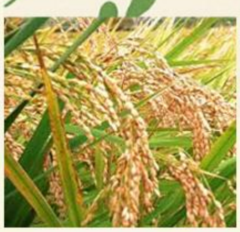
INNOVATIONS IN PLANT AND FOOD SCIENCES IPFS-2025

PLANT AND FOOD SCIENCES FOR SUSTAINABLE FUTURE – FROM BENCH TO FIELD

8-9 NOVEMBER 2025
GINGA HALL,
MORIOKA, IWATE, JAPAN

IPFS is a consortium of seven universities including, The United Graduate School of Agricultural Sciences, Iwate University (Japan), University of Saskatchewan (Canada), Fujian Agriculture and Forestry University (China), University of Dhaka (Bangladesh), Jilin University (China), and Dalhousie University (Canada).
The symposium is aimed at facilitating exchange and collaborative research among the faculty members, researchers, and students at these universities.




Organized by:

The United Graduate School of Agricultural Sciences (UGAS), Iwate University

INNOVATIONS IN PLANT AND FOOD SCIENCES IPFS-2025

PLANT AND FOOD SCIENCES FOR SUSTAINABLE FUTURE – FROM BENCH TO FIELD

Date: Saturday, November 8 through Sunday, November 9, 2025

Venue: Ginga Hall, Iwate University, Ueda Campus, Morioka, Iwate, Japan

Reception: The Morioka Grand Hotel, Morioka, Iwate, Japan
https://www.m-grand.jp/

Co-sponsor: Iwate University
https://www.iwate-u.ac.jp/english/index.html

IPSF-2025 information:
https://ugas.agr.iwate-u.ac.jp/en/schedule/international-symposium-innovations-in-plant-and-food-sciences-ipfs-2025/

Program Committee of the IPFS-2025 Symposium

Chairperson: Dr. Kikukatsu Ito, UGAS, Iwate University, Japan

Co-Chairperson: Dr. Abidur Rahman, UGAS, Iwate University, Japan

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Dr. Karen Tanino, University of Saskatchewan, Canada

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Dr. Yiling Miao, Jilin University, China

Dr. Shuang Wu, Fujian Agriculture and Forestry University, China

Dr. Balakrishnan Prithiviraj, Dalhousie University, Canada

Registration of Participants

Registration time:
Nov 8, 2025: 8:30 - 16:00
Nov 9, 2025: 9:00 - 12:00
Registration fee for domestic faculties and professionals: 3,000 yen (¥)
Registration fee for students: free
Registration fee for overseas participants: covered by IPFS-2025
※ Registration fee will include symposium materials, two lunches and drinks. The fee will be collected in cash during registration hours on November, 8-9, 2025.

Reception

November 8, 2025: 18:30 - 21:00, The Morioka Grand Hotel, Morioka (There will be a shuttle service from the symposium venue to hotel. The shuttle will depart from Building #1 of faculty of Science and Engineering at 18:10)
Reception fee for faculties and professionals: 10,000 yen (¥)
Reception fee for students: 5,000 yen (¥)
Reception fee for overseas participants- covered by IPFS
※ The fee will be collected in cash during registration hours on Nov 8, 2025.

Lunch

Lunch time:
Nov 8, 2025: 12:00 - 12:30
Nov 9, 2025: 12:00 - 12:30
Lunch will be served on the second floor of Ichiyu-Kaikan, close to the Ginga Hall from 12:00. We will prepare lunch boxes and drinks for all participants. Please refrain from bringing the lunch inside the Ginga Hall.

Drink Service during the Symposium

There are coffee and tea breaks between each session. We will serve free drinks and small snacks at the lobby of the Ginga Hall. However, you are requested not to bring the drinks inside the Ginga Hall.

