 17.1 cm in 2016 to 22.9 cm in 2024. Subsoil hardness dropped from 18.5 mm to 12.6 mm, indicating better structure and reduced compaction. Bulk density decreased from 1.29 Mg m^{-3} in 2016 to 1.12 Mg m^{-3} in 2020, slightly rising to 1.14 Mg m^{-3} in 2024. Organic matter rose from 56.9 g kg^{-1} in 2016 to 67.0 g kg^{-1} in 2020 but declined to 47.2 g kg^{-1} in 2024, likely due to changes in organic inputs, microbial activity, and decomposition. Overall, the physical properties of soils in greenhouse cultivation areas in Jeollanam-do generally remained within recommended standards. However, consistent and targeted management, particularly concerning organic matter supplementation, is necessary to sustain soil health and productivity in the long term.

PES-62

Greenhouse-Based Residue Dissipation Pattern and Age-Specific Dietary Risk of Propamocarb and Chlorfenapyr in Pumpkin

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With increasing regulatory emphasis on food safety and consumer protection, evaluating the behavior of pesticide residues and associated dietary risks in edible crops is critical. This study assessed the dissipation patterns and residual risks of two widely used pesticides propamocarb hydrochloride 66.5% EC and chlorfenapyr 10% SC in pumpkin (*Cucurbita moschata*) under greenhouse conditions. Both pesticides were applied twice at 7-day intervals, with samples of pumpkin fruit and leaves collected at 0, 3, 5, 7, and 14 days after the final application. Residue analysis was performed using validated QuEChERS-based methods, followed by detection with LC-MS/MS or GC-MS/MS. Residues of both compounds decreased over time, with propamocarb hydrochloride 66.5% EC falling below the limit of quantification in fruit by day 14. Chlorfenapyr 10% SC remained detectable in both matrices but complied with national maximum residue limits (MRLs). A dietary risk assessment across four age groups indicated that the hazard quotients (HQs) for both compounds were well below 100%, even for elderly consumers with the highest relative intake. These findings demonstrate the low chronic dietary risk associated with these pesticides when used appropriately, supporting their safe application in pumpkin production within Korean agricultural practices.

Poster Presentation

PES-63

Sustainable Option as Shifting Transplanting Date for Reducing Net Annual Global Warming Potential during Cropping and Fallow Seasons in a Mono Rice Paddy Field

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Shifting rice transplanting dates alters meteorological conditions and flooding periods, potentially influencing rice growth and greenhouse gas emissions (GHG; CH_4, CO_2, N_2O) throughout the year. This study evaluated the effects of modulating rice transplanting dates and deciphering key factors influencing GHG emissions and productivity in a mono rice paddy field during 2023 and 2024. Two different varieties (*Sindongjin* as late maturing and *Jomyeong no.1* as early maturing) were transplanted at four dates on May 10 (Time1), May 25 as locally recommended (Time2), June 9 (Time3), and June 24 (Time4). Regardless of cultivar or year, CH_4 emissions were highest in Time1 and gradually decreased by 24-87% with delayed transplanting, likely due to shortened flooded periods and reduced cumulative soil temperatures. CH_4 was the dominant GHG during the cropping season, while CO_2 prevailed during the aerobic fallow season. Interestingly, a positive relationship was observed between CH_4 and CO_2 emissions and residual root biomass after harvest, suggesting root derived carbon contributed to both emissions and may have a legacy effect in subsequent seasons. Rice yield increased with transplanting delay, peaking at Time3, and slightly decreased at Time4, with no significant loss compared to Time2. Conclusively, shifting the rice transplanting date could be a simple and sustainable way to effectively mitigate GHG emissions without significant productivity loss in paddy field ecosystem.

PES-64

A Study on the Analysis of the Impact of Agricultural Environmental Conservation Activities on Resources in the Agricultural Environmental Conservation Program

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The Ministry of Agriculture, Food and Rural Affairs (MAFRA) has been operating the Agricultural Environment Conservation Program (AECP) since 2019 to promote regional agricultural environment management measures. This program aims to raise farmers' awareness of agricultural environmental conservation and promote the conservation and improvement of the agricultural environment. AECP's agricultural environmental conservation activities are divided into individual and collective activities. Individual activities include using slow-release fertilizers, managing water in rice paddies, removing weeds without herbicides, and applying biochar, among over 20 other activities. This study analyzed the impact of these activities on the agricultural environment when performed on farmland. The resources evaluated were water, soil, water quality, energy, and carbon, with baseline indicators for each resource quantified as water usage, soil erosion, water quality load, energy usage, soil carbon storage, and greenhouse gas emissions. Each basic indicator was converted into evaluation indicators such as water conservation, soil conservation, water quality improvement, energy conservation, and carbon neutrality. Evaluation indicators are calculated based on the difference between baseline activities and agricultural environmental conservation activities. Each evaluation indicator was presented as a single value in the Integrated Evaluation Index (IEI), considering the weight values obtained through AHP/ANP analysis. This study can be used to evaluate the sustainability of agricultural environmental conservation activities by analyzing them across various resources.

PES-65

Phosphorus Control Using Metal-Modified Biochar Under Algal Bloom Conditions

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The increasing frequency of harmful algal blooms (HABs), driven by nutrient pollution and climate change, presents major challenges for water quality management by escalating treatment costs and operational complexity. Although copper sulfate is still the most commonly used algaecide, its toxicity to non-target aquatic life and potential for bioaccumulation highlight the urgent need for more sustainable mitigation strategies. This study investigates the potential of biochar both unmodified and metal-modified as a novel approach to control HABs through nutrient reduction. Initial tests showed that unmodified biochar reduced total nitrogen by 22.6% but unexpectedly increased total phosphorus by 76.9%, an undesirable outcome given phosphorus's key role in stimulating algal growth. To improve phosphorus removal, biochar was modified with metals including copper (Cu), zinc (Zn), iron (Fe), and cobalt (Co). While control, Fe-, and Co-modified biochars led to increased phosphorus concentrations, Cu- and Zn-modified biochars at 4 g/L achieved substantial phosphorus reductions of 78.5% and 83.7%, respectively. These were accompanied by sharp decreases in chlorophyll-a levels 95.1% and 98.3% after 6 days indicating strong inhibition of algal growth. The effectiveness of Cu- and Zn-biochars is likely due to their positively charged surfaces that enhance phosphate adsorption, combined with antimicrobial properties that suppress algal proliferation. These findings support their promise as sustainable alternatives to conventional algaecides.

PES-66

Assessment of the leaching potential and residues for pesticides from soils in rainfall simulations

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Pesticides applied to crops and soil are degraded, oxidised and metabolised by various factors, and the remaining pesticides are adsorbed/desorbed by the soil or leached through the soil into groundwater. Rainfall is one of the main sources of pollution that can lead to groundwater contamination, which can have serious consequences for human health and the environment. In this study, four rainfall patterns, which differed in duration and intensity, were applied nine times successively with an interval of three to five days on each soil sample. The analysis of leachate samples from each treated rainfall, was conducted over a period of more than 30 days to monitor the effect of rainfall patterns on pesticide leaching characteristics based on soil properties. Nine pesticides with various physicochemical properties (logKow, logKoc and solubilities etc.) were examined in soils. The potential for such pesticides was assessed by analyzing depth-dependent mobility and leaching from the soil by rainfall. In the rainfall events, the duration and intensity of precipitation, along with soil textures and their respective physico-chemical properties, exerted a significant influence on the leaching potential. It is anticipated that the present study will provide as a meticulous evaluation of the phenomenon of leaching, partitioning and residuals for pesticides in soils, with particular reference to their correlation with patterns of rainfall.

PES-67

Role of Green Manure in Promoting Humification and Soil Structure Stability in Paddy Systems

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Soil organic matter (SOM) is vital for soil health, carbon (C) sequestration, and climate change mitigation. In paddy fields, anaerobic conditions reduce decomposition rates, and SOM stability depends on carbon composition. This study evaluated the effects of green manure (GM) on soil carbon quality and stability compared to conventional NPK fertilizer. GM was introduced using a mixture of barley and hairy vetch as winter cover crops, while the control received only NPK. The GM-treated soils showed increased CO_2 and CH_4 emissions but also higher mean weight diameter (MWD), indicating improved soil physical properties. GM enhanced soil aggregate formation and stability, contributing to better soil structure than NPK. Moreover, carbon concentrations in aggregates increased with GM, especially reactive carbon in microaggregates (<0.25 mm). The GM treatment also elevated humic acid and stable carbon levels, reflecting enhanced SOM stability. These results suggest that incorporating GM in paddy soil management enhances soil structure and SOM stability, offering a promising approach for improving soil quality and promoting sustainable agriculture.

PES-68

Case study: Soil Health in Organic Conversion Vineyards

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Organic farming is based on maintaining and restoring soil health without the use of chemicals. In transition vineyards, assessing the soil health is essential to track changes and guide the transition process. However, there is a lack of studies on the transition period. Therefore, this study aims to 1)identify soil health indicators for vineyards in transition to organic farming, 2) investigate the soil physical, chemical and biological properties for three transition vineyards, and 3) analyze the correlations among the characteristics. The fourteen (14) parameters were selected; bulk density, aggregate, pH, EC, organic matter, nitrogen, available P_2O_5, exchangable cations, concentration of B-glucosidase, phosphatase, dehydrogenase, urease, and soil respiration, microbial biomass carbon. The investigation was conducted in one rain-sheltered vineyard and two greenhouse vineyards, and the results showed distinct characteristics depending on the management practices, respectively. Based on soil analysis results, it is necessary to develop soil management strategies during conversion period. Correlation analysis among soil parameters revealed that bulk density and total nitrogen had the highest average correlation values. It is required to monitor the changes throughout the transition period and to determine a minimal set of key soil indicators for future assessments.

PES-69

Enhancing Biochar Stability and Nutrient Content through Co-Pyrolysis Utilizing Plant and Animal By-Products

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Recently, the pursuit of carbon neutrality and the rising demand for biochar have led to its growing use in agriculture. However, due to economic constraints, the pyrolysis temperature of biochar is often kept below the standard threshold (350 °C), resulting in low carbonization stability. To address this limitation, co-pyrolysis of plant biomass (PB) with inorganic components has been proposed to enhance the stability and nutrient content of biochar; however, implementation is limited by the scarcity of inorganic resources. Therefore, in this study, animal by-products (AB), an organic waste material, were explored as a potential substitute for inorganic components to improve the stability of biochar through co-pyrolysis with PB. AB was mixed with PB at varying ratios from 0% to 100% and pyrolyzed at 350 °C for 2 h. Physicochemical properties were analyzed using XPS, TGA, FTIR, and SEM-EDS. As AB content increased, total carbon content decreased from 64.5% to 39.1%, while inorganic nutrients (N, P, K, and Ca) increased. The O/C ratio decreased from 0.22 to 0.17, indicating enhanced carbonization stability. Furthermore, XPS spectra confirmed a higher proportion of aromatic C=C bonds, underscoring the role of aromatic structures in stabilizing carbon. Thermal stability also improved with increasing AB content. Therefore, biochar produced by co-pyrolyzing plant-based biomass with animal by-products can be an alternative to enhance carbonization stability and nutrient content.

PES-70

Carbon stability to lime (CaO) and silicate (SiO_2) amendments across soil depths under upland conditions

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In arid, acidic upland soils, amendments such as lime (CaO) and silicate (SiO_2) are frequently applied to improve soil pH and physicochemical properties. However, their effects on the stability and sequestration potential of soil organic carbon (SOC) remain poorly understood. This study aims to evaluate the effects of lime and silicate fertilizers on SOC fractions and their stability at varying soil depths. Four treatments were applied: NPK alone, NPK with lime(CaO), NPK with silicate(SiO_2), and NPK with a reduced silicate dose (0.5 SiO_2) adjusted to match the CaO input level. Soil was incubated in columns at 40% water-filled pore space (WFPS) for 70 days, with continuous CO_2 emission monitoring. After incubation, SOC fractions including water-extractable C, acid-resistant C, particulate organic C (POC), mineral-associated organic C (MAOC), and permanganate-oxidizable C (POXC) were analyzed in both surface (0–15 cm) and subsoil (15–30 cm) layers. SOC increased by 22.50% in surface soils under amendment treatments compared to NPK alone. SiO_2-treated subsoils had the lowest SOC at 33.46 mg g^{-1}. POC was highest with CaO (46.69 g kg^{-1}), whereas MAOC was lowest under SiO_2. The lability index was highest in the 0.5 SiO_2 treatment at 1.6, indicating improved SOC quality. Overall, both amendments enhance SOC stabilization, with silicate particularly promoting C lability, contributing to improved soil quality and sustainable management in upland agricultural systems.

PES-71

Differential Physiological Responses to Plastoquinone Biosynthesis-Inhibiting Herbicides with Distinct Modes of Action in *Lactuca sativa* and *Lemna minor*

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Aclonifen, pyrazolynate, and clomazone are herbicides with different target sites of the plastoquinone biosynthesis, a pathway essential for carotenoid production and electron transport in photosynthesis. Inhibition of the pathway causes chlorophyll loss, impaired energy conversion, and visible bleaching, ultimately suppressing photosynthetic function.
To evaluate phenotypic responses to these herbicides, effect concentration 50% (EC_{50}) values were determined in *Lactuca sativa* (lettuce) based on bleaching symptoms using a rating scale. Aclonifen showed minimal phytotoxicity, while pyrazolynate and clomazone caused a strong bleaching symptom. EC_{50} values were 7.23 mg/L and 0.11 mg/L for Pyrazolynate and clomazone, respectively. Pigment contents (chlorophyll *a*, *b*, and total carotenoids) in lettuce were quantified via UV-Vis spectrophotometry following extraction with 95% ethanol. Concentrations were calculated using the method of Lichtenthaler and Wellburn. Despite phenotypic EC_{50}-based application, the total contents of pigment and individual profile were varied among herbicides. Among pigments, chlorophyll *a* gave the highest sensitivity towards pesticide treatments, indicating its potential as a phytotoxicity marker. To extend this assessment, *Lemna minor* (duckweed) was introduced as an aquatic model plant. The results clearly indicated that duckweed showed low sensitivity to clomazone but strong inhibition by aclonifen and pyrazolynate. Overall, these findings suggest notable interspecies variation in herbicide susceptibility. This supports the use of pigment-based endpoints and aquatic models for more comprehensive herbicide toxicity assessment.

PES-72

Evaluating the Effect of Enhanced Weathering Material on Lettuce Growth

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Enhanced weathering (EW) is a high-permanence technology for carbon dioxide (CO_2) removal (CDR), capable of storing CO_2 for over 10,000 years. Therefore, the present study aims to investigate the effect of EW materials on the growth of lettuce crop when applied to the soil. The EW materials used in the experiment were blast furnace slag (BFS), olivine (OV), basalt (BS), with doses corresponding to 0, 200, 500, 1,000, 2,000, 5,000, and 10,000 kg $10a^{-1}$ for each material. The results demonstrated that the fresh weight of lettice crop cultivated in the BFS, OV, and BS applied soil were within the range of 107.0 ~ 143.0, 110.3 ~ 149.0, and 82.7 ~ 142.0 g $plant^{-1}$, respectively. Furthermore, soil applied with EW materials increased the leaf length and width of the lettuce crops by 1.97 ~ 17.0% and 5.85 ~ 25.7%, respectively, compared to the untreated groups. This study suggests that the application of EW materials can enhance crop productivity by improving soil fertility and promoting sustainable agricultural pratices by mitigating atmospheric CO_2.

PES-73

Evaluation of Biochar as a Sustainable Exfoliating Agent for Replacing Microplastics and Natural Abrasives in Cleansing Foam

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Microplastics have been extensively used in cleansing products. However, due to their non-biodegradable nature, their use has been restricted worldwide. As alternatives, natural abrasives (walnut shells, avocado seeds, etc.) have been explored, but these often exhibit limitations such as inconsistent exfoliation efficacy, suboptimal texture, variability in particle size and cleansing performance. Although the exfoliating capability of biochar has been previously demonstrated, its functional performance in cleansing formulations has not been evaluated. This study aimed to develop an eco-friendly alternative material to replace microplastics and natural abrasives in cleansing products. The plant-based biochar was incorporated into cleansing foam formulations at varying concentrations (0.5–5.0%) with a particle size of 300 μm. The effects on skin-related parameters (oil content, sebum level, and pigmentation) and heavy metal content were analyzed. Oil removal efficiency increased proportionally with biochar concentration. Pigmentation and sebum removal rates peaked at 2.5% biochar, with respective improvements of 22.22% and 25.56% compared to the control. The removal efficiencies of cleansing foam with 2.5% biochar were 90.9–91.9% for oil, 97.0–99.0% for pigmentation, and 95.0% for sebum, indicating excellent cleansing performance. All biochar containing formulations complied with cosmetic safety standards regarding heavy metal content. These results suggest that biochar represents a promising substitute to microplastics and natural abrasives in cleansing products.

PES-74

Agronomic Effects of Livestock Manure Compost Produced from Biochar-Mixed litter

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In conventional cattle barns, litter materials like sawdust and rice husks have been used to control moisture, but issues such as odor and poor compost maturity have highlighted the need for alternatives. To address these problems, a biochar-mixed litter material was developed. However, its agricultural impact after use in barns and composting had not been reported. Therefore, this study aimed to assess the agricultural effectiveness of the developed biochar-mixed litter by applying it in cattle barns, composting it, and using the resulting compost (MC) in cabbage cultivation to evaluate its impact on crop growth and greenhouse gas mitigation. The experiment tested four treatments, which included Control, NPK+MC, NPK+SC (sawdust compost), and NPK+C (conventional compost). Each treatment was applied at a rate of 2000 kg/10a, and the experiment was conducted with three replicates. The fresh weight of cabbage increased by 95.8, 79.7, and 74.0% in the NPK+MC, NPK+SC, and NPK+C groups, respectively, compared to the Control. NPK+MC showed 8–12% higher fresh weight than the other compost treatments. Additionally, 30 days after planting, the NPK+MC treatment had 41.7 and 69.6% lower N_2O emissions than the NPK+SC and NPK+C treatments. These results indicate that biochar-mixed litter-based compost enhances crop growth and significantly reduces greenhouse gas emissions, demonstrating its potential as a sustainable alternative to conventional compost in livestock.

Poster Presentation

PES-75

Comparative Study on Pesticide Exposure Levels According to Formulation Type and Physical State During Mixing and Spraying by Pesticide Operator

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This study conducted a statistical analysis of pesticide exposure levels during mixing/loading and spraying according to formulation type and physical state (solid vs. liquid), using both the patch method and the whole-body dosimetry method. The data used in this study were collected from 2012 to 2023. The t-test was conducted to compare solids and liquids. In the whole-body dosimetry method, the t-value and p-value for mixing/loading were 0.553 and 0.585, respectively. For spraying, the t-value and p-value were 0.929 and 0.362. In the patch method, the t-value and p-value for mixing/loading were 0.719 and 0.475, respectively. For spraying, the t-value and p-value were 0.054 and 0.957. One-way ANOVA was conducted on formulation type. In the whole-body dosimetry method, the p-value and F-value for mixing/loading were 0.727 and 0.323, respectively. For spraying, the F-value and p-value were 0.508 and 0.608, respectively. In the patch method, the F-value and p-value for mixing/loading were 0.292 and 0.916, respectively. For spraying, the F-value and p-value were 1.092 and 0.371, respectively. Based on the results, it is concluded that there is no difference in pesticide exposure levels according to formulation type during mixing/loading and spraying.

PFS Food Sciences

PFS-1

Study on the Deodorizing and pH-Buffering Effects of Eggshell-Derived Calcium Carbonate Pads in Meat Storage

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As interest in eco-friendly food preservation increases, this study explores the potential of utilizing calcium carbonate ($CaCO_3$), the main component of eggshells, as a natural absorbent pad for pork storage. The pad was fabricated by combining ground eggshells with starch gel, creating a biodegradable material in line with food waste recycling and circular economy principles. Pork samples were divided into three groups: control (no pad), commercial absorbent pad, and $CaCO_3$-based pad, stored at 4°C for seven days. Odor suppression was assessed using ammonia test strips and sensory evaluation. The results showed that the $CaCO_3$ pad exhibited the lowest odor intensity throughout the storage period, while the control and commercial pad groups developed moderate to strong spoilage odors. pH measurements of meat exudate indicated that the $CaCO_3$ group maintained a pH approximately 0.7 units higher than the control, suggesting a buffering effect that delayed spoilage. Additionally, ammonia-sensitive paper exposed to the sample headspace showed lighter color changes in the $CaCO_3$ group, indicating suppression of volatile amine accumulation. These results suggest that $CaCO_3$ pads not only stabilize pH but also suppress the formation and release of odor-causing compounds, potentially through the physical adsorption or neutralization of ammonia. This study demonstrates that $CaCO_3$-based pads can function as practical food packaging materials, reducing reliance on synthetic materials while offering effective preservation solutions.

PFS-2

Preparation and Characterization of Tannase Immobilized Titanium Dioxide Nanoparticles

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Tannase-immobilized titanium dioxide nanoparticles (TITNP) was prepared by amino-functionalization and glutaraldehyde crosslinking on the surface of titanium dioxide nanoparticles (TNP) in anatase. The catalytic activity, thermal stability and reusability of immobilized tannases at various temperature or pH conditions were estimated by the tannase activity assay, which quantitates the gallic acid (GA) released after tannase-catalyzed hydrolysis reaction of tannic acid (TA) by capillary electrophoresis system. The amino-functionalized TNP intermediate was confirmed by the characteristic changes in fourier-transform infrared (FT-IR) spectrum, zeta potential and sedimentation behavior. Immobilized tannases retained its catalytic activity more than 60% at temperature range of 30 to 60°C or pH range of 3 to 6 with the optimum activity at 40°C and pH 5. In addition, immobilized tannases were thermally stable which retained 43% of tannase activity at 70°C during the incubation for 60 min. Finally, TITNP showed strong reusability maintaining 60% of initial enzyme activity even after 20 cycles of repeats. Thus, characteristic properties of TITNP might be useful for industrial application in food or medicine fields.

Poster Presentation

PFS-3

Research on Internationally Harmonized Usage of Sweeteners

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Food additives contribute to sustainable food security and are widely used in a wide range of food products, but different national standards of use act as non-tariff barriers, hindering smooth international trade. In particular, there is an urgent need for internationally harmonized use standards for sweeteners, which are increasingly used in response to consumers' growing preference for healthier foods. This study was conducted to systematically compare and analyze the usage standards of major sweeteners by country to provide a basis for the development of internationally harmonized usage standards. The study was conducted as aspartame, acesulfame potassium, sucralose, sodium saccharin, and neotame that are frequently used in Korea. First, the usage standards for each food type according to major countries(US, EU, Japan, etc.) and CODEX regulations were collected and compared by matching food types between countries. Second, more/less/new standard scenarios for similar foods with differences in use standards between countries. Third, the safety of the derived scenarios was evaluated using data from the National Health and Nutrition Examination Survey and the ADIs published in global. The results of this study can be used as a scientific basis for harmonizing international usage standards for sweeteners, and will be used to prepare international harmonized usage standards in the future by comprehensively considering the latest consumption trends, safety evaluation results, and industry interests.

PFS-4

Monitoring and Risk Assessment of Pesticide Residues in Shellfish Using GC and LC-MS/MS

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Aquatic products can be unintentionally contaminated by pesticides due to agricultural runoff and environmental exposure, necessitating continuous and comprehensive monitoring. In particular, shellfish such as clams and oysters are highly susceptible to accumulating contaminants because of their sedentary nature and habitat on the seafloor, where they are constantly exposed to suspended particles and sediments. In this study, a total of 40 shellfish samples—20 clams and 20 oysters—were collected based on actual consumer intake data. A total of 80 pesticides were selected for monitoring, including 51 pesticides analyzed by GC-MS/MS and 29 by LC-MS/MS, based on previous detection reports and contamination potential. As a result, no pesticide residues were detected in any oyster samples, while oxadiazon was found in 4 out of 20 clam samples at concentrations ranging from 0.008 to 0.009 mg/kg. For the detected pesticide, the estimated daily intake (EDI) was calculated and compared with the acceptable daily intake (ADI) to assess potential health risks. The resulting %ADI values ranged from 0.05% to 1.12%, indicating that even long-term consumption of the contaminated clams would pose no significant risk to human health.