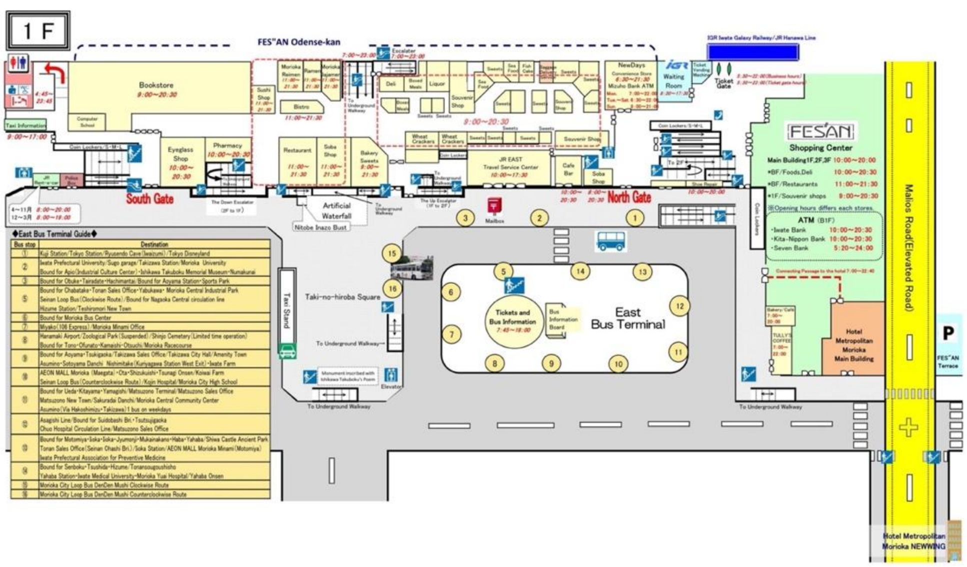
Guide Map (Ginga Hall, Iwate University)

Access to the Ginga Hall, Iwate University from Morioka train station

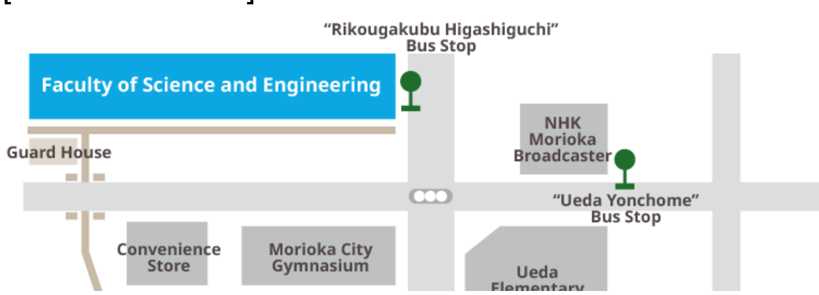
By bus: Morioka Station East Exit 11 bus stop (Iwateken Kotsu, Bus No. 307) → Ueda Yonchome (12-15 min), 270 yen (¥)/ person. a 4-min walk from Ueda Yonchome bus stop to the Ginga hall.

[Bus Schedule]
07:20, 07:35, 07:45, 07:55
08:05, 08:15, 08:25, 08:32, 08:42, 08:52
09:02, 09:12, 09:22, 09:37, 09:52

[Morioka train station East Exit 11 bus stop]



Bus station to get off
[Ueda Yonchome]



By taxi: Your hotel to faculty of Science and Engineering, the Ginga Hall, Iwate University
around 10 min, 1,000 to 1,500 yen (¥)/taxi

On foot: Morioka train station to the Ginga Hall, Iwate University around 40 min. Please check google map searched as "Ginga Hall, Iwate University " helping for you.

Oral Presentation

For keynote speakers, the allocated time of the presentation is 20 minutes which includes question and answer session. Please plan your talk within 15-16 minutes and keep the rest of the time for question-and-answer session. For other oral presentations in the sessions, the allocated time is 15 minutes including the question-and-answer session. Please plan your talk within 12 minutes and keep the rest of the time for question-and-answer session.

For the young scientist's session, the allocated time is 10 minutes including the question-and-answer session. Please plan your talk within 8 minutes and keep the rest of the time for question-and-answer session. Two best oral presentations will be awarded.

Poster Presentation

The main goal of the poster session is to gain a maximum benefit from the scientific work presented and to create a lively interaction between poster authors, judges (experts in the field) and interested symposium participants.

Poster session

Poster session will be held on Saturday, Nov 8, 2025 (12:30-14:25) and Sunday, Nov 9, 2025 (12:30 – 14:00).

Core time for poster presentation

Nov 8, 2025 (12:30-14:25)- odd numbered posters
Nov 9, 2025 (12:30-14:25)- even numbered posters
The presenter should be present in front of the poster during this time. Since best two posters will be awarded, the judges will walk around the posters and ask questions to the presenters. Please prepare yourself for a 5 min presentation and 3-5 min question- and-answer session.

Poster Size and Preparation

Please prepare your poster with A0 size paper (841 x 1189 mm). Symposium committee will provide the presenter with the poster number before the symposium. Poster boards will have numbers on it and the presenters are requested to mount their posters accordingly. Push pins for mounting the posters will be provided.
To prepare the poster, use a clear typeface. The poster should be readable from a distance of 2-3 meters. This means that all lettering should be at least 8 mm high. Graphs and diagrams should be drawn with a minimum line width of 1 mm. Please use proper color contrast.

Mounting and removing the poster

Please mount the poster by 11:00 am of Nov, 8, 2025. Please remove your poster by 15:00 pm of November 9, 2025. If posters are not removed within the time for dismantling, your poster will be removed and disposed of.

Venue for poster session

Poster session will be held on the 2nd floor of Ginga Hall.

Free Wireless LAN service

Free wireless LAN connection will be available in Ginga Hall
The ID and check the password will be provided at the reception desk during the symposium.

Program

Day 1- Saturday- November 8, 2025

8:30-16:00 Registration

9:30 - 9:35 Opening Remarks

Dr. Kikukatsu Ito Dean, The United Graduate School of Agricultural Sciences, Iwate University, and Chair of the IPFS-2025 Organizing Committee

Session 1: Developmental regulations in plants

Session Chairs: **Dr. Kikukatsu Ito** and **Dr. Abidur Rahman**

9:40 - 10:00 S-1-1K **Keynote Talk**

Dr. Bunyamin Tar'an (USask) Accelerated genetic improvement of flax

10:01 - 10:16 S-1-2O

Dr. Yuji Suzuki (UGAS, Iwate University) Effects of genetic manipulation of the Calvin–Benson cycle on photosynthesis in rice

10:17 - 10:32 S-1-3O

Dr. Yiling Miao (Jilin University) Genome-Wide Analysis of Rice Panicle Development

10:33 - 10:48 S-1-4O

Dr. Linzhou Huang (NWAFU) Starch metabolism contributes to the plasticity of rice plant architecture through modulating shoot gravitropism

10:50 - 11:25 **Coffee/Tea Break with Snacks**

11:26 - 11:41 S-1-5O

Dr. Bin Li (Jilin University) The role of tomato SNARE proteins in regulation growth and development and response to low temperature stress

11:42 - 11:57 S-1-6O

Dr. Yasuyuki Kawaharada (UGAS, Iwate University) Molecular regulation of symbiotic nodulation through interactions between the legume and *Rhizobium*

12:00 - 12:30 **Lunch Break**

12:30 - 14:25 **Poster presentations (Odd number)**

Session 2: Biotic and abiotic stress responses in plants

Session Chairs: **Dr. Arifa Rahman** and **Dr. Yuji Suzuki**

14:30 - 14:50 S-2-1K **Keynote Talk**

Dr. Yin-Gang Hu (NWAFU) Improving Drought Resistance in Bread Wheat

14:51 - 15:06 S-2-2O

Dr. Bill Biligetu (USask) Improving Salt Stress Resistance in Alfalfa: Integrating Genomic Insights with Breeding Strategies

15:07 - 15:22 S-2-3O

Dr. Qian Chen (FAFU) Viruses hijack salivary proteins of insect vectors to achieve transmission and pathogenesis in plant hosts

15:25 - 15:55 **Coffee/Tea Break with Snacks**

15:56 - 16:11 S-2-4O

Dr. Chengguo Jia (Jilin University) SlNAC12, A Key Regulator of Salt Stress Tolerance and Leaf Senescence in Tomato