PFS-5

Effect of drying methods on metaflumizone residues in Welsh onions

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This study examined the effects of three drying methods – hot-air drying, infrared drying, and freeze drying – on metaflumizone residue levels in Welsh onions. Metaflumizone (20% EC) was applied three times at 0.6 kg a.i./ha, with the final application occurring seven days before harvest. After removing the roots, outer layers, and washing, the harvested onions were sliced into 0.8 cm pieces to dry. Drying methods included hot-air and infrared at 75°C for 70 min, 70°C for 50 min, and 65°C for 90 min. Freeze-drying was done at -70°C for 52 h. Residue levels were measured using a validated method with a limit of quantification (LOQ) of 0.01 mg/kg. The method showed recovery rates of 79.3-92.2% in fresh samples and 91.0-97.9% in dried samples. Initially, fresh onions contained 0.22 mg/kg of residue. Post-drying, residues increased to 0.26-2.28 mg/kg (hot-air), 0.71-0.97 mg/kg (infrared), and 2.68-3.08 mg/kg (freeze-drying). These results indicate that drying significantly raises metaflumizone concentrations due to moisture loss, with hot-air yielding the lowest final residue levels among the methods tested.

PFS-6

Comprehensive analysis of metabolites and bioactivity from different cultivars of radish sprouts (*Raphanus sativus* L.)

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We aimed to compare different metabolite accumulation patterns and bioactivities in 3 different cultivars (green, red, and purple) of *Raphanus sativus* L. (common radish) sprouts. A total of 61 metabolites were identified, including amino acids, carotenoids, phenolics, sugars and their derivatives, TCA cycle intermediates, and organic acids. Among the cultivars, purple radish sprouts exhibited the highest accumulation levels of most metabolites. Using the KEGG *Arabidopsis thaliana* biosynthetic pathway database, we identified 14 significantly enriched metabolic pathways that distinguished radish cultivars. We focused on phenylalanine, known precursors of physiologically active phenolic compounds. In fact, the phenylpropanoid biosynthesis pathway emerged as one of the key differentiators among the cultivars. Subsequently, antioxidant assays demonstrated that purple radish sprouts, which showed higher accumulation of metabolites, such as amino acids and phenolic compounds, had higher bioactivities. In addition, total anthocyanin contents were confirmed higher in purple radish sprouts, followed by red, and not detected in green radish sprouts. These results suggest that purple radish sprouts possess superior nutritional and functional properties, highlighting their potential as valuable functional food ingredients for health-promoting diets. This work was supported by the Korea Institute of Planning and Evaluation for Technology in Food, Agriculture, and Forestry (IPET) through Cutting-edge Precision Breeding Development Program, funded by Ministry of Agriculture, Food and Rural Affairs (MAFRA) (RS-2025-02303365), Republic of Korea.

Poster Presentation

PFS-7

Comparison of immunomodulatory from lactic acid bacteria-fermented mountain-cultivated ginseng sprouts

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His study aimed to compare the changes in functional components and immunomodulatory activities between mountain-cultivated ginseng sprout (MCGS) and its fermented and aged form (FAMCGS), which was prepared through lactic acid bacterial fermentation. The fermentation process resulted in increased acidity (pH 3.77) and a significant elevation in the contents of deglycosylated ginsenosides Rg3 and compound K (each from 0.74 to 1.75 μg/g, and 0.35 to 3.03 μg/g, respectively), as well as an approximately threefold increase in total phenolic acids and flavonols. Along with a notable protective effect against oxidative DNA damage. *In vitro* studies using LPS-stimulated RAW264.7 macrophages confirmed that FAMCGS suppressed the expression of pro-inflammatory cytokines and regulated key inflammatory mediators such as COX-2 and iNOS through modulation of the NF-kB and MAPK signaling pathways. Notably, the key compound, compound K, demonstrated a novel anti-inflammatory mechanism through inhibition of the TREK-2 ion channel. *In vivo* experiments using an immunosuppressed mouse model revealed that FAMCGS restored body weight, spleen and thymus mass, immune cell populations, and NK cell activity. It also increased cytokine levels and NF-kB activation, indicating an overall improvement in immune function. These findings suggest that bioconversion enhances the immune-promoting properties of MCGS and support the potential of FAMCGS as a promising nutraceutical or nutraceutical ingredient.

PFS-8

Changes in metabolites and biological activities of isoflavone-enhanced mung bean leaves by bioprocessing stages

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Lactic acid bacteria fermentation harnesses microbial metabolism to transform substrate composition, enhancing bioactive compounds and functional properties in plant materials. This experiment measured changes in biometabolites and biological activity following three processing steps (dried, sterilized, and fermented with lactic acid bacteria) using metabolite-enhanced mung bean leaves (MEML). The analysis showed that fatty acids had higher saturated fatty acids in sterilized MEML (SMEML) and fermented MEML (FMEML) than dried MEML (DMEML), and unsaturated fatty acids tended to decrease. It was shown. According to free amino acids, their content decreased after sterilization, and several components, such as aminoadipic acid, γ-aminobutyric acid (GABA), and ornithine, increased after fermentation. The increase in the content of GABA may be of great significance, especially when comparing steam with fermentation (SMEML, 125.24 → FMEML, 154.10 mg/100g). Twelve isoflavone components changed dramatically after steam and fermentation. Glycosides decreased, resulting in increased aglycons (DMEML, 5,933.55 → SMEML, 5,277.92 → FMEML, 21,909.73 μg/g). This bioconversion occurs by the reaction of physical (high temperature) and biological (*β*-glucosidase). In addition, antioxidant and digestive inhibitory activity was highest in FAEML. In this study, we observed changes in biometabolites and biological activity and demonstrated the potential of FMEML as a functional food industry.

PFS-9

Optimization of fermentation conditions of isoflavone-enriched mung bean leaves with lactic acid bacteria

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In this study, fermentation conditions of metabolite-enhanced mung bean leaves (FMEML) using lactic acid bacteria (LAB) were optimized based on γ-aminobutyric acid (GABA) and isoflavone aglycone production. GABA content and glycoside-to-aglycone conversion were evaluated for 14 LAB strains isolated from kimchi. Among them, *Lacticaseibacillus paracasei*4557 (LAB47) showed the highest conversion efficiency and was selected for further experiments. *Lactobacillus brevis* WCP02 and *Lactiplantibacillus plantarum* DM083 (LAB02) were also employed to assess the effect of mixed-strain fermentation. LAB47 and WCP02 showed the highest aglycone conversion rates, while LAB02 significantly enhanced GABA biosynthesis. A three-strain mixture (LAB02, LAB47, WCP02) was evaluated in different inoculation ratios (1:1:1 to 1:1:2) across various fermentation durations (0–96 h). GABA levels increased steadily from 68.98 to 84.90 mg/100 g over 72 h. Isoflavone aglycones increased sharply after 12 h, reaching a peak conversion rate of 83.63% at 72 h, then slightly declined. The 1:1:2 ratio resulted in the highest combined yield of GABA and aglycones. These results suggest that 72 h fermentation using the 1:1:2 LAB blend is optimal for maximizing bioactive metabolite content. This optimized process offers a promising approach for the development of scalable functional mung bean leaf products with enhanced nutritional and physiological properties.

PFS-10

Comparisons in the nutritional and functional components of brown rice induced by fermentation with mushroom mycelia

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This study identified optimal mushroom mycelia to enhance protein content in brown rice via fermentation After fermentation and drying, changes in physicochemical properties (pH, acidity, reducing sugars, soluble protein), amino acids, phenolic acids, fourier transform infrared (FTIR) spectroscopy, and radical scavenging activity were analyzed. Results showed decreased pH, increased acidity, and elevated reducing sugars in all fermented samples. Soluble protein increased 1.32–1.74 -folds, particularly in *Flammulina velutipes* and *Tricholoma matsutake*. Free amino acids rose 3.69–6.82 folds, with essential amino acids increasing 2.69–14.75 folds. TMA exhibited the highest amino acid content (essential: 242.41 mg/100g; total: 218.91 mg/100g). Phenolic acids were highest in TMA (208.67 μg/g), followed by *Ganoderma lucidum* (124.44 μg/g) and *Cordyceps militaris* (106.13 μg/g). FTIR revealed increased transmittance in N-H, CH_2, and C=O regions, indicating component decomposition and new metabolite formation. These findings demonstrate that fermentation with mushroom mycelia effectively enhances the nutritional and functional components of brown rice. *T. matsutake* emerged as the most promising strain due to its superior ability to boost protein, amino acids, and antioxidant properties, making it a viable candidate for developing nutrient-rich fermented brown rice products.

Poster Presentation

PFS-11

Comparison of metabolites and biological activities in isoflavone-enriched soybean leaves by bioconversion with different mushroom mycelia

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Mushroom fermentation using edible fungi has emerged as a promising strategy to enhance the nutritional and functional qualities of plant-based materials. In this study, various mushroom strains were used to ferment isoflavone-enriched soybean leaves (IESL), following three processing stages: drying, steaming, and mushroom-mediated fermentation. The steamed IESL showed the highest β-glucoside isoflavone contents (1171.96 μg/g), while malonyl-β-glucosides were most abundant in dried samples (3500.82 μg/g), but disappeared after fermentation. Fermentation notably increased aglycone isoflavones, especially with *F. velutipes* (2340.00 μg/g), *G. frondosa* (2297.31 μg/g), and *P. ostreatus* (1531.88 μg/g). Mushroom bioprocessing also enhanced the leaves functional properties, boosting total phenolic and flavonoid contents and elevating antioxidant activity based on DPPH and ABTS assays. *F. velutipes* and *L. edodes* significantly increased phenolic and flavonoid levels, while *L. edodes* and *T. matsutake* improved antioxidant activity most effectively. These results highlight the metabolic enhancement potential of mushroom fermentation. By converting glycosides into aglycones, this method improves isoflavone bioavailability and physiological function. Additionally, it promotes the accumulation of total phenolics and flavonoids and enhances antioxidant properties. Overall, mushroom fermentation presents an effective microbial approach for producing bioactive compound-rich foods with potential health-promoting effects.

PFS-12

Comparison of functional components and biological activity in fermented white rice with edible mushroom mycelia

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This study aimed to evaluate the functional properties of white rice fermented with eight types of edible mushroom mycelia. Pre-treated white rice was inoculated with *Flammulina velutipes* (FVE), *Lentinula edodes*, *Tricholoma matsutake* (TMA), *Grifola frondosa* (GFR), *Pleurotus eryngii* (PER), *Pleurotus ostreatus* (POS), *Cordyceps militarys* (CMI), and *Ganoderma lucidum* (GLU). Changes in physicochemical characteristics, nutrient content, functional compounds, FTIR spectra, and antioxidant activity were assessed. Results showed that pH decreased and acidity increased across all treatments. Notably, FVE and CMI significantly improved nutritional values: soluble protein rose from 1.23 mg/g (control) to 23.13 and 3.78 mg/g; free amino acids increased to 209.23 and 91.10 mg/100 g, respectively. Antioxidant activity also improved. DPPH scavenging increased to 3.41 and 1.04 mg/g, and ABTS activity rose from 2.48 mg/g to 4.75, 1.47, and 1.55 mg/g in FVE, CMI, and PER. FTIR clearly showed compositional differences. These findings suggest that fermentation of white rice with mushroom mycelia enhances its functional properties, especially antioxidant activity, supporting its potential as a functional food ingredient for grain-based product development.

PFS-13

Effect of adding rice as a secondary ingredient on the hardness, antioxidant activity and aglycone isoflavone content of tempeh

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Tempeh is a traditional Indonesian food made by fermenting soybeans with the fungus Rhizopus. It is usually eaten after being fried, boiled, steamed or roasted. Since tempeh often breaks apart during cooking or secondary processing, achieving a certain level of hardness and firmness is necessary. In this study, we added rice as a secondary ingredient to increase hardness, examining how the main functional properties changed as the soybean content decreased. The rice was added in two forms: hard steamed rice and roasted rice flour. The hard steamed rice was added at 20% and 30% of the weight of the raw soybeans, and the roasted rice flour at 10% and 20%. Compared to the negative control, the hardness of all samples increased by between 1.15 and 1.5 times. Despite the soybean content decreasing with the addition of rice flour, the aglycone isoflavone content of tempeh containing 20% roasted rice flour remained similar to that of the control sample. Additionally, antioxidant activity increased in all samples after fermentation compared to before fermentation. The addition of roasted rice flour improved DPPH radical scavenging activity by 1.2-fold and ABTS radical scavenging activity by 1.3-fold, while also increasing total polyphenol levels by 1.4-fold. Consequently, adding roasted rice flour enhanced tempeh's usability as a food ingredient and improved its functionality.

PFS-14

Species Diversity of *Aspergillus* and *Fusarium* from Onion Bulbs in Korea

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The aim of this study was to evaluate the incidence of fungal pathogens in onion bulbs (*Allium cepa* L.). Fungal isolates were obtained from onion bulbs collected from 20 onion cultivated fields and storages in Muan. A total of 174 fungal colonies were isolated based on morphology and identified using marker genes. The dominant fungi in the onion bulbs were *Aspergillus* (3 species, 44.3%), followed by *Fusarium* (6 species, 33.9%) and *Penicillium* (15species, 14.9%). Other genera, including *Alternaria*, *Bipolaris*, *Chaetomium*, *Circinella*, *Circinella*, *Cladosporium*, *Coprinellus*, *Curvularia* and *Talaromyces*, were also detected. The predominant species was *A. welwitschiae* (42.0%), followed by *F. proliferatum* (24.7%), *P. brasilianum* (6.3%), *F. oxysporum* (5.2%), *P. glabrum* (5.2%), *A. montevidensis*, *F. commune* and *P. brevicompactum*. *A. welwitschiae* (94.8%) and *F. proliferatum* (72.9%) were the most prevalent species within the genus *Aspergillus* and *Fusarium*, respectively. The result could be used to develop control strategies for the protection of onion crops against pathogenic fungi during cultivation and storage. (This work was carried out with the support of “Cooperative Research Program for Agriculture Science and Technology Development (Project No. PJ01512801)” Rural Development Administration, Republic of Korea. And this study was supported by 2024 the RDA Fellowship Program of Allium Vegetable Research Center, Rural Development Administration, Republic of Korea.)

PFS-15

Sustainable Extraction of Anthocyanins from Mulberry (*Morus Alba* L.) By-Products Using Natural Deep Eutectic Solvents (NADES)

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Natural deep eutectic solvents (NADES) comprising choline chloride and organic acids have attracted attention as green solvents due to their biodegradability, low toxicity, and high efficiency in extracting bioactive compounds. Among these compounds, anthocyanins, water-soluble pigments found in fruits and vegetables, are renowned for their antioxidant activity and coloring ability. Mulberry (*Morus alba* L.) fruit pomace, a byproduct of juice processing, represents a source of anthocyanins. However, their stability is compromised by various factors. In this study, we optimized the extraction method for anthocyanins from mulberry pomace using NADES and evaluated the stability of the extracted anthocyanins under various temperatures, pH, and light conditions. Anthocyanin composition was analyzed using high-performance liquid chromatography (HPLC) and ultra-performance liquid chromatography coupled with quadrupole time of flight mass spectrometry (UPLC-qTOF-MS). Fourier transform infrared spectroscopy (FT-IR) and differential scanning calorimetry (DSC) analyses were conducted to reveal the molecular-level stability of the anthocyanins. The major anthocyanins of mulberry pomace were cyanidin-3-*O*-glucoside and cyanidin-3-*O*-rutinoside. The optimized NADES solvent was choline chloride-lactic acid (CC-LA). The stability study results indicate that pH and light exposure had a significant effect on the stability of the anthocyanins, while the anthocyanins remained stable below 45°C. These results provide a fundamental resource for understanding the NADES-based extraction systems and practical insights for the utilization of NADES-extracted anthocyanins within the food industry.

PFS-16

Characterization of volatile compounds in edible insect oils at different storage stages using HS-SPME-Arrow-GC/MS

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This study investigated the volatile compound profiles of oils extracted from three edible insect species: *Tenebrio molitor* (TM), *Gryllus bimaculatus* (GB), and *Zophobas atratus* (ZA), under accelerated oxidative conditions. Oils were obtained using an ultrasound-assisted extraction (UAE) method, with extraction yields of 26.41% for TM, 18.24% for GB, and 36.26% for ZA. Volatile compounds were identified and quantified at four stages of oxidation using headspace solid-phase microextraction arrow combined with gas chromatography–mass spectrometry. During storage, significant increases ($p < 0.05$) were observed in the concentrations of lipid oxidation products including hexanal, nonanal, benzaldehyde, and 2-methylbutanal. Hexanal is primarily generated from the oxidation of linoleic acid, while nonanal originates from oleic acid oxidation. These results show that lipids from edible insects are easily oxidized, which can reduce the quality of food made with these oils. Therefore, more research is needed to find effective ways to store and stabilize insect oils. The use of accelerated oxidation at 60°C provides a practical approach for estimating the shelf life of insect oils. These findings also suggest the potential of insect-derived oils as valuable resources in sustainable and upcycled food applications

PFS-17

Identification of Key Volatile Markers in Commercial Broth

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Headspace solid-phase microextraction arrow (HS-SPME-Arrow) combined with gas chromatography-mass spectrometry (GC-MS) was employed to investigate the volatile profiles of five commercial broth products. To evaluate the extraction efficiency of volatile compounds, three types of SPME-Arrow fibers were tested. Among them, the divinylbenzene/carboxen/polydimethylsiloxane (DVB/CAR/PDMS) fiber exhibited significantly higher peak areas than the others ($p < 0.05$). SPME-Arrow extraction conditions were optimized using response surface based on a Box–Behnken design, with equilibration time, extraction time, and extraction temperature as independent variables. The optimal conditions were determined to be 20 minutes of equilibration, 30 minutes of extraction, and an extraction temperature of 40°C. Under these conditions, a total of 18 volatile compounds were identified, with aldehydes being the most abundant group. Eleven compounds showed variable importance in projection (VIP) scores greater than 1, indicating their significant contribution to volatile differentiation. Multivariate statistical analyses effectively distinguished the samples based on their distinct volatile characteristics. The samples were classified into two groups: those dominated by fatty notes and those characterized by roasted or broth-like notes. Furthermore, beef flavoring ingredients exhibited unique volatiles such as pyrazines and methional, both known for their strong roasty and meaty sensory attributes. These findings contribute to a deeper understanding of volatile compound distribution in commercial broth products.

Poster Presentation

PFS-18

Seasonal and Regional Characteristics of Free Sugars and Crude Fat in Potatoes

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Potato is valued for its high nutritional composition and global significance as a food source. In this study, free sugars (sucrose, fructose, and glucose) were measured using UPLC in two cultivars (Geumseon and Eunseon) grown in Gangneung and harvested in autumn. In Geumseon, sucrose was the most abundant, followed by glucose and fructose, whereas Eunseon showed glucose as the most prevalent, with sucrose and fructose at similar levels. Two spring-harvested cultivars grown in three regions (Buan, Boseong and Gangneung) were analyzed for crude fat content using the Soxhlet extraction method. The highest fat content was observed in samples from Buan, followed by Boseong and Gangneung. Crude fat content did not differ significantly between Buan and Boseong for Geumseon, nor between Gangneung and Boseong for Eunseon ($p > 0.05$). To assess moisture content, a commercial potato was analyzed using both the conventional oven-drying method and a halogen moisture analyzer. No significant difference was observed between the two methods ($p > 0.05$), indicating that both are suitable for measuring moisture in peeled potatoes. Overall, these results provide a comprehensive basis for evaluating the nutritional quality characteristics of potatoes cultivated in different regions of Korea, based on their free sugar, crude fat, and moisture content.

Poster Presentation

PFS-19

Comparative Screening of Antioxidant and Anti-Inflammatory Activities Among Domestically Bred Carica papaya L. Hybrids Using Different Extraction Solvents

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Papaya (Carica papaya L.) is a tropical fruit with potential antioxidant and anti-inflammatory properties. This study aimed to evaluate the physiological activities of domestically bred papaya hybrids in comparison to Solo, an imported cultivar from the Philippines used as the control. Fruits from 12 trees representing three hybrid combinations 63 Red Lady × Holland Gold, 5th Bolyvia × 63 Red Lady, and 63 Red Lady × 5th Bolyvia were extracted using water, 70% ethanol, and absolute ethanol. Antioxidant capacity was assessed using DPPH, ABTS, and FRAP assays, while anti-inflammatory effects were determined by nitric oxide (NO) inhibition and cytokine analysis in LPS-stimulated RAW264.7 macrophages. Extracts obtained with 70% ethanol showed the highest overall activity. Significant differences were observed among the cultivars. Notably, one hybrid derived from 5th Bolyvia × 63 Red Lady showed enhanced antioxidant capacity, while another from 63 Red Lady × Holland Gold demonstrated stronger anti-inflammatory effects. These hybrids outperformed the Solo cultivar in multiple parameters. The findings highlight the potential of selected domestic hybrids as candidates for functional ingredient development and provide a foundation for future breeding and industrial applications.

PFS-20

Analysis of volatile components in Korean wheat flour with varying levels of added apple pomace based on drying method using an electronic nose

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Apple pomace is a waste product after the primary processing of apple juice that accounts for 25%–30% of the weight of apples and is estimated to generate more than 15,000 tons per year. Some is used for feed or compost, but most is wasted in the fields. This study aimed to identify the potential for high-fiber functional bakery products using byproducts derived from apples. Apple pomace was dried using hot air and freeze methods, then substituted with flour at levels of 0%, 10%, and 20%. The aroma composition was analyzed with an electronic nose. For the electronic nose analysis, 3 g of sample was placed into a 20 mL vial, sealed, heated to 50°C in the headspace, and incubated at 500 rpm for 2 min. A total of 5 mL was injected into the injector at a speed of 125 μL/s, and the aromatic compound ratio was measured by passing the sensor. For each column, a chromatogram indicating the intensity of each aromatic compound against its retention time for each sample was recorded, and the average peak areas were calculated by the software for data analysis. Additionally, principal component analysis (PCA), discriminant factorial analysis (DFA), and measurement of the distance between clusters were performed. The fragrance components could be categorized with a PCA1 and DFA1 contribution of 95%–99%.

PFS-21

Fermented Mixture of *Saccharina* and *Panax* Ameliorates Gentamicin-Induced Gut Dysbiosis via Modulation of the Gut Microbiota

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The recent overuse of antibiotics has led to a rise in antibiotic-induced gut microbiota dysbiosis, which is closely associated with increased risks of systemic inflammation and metabolic disorders. In response, fermented products containing postbiotics have garnered attention as safe and effective therapeutic alternatives. In this study, we evaluated the potential of a fermented mixture comprising *Saccharina japonica*, *Panax ginseng*, and *Panax ginseng* sprouts (FMSP) enriched with diverse bioactive compounds to restore microbial balance disrupted by gentamicin treatment, using an *in vitro* gastrointestinal digestion and fecal fermentation model. After one month of fermentation, FMSP exhibited approximately a 54% increase in total phenolic and flavonoid contents, which subsequently declined with extended fermentation to two months. Treatment with FMSP led to a partial restoration of gentamicin-induced reductions in gut microbial α-diversity, along with significant shifts in β-diversity. Notably, FMSP reduced the relative abundance of disease-associated bacteria, including Erysipelotrichaceae and *Holdemania*, while promoting beneficial genera such as *Bifidobacterium* and various short-chain fatty acid (SCFA)-producing microbes. Furthermore, the two-month fermented FMSP significantly enhanced total SCFA production. These results indicate that FMSP holds therapeutic potential for alleviating gut dysbiosis and may be utilized as a functional agent to support intestinal health.