16:12 - 16:27 S-2-5O

Dr. Karen Tanino (USask) The continuing journey into exploring the role of barriers in plant survival

16:28 - 16:43 S-2-6O

Sophie Duchesne (USask) Analyzing Heat Resilience in Interspecific Chickpea: A Genetic and Phenotypic Approach for Breeding

16:43 - 16:59 **Coffee/Tea Break with Snacks**

Session 3: Young Scientists Session 1

Session Chairs: **Dr. Yasuyuki Kawaharada** and **Dr. Karen Tanino**

17:00 - 17:10 YS-1-1O

Dr. Federica Higa (USask) Reduction of off - flavours in flaxseed proteins using adsorbent resins during protein extraction

17:11 - 17:21 YS-1-2O

Kalhari Manawasinghe (USask) Exploring the Impact of Canopy Architecture on Drought and Heat Stress Resilience in Spring Wheat (*Triticum aestivum* L.)

17:22 - 17:32 YS-1-3O

Dezheng Liu (NWAFU) Mining genomic regions associated with stomatal traits and their candidate genes in bread wheat through genome-wide association study (GWAS)

17:33 - 17:43 YS-1-4O

Botian Zheng (Jilin University) Transcriptomic Analysis Reveals a Regulatory Network and significance of VcWOXs During Adventitious Root Formation in Blueberry

17:44 - 17:54 YS-1-5O

Yihan Men (NWAFU) N^6-methyladenosine RNA modification regulates transcriptional and metabolic responses in wheat to drought stress

18:30 - 21:00 **Banquet at The Morioka Grand Hotel**

There will be a shuttle bus service from the symposium venue to the Morioka Grand Hotel. The shuttle will depart from Building #1 of faculty of Science and Engineering at 18:10

Day 2 – Sunday, November 9, 2025

9:00-12:00 Registration

Session 4: Food Science and Nutrition

Session Chairs: **Dr. Ahmad Al-Mallahi** and **Dr. Shu Taira**

9:30 - 9:50 S-4-1K **Keynote Talk**

Dr. Akira Nishimura (UGAS, Iwate University) Inhibitory mechanisms of proline utilization in yeast: A step toward proline-free wine

9:51 - 10:06 S-4-2O

Dr. Takuji Tanaka (USask) Value addition on the agriculture products towards sustainable food and feed supply

10:07 - 10:22 S-4-3O

Dr. Shu Taira (UGAS, Iwate University) Theanine Derived from Tea Leaves Modulates Monoamine Metabolism: A Single-Hair Analysis

10:23 - 10:50 **Coffee/Tea Break with Snacks**

10:51 - 11:06 S-4-4O

Dr. Ahmad Al-Mallahi (Dalhousie University) Creation of potato leaf samples under indoor conditions and using biostimulant for nutrient sensing development based on machine learning

11:07 - 11:22 S-4-5O

Dr. Pattama Wiriyasermkul (UGAS, Iwate University) Deciphering human transport systems for micronutrients and bioactives from foods

11:23 - 11:38 S-4-6O

Dr. Chunhong Yuan (UGAS, Iwate University) Advances in Precision Quality Control Technologies for Seafood: Insights from Shellfish Studies

11:40 - 12:30 **Lunch Break**

12:30 - 14:25 **Poster presentations (Even number)**

Session 5: Young Scientists Session 2

Session Chairs: **Dr. Takuji Tanaka** and **Dr. Pattama Wiriyasermkul**

14:30 - 14:40 YS-2-1O

Shangyi Xu (USask) Modification of the substrate specificity of *Lactococcus lactis* prolidase by rational design

14:41 - 14:51 YS-2-2O

Hao Chen (Jilin University) Deubiquitinase ZmUBP5 is essential for maize kernel development

14:52 - 15:02 YS-2-3O

Yosuke Akiba (Iwate University) Elucidating the molecular mechanism of auxinic herbicides, dicamba and picloram in *Arabidopsis thaliana*

15:03 - 15:13 YS-2-4O

Qifan Guo (NWAFU) Genetic and molecular basis of ABA response in wheat seedlings shared with mature-stage drought tolerance revealed by integrated GWAS and transcriptomics

15:15 - 15:30 **Coffee/Tea Break with Snacks**

15:31 - 15:41 YS-2-5O

Li Zhe (NWAFU) Genome-wide association study of novel genetic loci for cadmium accumulation and germplasm screening for low-cadmium accumulation in common wheat (*Triticum aestivum* L.)