PFS-22

Ellagic acid, an active compound of Rosa multiflora fruit, attenuates stress hormone-induced depression in mice by inhibiting monoamine oxidase

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Rosehip, the fruit of Rosa multiflora, has various biological properties; however, its role in alleviating stress-induced depression remains unclear. Excess glucocorticoid production may cause depression; thus, we aimed to investigate the antidepressant effects of R. multiflora fruit extract (RM) on corticosterone (CORT)-induced depressive-like behavior in mice and the molecular mechanisms underlying these effects. RM administration attenuated depressive-like behaviors by inhibiting monoamine oxidase (MAO)-B expression and astrocyte hypertrophy in the hippocampus of CORT-injected mice; this observation was consistent with in vitro results in neuronal and astrocytic cells. Ellagic acid (EA), an active compound of RM, alleviated depressive-like behaviors by inhibiting MAO-B expression and preventing synaptic loss; this finding was consistent with the molecular docking analysis results. Overall, these findings suggest that RM and EA have antidepressant effects in CORT-induced depressive mice, which are mediated by the MAO-B pathway. RM and EA may be natural antidepressants.

Poster Presentation

PFS-23

Functional Analysis of the Ectopically Expressed Olfactory Receptor OR2AT4 in Leukemic Cells

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Olfactory receptors (ORs) constitute the largest family of mammalian G protein-coupled receptors (GPCRs), and GPCR containing ORs are the most important drug targets. Various ORs are expressed in cancer cells and several parts of the body, and it is emerging that they may be associated with cell progression or cancer biomarkers. In particular, it is known that OR2AT4 can suppress cancer in leukemia cells by regulating cellular signaling pathways. However, the function of the novel OR2AT4 ligand in leukemia cells is poorly understood. Here, we expressed and purified the recombinant protein, identified a novel ligand, and confirmed its function in K562 leukemia cells. In particular, the surface plasmon resonance (SPR) method was used to search for novel OR2AT4 ligands, and compound A was identified as an OR2AT4 ligand that modulated the calcium levels, proliferation, and apoptosis in K562 cells. This study highlights the importance of compound A as an anti-cancer agent against leukemia, making it a new anti-cancer target. Our results suggest that novel OR2AT4 ligands offer new cancer treatment and drug development possibilities.

PAM Applied Microbiology

PAM-1

Ferrous Ion-Induced Antifungal Activity of *Metschnikowia persimmonesis* Against *Colletotrichum gloeosporioides*

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Metschnikowia persimmonesis (Mp), a novel endophytic single cell yeast isolated from persimmon fruit calyx part, exhibited a potential biocontrol agent against spoilage pathogen. The current study aimed to investigate the correlation between pulcherrimin production and antifungal activity of *M. persimmonesis* against *Colletotrichum gloeosporiodies* (Cg) and *Colletotrichum fructicola* (Cf), the causal anthracnose in persimmon tree. An *invitro* dual assay was conducted using five different media: Luria-Bertoni (LB), Potato Dextrose (PD), PD + glucose (PDrich), Minimum media (MM), and MM supplemented with Tween80 (MMT). *M. persimmonesis* demonstrated the highest antagonistic activity against Cg in MMT media (around 23% inhibition rate) followed by MM media (around 15%). The presence of ferrous ion in MM and MMT appeared to stimulate pulcherrimin biosynthesis. Furthermore, the presence of Tween80 may have facillitataed intracellular transport of pulcherrimin which increase utilization of ferrous ion as essential nutrient for pathogen growth. Ferrous supplementation significantly influenced the antifungal efficacy of *M. persimmonesis* against plant pathogen. However, no significant differences in inhibition rates were observed against Cf among the tested media, suggesting a possible resistance mechanism by Cf against the endophytic yeast. These finding provide fundamental insight for developing eco-friendly biopesticide, particularly for managing anthracnose in persimmon cultivation. This work was supported by (NRF) (NSN2313020: NRF 2023R1A2C3004706, RS-2023-NR077258) & Korea Institute of Oriental Medicine(KSN2511030), Republic of Korea.

PAM-2

Analysis of the characteristics of Carbapenem-resistant Enterobacterales (CRE) infections in southern Gyeonggi-do

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Among Carbapenem-resistant Enterobacterales (CRE) infections, there are Carbapenemase-producing Enterobacterales (CPE) that exhibit antibiotic resistance by producing carbapenemase enzymes. CPE infections can spread within healthcare settings and communities through the transmission of resistance genes, underscoring the importance of continuous monitoring. This study analyzed 15,338 clinical specimens submitted to the Gyeonggi Province Institute of Health and Environment between 2021 and 2023, focusing on the prevalence of CRE infections in southern Gyeonggi-do, the distribution of carbapenemase gene types, and their regional and institutional patterns. The number of CRE specimen submissions has increased annually, with a concurrent rise in the detection rate of CPE. The detection rate of CPE in southern Gyeonggi-do was higher in males than in females, with the predominant age group being those aged 60 and above. Among carbapenemase types, KPC was the most commonly detected, and the subtype KPC-2 accounted for over 80%. In the study, it was observed that areas with a high number of medical institutions had a higher rate of specimen referrals and CPE positivity. Continuous laboratory monitoring of causative agents, coupled with strong cooperation among relevant institutions, is crucial for the effective management of CRE infections

Poster Presentation

PAM-3

Metagenomic Insight into the Gut Dysbiosis and Its Association with Non-Alcoholic Fatty Liver Disease in Humans

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Non-alcoholic fatty liver disease (NAFLD) is associated with gut microbiota dysbiosis, metabolic dysfunction, and systemic inflammation, highlighting the gut-liver axis as a pivotal therapeutic target. Gut microbiota profiles were analyzed in NAFLD patients, healthy controls, and treatment groups receiving prebiotic. Raw sequencing (16S rRNA) data were retrieved from the NCBI database processed through QIIME2. Visualization and advanced statistical analyses were performed using R. Results revealed significant gut dysbiosis in NAFLD patients, with notable alterations in the relative abundance of key microbial taxa including *Bifidobacterium*, *Firmicutes* and *Faecalibacterium* — genera associated with anti-inflammatory and metabolic homeostasis functions. An observed an enrichment of lactic acid-producing bacteria (such as *Lactobacillus*) in patients with NAFLD. Prebiotic supplementation markedly improved microbial diversity metrics and restored the abundance of beneficial gut commensals, and other SCFA-producing bacteria. The observed modulation of microbial communities and functional pathways highlights the potential of prebiotics to restore gut microbiota balance. These findings advocate further clinical research to explore the gut-liver axis as a critical target for NAFLD management and the development of prebiotic-based therapies

PAM-4

Metatranscriptomic analysis of plant viruses infecting pepper in Indonesia

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Pepper (Capsicum annuum L.) is an essential crop widely cultivated in Indonesia and contributes significantly to the agricultural economy. This study is the first to comprehensively investigate viral pathogens affecting Indonesian pepper plants using next-generation sequencing (NGS) technology. We performed metatranscriptomics analysis through RNA sequencing, followed by bioinformatics analyses, to identify viral species present in six libraries collected from different geographical regions of West Java. A total of 13 viruses were identified, with Cucumber mosaic virus (CMV) being the most prevalent, showing an average occurrence exceeding 95% across all libraries. Unidentified viruses were consistently detected in all samples, reflecting the need for further investigation. Notably, Pepper cryptic virus 2 (PCV2) and Capsicum annuum amalgavirus 1 (CaAV1) were detected for the first time in Indonesia. Phylogenetic analyses revealed close genetic ties between the identified viruses and strains from Asia, Europe, and Australia, suggesting potential regional and intercontinental transmission routes. Validation through RT-PCR confirmed the accuracy of virus detection using RNA sequencing. These findings provide comprehensive insights into the diversity, prevalence, and geographic distribution of viral pathogens affecting pepper crops in Indonesia, emphasizing the need for continued viral monitoring and implementation of region-specific management strategies to protect crop productivity.

PAM-5

Evolutionary and pathogenic characterization of the cucurbit aphid-borne yellows virus population in Korea

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Cucurbit aphid-borne yellows virus (CABYV), a member of the genus *Polerovirus*, is emerging as an important pathogen affecting cucurbit crops in Korea. In this study, we sequenced the complete genomes of 29 CABYV isolates collected from various cucurbit plants exhibiting symptoms such as yellowing, leaf mosaic, and irregular netting in Korea between 2020 and 2024. Using these complete genome sequences, we conducted an evolutionary analysis to determine the genetic relationships among the newly identified isolates and previously reported CABYV populations. Our analyses revealed that the CABYV Korean population exhibited significantly lower genetic diversity compared to the Mediterranean population. Phylogenetic analysis suggests that the newly identified isolates have evolved from pre-existing CABYV populations within Korea, rather than being introduced from abroad. To explore potential pathogenic variation within the CABYV Korean population, we constructed full-length cDNA clones of two genetically distinct Korean isolates, CABYV-NW and CABYV-PC (designated as pCABYV-NW and pCABYV-PC), using an *Agrobacterium*-mediated inoculation system. Agroinfiltration of melon plants with either construct successfully established systemic infection. Ongoing studies aim to characterize the differences in pathogenicity between pCABYV-NW and pCABYV-PC to better understand the biological relevance of genetic diversity within the CABYV Korean population.

PAM-6

Unraveling Environmental Immunomodulation: Multi-Omics Study of Microbiome-Mediated Plant Disease Suppression using Gnotobiotic Systems

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Cucumber production faces significant threats from powdery mildew (PM), caused by the fungal pathogen *Podosphaera xanthii*, severely reducing crop yields and prompting reliance on chemical pesticides with ecological consequences. This study investigated the potential of microbiome-mediated disease suppression using multi-omics approaches within a gnotobiotic system (GnotoPot). We initially screened 30 commercial cucumber cultivars for PM resistance, identifying highly resistant and susceptible cultivars. These were studied under controlled microbial conditions (axenic vs. holoxenic) and PM infection. Metagenomic analysis revealed distinct phyllosphere microbial shifts associated with PM infection, notably the increase of antifungal genera such as *Pseudomonas*. Transcriptomic profiling identified differential gene expressions related to plant immunity modulated by microbial presence, and metabolomics highlighted microbial metabolites potentially inhibiting fungal pathogens. Quantitative microbial profiling using ddPCR further confirmed the role of specific microbial taxa in reducing disease severity. Our integrated analysis demonstrated that the microbiome significantly enhanced disease resistance beyond genetic cultivar differences, indicating its potential as a universal regulator of PM resistance. This research presents a sustainable framework for PM control in cucumbers by leveraging microbiome-driven immune modulation, reducing chemical pesticide dependency, and fostering eco-friendly agricultural practices.

Poster Presentation

PAM-7

Microbial Network and Functional Analysis in Rhizosphere Soils Cultivated Wild-Simulated Ginseng

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Soil bacterial communities play an important role in the growth and biosynthesis of active compounds of various medicinal plants. In the cultivation of wild-simulated ginseng (WSG, *Panax ginseng* C.A. Meyer), it is well known that soil bacteria influence the growth and ginsenoside content of WSG. Microbial network analysis reveals functional redundancy and keystone taxa among bacterial and fungal communities. Therefore, this study aimed to investigate functions and microbial network to discover relationships between WSG cultivation environments and WSG growth. Treatment of bacterial strain ‘75’ in WSG increased the activity of nitrogen cycle and degradation of organic matter. Microbial network analysis confirmed six and five major modules in the bacterial and fungal communities, respectively. In bacterial modules, modules ‘1’, ‘2’, and ‘3’ showed significantly negative correlations with soil chemical properties indicating they can be important in poor environments. In the fungal modules, the modules ‘3’, ‘4’, and ‘5’ showed significant positive correlations with soil chemical properties. Furthermore, module ‘2’ showed positive correlations with dry weight, fresh weight, number of rootlets, and root diameter. Among the fungal modules, the module ‘5’ had 6 keystone taxa, indicating that this module is critical for the stability of the fungal community in the rhizosphere soils. These results of this study indicate the vital role of microbial community to the WSG cultivation environments.

PAM-8

Exploration of Nitrogen-fixing and Nitrous oxide-reducing Bacteria from Legume Roots and Soils

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To promote sustainable agriculture, microbial-based technologies that reduce dependence on chemical fertilizers and lower greenhouse gas emissions are gaining attention. This study aimed to identify soil microorganisms with both nitrogen fixation and nitrous oxide (N_2O) reduction capabilities. Soil samples were collected from agricultural lands and natural environments in Korea and cultivated for one month. Root nodules and rhizosphere soils of plants were inoculated on Modified Arabinose-Gluconate (MAG) medium, leading to the isolation of viscous, white colonies. These isolates were screened for nitrogen fixation using a Bromothymol blue-based assay. Strains showing color change were selected and identified via 16S rRNA gene sequencing. Phylogenetic analysis revealed that the isolates belonged to the genera *Pseudomonas*, *Erwinia*, *Rahnella*, and *Bacillus*. To assess N_2O reduction ability, PCR targeting Clade I and II of the N_2O reductase gene (nosZ) was conducted for each strain. Results showed the potential of some strains to harbor nosZ genes, suggesting their role in reducing N_2O emissions. This study indicates the potential of isolating diverse soil bacteria with dual functions-nitrogen fixation and greenhouse gas mitigation. Such microbial resources can contribute to developing eco-friendly agricultural practices and reducing the environmental impact of conventional farming methods.

PAM-9

Vesicle-Based Delivery of *Bacillus*-Derived Lipopeptides Improves Stability and Enhances Antifungal Efficacy in Field Application

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Cyclic lipopeptides (CLPs) produced by *Bacillus velezensis* KB21—primarily fengycin, iturin, and surfactin—exhibit strong antifungal activity. However, their low water solubility and environmental instability limit field-level application. This study developed a vesicle-based delivery system using phospholipids and polysaccharides to improve the stability and efficacy of CLPs. Formulation parameters were optimized for particle integrity, encapsulation efficiency, and sustained release. Transmission electron microscopy and Fourier-transform infrared spectroscopy confirmed successful incorporation of CLPs and chemical interactions with coating materials. Dynamic light scattering showed increased particle size and reduced polydispersity with increasing coating concentrations, indicating stabilization. In vitro assays demonstrated dose-dependent inhibition of *Colletotrichum acutatum* and *Magnaporthe oryzae*. Field trials, including drone-assisted application, showed significant disease suppression and enhanced plant health. A strong positive correlation ($R > 0.9$, ***$P < 0.001$) was observed between filtrate concentration, surface tension reduction, and fungal inhibition. These results support the use of vesicle-based delivery systems to enhance the environmental performance of microbial metabolites and highlight their potential for sustainable crop protection in real-world conditions.

PAM-10

Structure-guided Engineering of TtgR-based Whole-cell Biosensors for Selective and Quantitative Detection of Flavonoids

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TtgR, a transcriptional repressor from *Pseudomonas putida*, plays a key role in regulating multidrug resistance by controlling the expression of genes such as the *ttgABC* efflux pump in response to various ligands. Despite its broad specificity—interacting with antibiotics, phloretin, and flavonoids like quercetin and naringenin—TtgR represents a promising candidate for the development of transcription factor (TF)-based biosensors. In this study, we utilized TtgR and its native promoter region (P_{ttgABC}) as genetic components to construct TF-based biosensors in *Escherichia coli*. By coupling TtgR and P_{ttgABC}, we developed a biosensor responsive to diverse flavonoids, including flavanones, flavones, and flavonols. To enhance the selectivity and specificity of the biosensor, we performed genetic engineering on the TtgR binding pocket, targeting residues critical for ligand recognition. Notably, biosensors based on wild-type TtgR and the TtgR N110F mutant were capable of quantifying resveratrol and quercetin at concentrations as low as 0.01 mM with over 90% accuracy. Although the precise molecular mechanisms remain to be fully elucidated and further optimization is needed, the biosensors developed in this study demonstrate strong potential for application in a wide range of fields. This work lays the foundation for future research that could extend the utility of TtgR-based biosensors in synthetic biology, metabolic engineering, and beyond.

Poster Presentation

PAM-11

Effect of streptomycin on the growth characteristics of soil-isolated microorganisms

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In an agricultural environment, antibiotics such as streptomycin (ST) are commonly used to treat crop and livestock diseases. However, their use poses a risk of residual accumulation in soil and water systems. Bioaugmentation using microorganisms is a promising strategy for mitigating such antibiotic residues. This study aimed to identify soil-derived microorganisms with the potential to degrade ST and to investigate their growth characteristics under ST exposure. Three ST-resistant strains – MFB1, MFB5, and 2MFB – were isolated from agricultural soil. The minimum inhibition concentration (MIC) for MFB1, MFB5, and 2MFB were approximately 0.2, 1.6, and 15.6 µg/mL, respectively. Growth response assays revealed that MFB1 and MFB5 exhibited decreased growth with increasing ST concentrations. In contrast, 2MFB showed five distinct growth patterns depending on ST concentrations: complete inhibition, delayed death, delayed growth, overgrowth, and normal growth. Biofilm formation analysis showed no significant change in MFB1. In MFB5, ST treatment enhanced biofilm formation, with biofilms quantity inversely proportional to ST concentration. Notably, 2MFB exhibited maximal biofilm formation at concentrations near its MIC. These findings provide insights into the response mechanisms of soil microorganisms to ST and suggest their potential utility in bioaugmentation. Further studies are necessary to evaluate their applicability under diverse environmental conditions and to optimize their use in antibiotic-contaminated sites.

PAM-12

Robustness of Cellulase Activity Under Limited Water Condition

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Cellulase uses water to break down cellulose into glucose. Cellulase activity, therefore, can be modulated by soil water content. Yet, we lack knowledge about how cellulase activity changes along a gradient of soil water content, a common condition under changing precipitation (e.g., drought and rain). Here we assessed cellulase activity in two artificial soils (loam and silt loam) as gravimetric water contents (GWC) decreased 40% to 5%. The experimental setup included endo-1,4-β-glucanase as cellulase and 4,6-O-3-ketobutylidene-4-nitrophenyl-β-D-cellopentaoside as substrate. Cellulase was active even at 5% GWC, retaining approximately 75% of the activity compared to that at 40% GWC. The sustained enzymatic activity led to the accumulation of glucose in dry soil, which may serve as a substrate for microbial respiration once the dry condition is relieved by rain.

PAM-13

Activation of plant defense responses by a chitinase-producing rhizobacterium mitigates cobalt stress in soybean (*Glycine max* L.)

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Although chitinase-producing bacteria hold promise for agricultural applications, their role in alleviating abiotic stress has not been fully elucidated. In this study, we evaluated the effect of combined treatment with chitin and a chitinase-producing bacterium on cobalt (Co) resistance in soybean. The chitinase-producing *Pseudomonas iranensis* JS80 exhibited chitinase activity of 144.55 U/mL and Co tolerance (>3 mM). Chitin treatment alone significantly upregulated the expression of *CERK1* and *RLCK* by 245% and 47%, respectively, whereas co-treatment with JS80 further enhanced their expression to 287% and 194%. Their activation was accompanied by increased expression of *MAPK3-1*, *MAPK6-1*, and *CaMK1*, which were upregulated by 11%, 135%, and 123%, respectively. Moreover, defense-related genes also upregulated. Simultaneously, Co stress altered phytohormonal levels—salicylic acid (SA) increased by 101%, while abscisic acid (ABA) and jasmonic acid (JA) decreased by 13% and 51%, respectively. The combined treatment further elevated SA levels by 34% and significantly reduced ABA and JA levels by 22% and 15%, respectively. These results suggest that co-application of chitin and a chitinase-producing bacterium reprograms pattern-triggered immunity (PTI) signaling and phytohormone crosstalk, supporting its potential utility in enhancing plant resilience under abiotic stress conditions.

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PAM-14

Whole-Genome Sequencing of the Bacterium *Bacillus amyloliquefaciens* PgBE99, with antifungal activities against fungal disease associated with ginseng leaves

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Panax ginseng is cultivated in shaded fields at a single location for 4 to 6 years, during which time fungicides with identical or similar active ingredients are repeatedly applied to control aerial diseases. This practice can lead to the emergence of fungicide-resistant pathogens, highlighting the importance of using biological control methods for safer disease management. In our previous study, we isolated endophytic bacteria from various tissues, ages, and cultivars of ginseng. Among the 311 isolates, 15 strains inhibited the hyphal growth of all tested pathogens. Notably, *Bacillus amyloliquefaciens* PgBE99 exhibited antifungal activity in a detached leaf assay. Furthermore, we analyzed the whole genome sequence of PgBE99, which revealed a single contig with a genome size of 4,413,514 bp and a GC content of 45.8%. Several gene clusters related to antifungal activity were predicted. Based on these findings, *B. amyloliquefaciens* PgBE99 is considered a promising candidate for development as a biocontrol agent to protect ginseng from airborne fungal pathogens.

Poster Presentation

PAM-15

Microalgae Anaerobic Digestion for Enhanced Methane Production

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Anaerobic digestion of microalgae presents a promising strategy for renewable methane production while contributing to atmospheric CO_2 reduction. This study assessed the methane production potential of two strains of the green microalga *Tetradesmus obliquus* (AG60 and AG10) using seed sludge from a municipal wastewater treatment plant as the microbial inoculum. To enhance biomass degradation, zero-valent iron (ZVI, Fe^0) was added to facilitate improved hydrolysis of microalgal cells. Methane yields from both microalgal treatments significantly exceeded the control (93.2 mL/g volatile solids [VS]), with AG60 and AG10 producing 139.7 mL/g VS and 261.7 mL/g VS, respectively—levels comparable to those achieved with pretreated microalgae. Quantification of the methanogen-specific *mcr*A gene revealed an increase in methanogenic populations, particularly hydrogenotrophic methanogens such as *Methanobacterium*, suggesting a shift toward hydrogenotrophic methanogenesis. Microbial community analysis showed an enrichment of cellulolytic bacteria, indicating effective microalgal biomass degradation that likely contributed to enhanced methane production. These findings demonstrate the feasibility of using *T. obliquus* as a substrate for anaerobic digestion and provide valuable insights into microbial dynamics that support the development of efficient biogas systems for renewable energy generation and climate change mitigation.

PAM-16

Comparative Analysis of Scalp Microbiome Across Healthy, Problematic, and Alopecic Conditions

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The scalp microbiome plays a critical role in regulating scalp health, including sebaceous activity, inflammation and hair loss. However, comprehensive studies comparing microbial shifts across different scalp conditions remain limited. This study aimed to analyze compositional and functional differences in scalp microbiome among healthy, problematic, and alopecic Korean individuals. Scalp samples were collected from 123 Korean female adults and categorized into three groups. Microbiome analysis was conducted based on long read 16S rRNA amplicon sequence data, generated by the PacBio Sequel IIe system. Sebum measurements revealed significantly higher oiliness in both the problematic and alopecic scalp groups compared to the healthy controls, suggesting a physiological association between excess sebum and scalp conditions. Microbial taxonomic analysis showed that while *Cutibacterium acnes* was predominant in the healthy group, both problematic and alopecic groups exhibited a marked shift toward *Cutibacterium namnetense* dominance. This species-level displacement may reflect microenvironmental changes related to altered lipid content or inflammatory status. In terms of microbial diversity, the alopecic group showed significantly higher α-diversity compared to the healthy controls, indicating a more heterogeneous and possibly dysbiotic microbial community. These findings demonstrate that increased abundance of *C. namnetense* in problematic and alopecic scalps, alongside elevated sebum levels and microbial diversity, suggests that dysbiosis and altered lipid metabolism may contribute to scalp inflammation and hair loss.

PAM-17

Transcriptomic Analysis of *Xanthomonas oryzae* pv. *oryzae* Under Microgravity: Insights into Pathogenicity Modulation and Adaptive Strategies

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Space agriculture has been emerging as a crucial technology for sustainable long-term space exploration and habitation. To do so, we first need to understand the physiological, pathological, and ecological changes that occur in crop plants, pathogens, beneficial microorganisms, and their interactions under the unique environmental factors of space, such as microgravity and UV-rich light conditions. This study aims to investigate the changes of a pathogenic bacteria (*Xanthomonas oryzae* pv. *oryzae*, *Xoo*) under microgravity. We analyzed the transcriptome of *Xoo* cultured in microgravity to elucidate the changes most likely to occur in space conditions. Transcriptomic analysis revealed that oxidative stress responses, defense mechanisms, and epigenetic regulation enhanced metabolic pathway activation, while signal transduction, pathogenicity regulation, amino acid, and lipid metabolism were suppressed. These results suggest that under microgravity conditions, *Xoo* activates energy metabolism and oxidative stress defense mechanisms while simultaneously suppressing its virulence and signaling capabilities, indicating an adaptive strategy to environmental changes. This implies a potential shift in the survival strategy and a reduction in pathogenicity of the bacterium under space conditions. Future results from this study will not only provide information on changes in the biology of crops and microorganisms in space environments, but also help develop optimized crop cultivation technologies suitable for closed-ecosystem agricultural systems in both space and terrestrial extreme environments.

PAM-18

The Characteristics of Microbial Communities in Greenhouse Cultivation Soils in Jeonnam Province

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Soil microbes play an important role for the soil health and material (nutrient) circulation and agricultural ecosystem. Therefore, in order to predict and prepare for future changes in the agricultural environment, it is necessary to investigate the distribution pattern and diversity of soil microorganisms, which are important indicators of the soil ecosystem. This study was conducted to evaluate the characteristics of microorganisms distributed in greenhouse cultivation soils in the province. Topsoil from twenty-five greenhouse cultivation soils in the Jeonnam province was collected and analyzed for Biomass C and dehydrogenase activity, and microbial distribution and diversity were analyzed through illumina NGS analysis. The microbial biomass C of greenhouse cultivation soils was 436.1 kg^{-1} and dehydrogenase activity was 219.1 μg TPF g^{-1} 24h^{-1}. As a result of quantifying the richness estimators for bacteria, the ACE index was 3,497 species and the Chao index was 3,701 species. For fungi, the ACE index was 698 species and the Chao index was 753 species, which were found to be somewhat higher compared to those in Korea. As a result of analyzed bacteria at the phylum level, Firmicutes was the highest with 36.01%, followed by Proteobacteria 20.31% and Actinobacteriota 12.96% and Chloroflexi 6.58%. At the fungi, Ascomycota was the highest with 49.32%, followed by Mortierellomycota 14.95%, Basidiomycota 7.33%, Mucoromycota 2.35%.

PAM-19

Isolation of Laccase-producing Bacteria from Diverse Environments and Their Application to Decolorize Textile Dyes

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Laccase is a multicopper oxidase that directly extracts one electron from substrates and transfers it through a continuous process within the enzyme to O_2. Additionally, it produces only H_2O as a byproduct of the enzymatic reaction without requiring cofactors. In this study, our aim is to explore laccase-producing bacteria from diverse environmental and determine their potential for the biodegradation of textile dyes. Environmental sources were collected including waste plastic, straw, wood, and soil. Samples were enriched with guaiacol. Pure isolates were screened using 2,6-dimethoxyphenol. laccase activity was determined using the supernatant of the isolates using Cu^{2+} to induce favorable enzyme conformation. Additionally, decolorization of common textile dyes was investigated using the isolates, including triarylmethane and azo dyes. Notably, total thirteen isolates were identified as *Pseudomonas* spp.. Interestingly, the isolates showed increased enzyme activity in the presence of Cu^{2+}. Among them, Pseudomonas sp. strain B3 (3.11 μmol/min) and C5 (3.28 μmol/min) exhibited the highest laccase activity against 2,6-DMP, which were isolated from the surface of straw and waste plastic, respectively. Furthermore, strain A4-A2, B3, C4, and C5 decolorized 0.137 mM of triarylmethane and azo dyes. Taken together, the results of this study highlight that laccase-producing bacteria, *Pseudomonas* spp. isolated from diverse environments have the broad substrate ranges from simple lignin-mimicking molecules to various dyes, and promising potential in biotechnology.

PAM-20

Characterization of indole-3-acetic acid (IAA)-producing rhizobacteria with potential to alleviate salt stress in plants

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Inappropriate irrigation, climate change, and other factors have led to the aggravation of salinity in soils, posing significant challenges to sustainable agriculture. Salinity stress is an important abiotic factor that seriously affects crop growth and productivity. Some plant growth-promoting rhizobacteria (PGPR) produce indole-3-acetic acid (IAA), which promotes root development and enhances water and nutrient uptake efficiency, improving plant tolerance to salinity. To identify the microbial candidates which potentially alleviate saltinity stress in crops, we isolated IAA-producing PGPR and evaluated their salt tolerance. 109 bacterial strains were isolated from the rhizosphere collected in Busan and Miryang, Korea. We evaluated multiple plant growth promoting traits, including exopolysaccharide production, phosphate solubilization, siderophore production and IAA production. Based on the result, 41 promising isolates were selected. They were exposed to high-salinity conditions (3, 10, and 20% NaCl). Among them **JY81** exhibited the highest salt tolerance and was subsequently selected for further investigation. JY81 was subjected to 16S rRNA sequencing, which revealed a 99% similarity to *Rossellomorea arthrocnemi*. Our results showed that **JY81** produces IAA at 34.30 ng/mL and secretes metabolites demonstrate the potential of **JY81** to alleviate salt stress in crops, highlighting its applicability to sustainable agricultural production under saline soil.

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PAM-21

Effects of Oil Cake Fertilization on Soil Chemistry and Bacterial Communities in a Jujube Orchard

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The application of organic fertilizers, such as oil cake (OC), is known to improve soil microbial processes, fertility, and crop yield. This study compared the effects of OC and chemical fertilizer (NPK) on soil bacterial diversity, community structure, and enzyme activity in a jujube orchard. OC-treated soils showed higher microbial diversity and distinct community compositions compared to NPK-treated soils, likely due to changes in soil pH, calcium, and magnesium levels. Bacterial groups such as Proteobacteria, Verrucomicrobia, and Bacteroidetes were significantly more abundant in OC-amended soils. These microbial shifts were observed from the phylum to the genus level and were associated with changes in soil chemical properties. Additionally, OC-treated soils contained higher predicted gene abundances related to biogeochemical cycling, organic matter decomposition, and plant growth promotion. Ordination analyses further highlighted the clear separation between treatments based on microbial community profiles and soil chemistry. Overall, the study demonstrates that oil cake fertilization can beneficially influence soil microbial diversity and ecosystem functions, supporting its use as a sustainable alternative to chemical fertilizers in jujube orchards.

PAM-22

Bacterial Carbonate Precipitation by Urease-Producing *Priestia* sp. Strain GS1 in Alkaline Conditions

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Urease is an enzyme that catalyzes the hydrolysis of urea into ammonia and carbon dioxide, leading to an increase in pH and the accumulation of insoluble calcium carbonate ($CaCO_3$) in the environment. This mineral plays an important role in soil aggregation and can be microbially induced under alkaline conditions. In this study, urease-producing bacteria were isolated from agricultural soil in Gangwon state, South Korea, to evaluate their potential for microbial-induced carbonate precipitation (MICP). Among ten isolates screened on Christensen's urea medium, strain GS1 showed the highest urease activity and visible $CaCO_3$ formation. The strain was identified as *Priestia* sp. based on 16S rRNA sequencing. Growth was optimized in tryptic soy broth (TSB) at pH 7−9, with peak biomass observed within 24 hours. Urease activity was quantified using the indophenol method, producing 3.263 mM of ammonium ions (0.027 U). Scanning electron microscopy (SEM) and energy-dispersive X-ray spectroscopy (EDS) analysis revealed irregular, angular $CaCO_3$ crystals smaller than 5 μm. These results indicate that *Priestia* sp. GS1 is capable of surviving in alkaline environments and can serve as a promising microbial resource for eco-friendly applications based on MICP.

Poster Presentation

PAM-23

Effect of Organic Fertilizer on Soil Bacterial Community Structure in a Jujube Orchar

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This study evaluated the impact of oil-cake (OC) organic fertilizer on soil bacterial diversity, community structure, and enzyme activity in a jujube orchard, compared to chemical fertilizer (NPK). Results showed that OC application significantly increased microbial diversity and altered community composition, likely due to long-term changes in soil chemical properties such as pH, calcium, and magnesium. Ordination analysis revealed distinct clustering of microbial communities between OC and NPK treatments, reflecting the influence of soil chemistry. OC-amended soils exhibited higher abundances of Proteobacteria, Verrucomicrobia, and Bacteroidetes, as well as greater predicted gene content related to biogeochemical cycling, organic matter decomposition, and plant growth promotion. These changes were evident from the phylum to the genus level. Overall, the use of OC fertilizer led to improved microbial diversity and enhanced soil ecosystem functions. The findings support OC as a beneficial organic amendment that can positively reshape soil microbial communities and support sustainable agriculture in jujube orchards.

PAM-24

Screening and Characterization of Polyhydroxyalkanoates (PHAs)-producing Bacteria Isolated from Diverse Environments and Their Potential for Bioplastic Production

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Polyhydroxyalkanoates (PHAs) are biodegradable polyesters produced by microorganisms under nutrient-limited conditions or an excess carbon source. PHAs are considered a promising alternative to conventional plastics due to their biodegradability. Among PHAs, polyhydroxybutyrate (PHB) is known for high thermal stability and applications, but commercialization is limited by high production costs and poor mechanical properties. This study aimed to isolate PHA-producing bacteria from oil-contaminated soil, rice straw, and waste plastic. One hundred colonies were screened on PHA-detection agar containing 2% glucose and Nile blue stain. PHA production was confirmed by Nile Blue A, Sudan Black B, and Nile Red staining. To determine optimal growth medium, isolates were incubated in LB, NB, TSB, and YPD. Three strains (JE1, JE2, and JE3) with rapid growth and strong UV absorbance at 312 nm were selected. These strains showed characteristic blue, black, and red signals in respective stains, confirming PHA accumulation. Identified as *Pseudomonas* spp., they showed optimal growth in YPD at 30°C after 24 h. A cell dry weight of 0.032 g/L was obtained from 500 mL culture. PHA production was further verified by Py-GC/MS, FTIR, and XRD, supporting their potential in bioplastic applications.

PAM-25

Exploration of Laccase-producing Bacteria from Alkaliphilic Environments and Their Decolorizing Activity against Industrial Synthetic Dyes

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Azo and triarylmethane dyes, a major synthetic dyes, have been widely used in textile industries. The dyes are recalcitrant to be degraded due to high chemical stability, especially under alkaline condition. Laccase, a multicopper oxidase, capable of oxidizing wide ranges of aromatic compounds, can be used for mild and biological strategies for biodegradation. This study was investigated to explore laccase-producing bacteria from diverse alkaliphilic environments and assess their potential to degrade industrial synthetic dyes. Alkaliphilic laccase-producing bacteria were screened from soils in Gangwon State and Busan, South Korea, using guaiacol and 2,6-dimethoxyphenol as substrates. Isolates were identified through 16S rRNA gene sequencing, and their enzymatic activities were evaluated in the presence of Cu^{2+}. In addition, the isolates were grown on agar plates containing five dyes, including aniline blue, methyl orange, methyl red, methyl blue, and malachite green. Among 12 isolates, 9 were identified as Pseudomonas spp. and the others were Brucella sp., Agrobacterium sp., and Bacillus sp. All isolates produced extracellular laccase, showing increased enzyme activity in the presence of Cu^{2+}. Notably, Pseudomonas sp. strain B4 and B5 exhibited a threefold increase in laccase activity with the addition of Cu^{2+}. Both strains effectively decolorized 0.137 mM of all dyes tested in this study. Further study should be performed to determine a potential application in the bioremediation of dye-contaminated industrial wastewater.

PAM-26

Silicate-solubilizing rhizobacteria enhance drought resilience in wheat (*Triticum aestivum* L.)

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Silicon enhances growth and productivity in wheat (*Triticum aestivum* L.) under drought stress by alleviating stress-induced damage. However, silicon in soils typically exists in insoluble silicate forms. Silicate-solubilizing rhizobacteria facilitate the bioavailability and uptake of silicon by converting insoluble silicates into plant-accessible forms. This study aimed to enhance the growth and yield performance of wheat through the application of various silicate-solubilizing bacterial strains — *Enterobacter kobei* MY1, *Enterobacter sichuanensis* MY2, *Pseudomonas kurunegalensis* MY3, and *Pseudomonas umsongensis* MY4, under pot experiments. These microbial strains were isolated from paddy field and screened for their ability to solubilize silicate. The isolates with superior ability were further characterized for multiple plant growth-promoting traits, revealing their potential as effective microbial inoculants for wheat cultivation. Pot experiments were conducted to evaluate the strain-specific effects on wheat morphology and physiology under drought stress. The results demonstrated that MY3 significantly promoted wheat growth, notably increasing shoot length (14.3%) and fresh weight (66.6%) under drought conditions. Moreover, chlorophyll content increased by 33.4%, with electron transport efficiency also enhanced. This study suggests that our strains exhibited the capacity to enhance wheat resilience and productivity under drought stress, highlighting their potential bio-inoculants as a sustainable strategy for improving crop performance under water deficit.

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Poster Presentation

PAM-27

Increasing Fucoxanthin Concentration in *Phaeodactylum tricornutum* by Optimization of Culture Conditions Using Response Surface Methodology

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Microalgae appear as an alternative source of fucoxanthin to meet the increased global demand for fucoxanthin-containing products. Fucoxanthin, exhibiting numerous health-promoting properties, is the most predominant carotenoid found in marine diatom *Phaeodactylum tricornutum*. Our study aimed to optimize light intensity, nitrate concentration, and cultivation time for enhancing fucoxanthin concentration in *P. tricornutum* using response surface methodology - central composite design (CCD). Particularly, following a three-factorial CCD design with three independent variables: light intensity (8.18–41.8 μmol photons/m^2/s), nitrate (0.0882–16.23 mM), and cultivation time (4–14 days), twenty experiments were conducted. The dependent variables considered for optimization included biomass concentration (g/L), fucoxanthin content ($mg/_{gdw}$), and fucoxanthin concentration (mg/L). In results, the highest fucoxanthin concentration of 10.44 mg/L, fucoxanthin content of 16.69 $mg/_{gdw}$, and biomass concentration of 1.11 g/L were obtained. ANOVA analysis revealed the significant effects of independent factors and the interaction between light intensity and cultivation time on fucoxanthin concentration ($p<0.05$). In validation test, *P. tricornutum* grown under the optimized conditions (light intensity, 25 μmol photon/m^2/s; nitrate concentration, 10.04 mM; cultivation time, 12 days) produced the maximum fucoxanthin concentration of 10.804±0.11 mg/L, which closely aligned to the predicted value of 10.813 mg/L. Thus, the error percentage between experimental and predicted values was approximately 0.083%, demonstrating the reliability of this model.

PAM-28

Integrated Biocontrol and Abiotic Stress Tolerance via *Bacillus*-Derived Lipopeptides and Functional Genomic Trait

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Bacillus velezensis KB21 and *B. amyloliquefaciens* HN7 produce cyclic lipopeptides (CLPs) that suppress pathogens and enhance plant tolerance to abiotic stress. This study investigated how fermentation optimization and strain-specific genomic features influence CLP production and stress adaptation. Under natural polymer-supplemented conditions, HN7 produced higher fengycin levels, exhibiting strong inhibition against *Fusarium oxysporum*, while KB21-derived iturin suppressed *Colletotrichum acutatum* and reduced pepper fruit lesions. KB21 treatment induced systemic resistance by upregulating PAL, GLU, and LOX genes. Genomic analysis revealed clusters for CLP biosynthesis, IAA/GA production, ion transport, and oxidative stress regulation. Under the salt stress, KB21 significantly improved cucumber growth by enhancing SOD, CAT, and POD activities and modulating key stress-related genes, including NHX, HKT, AQP, NCED, and CYP. Ion homeostasis improved via reduced Na^+ uptake and increased K^+ accumulation. These results demonstrate that *Bacillus*-derived lipopeptides act as multifunctional agents, enabling integrated pathogen control and abiotic stress tolerance through coordinated transcriptional and physiological responses. The findings provide a foundation for developing Bacillus-based biocontrol systems applicable to both biotic and abiotic challenges in sustainable agriculture.

PAM-29

Valorization of sulfonated polyethylene via Bio-Fenton reaction supported by *Desemzia* sp. strain C1

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The valorization of polyethylene has been widely studied as a strategy to upcycle plastic waste into value-added chemicals. However, conventional approaches such as pyrolysis typically require high temperatures and pressures along with costly catalysts, which require energy consumption and the utilization of fossil fuels. Hence, it increases the costs for operation but also raises the potential environmental concerns. As an alternative strategy, in this study, polyethylene activated by sulfonation was degraded via Bio-Fenton reaction supported by *Desemzia* sp. strain C1 at 30°C and pH 7, resulting in the production of oxalate. The oxalate production as a degradation metabolite of sulfonated polyethylene was verified by tracing the presence of ^{13}C-isotopes produced from Bio-Fenton degradation of ^{13}C-labeled sulfonated polyethylene. We believe this study suggests a new insight for the valorization of polyethylene via activation and a bacteria-mediated oxidative degradation system.

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PAM-30

Conferring non-strain-specific resistance to a potyvirus via overexpression of mutant potyviral coat proteins in soybean

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R-gene-mediated resistance in plants provides specific defense against pathogens but is often rapidly overcome by highly mutable plant viruses like potyviruses. To achieve durable, broad-spectrum resistance, we investigated a novel strategy targeting the cell-to-cell movement of viruses by disrupting virion assembly. Potyviruses, including soybean mosaic virus (SMV), move intercellularly as virions, and mutations in the coat protein (CP) that prevent virion formation can inhibit this movement. We examined the effect of expressing CP mutants (CP$_{R245A}$, CP$_{H246A}$, CP$_{D250A}$) in soybean. Transgenic soybean lines expressing CP$_{D250A}$ showed no systemic SMV infection and significantly reduced cell-to-cell movement, despite normal growth and development. This resistance was not due to RNA silencing, as CPD$_{D250A}$ lines did not accumulate CP-derived siRNAs or viral RNA, yet allowed SMV replication in initially infected cells and protoplasts. Importantly, CP$_{D250A}$-transgenic plants were resistant to multiple SMV strains, indicating non-strain-specific resistance. Conservation of CP$_{D250A}$-corresponding residues among potyviruses led to similar mutations in pepper mottle virus (PepMoV) and zucchini yellow mosaic virus (ZYMV), which also disrupted their systemic spread and intercellular movement. These findings support a model in which virion assembly is essential for potyviral movement, and disrupting this process through CP mutations can confer durable, broad-spectrum resistance. This strategy offers a promising alternative to R-gene-based resistance for controlling diverse potyvirus infections in crops.

Poster Presentation

PAM-31

Agricultural Applications of Pyrrolnitrin-Producing Burkholderia sp.: Effects on Plant Growth and Fungal Suppression

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Burkholderia is a genus within the phylum *Pseudomonadota*, commonly found in soil environments. These bacteria are known for producing diverse secondary metabolites, including pyrrolnitrin, a phenylpyrrole fungicide. Although pyrrolnitrin is rapidly photodegraded, it exhibits reactive oxygen species (ROS)-generating effects that match or exceed those of commercial fungicides like fludioxonil and fenpiclonil. This study aimed to evaluate the plant effects and disease control potential of pyrrolnitrin when applied through microbial treatments. Pyrrolnitrin was extracted from *Burkholderia* sp. O33 (KACC12815), cultured in nutrient broth for seven days, and purified via ethyl acetate extraction and column fractionation. Fractions without pyrrolnitrin were also tested against *Botrytis cinerea* (KACC43524). Potato dextrose agar was supplemented with pyrrolnitrin at its IC_{50} concentration, and fungal growth was monitored after 120 hours. The effects of *Burkholderia* sp. and pyrrolnitrin on lettuce seed germination and growth were assessed using OECD guidelines, with five concentrations differing by tenfold. Germination rates were recorded at 24-hour intervals, and growth was measured after 120 hours. Additionally, wounded lettuce leaves were treated with pyrrolnitrin or *Burkholderia* suspensions, followed by inoculation with *B. cinerea* to observe pathogen growth. Comparative analyses between treated and untreated lettuce were performed to determine in planta disease suppression. These results provide valuable insights into the agricultural potential of *Burkholderia* sp.

PAM-32

Microbial carbon availability decreases, but the degree of carbon limitation remains invariant along soil depth profiles

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Microbial carbon availability influences the rate of soil organic carbon decomposition. However, it remains unclear how much carbon is available to microbes and whether soil organic carbon content influences microbial carbon limitation. Here, we used the Michaelis–Menten parameters to estimate the available carbon to microbes and the degree of microbial carbon limitation along soil depth intervals (0-20, 20-40, 40-60 cm) at two sites with different soil organic carbon contents (H-SOC and L-SOC). Soil organic carbon and available carbon decreased across soil depth intervals at both sites. However, the proportion of estimated available carbon to the soil organic carbon remained unchanged across sites and soil depth intervals. Overall, microbes only decomposed 0.11% of soil organic carbon. Furthermore, the degree of carbon limitation was consistent across the soil depth profile and sites, indicating a common pattern of carbon limitation. These findings suggest that microbes may have utilized only a small fraction of soil organic carbon and experienced similar levels of carbon limitation regardless of soil organic carbon content.

PAM-33

A Novel Secreted Effector MGG40 from *Magnaporthe oryzae* Triggers Immune Responses and Cell Death in Rice

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Rice blast, caused by *Magnaporthe oryzae*, is a devastating disease that leads to annual yield losses of up to 30% in rice. In this study, we conducted a transcriptomic analysis to identify candidate fungal effectors involved in rice susceptibility. A total of 376 genes were differentially expressed during infection, among which 52 were predicted to encode secreted proteins using SignalP. Eight candidates with low molecular weight and signal peptides were selected as putative effectors. One of these, designated MGG40, localized to the extracellular space and induced cell death in *Nicotiana benthamiana* upon agro-infiltration. Recombinant MGG40 protein also triggered cell death and reactive oxygen species accumulation in rice suspension cells. Co-treatment with jasmonic acid further enhanced the immune response. Gene diversity and synteny analysis revealed that MGG40 is specifically conserved in rice-infecting *M. oryzae* strains. A deletion mutant of MGG40 exhibited no significant differences in vegetative growth, appressorium formation, or pathogenicity. However, MGG40 expression was strongly induced 48 hours post-inoculation, corresponding to the transition from biotrophy to necrotrophy. Furthermore, a yeast two-hybrid screen identified the rice protein OsDSK2a as an interactor of MGG40, which was further supported by AlphaFold structural prediction. These findings suggest that MGG40 functions as a rice-specific effector contributing to the modulation of host immune responses during *M. oryzae* infection.

PAM-34

Co-application of a Silicate-Solubilizing *Burkholderia* Strain and Slag Silicate Fertilizer Boosts Maize Biomass and Restructures the Rhizosphere Microbiome

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Silicate fertility in maize can be improved biologically as well as chemically. We tested this idea in pots by pairing a silicate-solubilizing *Burkholderia cepacia* strain (CD2) with a slag-based Si fertilizer. Plants given the microbial inoculant plus slag accumulated roughly 45 % more shoot biomass and 30 % more root biomass than those supplied with slag alone. Amplicon sequencing of 16S rRNA genes revealed that the combined treatment reshaped the rhizosphere, selectively amplifying classic P-mobilizers such as *Burkholderia*, *Bacillus* and *Pseudomonas*. The shift coincided with elevated signatures of organic-acid release and siderophore production, implying a multi-nutrient facilitation mechanism. These results suggest that co-delivery of Si-solubilizing bacteria and industrial slag could serve as a low-input route to higher maize yields while fostering a nutrient-efficient microbiome.