15:42 - 15:52 YS-2-6O

Xinjie Yu (USask) Tapping the flax gene pool: from domestication traits to hybridization barriers

15:53 - 16:03 YS-2-7O

Yan Yu (NWAFU) Correlation study between canopy temperature (CT) and wheat yield and quality based on infrared imaging camera

16:04 - 16:14 YS-2-8O

Subarna Sharma (UGAS, Iwate University) Robust and affordable root phenotyping approaches for early-stage wheat growth

16:15 - 16:25 YS-2-9O

Hao Ren (NWAFU) Novel QTLs/genes affecting single stem elasticity, stem strength, and three lodging indices in bread wheat (*Triticum aestivum* L.) identified by genome-wide association analysis

16:30 - 16:44 **Coffee/Tea Break with Snacks**

Closing session

16:45 - 16:55 Award ceremony

16:55 - 17:00 Closing Remarks

Dr. Karen Tanino (USask)

UGAS; The United Graduate School of Agricultural Sciences

USask; University of Saskatchewan

FAFU; Fujian Agriculture and Forestry University

NWAFU; Northwest Agriculture and Forestry University

Dalhousie University

Iwate University

Poster session

Day 1 Saturday November 8, 2025
12:30-14:25 **Poster presentations (Odd number)**

P01. Reo Sato (The United Graduate School of Agricultural Sciences, Iwate University) Which fertilization component enhances cold tolerance in highly cold tolerant rice varieties "Tohoku PL1-3", "Ouu PL4,5"? -Estimation of fertilization process using anther morphology-

P03. Md Arafat Hossain (The United Graduate School of Agricultural Sciences, Iwate University) Nighttime-heating exposure at above ground and below ground; which is more influential on rice yield?

P05. Xiangfeng Wang (The United Graduate School of Agricultural Sciences, Iwate University) Regulation of Efferocytosis as a Key Mechanism in the Anti-Atherosclerotic Effects of Resveratrol

P07. Yusuke Sawamura (Department of Plant Bio Sciences, Faculty of Agriculture, Iwate University) Indole-3-butyric Acid (IBA) functions as an independent hormone to regulate the lateral root developmental process in *Arabidopsis thaliana*

P09. Ririko Sato (Graduate School of Arts and Sciences, Iwate University) Identification of novel cadmium uptake transporters in *Arabidopsis thaliana*

P11. Satomi Arakida (Graduate School of Arts and Sciences, Iwate University) Effect of soil inoculation on rice productivity under different soil and water conditions

P13. Dr. Takumi Tezuka (Faculty of Agriculture, Iwate University) Analysis of the dorsal-ventral axis formation in rice embryos as a model for monocots

P15. Rui Tian (The Graduate School of Agricultural Sciences, Fukushima University) Temporal Variation of GABA Levels in Tomatoes During Ripening in Mori Town, Hokkaido

P17. Ayano Miyabayashi (The Graduate School of Agricultural Sciences, Fukushima University) Administration of Vitamins (A_1, B_1, B_6) prevent a Parkinson's Disease Symptom

P19. Dr. Maya Matsunami (Faculty of Agriculture, Iwate University) Effect of two-depth split application of liquid fertilizers on rice root system architecture

P21. Soichiro Yamada (The United Graduate School of Agricultural Sciences, Iwate University) Localization Analysis of Toxic Components in Higher Plants Using Imaging Mass Spectrometry (IMS)

Day 2 Sunday November 9, 2025
12:30-14:25 **Poster presentations (Even number)**

P02. Issa Ousmane Mamadou (The United Graduate School of Agricultural Sciences, Iwate University) Genotypic variation in phenotypic plasticity of 23 rice accessions: Both root and shoot responses to low planting density