PAM-35

Comparison Growth and Antioxidant Activity of *Lysimachia mauritiana* Lam. by IAA Pruduction Optimized *Bacillus toyonensis* WS2-2

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Plant growth-promoting rhizobacteria(PGPR) is known to be involved in the growth and antioxidant activity of several plants. *Lysimachia mauritiana* Lam. is a medicinal plant native to Korea and is known to have antioxidant, antibacterial and antiviral activities. Several strains producing indole-3-acetic acid (IAA) were isolated from the rhizosphere soil of *Abelia spathulata*(NIBR0000120879). Among the isolated strains, *Bacillus toyonensis* WS2-2, which exhibited the highest IAA production, was selected for further study. The conditions for maximum IAA production were optimized for *B. toyonensis*. The conditions are temperature, pH, agitation rate, tryptophan concentration, carbon and nitrogen source. The conditions were confirmed to be 30°C, pH 7, 200 rpm, 15mM tryptophan, 1% saccharose and 1% tryptone. *B. toyonensis* cultured under those conditions was diluted 50-, 100-, 200- and 500-fold and treated with *L. mauritiana*, then growth and antioxidant activity were compared. As a result, compared to the control, shoot fresh weight was the highest at 1.27-fold in the 50-fold dilution, and root fresh weight was the highest at 1.1-fold in the 500-fold dilution. Antioxidant activities were higher in roots than in shoots, and the activities were higher in the order of 100, 50, 200, and 500-fold dilution. These results suggest that *B. toyonensis* WS2-2 possesses significant potential as PGPR capable of enhancing both biomass production and antioxidant activity in medical plants.

PAM-36

Effect of *Rahnella bruchi* DSM 27398^T Cultured for Maximum IAA Production on *Lysimachia mauritiana* Lam. Growth

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Lysimachia mauritiana Lam., a medicinal plant endemic to Korea, has been reported to possess significant antioxidant, anticancer, antibacterial, and antiviral activities. In this study, indole-3-acetic acid (IAA) producing bacterial strains were isolated from the rhizoplane soil of *Aster* × *chusanensis* native to Ulleungdo, Korea. Among them, *Rahnella bruchi* DSM 27398^T showed the highest IAA production and was selected for further study. Optimal conditions for IAA production were determined using different parameters, including temperature, pH, agitation speed, tryptophan concentration, and various carbon and nitrogen sources. Maximum IAA yield was found at 25°C, pH 7, 200 rpm, 18 mM tryptophan, 0.5% glucose, and 3% tryptone. Following cultivation under optimized conditions, *R. bruchi* was diluted at ratios of 1:50, 1:100, 1:200, and 1:500, and applied to *L. mauritiana* to evaluated its effects. Compared to the control, both shoot (1.11-fold) and root (1.10-fold) fresh weight increased the most at 500-fold dilution. Antioxidant activities were higher in the root parts than in the shoot parts, with the highest activity observed at a 200x dilution, followed by 100x, 500x, and 50x.

PAM-37

Microbial Engraftment and Symptom Improvement Following FMT in Dogs with Chronic Enteropathy

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Chronic enteropathy (CE) is a persistent gastrointestinal disorder that affects companion animals such as dogs. This study explored the therapeutic potential of fecal microbiota transplantation (FMT) in dogs diagnosed with CE. A healthy donor dog was selected after polymerase-chain-reaction screening for 12 common canine enteric pathogens and confirmation of normal urine and blood panels. Donor feces were processed into oral FMT capsules and administered to 16 CE-affected dogs. Fecal samples were collected at baseline and at 10, 30, and 60 days after FMT, then analyzed by 16S rRNA gene sequencing on the MiSeq platform. Alpha diversity, a metric describing within-sample richness and evenness, increased steadily throughout the study, indicating recovery of gut ecological complexity. Beta diversity, which compares microbial community composition between samples, shifted toward the donor profile, showing that recipient microbiotas became more similar to that of the healthy donor. SourceTracker analysis confirmed robust engraftment of donor-derived taxa. Clinically, most recipients exhibited marked improvement in gastrointestinal signs following FMT. These findings demonstrate that oral FMT is a safe and promising intervention for managing CE in dogs by re-establishing a health-associated gut microbiome, underscoring the growing potential of microbiota-based therapies in veterinary medicine.

PAM-38

Comparative Analysis of Microbial Community Structure and Pathogen Persistence in Municipal Wastewater and Livestock Manure Treatment Facilities

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This study conducts a comparative evaluation of microbial community dynamics and pathogen retention across treatment processes in a livestock manure treatment plant (LMTP) and a municipal wastewater treatment plant (WWTP), each receiving distinct influent substrates. High-throughput 16S rRNA gene sequencing combined with quantitative PCR was employed to characterize microbial composition and to quantify absolute abundances of key potential pathogens. In the LMTP influent, anaerobic fermentative and methanogenic taxa—most notably *Candidatus Cloacamonas* and *Methanobrevibacter*—dominated, then gradually declined in abundance through successive treatment stages. Conversely, the WWTP influent was enriched in intestinal-origin genera such as *Faecalibacterium* and *Blautia*. Within the WWTP's sludge treatment, nitrifying bacteria like *Nitrospira* selectively proliferated, while during anaerobic digestion, methanogens such as *Methanothermobacter* became more abundant, reflecting functional reorganization under changing physicochemical conditions. Overall, both facilities exhibited markedly different initial community structures corresponding to their influent characteristics, and these communities underwent substantial compositional and functional shifts as treatment progressed. Although total microbial loads were significantly reduced in final effluents, pathogenic genera—including *Legionella* and *Acinetobacter*—persisted at low but detectable levels. These findings underscore the necessity for precise operational control, continual microbial surveillance, and the integration of advanced treatment technologies to mitigate pathogen release.

PAM-39

The Crosstalk between Vaginal, Urinary, and Anal Microbiome in Female Urogenital Tract Health

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The health of the female genitourinary tract (FGT) is closely associated with the structure of its resident microbial communities, which play a crucial role in defending against pathogens and maintaining physiological balance. This ecosystem is shaped by dynamic interactions among the vaginal microbiome (VM), urinary microbiome (UM), and gut microbiome (GM). The VM is categorized into community state types (CSTs) based on the predominant bacterial taxa, and disruptions in this balance have been linked to various FGT-related conditions. These microbial niches not only influence local host environments but also serve as reservoirs for the exchange of microbial strains facilitating microbial adaptation. In this study, matched triplet samples—vaginal and anal swabs, along with urine specimens—from 40 participants were analyzed using whole metagenome sequencing to characterize microbiome compositions across anatomical sites. Based on vaginal CSTs, the UM exhibited distinct compositional differences and strong correlations with vaginal CSTs. Notably, the presence of Lactobacillus crispatus and Gardnerella vaginalis strongly influenced both the VM and UM. Lactobacillus spp., Prevotella spp., and Streptococcus spp. were the most commonly shared genera across the vaginal, urinary, and anal sites. These findings underscore the intricate interplay of microbiota within the female urogenital tract and its disruption during dysbiosis, revealing potential ecological links between anatomical niches and emphasizing the importance of translational research for therapeutic and preventive strategies.

PAM-40

Time Course for Solubility of Imipenem as an Antibiotic against *Pseudomonas aeruginos*

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Imipenem is a broad-spectrum beta-lactam antibiotic from the carbapenem class, effective against severe bacterial infections caused by various organisms. However, it is rapidly inactivated in the kidneys by the enzyme renal dehydropeptidase I (DHP-I), which limits its effectiveness. To enhance its efficacy, Cilastatin is co-administered with Imipenem. Cilastatin inhibits DHP-I, preventing the breakdown of Imipenem and thereby increasing its effectiveness and safety. The chemical structure of Imipenem degrades through various mechanism including hydrolysis, oxidation, and photolysis. Thus, the stability and kinetics of degradation of imipenem was investigated. The observation of Imipenem solution was monitored at regular time intervals for 48 hours, showing a gradual color change from yellow to deep red. Imipenem gradually decreased at the same conditions over the dissolution time by HPLC analysis at the wavelength of 293 nm. In addition, the results of measuring the antibacterial activity of imipenem samples against *Pseudomonas aeruginosa* by dissolution time showed that the antibacterial activity decreased during the dissolution time, in a dependent manner.

PAM-41

Chronic PET-Microplastic Exposure Triggers Hyperphagia and Gut Microbiome Perturbation: Implications for Metabolic Health

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Microplastic pollution has emerged as a significant environmental concern, with increasing evidence suggesting its adverse effects on human health. However, the mechanisms linking microplastic exposure to metabolic disruption remain poorly understood. Here, we demonstrate that chronic microplastic exposure in mice leads to significant alterations in feeding behavior through disruption of the gut-brain axis. Using a 15-week exposure model with microplastics we found that microplastic treatment resulted in increased food consumption without initial changes in body weight. Notably, ddPCR analysis revealed a significant reduction in gut microbial populations, suggesting compromised mucosal habitat. We hypothesize that these alterations in the mucosal microbiome lead to disrupted microbe-host interactions, subsequently affecting gut hormone secretion. DEXA analysis showed increased fat accumulation and decreased lean mass ratio in MP-treated mice, accompanied by reduced energy expenditure. Our findings reveal a novel mechanism whereby microplastic exposure impairs the gut mucosal microbiome, leading to dysregulation of host-microbe interactions, altered gut hormone signaling, and subsequent hyperphagia. This study provides crucial insights into how environmental microplastic exposure may contribute to metabolic disorders through disruption of the gut-brain axis.

PAM-42

Differential Impacts of Dietary Fibers on the Human Gut Microbiome in an *In Vitro* Fermentation Model

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Dietary fiber plays a critical role in modulating human gut health, primarily by serving as a substrate for microbial fermentation within the intestinal environment. Fermentation of fiber is known to result in the production of short-chain fatty acids (SCFAs), shifts in gut microbiota composition, and potential enhancement of intestinal barrier function. However, the effects of different types of dietary fiber on the human gut microbiome remain incompletely understood. In this study, we aim to investigate how various types of dietary fiber influence the human gut microbiota using an in vitro fecal fermentation model. By comparing the fermentability of individual fibers and their combinations, this research seeks to provide novel insights into fiber-driven microbial dynamics. The findings are expected to contribute to a deeper understanding of fiber–microbiome interactions and support the development of fiber-based dietary strategies to promote gut health.

Poster Presentation

PAM-43

First-Crop or Replant? Microbial Fingerprints Decode Ginseng Soil History and Rusty Root Risk

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Repeated cultivation of Korean ginseng (*Panax ginseng* C.A. Meyer) accelerates soil fatigue and heightens the risk of Ginseng Rusty Root (GRR). Because replanted (연작지) fields often appear healthy until symptoms emerge, the ability to distinguish them from first-crop (초작지) fields is critical for timely management. We sampled bulk soils from first-crop, healthy-replanted, and GRR-replanted plots in four Korean provinces and profiled the V4 16S rRNA region with QIIME2. Relative-abundance tables were adjusted for site-level covariates using multivariable association modelling, then subjected to a machine-learning pipeline: (i) ensemble classification, (ii) feature ranking by mean decrease accuracy, (iii) recursive feature elimination to derive a minimal predictor set, and (iv) SHAP interpretation to visualise taxon-level contributions. Our workflow culminated in a concise panel of microbial indicators capable of separating first-crop from replanted soils regardless of geographic origin or disease status. These candidate biomarkers lay the groundwork for a rapid diagnostic index that can flag high-risk fields, guide sustainable soil management, and ultimately reduce GRR incidence in ginseng cultivation.

PAM-44

Soil Microbial Community Responses to Biofumigation Using *Brassica juncea*: A Temporal Comparison Based on the Presence or Absence of Glucosinolates

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Biofumigation, utilizing isothiocyanates released from glucosinolate hydrolysis in cruciferous plants, offers a sustainable alternative to chemical fumigation. In addition to its biocidal effects, it also contributes organic matter, potentially enhancing beneficial microbial activity and suppressing soilborne pathogens. However, its efficacy is influenced by biomass handling methods and environmental factors, requiring site-specific evaluation.

This study investigated the effects of Brassica juncea-based biofumigation on soil microbial communities. A four-week treatment period was established, followed by comprehensive profiling of soil microbial communities. Six treatments were designed to assess application strategies and glucosinolate volatilization:

(1) In situ biofumigation (ISBF);
(2) Ex situ biofumigation (ESBF);
(3) In situ biofumigation with volatilized biomass (ISBF-V), where biomass was chopped and left for 24 hours prior to incorporation;
(4) Ex situ biofumigation with volatilized biomass (ESBF-V);
(5) In situ non-fumigated control (ISNF);
(6) Ex situ non-fumigated control (ESNF).

By comparing microbial dynamics across treatments, this study aims to elucidate how biofumigation and biomass preparation influence soil microbiota. The results will contribute to understanding the ecological mechanisms of biofumigation and inform sustainable soil management practices tailored to temperate cropping systems.

PBD Bio-health/Drug development

PBD-1

Distinct Microglial Responses to Non-Neurotropic and Neurotropic Influenza A Virus Strains Under Innate Immune Priming

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Influenza virus infection in the central nervous system (CNS) can trigger neuroinflammation linked to neurodegenerative diseases. Microglia, the CNS's resident immune cells, play key roles in detecting pathogens and regulating inflammation. This study compared the responses of human microglial cells (HMC3) to two influenza A virus strains: non-neurotropic A/PR/8/34 (PR8) and neurotropic A/NWS/33 (S33), under both basal and LPS-primed immune conditions. Microglia were pre-treated with lipopolysaccharide (LPS; 10 µg/mL) for 24 hours prior to infection (MOI 0.1). PR8 induced pro-inflammatory cytokines (CCL2, IL-6, TNF-α, IL-1β) and activation markers (CD40, CD68, CD86, CD206, HLA-II), with TNF-α strongly upregulated in non-primed conditions. S33 triggered robust production of CCL2, IL-6, and TNF-α, along with significant upregulation of CD40, CD68, CD206, and HLA-I in both primed and unprimed cells. Notably, CCL2 levels peaked in LPS-primed S33-infected cells, indicating a heightened inflammatory response. Moreover, S33 infection resulted in greater viral nucleoprotein (NP) expression and HLA-I surface presentation than PR8, suggesting enhanced replication and antigen processing. These findings reveal distinct microglial activation patterns depending on influenza strain neurotropism and immune priming, emphasizing their role in shaping CNS immune responses during infection.

PBD-2

Avian Diversity in Ephemeral and Permanent Wetlands of Jeju Island

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Mountain wetlands support diverse avian communities, yet their ecological dynamics differ markedly depending on hydrological regimes. This study compared avian diversity and environmental conditions in two contrasting high-altitude wetlands on Jeju Island, South Korea: the ephemeral Soejilmot and the permanent Mulchat Oreum. From 2018 to 2023, we conducted monthly bird surveys, climate monitoring, invertebrate sampling, and fish assessments. In Soejilmot, avian diversity was positively correlated with invertebrate abundance, humidity, and precipitation. In contrast, diversity in Mulchat Oreum declined with increasing invertebrate abundance and wind speed. Fish presence, predominantly in the permanent wetland, was significantly associated with reduced invertebrate availability and lower avian diversity, suggesting trophic suppression effects. Vegetation composition showed no significant influence on species richness or diversity indices. Diet analysis indicated a higher proportion of insectivorous birds in the ephemeral wetland and more frugivorous species in the permanent one. These findings highlight the differential ecological functions of ephemeral and permanent wetlands. In particular, the ephemeral Soejilmot wetland supported higher species richness and provided favorable conditions for insectivorous birds, likely due to reduced fish predation and increased invertebrate availability. These results underscore the ecological significance of temporary wetlands, which may play a disproportionately important role in sustaining avian biodiversity under fluctuating environmental conditions.

Poster Presentation

PBD-3

Selective Thyroid Uptake of Technekitty injection (Tc-99m) in Feline Hyperthyroidism

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Feline hyperthyroidism is a common endocrine disorder in older cats, and early diagnosis is critical for effective treatment and improved prognosis. Therefore, the development of accurate and safe radiopharmaceutical-based diagnostic tools is essential. This study evaluated the cellular uptake characteristics of the Technekitty injection (Tc-99m), a diagnostic radiopharmaceutical developed for feline hyperthyroidism. In vitro experiments using FRTL-5 thyroid follicular cells and Clone 9 hepatocytes showed that the uptake of Tc-99m in FRTL-5 cells was 0.182±0.018%, approximately six times higher than in hepatocytes, indicating selective thyroidal accumulation. When combined with sodium iodide, the absorption was reduced by 38.2%. This suggests that, like iodine, Tc-99m is absorbed into thyroid cells via the sodium iodide transporter (NIS). In addition, in vivo biodistribution studies also confirmed specific accumulation of Technekitty injection (Tc-99m) in the thyroid gland. Containing only sodium pertechnetate (Tc-99m) as the active ingredient, the formulation shares identical pharmacological properties with Tc-99m products already in clinical use in the United States and Europe. Based on its selective thyroidal uptake and favorable pharmacokinetic profile, the Technekitty injection (Tc-99m) is expected to serve as a safe and effective radiopharmaceutical for the clinical diagnosis of feline hyperthyroidism.

PBD-4

Predicting the Fine-scale Habitat Suitability of an Endemic Species, Jeju Striped Field Mouse (*Apodemus chejuensis*) in Jeju Island, South Korea

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Species distribution modeling plays a crucial role in the conservation and management of wildlife, particularly for rare and endemic species. The Jeju Striped Field Mouse (*Apodemus chejuensis*) is a rodent species endemic to the Jeju Island of South Korea that requires targeted conservation efforts. This study aims to model habitat suitability of *A. chejuensis* in Jeju Island utilizing the Maximum Entropy (MaxEnt) algorithm to identify the key environmental variables influencing its distribution. After testing for multicollinearity, 48 occurrence records were integrated with 12 fine-scale environmental variables for the final projection. The model performance was evaluated by using the area under the receiver operating characteristic curve (AUC), response curves, variables relative importance, jackknife test and suitability map. The model demonstrated excellent predictive performance, yielding an AUC score of 0.82 ± 0.03. The model revealed that distance to Oreum (volcanic cone), grassland, and slope were the strongest predictors for its distribution. The model predicted that 2.12% of Jeju Island constitutes highly suitable habitat, while 4.06% is suitable. *A. chejuensis* was found to have a heterogenous distribution, predominantly concentrated in the island's mountainous region. These findings provide valuable insights into the conservation planning and implementation of monitoring and early-warning systems, particularly in human-dominated landscape where *A. chejuensis* faces increasing threats.

PBD-5

pH-Dependent Modulation of Nitrous Oxide Emission in *Nitrospira inopinata*

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Complete ammonia-oxidizing (comammox) bacteria, such as *Nitrospira inopinata*, are pivotal in the nitrification process. This study explored the effects of pH (5.5 – 9.0) on ammonia oxidation, NH_2OH and N_2O production, cellular growth, and transcriptomic profiles in N. inopinata. The organism demonstrated effective ammonia oxidation across a broad pH range, with optimal activity between pH 6.5 and 8.5. Ammonia oxidation rates and nitrate production peaked at pH 7.5, while maximal growth rates gradually transitioned from pH 6.5 to 7.5 during incubation. NH_2OH accumulation was highest at pH 7.5, whereas abiotic N_2O formation was notably enhanced at low pH, potentially due to chemical interactions between NH_2OH and NO_2^-. Transcriptomic analysis revealed significant upregulation of core nitrification genes (amoA, nxrA, nirK) at pH 6.5, along with increased expression of genes related to carbon metabolism and ATP synthesis. These transcriptional changes suggest an active metabolic adaptation under acidic stress. These findings provide novel insights into the physiological flexibility of *N. inopinata* and its adaptive responses to pH variation, contributing to a better understanding of pH-dependent nitrification and nitrogen oxide dynamics.

PBD-6

Bisphenol A Drives Exosome-Mediated Neuron-to-Glia Mitochondrial Transfer, Accelerating Neurodegeneration

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Bisphenol A (BPA), an industrial chemical prevalent in food and water containers and many consumer products, is a well-known endocrine disruptor owing to its estrogen-mimetic activity. BPA readily accumulates in the brain, where it induces mitochondrial dysfunction including elevated mitochondrial reactive oxygen species (mtROS) and dysregulated mitophagy. Here, we examined how these perturbations reshape exosome-mediated mitochondrial transfer and promote neurodegenerative phenotypes. In human SH-SY5Y neuroblastoma cells, high-dose BPA (100 µM) markedly increased mtROS and mitophagy; both effects were mediated by reduction in membrane estrogen receptor (mER) due to internalization by BPA. BPA also upregulated CHMP2B, a core component of the ESCRT-III complex that drives mitochondrial release, as evidenced by elevated TOMM20 protein and oxidative-phosphorylation mitochondrial RNAs (ND1-ND6, COX1-COX3) in the exosome fraction. In a HT-22 – astrocyte co-culture, BPA stimulated neuronal release of mitochondrial cargo into the medium, which was subsequently taken up by astrocytes. This neuron-to-glia mitochondrial transfer coincided with a significant rise in astrocytic GFAP, indicating reactive astrogliosis. Collectively, our data suggest that BPA triggers CHMP2B-driven exosomal export of neuronal mitochondria, depleting neuronal mitochondrial reserves, activating glia, and ultimately fostering neurodegenerative change.

Keyword: BPA, Exosome Secretion, Neurodegeneration, Mitochondrial transfer

Poster Presentation

PBD-7

Hepatocyte TonEBP promotes metabolic dysfunction-associated steatohepatitis by transcriptionally activating multiple neutrophil-attracting chemokines

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Metabolic dysfunction-associated liver disease (MASLD) is a chronic metabolic disorder primarily driven by overnutrition, which can progress to metabolic dysfunction-associated steatohepatitis (MASH) and, eventually, hepatocellular carcinoma (HCC). The transcription factor tonicity-responsive enhancer-binding protein (TonEBP) has been implicated as a risk factor associated with poor prognosis, tumor recurrence, and metastasis in HCC patients. However, its role in the pathogenesis of MASLD and MASH remains poorly understood. Here, we investigated the potential involvement of hepatic TonEBP in the development of diet-induced MASLD and MASH using a hepatocyte-specific TonEBP-knockout mouse model. TonEBP promoted the progression of MASLD/MASH in a nutrition-dependent manner. Deletion of TonEBP ameliorated steatohepatitis, as well as associated inflammation, fibrosis, and tumorigenesis, leading to improved liver function. Neutrophil chemotaxis-related genes, including *IL-8*, *CXCL1*, and *CXCL2*, were identified as direct transcriptional targets of TonEBP in hepatocytes. These findings reveal that TonEBP promotes hepatic neutrophil infiltration, a key process in the pathogenesis of MASLD/MASH. Our results suggest that hepatocyte-specific TonEBP inhibition is a promising therapeutic strategy to mitigate MASLD/MASH and reduce the risk of progression to HCC.

PBD-8

Polymethoxyflavones from *Citrus sunki* Leaves Attenuate Renal Dysfunction in Oxidative Stress-Induced Acute Kidney Injury

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Acute kidney injury (AKI) caused by ischemia/reperfusion (I/R) is a serious clinical condition with high morbidity and mortality, and currently lacks effective therapeutic strategies. Polymethoxyflavones (PMFs), a class of flavonoids abundant in citrus and traditionally used in herbal medicine, possess diverse pharmacological properties, including antioxidant and anti-inflammatory activities. This study aimed to investigate the renoprotective effects of a PMF-enriched fraction derived from *Citrus sunki* leaves—containing high levels of tangeretin and nobiletin—against I/R-induced AKI in mice. Additionally, the underlying molecular mechanisms of the protective effects were explored. Oral administration of the PMF-enriched leaf extract (PMFL) prior to I/R injury significantly reduced serum creatinine levels and improved glomerular filtration rate, indicating attenuation of renal dysfunction. In vitro, under hypoxia/reoxygenation conditions mimicking ischemia, both PMFL and nobiletin enhanced cell viability in human renal tubular epithelial cells. Mechanistically, treatment with PMFL or nobiletin upregulated heme oxygenase-1 (HO-1), a key antioxidant enzyme, along with its upstream regulator, nuclear factor erythroid 2–related factor 2 (Nrf2). These findings suggest that *Citrus sunki* leaves are a promising source of bioactive PMFs. PMFL and its major component, nobiletin, confer significant protection against oxidative stress–induced renal injury, likely through activation of the Nrf2/HO-1 antioxidant pathway. Further studies are warranted to elucidate the detailed mechanisms and assess the therapeutic potential of PMFL in clinical settings.

PBD-9

Optimization of Estrogen Analysis Using Liquid–Liquid Extraction and Derivatization Protocol

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Quantitative determination of estrogens in biological matrices is critical for both clinical diagnostics and monitoring, as estrogens are key regulators of endocrine function and are associated with various hormone-related disorders. Accurate measurement is essential for diagnosing hormonal imbalances. Although solid-phase extraction (SPE) has traditionally been used to isolate free estrogens from their glucuronide and sulfate conjugates, it requires multiple processing steps and specialized cartridges, making the procedure time-consuming and labor-intensive. To improve detection sensitivity, derivatization with dansyl chloride has been widely employed in estrogen analysis. Two principal derivatization strategies have been reported: one using acetone and aqueous potassium carbonate to selectively target phenolic hydroxyl groups, and another employing dichloromethane, *N*,*N*-diisopropylethylamine (DIPEA), and 4-dimethylaminopyridine (DMAP) to derivatize all hydroxyl moieties. Despite their widespread application, these two methods have not been systematically compared under controlled conditions. In this study, a simplified liquid-liquid extraction (LLE) protocol was developed for the efficient separation of free and conjugated estrogens. In addition, the two derivatization methods were optimized and comparatively evaluated with respect to reaction conditions, including reagent concentrations and incubation time. The objective of this work is to establish a streamlined, sensitive, and reproducible workflow for estrogen quantification, thereby improving analytical precision and method robustness.

PBD-10

ZjGIGANTEA Negatively Regulates Osmotic Stress Tolerance in *Zoysia japonica*

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The growth of *Zoysia japonica*, a temperate turfgrass species widely used in lawns and sports landscapes, is severely inhibited by osmotic stress under drought conditions. Despite its ecological and commercial significance, the molecular mechanisms underlying its drought tolerance remain poorly understood. In this study, we identified and functionally characterized *ZjGI*, a homolog of the *GIGANTEA* (*GI*) gene, which is known to regulate circadian rhythms, flowering time, and stress responses in various plant species. Using CRISPR/Cas9-mediated genome editing, we successfully generated *zjgi* knockout mutants and conducted both physiological and transcriptomic analyses. The *zjgi* mutants exhibited markedly reduced expression of key circadian genes, including *ZjCCA1* and *ZjLHY*, resembling gene expression patterns observed in *gi* mutants of Arabidopsis and rice. Interestingly, these mutants also showed enhanced tolerance to osmotic stress induced by polyethylene glycol (PEG) treatment. This improved tolerance was accompanied by substantial transcriptional reprogramming of multiple stress-responsive regulatory genes, suggesting that disruption of *ZjGI* alters core regulatory networks involved in both circadian and stress response pathways. Together, these findings suggest that *ZjGI* acts as a negative regulator of osmotic stress tolerance in *Z. japonica*. Our study provides new insights into the molecular basis of drought resistance and identifies ZjGI as a promising genetic target for developing turfgrass varieties with enhanced abiotic stress tolerance.

PBD-11

ZjWRKY75 Transcription Factors Mediate Stress-Induced Leaf Senescence via Hormonal Regulation in *Zoysia japonica*

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Environmental stresses such as darkness and salinity accelerate premature leaf senescence in *Zoysia japonica*, a widely used warm-season turfgrass. This stress-induced senescence not only compromises its aesthetic value but also limits its ecological and commercial lifespan. Understanding the roles of transcription factors (TFs) involved in this process offers valuable insights for enhancing stress resilience and extending the plant's green phase. We identified *ZjWRKY75a* and *ZjWRKY75b* as key WRKY TFs upregulated during dark-, salt-, and age-induced senescence. Protoplast-based reporter assays revealed that *ZjWRKY75a* significantly activated the early senescence marker promoter *pZjPCAP-LUC* while repressing the late senescence marker *pZjSGR-LUC*, suggesting a complex role in regulating senescence progression. Functional characterization using transgenic Zoysia lines revealed that overexpression of *ZjWRKY75a* accelerated leaf yellowing and reduced photosynthetic efficiency under dark- and salt-induced stress, whereas CRISPR-Cas9-induced *ZjWRKY75a/b* double mutants exhibited delayed senescence phenotypes. Gene expression profiling indicated that *ZjWRKY75* modulates components of salicylic acid and abscisic acid signaling pathways. Taken together, these results support a model in which *ZjWRKY75* functions as a regulator that integrates hormonal signaling pathway to mediate stress-induced leaf senescence in *Z. japonica*.

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PBD-12

Benchmarking AI Applications in Screening: Evaluating AlphaFold3 as a Tool for Drug Discovery

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Since the release of AlphaFold, the field of structural bioinformatics has rapidly evolved from solving individual protein structures to predicting complex protein–protein and protein–compound interactions. AlphaFold3, the latest version, incorporates the prediction of macromolecular interactions, prompting new possibilities in drug discovery, particularly in virtual screening. This study aims to benchmark AlphaFold3 as a potential screening tool by comparing its applicability with traditional molecular docking software such as DiffDock and AutoDock Vina. Using the PDBbind dataset, which provides experimental binding data for various compounds against target proteins, we evaluated the predictive performance, limitations, and practical implications of AlphaFold3 in modeling protein–ligand interactions. By establishing a comparative framework, this benchmark provides insights into the strengths and limitations of AI-based structure predictors in drug screening workflows.

PBD-13

Polygonum cuspidatum Extract Containing Emodin Suppresses Lung Cancer-Induced Cachexia by Suppressing TCF4/TWIST1 Complex-Induced PTHrP Expression

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Cachexia, which is characterised by the wasting of fat and skeletal muscles, is the most common risk factor for increased mortality rates among patients with advanced lung cancer. PTHLH (parathyroid hormone-like hormone) is reported to be involved in the pathogenesis of cancer cachexia. However, the molecular mechanisms underlying the regulation of PTHLH expression and the inhibitors of PTHLH have not yet been identified. The interaction between TCF4 (Transcription Factor 4) and TWIST1 and the binding of the TCF4–TWIST1 complex to the PTHLH promoter were analysed using co-immunoprecipitation and chromatin immunoprecipitation. The results of the mammalian two-hybrid luciferase assay revealed that emodin inhibited TCF4–TWIST1 interaction. The effects of *Polygonum cuspidatum* extract (Pc-Ex), which contains emodin, on cachexia were investigated in vivo using A549 tumour-bearing mice. Ectopic expression of TCF4 upregulated PTHLH. Conversely, TCF4 knockdown downregulated PTHLH expression in lung cancer cells. The expression of PTHLH was upregulated in cells ectopically co-expressing TCF4 and TWIST1 when compared with that in cells expressing TCF4 or TWIST1 alone. Emodin inhibited the interaction between TCF4 and TWIST1 and consequently suppressed the TCF4/TWIST1 complex-induced upregulated mRNA and protein levels of PTHLH and PTHrP. Meanwhile, emodin-containing Pc-Ex significantly alleviated skeletal muscle atrophy and downregulated fat browning-related genes in A549 tumour-bearing mice. Emodin-containing Pc-Ex exerted therapeutic effects on lung cancer-associated cachexia by inhibiting TCF4/TWIST1 complex-induced PTHrP expression.

PBD-14

Functional study of Fermented Silk Sericin by Marine Extremophiles from the High Seas

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Silk sericin is a natural polymer produced by silkworm, *Bombyc mori*. Sericin is usually removed from the raw fiber and discarded by silk producers. Besides all the beneficial effects and possible applications of silk sericin, it presents some limitations that restrict its application. This study aimed to investigate the potential of open-ocean marine microorganisms in depolymerizing silk sericin, with the goal of developing novel bioactive materials, enhancing its bioactivity, and exploring its potential for industrial applications. A total of 70 marine microorganisms (51 species) were used in this study. Among them, 14 strains exhibited the ability to degrade silk sericin under experimental conditions. *Idiomarina loihiensis* and *Alteromonas macleodii* exhibited superior growth, sericin-degrading activity, and higher antioxidant properties. Fermented silk sericin extracts exerted anti-inflammatory effects on LPS-induced RAW 264.7 macrophage cells, downregulating pro-inflammatory mediators including IL-6, IL-1β, and TNF-α without toxicity. Anti-osteoporotic activity was evaluated using MC3T3-E1 osteoblastic cells, measuring cell proliferation, alkaline phosphatase (ALP) activity, mineralization, and osteoprotegerin (OPG) and receptor activator of nuclear factor κB ligand (RANKL) levels. Results indicated significant improvements in all parameters. In conclusion, this study demonstrates that marine microorganisms can depolymerize sericin, enhancing its antioxidant, anti-inflammatory, and anti-osteoporotic activities, and suggesting its potential as a biomaterial for industrial applications.

PBD-15

Bacillus licheniformis CP6 fermented *Abelmoschus Manihot* ameliorates bone loss in ovariectomized rats and promotes osteoblast differentiation through BMP/Runx2 signaling pathway

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Osteoporosis is a common skeletal disease characterized by decreased bone mass, which increases the risk of bone fracture. In this study, the preventative effects of *Bacillus licheniformis* CP6-fermented *Abelmoschus Manihot* extract (FAME) on bone loss were determined in ovariectomized (OVX) rats, and the mechanisms by which FAME promote osteoblastogenesis were investigated. Female Sprague-Dawley rats were randomly assigned to the sham-operated and four OVX experimental groups, G1:SHAM, G2:OVX, G3:OVX+incubated-*A. Manihot* extract (100 mg/kg, IAME), G4:OVX+FAME (100 mg/kg, FAME) and G5:OVX+17β-estradiol (10 μg/kg, E2). Oral administration of FAME significantly increased uterine weight, bone mineral density and bone biomechanical properties in OVX rats. The levels of serum bone turnover markers in FAME group decreased compared with IAME group. Furthermore, FAME activated BMP/Runx2 signaling pathpway and then promoted the transcription of osteogenic related factors including type 1 collagen, ALP, osterix, BMP2 and Runx2 in 3T3-E1 osteoblasts. Our data suggests that fermentation may be a useful strategy for improving the biological properties of raw materials including their anti-osteoporosis properties. Taken together, FAME, more than IAME, protects against OVX-induced bone loss and stimulates osteogenic differentiation by BMP2/Runx2 signaling pathway in 3T3-E1 cells. These findings suggested FAME could be a potential therapeutic agent for the treatment and prevention of osteoporosis.

Keywords: Abelmoschus Manihot Jinhuakui, Bacillus licheniformis, Anti-osteoporosis

PBD-16

Role of bean yellow mosaic virus P1 and HC-Pro in enhancing gene expression and suppressing RNA silencing in *Nicotiana benthamiana*

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Potyviruses, a major group of plant viruses, utilize HC-Pro, a multifunctional protein, to suppress RNA silencing, a crucial plant defense mechanism. This study investigated the role of P1 and HC-Pro from bean yellow mosaic virus (BYMV), a potyvirus with a broad host range, in enhancing gene expression and suppressing RNA silencing in *Nicotiana benthamiana*. We observed that BYMV HC-Pro significantly enhanced reporter gene expression, likely through suppression of RNA silencing pathways. This effect was further augmented by the presence of the P1 protein, another viral protein. Analysis of HC-Pro mutants revealed that the conserved FRNK box within HC-Pro is crucial for its activity and its impact on gene expression. Furthermore, HC-Pro significantly downregulated the expression of key RNA silencing genes, including *DCL2*, *DCL4*, *RDR6*, *AGO1-1*, *AGO1-2*, and *AGO2*. These findings demonstrate that BYMV P1::HC-Pro is a potent suppressor of RNA silencing and a promising tool for enhancing gene expression in plants. The results have significant implications for developing novel strategies to improve plant biotechnology, including the production of high-value recombinant proteins.

Keywords: Potyvirus, HC-Pro, RNA silencing suppressor, Gene expression, Plant biotechnology

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PBD-17

Development of Reverse-Aging Cosmetic Ingredients Using Plant Cell Library and SMART-RC^2 Bioreactor System

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Reverse-aging technology, recognized among the top 10 promising biotechnologies in 2023, is, as of 2025, transforming the global skincare industry with its focus on regenerative and longevity-based solutions. However, rapid loss of plant biodiversity due to industrialization poses a major challenge in sourcing high-efficacy cosmetic ingredients. Using the SMART-RC^2 bioreactor system, 25 high-potential cell lines were mass-cultivated under standardized conditions. From these, extracts and extracellular vesicles (EVs) were obtained and functionally characterized. To validate efficacy, the Multiple Cellular Senescence Scoring (MCSS) platform was applied for high-throughput screening of reverse-aging effects in human skin cells. Several callus lines showed remarkable efficacy in reducing cellular senescence markers and promoting antioxidant activity, collagen production, and skin cell regeneration. This convergence of bioengineered plant resources with advanced screening technology offers a scientifically validated, scalable, and globally competitive solution for cosmetic actives. The platform supports not only production and safety validation but also formulation and commercialization, paving the way for innovation in the reverse-aging skincare market.

Keywords: Plant callus culture, Reverse-aging, SMART-RC^2, Plantomics, Phytochemicals, Anti-aging, Cosmeceuticals

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PBD-18

Inhibitory Effect of Ganoderma Lucidum Spore Oil Extracted by CO2 Supercritical fluid on Osteoarthritis

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Osteoarthritis (OA) is a chronic joint disease characterized by inflammation and cartilage degradation, with no curative treatment currently available. Long-term use of conventional medications often leads to side effects, highlighting the need for safer alternatives. Ganoderma lucidum (GL), a traditional medicinal mushroom, has been used to treat inflammatory conditions, including autoimmune diseases like rheumatoid arthritis (RA). Its spores are known for their immunomodulatory and anti-aging properties, but their potential effects on arthritis remain unclear. In this study, we investigate the therapeutic effects of Ganoderma lucidum spore oil (GLSO), extracted using supercritical CO_2, in a destabilization of the medial meniscus (DMM)-induced OA mouse model. Metabolomic profiling revealed that GLSO is rich in fatty acids, predominantly oleic acid (52.12%) and linoleic acid (16.77%). We aim to evaluate whether GLSO can attenuate cartilage degeneration and synovial inflammation in OA. Histological analyses will be performed to assess OARSI scores, osteophyte formation, and synovitis, which are key pathological features of OA. Additionally, we will examine GLSO's effect on the expression of inflammatory cytokines induced by LPS or TNF-α in cultured chondrocytes. Our study suggests that GLSO may serve as a promising natural therapeutic agent for arthritis, potentially improving patient quality of life while supporting the development of safe, plant-based anti-inflammatory treatments.

PBD-19

PARP-1 activation prevents OA pathogenesis by inhibiting apoptosis in chondrocytes

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Osteoarthritis (OA) is a progressive degenerative joint disorder characterized by cartilage breakdown, synovial inflammation, and altered bone structure. Chondrocyte apoptosis contributes significantly to cartilage degradation in OA. Poly(ADP-ribose) polymerase-1 (PARP-1) plays a crucial role in DNA damage repair and the regulation of apoptosis. However, the relationship between PARP-1 expression and OA remains unclear. This study investigated the effects of PARP-1 on OA pathogenesis in PARP-1 knockout (KO) mice and primary chondrocytes. Destabilization of the medial meniscus (DMM) was performed to induce OA in wild-type (WT) and PARP-1 KO mice. Histological analysis revealed increased cartilage degeneration in PARP-1 KO mice compared to that in WT controls. TUNEL assay demonstrated a significant increase in apoptotic cells in the cartilage and synovium of PARP-1 KO mice. In vitro, PARP-1 inhibition by 3-aminobenzamide (3-AB) or PARP-1 KO enhanced apoptosis in primary chondrocytes, as evidenced by increased TUNEL-positive cells and elevated levels of cleaved PARP-1, poly(ADP-ribose) (PAR), and caspase-3. Furthermore, PARP-1 deficiency disrupts the balance between anabolic and catabolic factors under inflammatory conditions, thereby promoting cartilage degradation. These findings suggested that PARP-1 activation exerts protective effects against OA pathogenesis by inhibiting chondrocyte apoptosis. Targeting PARP-1 may be a novel therapeutic strategy for OA prevention and treatment.

PBD-20

Phytochemical composition and antioxidant activity of fermented extracts from *Olea europaea* L. leaves

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Olea europaea L. has been extensively cultivated throughout the Mediterranean countries for centuries. This species is characterized by the presence of various phenolic compounds, including oleuropein, luteolin-7-glucoside, and verbascoside, which are important for resisting diseases and protecting against pests. We investigated the chemical composition and antioxidant activity of olive leaf extract and its fermented forms using *Saccharomyces*, *Galactomyces*, and *Lactobacillus* strains. The overall chemical profiles of the olive leaf samples were similar, with oleuropein identified as the main compound. The extract fermented with *Saccharomyces* showed the highest oleuropein concentration (41.9 mg/g ext.). Antioxidant properties were assessed through DPPH radical scavenging, total phenolic content, and total flavonoid content, with the *Saccharomyces*-fermented extract exhibiting the greatest antioxidant activity. These results suggest that fermentation with *Saccharomyces* can significantly enhance both the oleuropein content and antioxidant potential of olive leaf extract compared to the unfermented extract.

Keywords: *Olea europaea* L., fermentation, *Saccharomyces*, *Galactomyces*, *Lactobacillus*, antioxidant activity, oleuropein

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PBD-21

Comparative Analysis of Phytochemicals and Antioxidant Activity in *Hibiscus hamabo* plant parts

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Hibiscus hamabo Siebold & Zucc., commonly known as "Hwang-geun," is a small tree from the Malvaceae family, reaching approximately 3 meters in height. It is the only native species of the *Hibiscus* genus found in Korea. Designated as a Class II Endangered Wild Species in 1988, it was delisted in 2023 following successful seed restoration efforts. Despite its ecological significance, there are limited pharmacological and phytochemical studies on this plant. This study aims to evaluate the biological activity of *H. hamabo* and analyze its bioactive compounds to explore its potential as a medicinal resource and functional material. The chemical properties of each part of *H. hamabo* were compared using HPLC-PDA and UHPLC-Q-ToF-MS. Antioxidant activity was assessed through DPPH, ABTS, TPC, and TFC assays. Results showed the highest activity in the leaves and petals, while the pedicels and roots exhibited the lowest activity. Main peaks observed in the HPLC chromatograms of the flowers and petals were isolated via PREP-LC, and their antioxidant activities were comparable to that of L-ascorbic acid (LAA). Future studies will focus on the structural identification of the main peak using NMR spectroscopy, as well as the assessment of its anti-inflammatory activity.

Keywords: *Hibiscus hamabo*, antioxidant activity, HPLC-PDA, plant parts

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PBD-22

Investigation of the Anti-Inflammatory Properties of *Tetragonia tetragonoides* (Pall.) Kuntz in Mouse Macrophages

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Tetragonia tetragonoides (New Zealand spinach) is a perennial plant of the Aizoaceae family that has been traditionally used as an herbal remedy for treating and preventing of stomach disorders, such as gastritis and peptic ulcers. It is also known to contain a variety of bioactive compounds, including flavonoids, and alkaloids. In this study, we investigated the anti-inflammatory effects of *T. tetragonoides* extracts by comparing its HPLC profiles and evaluating its impact on LPS-stimulated J774 macrophages. Expression levels of key inflammatory markers—iNOS, COX-2, as well as pro-inflammatory cytokines including IL-1β, IL-6, and TNF-α—were assessed. The results showed that LPS stimulation significantly upregulated the expression of inflammatory markers. However, *T. tetragonoides* extract dose-dependently modulated key inflammatory indicators such as IL-1β, IL-6, iNOS, TNF-α, and NO. In addition, four methoxy kaempferol glycosides (compound **1-4**) were isolated from the extract *T. tetragonoides* using column chromatography. These results suggest that *T. tetragonoides* exhibits notable anti-inflammatory effects, likely mediated through the modulation of inflammatory signaling pathways. The identified methoxy kaempferol glycosides may play a key role in this activity and represent promising candidates for the development of plant-based therapeutics for inflammatory diseases.

Keywords: *Tetraagonia tetragonoides* (Pall.) Kuntz; anti-inflammatory activity; methoxy kaempferol glycosides

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PBD-23

Targeting the SARS-CoV-2 Nsp3 Macrodomain with Evolutionary Chemical Binding Similarity (ECBS): Insights from the CACHE#3 Challenge

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The macrodomain within SARS-CoV-2 nonstructural protein 3 (Nsp3) plays a critical role in coronavirus pathogenesis, making it a promising target for antiviral drug development. In the third CACHE challenge, we focused on the ADP-ribose (ADPr) binding site of the Nsp3 macrodomain (Mac1) using an in-house hybrid virtual screening pipeline. Our approach integrates Evolutionary Chemical Binding Similarity (ECBS), which exploits evolutionary relationships among targets, with structure-based docking and machine learning methods to prioritize potential small-molecule inhibitors. We utilized the Target-Specific ensemble ECBS (TS-ensECBS) model to screen compounds from the ZINC and Mcule databases, followed by refinement with AutoDock, DOCK, and RASPD+ docking programs. Consensus scoring and ADME profiling using SwissADME further guided hit selection. Among 73 candidate molecules predicted across Rounds 1 and 2, nine demonstrated ADP-ribose peptide displacement in an HTRF assay. Four compounds were confirmed as binders by SPR assay, with one showing a dissociation constant (KD) below 28 μM, ranking among the top hits of the challenge and representing a novel chemical scaffold. Our findings highlight the effectiveness of combining ECBS with structure-based and machine learning methods for discovering potent, novel inhibitors and advancing drug discovery.

PBD-24

Phytochemical analysis and biological activities of *Idesia polycarpa*

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Idesia polycarpa Maxim. is a deciduous tree of the Flacourtiaceae family, native to China, Japan, Taiwan and Korea. The fruits of *I. polycarpa* are a valuable source of edible oil rich in polyphenols. Previous studies have found that *I.polycarpa* fruits possess various biological activities including antioxidant, anti-adipogenic and whitening properties. However, the antioxidant and anti-inflammatory effects of *I.polycarpa* leaves have not been investigated. In this study, we explored the antioxidant and anti-inflammatory potential of *I. polycarpa* leaves. In order to identify the chemical components of the leaves, they were extracted with 70% EtOH and different fractions were prepared. In this study, HPLC-PDA and UHPLC-Q-ToF-MS were used to compare the chemical compositions, while the isolation of compounds was performed using medium pressure liquid chromatography (MPLC). The antioxidant activity of the extracts was evaluated using several assays, including DPPH radical scavenging activity, ABTS radical scavenging activity, ferric reducing antioxidant power (FRAP), total phenolic content (TPC), and total flavonoid content (TFC). Among the fractions, the methylene chloride fraction showed the strongest antioxidant activities. The results of our study suggest that the *I. polycarpa* leaf extract has potential antioxidant effects.

Keywords: *Idesia polycarpa* Maxim; antioxidant activity; HPLC-PDA; MPLC; LC-MS; UHPLC-Q-ToF-MS

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PBD-25

Immune-Enhancing Screening of Proteins from a gut bacterium, BP, in RAW 264.7 Macrophages

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Pancreatic cancer is notorious for its non-responsiveness to cancer immunotherapy due to highly immunosuppressive tumor microenvironment. This study aimed to screen recombinant proteins derived from a gut bacterium, BP, for their immune-enhancing potential using the RAW 264.7 murine macrophage model. A total of 16 candidate proteins were identified based on a previous study, of which 14 were successfully expressed in *Escherichia coli* BL21 (DE3). Proteins were purified using His-tag affinity chromatography (IMAC) and validated by SDS-PAGE. To ensure suitability for immunological testing, all protein samples underwent endotoxin removal using poly(ε-lysine) as the affinity ligand. Initial optimization of endotoxin removal was performed on the first eight proteins, achieving partial clearance in the range of 80–90%. An immune-enhancing assay was then conducted by stimulating RAW 264.7 cells with each protein, followed by nitric oxide (NO) quantification using the Griess assay, a standard marker of macrophage activation. Several BP-derived proteins (Ndo, Gen, Cop, Ino, Sbs, C-domain, and Nu) significantly increased NO levels. Notably, their responses remained consistent before and after partial endotoxin removal, suggesting intrinsic immune-stimulating potential. Endotoxin removal optimization is ongoing to meet acceptable levels for in vitro immunoassays. Proteins showing strong activity will be advanced to additional immune-enhancement methods and in vivo models to evaluate their relevance in inflammation-associated tumor progression.

PBD-26

Synthesis of Novel Carboxylic Acid Derivatives Targeting the ROS-TGFβ1-HIF-1α Axis for Idiopathic Pulmonary Fibrosis Treatment

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Idiopathic pulmonary fibrosis (IPF) is a progressive interstitial lung disease driven by recurrent cellular injury and abnormal repair. The currently approved therapeutics, Pirfenidone and Nintedanib, slow disease progression but do not reverse established fibrosis and are often associated with side effects, highlighting the need for new treatments. Oxidative stress induces TGF-β1, a central mediator of fibrosis that also stabilizes HIF-1α under normoxic conditions. This ROS–TGF-β1–HIF-1α axis promotes fibroblast activation and extracellular matrix deposition. Targeting both oxidative stress and HIF-1α may provide a more effective therapeutic strategy. We designed and synthesized carboxylic acid derivatives containing pyrrole and imidazole rings with dual antioxidant and HIF-1α inhibitory activities. These compounds showed strong radical scavenging activity in DPPH and DCFDA assays, supported by density functional theory calculations. Compounds 2a and 2b significantly inhibited HIF-1α and reduced fibrotic marker expression in vitro. In a bleomycin-induced IPF mouse model, compound 2a markedly decreased collagen and fibronectin deposition. Mechanistic studies revealed that 2a modulated both Smad and non-Smad profibrotic pathways. These results identify compound 2a as a promising dual-target therapeutic for IPF, offering antioxidant and anti-fibrotic effects by disrupting the ROS–TGF-β1–HIF-1α axis and supporting its potential for future clinical development.

Keywords: Idiopathic pulmonary fibrosis, Dual-target therapy, HIF-1α inhibitors, Antioxidants

PBD-27

Application of a Genotoxicity Assessment Framework to Pesticide Evaluation: Case Studies

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Genotoxicity evaluation is a critical toxicological endpoint essential for protecting human health and ensuring compliance with pesticide registration regulations, as genotoxicity can preclude registration. Toxicity assessment has traditionally relied on animal testing, but predictive accuracy is now being improved through the use of new approach methodologies(NAMs). This study developed a genotoxicity assessment framework for pesticides based on NAMs and evaluated the applicability through case studies. The framework consists of five steps: (1) exposure assessment, (2) evaluation of existing genotoxicity data, (3) application of predictive tools, (4) testing, and (5) dose-response analysis. Substances for the case studies were selected by reviewing their classification as genotoxic and/or carcinogenic in the PAN High Hazardous Pesticides list, considering regulatory assessment results, the availability of NAMs data and other relevant factors. For the case studies, it was assumed that no prior toxicological information was available and the evaluation started from step 3. Pesticide A, classified as genotoxic and carcinogenic in regulatory assessments, was also classified as genotoxic by the framework, which provided a more conservative evaluation in comparison of the reference values. Pesticide B, negative for both toxicity endpoints, was predicted to be non-genotoxic. For pesticide C, which was classified as non-genotoxic but carcinogenic, the framework predicted it to be genotoxic. These results demonstrate the successful application of the framework for systematic genotoxicity assessment.

PBD-28

ACF-01 downregulates HIF-1α and potentiates the antitumor effect of Lenvatinib by inducing apoptosis in hepatocellular carcinoma

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Hepatocellular carcinoma (HCC) is one of the most prevalent solid tumors and a leading cause of cancer-related mortality worldwide. Although sorafenib and lenvatinib are currently FDA-approved as first-line therapies, the emergence of drug resistance severely limits their long-term effectiveness. Thus, there is an urgent need to identify novel therapeutic agents that can enhance the efficacy of existing treatments. In this study, we evaluated the antitumor activity of ACF-01, a synthetic compound derived from catechol and 4′,6,7-trimethoxyisoflavone, in HCC cell lines. ACF-01 demonstrated dose-dependent growth inhibition, with IC_{50} values of 44.2 μM in HepG2 and 32.27 μM in Huh7 cells after 48 hours of treatment. Importantly, ACF-01 suppressed the expression of hypoxia-inducible factor-1 alpha (HIF-1α) in a concentration-dependent manner. Notably, ACF-01 exhibited synergistic effects when combined with lenvatinib, a standard first-line targeted therapy for HCC. The combination treatment significantly inhibited cell proliferation and induced apoptosis more effectively than lenvatinib alone. Furthermore, the protein levels of HIF-1α were markedly reduced in cells receiving the combination treatment. Taken together, these findings suggest that ACF-01 is a promising candidate for combination therapy in HCC. By downregulating HIF-1α and promoting apoptosis, ACF-01 may enhance the therapeutic efficacy of lenvatinib and help overcome drug resistance in hepatocellular carcinoma.

PBD-29

Daphne jejudoensis leaf extract Attenuate Psoriatic symptoms by Mitochondrial modulation of Th17 cells

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Th17 cells play a critical role in host defense against extracellular pathogens. However, their dysregulated activity drives chronic inflammation and autoimmune diseases. Although various therapies have been developed to target Th17 cells, these often have side effects and limitations. Recently, plant-based extracts have gained attention as alternative strategies. In this study, we investigated the effects of Daphne jejudoensis leaf extract (DJLE) derived from a plant native to Jeju Island on Th17 cells differentiated from naïve CD4+ T cells. We confirmed that DJLE significantly inhibited IL-17A production. At the molecular level, DJLE downregulated mRNA expression of Th17-associated transcription factors, including RORγt, IRF4, RORα, and BATF, and reduced the phosphorylation of STAT3. Furthermore, DJLE decreased mitochondrial mass and membrane potential, as well as the expression of genes related to mitochondrial function. To demonstrate the effect of the DJLE in vivo, we adopted the imiquimod-induced psoriasis model. DJLE treatment mitigated symptoms of psoriasis, including ear keratin, thickness, and erythema. Moreover, the IL-17A, IFN-γ, and TNF-α protein levels were reduced in tissue lysates following DJLE treatment. Collectively, our findings suggest that DJLE regulates Th17 cell response through mitochondrial function, supporting its potential as a therapeutic candidate for autoimmune and inflammatory diseases such as psoriasis and other Th17-driven autoimmune diseases.

PBD-30

High-fat diet alters Colonic CD4+ T Cells with Reprogramming of Inflammatory and Metabolic gene signatures

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Dietary composition critically modulates metabolic function and mucosal immune homeostasis, particularly in the intestine where diet-derived cues influence immune cell differentiation. High-fat diet (HFD)–induced caloric excess is associated with increased risk of colorectal cancer and inflammatory diseases, yet its specific impact on colonic $CD4^+$ T cell homeostasis remains unclear. To investigate this, high-dimensional flow cytometric profiling was performed on immune cells from multiple organs of mice fed either normal diet (ND) or HFD. HFD-fed mice exhibited pronounced remodeling of the colonic $CD4^+$ T cell compartment, notably a significant reduction in $ROR\gamma t^+$ regulatory T cells (Tregs), a subset essential for sustaining mucosal tolerance and metabolic balance. Concurrently, conventional $CD4^+$ T cells showed diminished expression of co-inhibitory receptors PD-1 and CTLA-4, suggesting impaired immune checkpoint signaling and a reduced threshold for inflammatory activation. Complementary transcriptomic analysis of colonic tissue from HFD-fed mice revealed coordinated downregulation of genes involved in oxidative metabolism, epithelial ion transport, and stress responses, along with enrichment of inflammatory signaling pathways. These findings collectively demonstrate that HFD perturbs colonic $CD4^+$ T cell homeostasis by depleting regulatory subsets and disrupting immune tolerance, thereby predisposing the gut to inflammation. Ongoing studies aim to elucidate the role of diet-altered metabolites and their molecular targets within $CD4^+$ T cells that may mediate these immunological perturbations.

PBD-31

Sobrerol (NRM-331) Alleviates Ischemic Stroke and Cognitive Disorder via Multi-Target Mechanisms

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Ischemic stroke induces secondary brain injury through oxidative stress and neuroinflammation, with excessive autophagy accelerating neuronal death. Post-stroke accumulation of p-tau and Aβ proteins promotes vascular dementia, causing cognitive decline. This study aimed to elucidate the anti-inflammatory and autophagy inhibitory effects of NRM-331 in ischemic stroke, and the cognitive function improvement effect through tau/Aβ inhibition. In addition to experiments using a cell culture system, *in vivo* studies, transient middle cerebral artery occlusion (tMCAO) model and scopolamine-induced amnesia model were performed in male C57BL/6 mice. *In vitro*, NRM-331 significantly attenuated inflammatory cytokines (CCL-2, CCL-3, TNF-α). In the oxygen-glucose deprivation model, NRM-331 suppressed autophagy signaling, reducing phosphorylated p62 expression and LC3-II accumulation by 69% and 49%, respectively. *In vivo*, NRM-331 decreased infarct volume by approximately 50% and enhanced motor function by 27% (foot fault test). In the scopolamine-induced amnesia model, NRM-331 significantly improved spatial learning and memory performance in the Morris water maze. Serum Aβ levels were reduced by 50%, and brain AChE activity decreased by 84%. Furthermore, the 19% increase in hippocampal neuronal survival was associated with reduced p-tau levels, underscoring NRM-331's neuroprotective efficacy. NRM-331 mitigates ischemic stroke by suppressing inflammation and autophagy, and prevents vascular dementia progression through tau/Aβ reduction, enhancing cognition via cholinergic signaling. NRM-331 has demonstrated multi-target therapeutic potential. Further clinical studies are warranted.

PBD-32

A novel compound ACF-01 synergistically enhances the anticancer effects of doxorubicin in MDA-MB-231 cell variants with stem cell properties

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Triple-negative breast cancer (TNBC) is a highly aggressive subtype of breast cancer, characterized by an enrichment of cancer stem-like cells, high metastatic potential, and poor clinical prognosis. Although chemotherapeutic agents such as doxorubicin are widely used, their efficacy is often limited due to the development of drug resistance. Notably, cancer stemness, epithelial–mesenchymal transition (EMT), and drug resistance are interrelated processes that collectively contribute to a more malignant and therapy-resistant phenotype. In this study, we investigated the anticancer effects of a novel compound, ACF-01, using MDA-MB-231 cells with stem cell properties (MDA-MB-231/SCP), established by sorting $CD44^+/CD24^-$ subpopulations from parental MDA-MB-231 cells. ACF-01 significantly reduced stemness features, including self-renewal capacity, clonogenicity, chemoresistance, and EMT-associated traits, while promoting apoptotic cell death. Importantly, combination treatment with ACF-01 and doxorubicin showed a synergistic effect (combination index < 1.0), resulting in enhanced apoptosis and further suppression of stem-like characteristics. This combinatorial treatment also led to increased nuclear accumulation of doxorubicin and reduced drug efflux activity compared to doxorubicin alone, suggesting that ACF-01 sensitizes cells to doxorubicin by modulating drug resistance mechanisms. These findings suggest that ACF-01 is a promising therapeutic candidate for targeting stem-like cancer cells and improving the efficacy of chemotherapy in TNBC.

PBD-33

Antiviral Activity Analysis of *Abies nephrolepis* Extract

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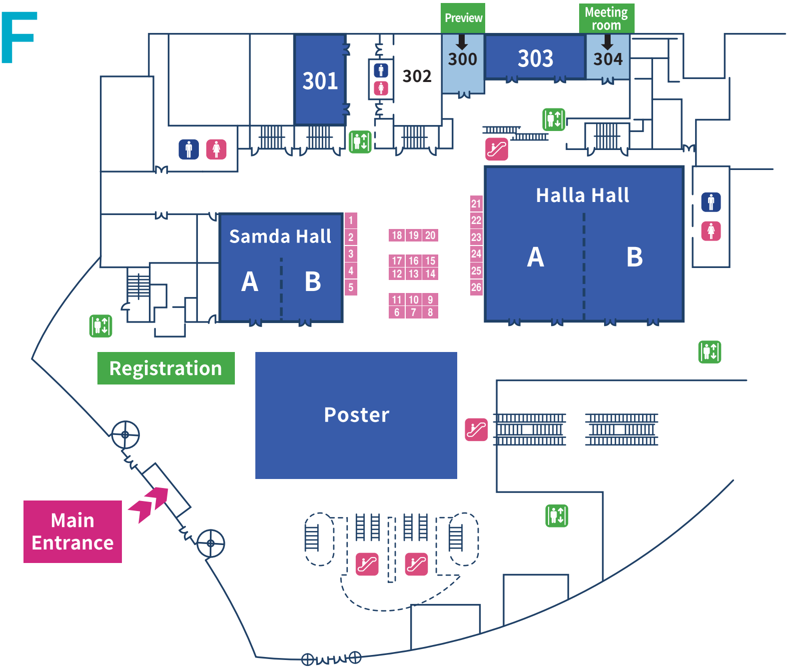
Both influenza virus and coronavirus are viruses that have caused worldwide pandemic diseases. In this study, we investigated the antiviral efficacy of evergreen conifers growing in Gyeonggi-do to develop antiviral agents for coronaviruses for which there are no antiviral agents. Cell viability was measured by MTT assay (Modified ISO 10993-5), and antiviral activity was measured by a modification of ASTM E1052-20. To investigate the effect of *Abies nephrolepis* extract on cells, the cell viability of the host cells of H1A1 influenza virus and coronavirus was measured. As a result, it did not show cytotoxicity in the influenza host cells, but cytotoxicity was shown in the host cells of coronavirus at high concentrations. As a result of measuring the antiviral activity of *Abies nephrolepis* extract against H1A1 and coronavirus, it showed a virus reduction rate of 99.999% in the case of H1A1, and 92.06% and 98.59% in the case of FCoV and HCoV, respectively. Accordingly, *Abies nephrolepis* extract is expected to be used as a substance for the treatment or prevention of infections caused by H1A1, FCoV, and HCoV.

Exhibition

3F



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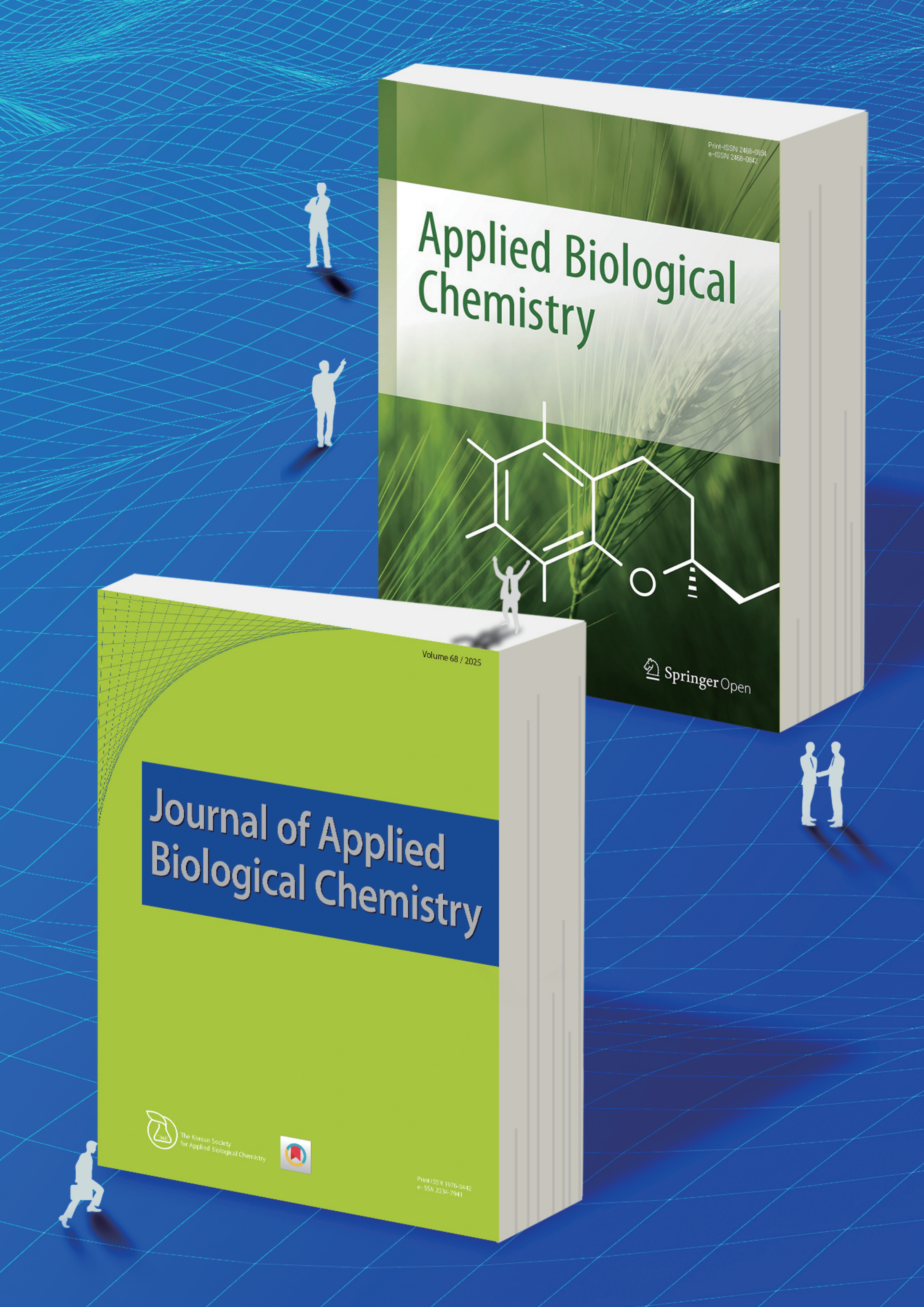
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신규제품 개발지원

신규제품 개발지원

고품질 안정적 천연소재 원료 공급

농가 재배 수요 및 일자리 창출, 소득증대 기여

- 사업명: 천연물소재 전주기 표준화 허브 구축 사업
- 사업기간: 2024년-2028년
- 수행기관: (재)강원테크노파크 (강원도, 강릉시)
- 참여기관: KIST 천연물연구소, 서울대 GBST, 강원ICT융합연구원
- 사업예산: 450억원
  - 건축 340억원, 시설장비 160억원, 시범사업 50억원

Progress Solution

Value Chain 기반 '표준화 애로 해소'
- 원재료 수급, 품질 안정화
- 표준화 단계별, 수요 맞춤형 서비스 제공

국내 최고 수준의 '핵심기술력 제공'
- NPI finder, HTS 등 국내 최고 수준 기술, 인력 지원
- 글로벌 수준의 첨단장비 지원

천연물산업 성과를 위한 '생태계 지원'
- 계약재배 프로그램 협력 지원
- 천연물소재 표준화 사업비 지원
- 세제혜택, 장비이용 지원 등 인센티브 제공

글로벌 인증 및 수출 성과 '농업-기업 동반 시너지'
- KIST 유럽분원, 인데나 등 글로벌 Top tier 네트워크 지원
- 소재작물 재배 확대 등을 통한 농업 부가가치 창출

천연물소재 전주기 표준화 시범사업 기술 지원 현황(2024-2025)

기업-농가(생산자 단체) 22개소 / 49건 / 총 14억원 기술지원 ☞ 기업당 최대 1억원 지원

※ 지자체 정책방향에 따라 지원 내용 및 범위가 변경될 수 있음

No	기업-농가명	지원 품목/제품	지원분야					
			원료 생산 표준화	원재료 규격관리	맞춤형 원료 표준화	원료기능성 평가	제조공정 컨설팅	분석검증
1	경희한약	맥문동 외 4종			●			
2	주식회사 바오젠	야생버섯,야생콩 4종			●			●
3	농업회사법인 흥 주식회사	와사비(고추냉이)			●	●	●	
4	농업회사법인 ㈜제주천지	바늘엉겅퀴			●			●
5	평창산양삼특구 영농조합법인	산양삼	●					●
6	주식회사 로지앤엘	한약재 발효액	●			●		
7	셀모티브 주식회사	우산이끼	●					●
8	농업회사법인 수예평창오가피(주)	오가피 잎						●
9	메타오가닉테크놀러지 주식회사	홍삼박						●
10	예인미코스메틱	홍삼박				●		
11	마이크로알지에스크어스	미세조류 유래 제품			●	●		
12	㈜비체담	BCD101			●			●
13	주식회사 알지프로나	미세조류 유래 엑토좀			●	●		●
14	비아루트㈜	개구리밥(부평초)				●		●
15	농업회사업인 고려홍삼원㈜	완두콩, 병아리콩				●		●
16	㈜네이처사이언스	NC-1			●			
17	㈜지원바이오	천연혼합추출물			●	●		
18	농업회사법인 흥 주식회사	고추냉이	●	●				
19	㈜케이메디켐	오가피 나무						●
20	유한회사 소미노	아주까리밤콩						●
21	농업회사법인 ㈜병풀농원	병풀 3개 품종	●					●
22	진부농업협동조합	당귀	●					●

강원 천연물소재 전주기 표준화 기술지원 문의처

(재)강원테크노파크 미래사업단 한재현 과장 ☞ e-mail. jay82@gwtp.or.kr

그린국제특허법률사무소는 20년의 노화우를 바탕으로 생명공학/종자산업 분야에 대한 높은 신뢰도의 서비스를 제공합니다.

기관 강점

20년 이상의 전문분야 업력

- 바이오 등 관련분야 전문인력 77%
  (변리사 7명, 박사 6명, 석사 9명)
- 바이오 등 특허출원 비중 85%
- 발명자 아이디어 문서화 능력 우수

특허등록률·품질 특허업계 최고

- 장기 근속기반 안정적 특허관리
  (변리사 특허경력 28년/명세사 근속연수 9년)
- 특허등록률 80%(4,332건/5,413건)
- BT분야 특허품질(SMART3) 최고획득
  (경상국립대, 전체 5.43점 vs. 그린 5.92점)

품종보호 출원 전문 서비스 可

- UPOV 총회 의장 및 종자원 지원장 역임
  최근진 이사 중심 컨설팅
- 품종보호 출원 및 기술이전 업무 위탁 가능

연구기관 특허 이해도 및 경험 高

- 대학 및 연구기관 전담사무소 수행경험 有
  (대학 7개 기관, 연구소 6개 기관)
- IP-R&D, IP분석 등 과제 다수수행
  ('23 차세대바이오그린21사업, 농과원, 원예원 등)
- 국유특허 특허출원, 기술이전 전문가 보유

기술이전·사업화 토탈 서비스 可

- 아이디어 상담부터 IP 창출 및 활용전략
  (기술이전, 사업화) 수립까지 전주기적 컨설팅
- 기술이전 및 사업화기관인 ㈜아이피온 및
  투자회사 WP와 전략적 제휴 파트너 구축

대전지역 소재 등

- 연구자 원활한 대면 미팅 가능
- 특허청 인근 소재(도보 5분) → 심사관 면담 용이
- 특허청 심사관 출신 대표 변리사
  → 심판 등 중요사건 처리 용이

기관 연혁

2005	그린국제특허법률사무소 설립(대전시 둔산동)
2007	국가연구개발 특허기술동향조사사업 기관 선정
2010	농업기술실용화재단 특허전담사무소 선정
2011	식물분자육종사업단, 차세대유전체연구사업단 기술동향분석 수행기관 선정
2012	정부 R&D 골든씨드프로젝트사업 컨설팅 기관 선정
2014	국가특허전략 청사진사업 농림수산식품분야 수행기관 선정
2015	연구성과실용화진흥원 대형사업단 성과활용 지원사업 수행기관 선정
2016	산업통상자원부 경제협력권 육성사업 참여기관 선정
2017	지역지식재산창출지원사업(특허-화학·바이오 분야) 수행기관 선정
2017	차세대바이오그린21사업 정책기획과제 수행기관 선정
2018	스타트업 지식재산바우처 사업 IP 서비스 기관 선정
2018	식물분자육종사업단 연구과제 수행기관 선정
2018	시스템합성농생명공학연구사업단 연구과제 수행기관 선정
2018	농업생명공학연구단 연구과제 수행기관 선정
2020	신육종기술실용화사업단 연구과제 수행기관 선정
2021	연구개발전담부서 지정
2021	산업재산권 진단기관 선정
2021	수출지원기반활용사업 수출바우처사업 수행기관 지정

전담사무소 및 용역기관 등록 현황

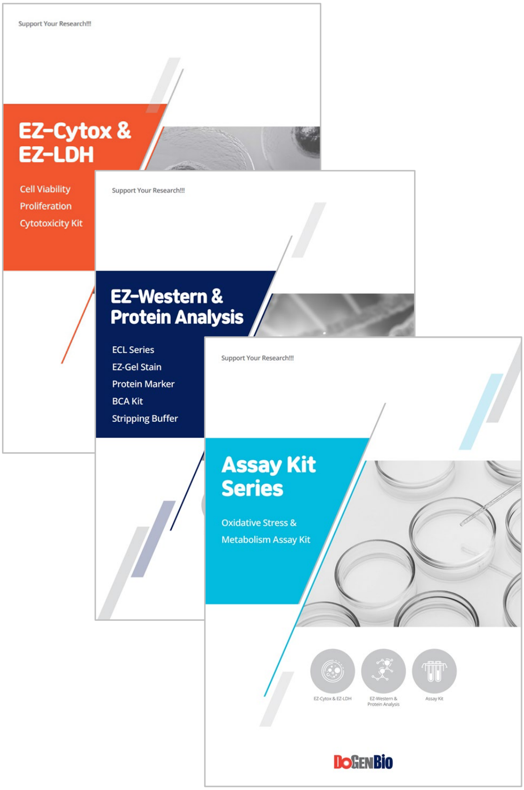
- 한국한의학연구원 특허업무 전담사무소
- 경상국립대학교 특허업무 전담사무소
- 한국생명공학연구원 특허업무 전담사무소
- 충남대학교 특허업무 전담사무소
- 영남대학교 특허업무 전담사무소
- 충북대학교 특허업무 전담사무소
- 전북대학교 특허업무 전담사무소
- 한남대학교 특허업무 전담사무소
- 한국농업기술진흥원 특허업무 전담사무소
- 바이오그린21 식물분자육종사업단 특허업무
- 전주농생명소재연구원 특허업무
- 서울과학기술대학교 특허업무
- 한국해양과학기술원 특허업무

구성원 현황 변리사/전문인력

최규환	박성용	김찬주	한진희	신경아	최진남	최근진
대표변리사/기술거래사	변리사/기술거래사	변리사/기술거래사	변리사	변리사/기술거래사	서울대 농학박사	서울대 농학박사
서울대 농학박사	서울대 농학사	고려대 이학사	고려대 이학사	도쿄대 농학박사	분자생물학 전공	UPOV 의장
유전육종학 전공	농생물학 전공	생명과학 전공	서울대 이학석사	응용생명공학 전공	㈜진로연구소	국립종자원
특허청 수석심사관	㈜아이피온 대표이사	고려대 법학박사(수료)	생명분자유전공학전공	특허청 특허심판관		
		한국농업기술진흥원	김앤장 법률사무소			

그린국제특허법률사무소
Green International Patent & Law Office

DoGenBio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Cell Viability
Proliferation
Cytotoxicity Kit

Support Your Research!!!

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ECL Series
EZ-Gel Stain
Protein Marker
BCA Kit
Stripping Buffer

Support Your Research!!!

Assay Kit Series

Oxidative Stress & Metabolism Assay Kit

EZ-Cytox

MTT 보다 간편하고 빠르게! MTS, XTT 보다 정확하게
Cell viability, proliferation, cytotoxicity를 측정하는 kit

EZ-LDH

상층액을 이용하여 보다 정확한
cytotoxicity를 측정할 수 있는 kit

Metabolism Assay Kit

01 EZ-Lactate Assay Kit
02 EZ-Acetylcholinesterase Assay Kit
03 EZ-Ascorbic Acid Assay Kit
04 EZ-ATP Assay Kit
05 EZ-Free Fatty Acid Assay Kit
06 EZ-Free Glycerol Assay Kit
07 EZ-Glucose Assay Kit
08 EZ-HDL, LDL/VLDL Assay kit
09 EZ-Total Cholesterol Assay Kit
10 EZ-Triglyceride Quantification Assay Kit
11 EZ-Nitric Oxide Assay Kit

Oxidative Stress Assay Kit

01 EZ-Superoxide Dismutase (SOD) Assay Kit
02 EZ-Glutathione (GSH/GSSG, Total) Assay Kit
03 EZ-Catalase Assay Kit
04 EZ-Hydrogen Peroxide/Peroxidase Assay Kit
05 EZ-Lipid Peroxidation (TBARS) Assay Kit
06 EZ-Total Antioxidant Capacity (TAC) Assay Kit
07 EZ-DPPH Antioxidant Assay Kit

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브리즈 사이언스 breezesc@naver.com

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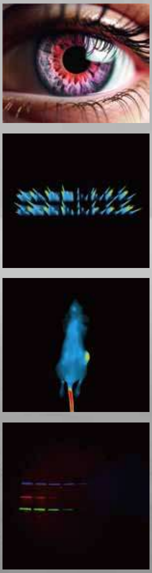
- **65,535 gray levels** research level protein quantification



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S. Sensitive
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Natural Product Central Bank

홈페이지
https://kobis.re.kr/npcb

홍보
동영상 1

홍보
동영상 2

(부가세 별도)

서비스 유형	세부 서비스 유형	서비스 내용	신청 절차	추가 제공 정보		분양 수수료 (추출물/원시료)	정보 이용료 (효능정보)	담당자
				분석 정보	효능 정보			
천연물 분양서비스	국내식물 전략소재	개별시료 : 70% 발효주정 추출물 10mg	천연물중앙은행 홈페이지 (kobis.re.kr/npcb)에서 분양신청 1. 소재분양신청 회원가입 ▶ 분양신청 ▶ 접수 ▶ 분양수수료 청구 ▶ 발송 ▶ 연구결과 Feedback 2. 분석정보 검색 회원가입 ▶ 소재/성분정보검색 ▶ 분석정보열람 신청 ▶ 분석 정보 열람 ▶ 분석정보 신청 3. 효능정보 검색 회원가입 ▶ 효능정보 신청 (효능정보 활용협약서 작성필수) ▶ 접수 ▶ 분양수수료 청구 ▶ 발송 ▶ 연구결과 Feedback	HPLC/UPLC Chromatogram (MS/UV/ELSD) 및 구성성분 정보	효능 I	10,000원	10,000원 / 바이오마커	김정희 043–240–6121 plantext@kribb.re.kr
		대량추출 : 70% 발효주정 추출물 1g				500,000원		
		원시료 : 추출물 1g 상당의 원시료				150,000원		
	해외식물 전략소재	개별시료 : 70% 발효주정 추출물 10mg		UPLC–MS Chromatogram	효능 I 산업화 후보소재 대상으로만 '24.~ '26.에 구축예정	10,000원		
		대량추출 : 70% 발효주정 추출물 1g				500,000원		
		원시료 : 추출물 1g 상당의 원시료				150,000원		
	국내식물 (舊)한국식물 추출물은행	개별시료 : 99.9% MeOH 추출물 20mg				6,000원		
		대량추출 : 99.9% MeOH 추출물 1g				300,000원		
		원시료 : 추출물 1g 상당의 원시료				100,000원		
	해외식물 (現)해외생물 소재센터	개별시료 : MeOH, EtOH, 추출물 20mg			효능 II	3,000원		
		분쇄시료 : 담당자에게 문의				10,000원		
		대량시료 : 담당자에게 문의				협의		
천연물 분리 분석서비스	용매 분획서비스	식물추출물을 Hexane, Chloroform, Ethyl acetate, Buthyl alco–hol, Distilled water로 단순 용매분획하여 제공하는 서비스	천연물중앙은행 홈페이지(kobis.re.kr/npcb)에서 분획 신청			1,000,000원 / 추출물 1–10g 기준		안종민 043–240–6143 jmahn@kribb.re.kr
	Column을 이용한 분획서비스	Column을 이용하여 식물추출물을 UV(254nm) peak 기준으로 5–10개의 Fraction을 제공하는 서비스				5,500,000원 / 추출물 1–5g 기준		
	Mass 분석서비스	UPLC–QTOF–MS(Waters 社)를 이용하여 식물추출물 또는 분획물의 주요 화합물의 Mass data 분석을 통해 잠정적으로 확인(Tentative Identification) 해주는 서비스 ※ 정량분석 가능(표준품 제공필수)	회원가입 및 분석신청(http://www.zeus.go.kr/main) ※ 장비명 : 이온 모빌리티 Q–TOF Mass Spectrometer (시설장비등록번호 : NFEC–2020–10–265378 장비선택)			1단계 : 400,000원 / 점 2단계 : 400,000원 / peak 3단계 : 400,000원 / peak		
소재기탁 서비스	천연추출물 및 원시료 기탁	국가연구개발사업을 통해 확보된 식물소재를 천연물중앙은행에 기탁하여 다른 연구자들이 기탁된 소재를 공유하여 연구할 수 있도록 하는 기탁서비스	회원가입 및 기탁접수(연구성과물 웹사이트, https://biorp.kribb.re.kr/) ▶ 서류검사(기탁가능 여부심사) ▶ 실물자원 접수 ▶ 자원확인 ▶ 기탁번호부여 ▶ 연구성과물 기탁필증 발행			무료 (기탁자 동의 시)		김정희 043–240–6121 plantext@kribb.re.kr

〈추가제공정보 참고사항〉

- **분석정보** 1) 분석데이터의 저작권은 '천연물중앙은행' 에 있으며, 분석데이터는 회원에게 무료공개를 원칙으로 하나, 무단캡처, 배포 및 2차 가공을 통한 재배포를 금지 2) 논문, 특허작성용으로 사용될 분석데이터를 원하시면 'Mass분석서비스'를 이용
- **효능정보** **효능 I .** MAO A, MAO B, 뇌신경세포생존율, ACE, IL–6, sICAM–1, DPP–4, IL–8, DPPH, ABTS, TARC, β–hexosaminidase, MUC5AC, IL–5, NO, Cell viability, IL–1β, ALP, 지방세포분화, Cell viability, ROS, IL–8, MMP–1, Procollagen
  1) 효능정보의 저작권은 '천연물중앙은행'에 있으며, 효능정보는 지식재산권의 보호를 위해 홈페이지에 미공개
  2) 효능정보는 '천연물중앙은행 효능정보 활용협약서'를 작성한 후, 회원에게 유료제공

  효능 II . 항염, 세포생존율, 살충, 항산화, 항당뇨, 미백, 항뎅기열, 항암

조선대학교 G-LAMP 사업단, 건강한 100세 시대를 여는 혁신의 시작

조선대학교 G-LAMP 사업단이 대한민국의 건강한 내일을 만들어갑니다.

국내 최대 규모의 딥&빅데이터로 연구의 패러다임을 바꾸다

조선대학교 G-LAMP 사업단은 **국내 최대 뇌 노화 딥&빅데이터를 기반**으로 '웰에이징-뇌 아바타' 모델을 개발하여, **노인성 뇌질환의 위험을 예측하고 조기진단 및 최적의 치료 방안을 제시합니다.**

건강한 100세를 위한 새로운 패러다임 제시

생명과학, 수학·통계, 생물정보학, 의공학 등 **다양한 학문이 융합된 혁신적인 연구**로 기초 과학과 의학의 융복합을 통해 **새로운 연구 생태계를 구축**하고 조기진단과 치료 예측 통합 시스템을 개발하여 건강한 고령사회를 실현합니다.

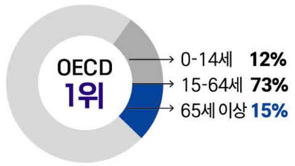
뇌질환 정밀 진단과 치료의 새로운 길

최첨단 생체/디지털 아바타 기술을 접목하여 뇌질환 병리와 치료 가능성을 심층연구합니다. 이는 노령화 사회에 필수적인 예측 후 예방과 정밀 의료 시스템 구축으로 이어질 것입니다.

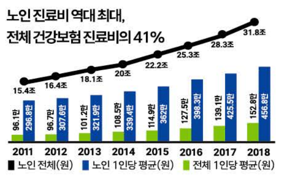
지역과 함께, 미래를 향해

조선대학교 G-LAMP 사업단은 뇌·신경과학 및 기초의학 분야의 전문 인재를 양성하며, **지역 산업 생태계의 발전과 미래 먹거리를 제공하는 초석**이 되고자 합니다. 이를 통해, 광주와 호남권을 중심으로 글로벌 연구의 선두에 서겠습니다.

노인성 질환의 심각한 사회적 문제 대두

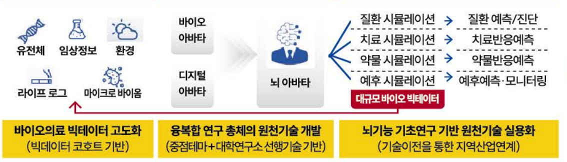


한국의 고령화 속도 OECD국가 중 1위
현재 고령사회에서 초고령사회로 진입 중



노인성/퇴행성 신경질환에 의한
사회경제적 문제 심각

광주 • 전남지역 고령인구는
전국 고령인구의 35.2%로 압도적 1위

비전	디지털 바이오 • 의료 연구혁신 생태계 거점 조성 및 건강한 지역사회 구현
전략	**L** 글로벌 연구리더 양성 Leadership **I** 노인성 질환 인프라 구축 Infrastructure **G** 대학주도 연구플랫폼 구축 Guardiance **H** 혁신적 초격차 원천기술 개발 High-tech **T** 신진인력의 동반성장 Teamwork
세부내용	 바이오의료 빅테이터 고도화 (빅데이터 코호트 기반) 융복합 연구 총체의 원천기술 개발 (중점테마+대학연구소 선행기술 기반) 뇌기능 기초연구 기반 원천기술 실용화 (기술이전을 통한 지역산업연계) 뇌기능 기초연구 인프라 구축 및 실용화
파급효과	건강한 초고령화 사회 확립 초격차 대학 중점 테마연구소 운영 뇌·신경과학 및 기초의학 연구 인프라 허브 제공 타 지역의 인재를 유인하는 대학의 연구 브랜드

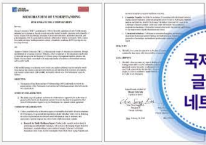
자세히 보기

교육부 NRF 한국연구재단 광주광역시 조선대학교 조선대학교 G-LAMP 사업단 CHOSUN UNIVERSITY G-LAMP Well-Aging Medicare Institute

조선대학교 **G-LAMP 사업단**, 건강한 100세 시대를 여는 **혁신의 시작**

공동연구 네트워크

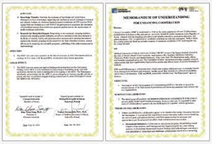
한미 공동 한국-미국 MOU 시행(조선대-보스턴 의과대학)



뇌 • 신경과학 및 기초의학분야 포함한 공동협력네트워크 구축 및
연구소 교류협력 진행

국제협력
글로벌
네트워킹

한EU 공동 한국-폴란드 MOU 시행(조선대-사일레지아 의과대학)



중점테마연구소 참여인력의 교류, 글로벌 협력센터 설립으로
국제공동연구 기획 및 수행 등 논의

2023.10. → 2024.08.

- '24.04 조선대-(주)메디노 MOU
- '24.04 조선대-휴덴스바이오 MOU
- '24.06 조선대-엑스켈리버 MOU
- '24.07 조선대-KBSI MOU
- '24.08 조선대-IBS MOU
- '24.12 조선대-생물의약센터 조선대-국립호남권생물자원관 섬야생생물소재 선진화 연구단
- '25.01 조선대-아이온셀(주)
- '25.02 조선대-(주)브레디스헬스케어

제도•인재양성 프로그램 인프라

제도 구축

- 1차년도 (2023) 사업단 구성 근거 마련 (부서 설치/운영 기준/강의책임사수)
- 2차년도 (2024) 사업단 운영 및 평가 근거 마련 (조직 구성/인사관리/연구소 평가)

2023 → 2025

- '23.9 조선대 LAMP사업 선정 (지방사립 유일)
- '23.11 LAMP 사업단 구성 근거 마련
- '24.02 사업단 운영 세칙 제정
- '24.03 G-LAMP 사업단 부서 설치
- '24.07 G-LAMP 사업단 -연구 지원 조직개편 -인구인력 인사 지침 제정
- '24.11 G-LAMP 사업단 -학내 연구소 평가 지침 제정

초청 세미나 개최

인재 양성 프로그램 진행

[중점테마 및 학내연구소 인턴십 프로그램(학사)
(`24. 07.~`24. 08.) 하계 방학]

[새싹 프로그램(석·박사),
(`24. 09.~`25. 01.)]

연구소 인프라 구축

홍보 • 성과 공유

사업단 홍보

조선대 램프사업 선정
('23.10)

기초과학 분야 '포닥' 공동연구 지원하는 '램프 사업' 8개교 예비 선정

캐릭터 제작
(`24.05-08)

광주 EXPO 홍보
(`24.06)

홈페이지 구축
(`24.08-11)

램프 포닥 전임교원 임용
(`23.09)

광주 MBC 라디오 홍보
(김정수, 박정희)

광주MBC 캠페인

2023.10. → 2024.12.

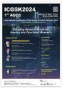
학회 공동개최 성과공유회

제57차
KSCB 공동개최
(`24.01)

7차
NFAD 공동개최
(`24.02)

제58차
KSCB 공동개최
(`24.08)

ICGSK2024
공동개최
(`24.10)



조선대 G-LAMP
사업단 개소식
(`24.10)

CSU-G-LAMP
FESTA 2024
(`24.10)

2024 G-LAMP
성과공유회
('24.12)

교육부 NRF 한국연구재단 광주광역시 조선대학교 조선대학교 G-LAMP 사업단 CHOSUN UNIVERSITY G-LAMP Well-Aging Medicare Institute

한경국립대학교
Hankyong National University

한경국립대학교 산학협력단 **한살림농식품분석센터**는 독자적인 **분석 시스템**을 구축하여 농식품의 품질 **안전성과 신뢰성**을 높이기 위해 노력합니다.

안전성검사기관 (농산물품질관리원,제49호) : 농산물 및 식품 등 **잔류농약 분석**

유기농업자재 시험연구기관 (농산물품질관리원,제57호)

농약시험연구기관(농촌진흥청, 제67호)

유해물질 분석: 방사성 물질 & 벤조피렌 & 동물용의약품 & 생물독소류 등

연구사업: 농축산물 잔류, 오염 유해물질 성분 프로파일링

보유 분석기기: LC/GC-QTOF & 2D-GCMS & LC/GC-MSMS & LC-MS & GC-MS & HPGe 감마핵종분석기기 등

분석 가능 성분 : 휘발성물질 및 PAH 등 유기화합물질 상담을 통해 진행 가능

분석의뢰 및 상담 _ 경기도 수원시 영통구 월드컵로150번길 56 경기친환경농업연구센터 5층
T.070-4489-8604~8609 / F. 031-213-9121

현성바이오 HSBIO

실험실 기자재, 시약 및 소모품 판매기업

견적문의
Tel.055)763-4525 / hsbio82@naver.com
경남 진주시 촉석로211번길 7

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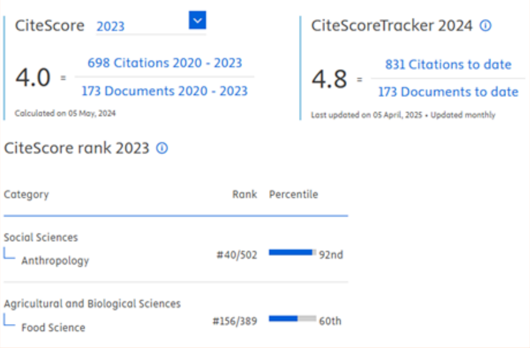
Journal Metrics



CiteScore 2023

4.0 = 698 Citations 2020 - 2023 / 173 Documents 2020 - 2023

Calculated on 05 May, 2024

CiteScoreTracker 2024

4.8 = 831 Citations to date / 173 Documents to date

Last updated on 05 April, 2025 • Updated monthly

CiteScore rank 2023

Category	Rank	Percentile
Social Sciences Anthropology	#40/502	92nd
Agricultural and Biological Sciences Food Science	#156/389	60th

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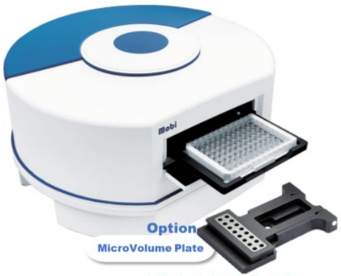


AVITI 24
AVITI


Next Gen Sequencing
Whole Genome
Exomes
Exon 1
Exon N
RNA-Seq
Metagenomics
Targeted sequencing
Gene 1
Gene 2
Gene N
Teton CytoProfiling
In situ multiomics
Drug screens
High content imaging
Pathway analysis
CRISPR screens
AVITI 24
AVITI

제주대학교 지역혁신클러스터육성사업단이 산학협력 현장착근형 인재양성을 책임지겠습니다.

계약Lab 운영 지원사업

- 제주지역혁신클러스터 내 바이오산업 및 전후방산업 특화산업 관련 기업과 대학이 공동으로 기업의 수요 발굴 후 문제해결형 산학협력 공동프로젝트 수행을 통한 맞춤형 인력양성 및 취업 연계지원
- 참여기관(팀)별 최대 28,000천원 이내(학생인건비 및 연구활동비 별도 지원)

산학협력 프로젝트Lab 운영 지원사업

- 대학-사업체 협력 운영체계 구축을 통한 현장중심 교육과정 개설 및 전문기술 인력양성
  지도교수 및 기업 전문가의 연구 지도하에 과제참여 학생들의 기술개발 과정 참여기회 부여
  클러스터 내 유망기업의 수요중심의 산학협력을 통하여 애로기술 해결 및 신기술 개발 지원
- 참여기관(팀)별 최대 10,000천원 이내(학생인건비 및 연구활동비 별도 지원)

유망기업 혁신인재 재직자교육 프로그램

- 클러스터 내 네트워크 활용 성장육성형 중심의 맞춤형 바이오산업 기술역량 강화를 통한 기술혁신형 강소기업 육성 기반 마련
- 1개 프로그램, 4주 진행(2025년 7~8월 중, 교육 당 4시간)

산업통상자원부
Ministry of Trade, Industry and Energy

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한국산업기술진흥원

Jeju 제주특별자치도
Jeju Special Self-Governing Province

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