P04. Shun Iketani (Department of Plant Bio Sciences, Faculty of Agriculture, Iwate University) Potential roles of lipid transport family protein in the cold stress response of *Arabidopsis thaliana*

P06. Mahbubah Jannat (The United Graduate School of Agricultural Sciences, Iwate University) *Bradyrhizobium ottawaense* Type III Secretion System mediated Compatible and Incompatible Nodulation in *Vigna* species

P08. Tomo Kitabayashi (Department of Plant Bio Sciences, Faculty of Agriculture, Iwate University) Elucidating the response mechanism of tomato roots to cold stress response

P10. Rinto Enya (Faculty of Agriculture, Iwate University) Control of seed dormancy using iron-powder coating in rice

P12. Yukino Kominami (Graduate School of Arts and Sciences, Iwate University) Yield potential of a BNI elite wheat line under cool climate

P14. Manaka Kumagai (Graduate School of Arts and Sciences, Iwate University) Development of High-Value-Added Products from Sanriku Sea Cucumbers Based on Their Biochemical Characteristics

P16. Yuya Kuwaba (The Graduate School of Agricultural Sciences, Fukushima University) Stress Biomarkers in Mouse Fur under Low Gravity Conditions on the International Space Station (ISS)

P18. Akane Higuchi (Graduate School of Arts and Sciences, Iwate University) Analysis of the efficacy of phenethyl isothiocyanate on recovery from skeletal muscle atrophy induced by disuse

P20. Kotone Yoneda (The Graduate School of Agricultural Sciences, Fukushima University) Visualization of Stress Levels from a Single Strand of Hair Using IMS

Abstract

S-1-1K

Accelerated genetic improvement of flax

Megan. A. House[1], Frank. M. You[2], Bunyamin Tar'an[1*]

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[2] Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON, K1A 0C6, Canada

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Abstract
Accelerated breeding approach allows to reduce breeding cycle, reduce costs, and enhance genetic gain to meet market demands. We developed accelerated breeding protocol for flax (*Linum usitatissimum*) using a combination of high temperatures and long-day conditions that enabled us to develop novel advanced breeding lines and inbred populations in a relatively short period. Mature seeds can be reliably collected up to nine days earlier under accelerated breeding conditions compared to under normal conditions. We applied accelerated breeding approach to develop advanced breeding lines using a combination of speed breeding and (a) phenotypic selection for high value traits such as seed size and short plant stature, and (b) molecular marker-assisted selection for disease resistance and seed quality traits. We combined speed breeding with a high plant-density growth system to quickly develop large recombinant inbred line populations. With this approach, the average generation time is reduced by one to one and half months, allowing the completion of 5-6 generations in one year. In addition, we also examined the potential of genomic selection (GS) in flax breeding by testing the prediction accuracy of several GS models, marker types, and training populations for seed yield. Using a subset of the flax core collection as the training population, genome wide single nucleotide polymorphism (SNP) markers, SNP-based haplotypes, principal component markers, and five-fold cross-validation methods, we obtained prediction accuracy as high as 0.84. Across-population prediction using historical data to evaluate new breeding lines achieved accuracy of up to 0.83 highlighting the potential of GS for predicting flax yield.

S-1-2O

Effects of genetic manipulation of the Calvin–Benson cycle on photosynthesis in rice

Yuji Suzuki[1,*], Chikahiro Miyake[2], Amane Makino[3]

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[2] Graduate School of Agricultural Science, Kobe University, Kobe 657-8501, Japan
[3] Graduate School of Agricultural Science, Tohoku University, Sendai 980-8572, Japan

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Abstract
Improving photosynthesis is an effective means for improving plant productivity. One of the target is CO_2 assimilation by the Calvin–Benson cycle. The CO_2-fixing enzyme Rubisco is thought to limit CO_2 assimilation rate (*A*) at low to normal CO_2 levels. However, its overexpression did not markedly increase *A* at these conditions. Other factors such as the regeneration of another Rubisco substrate, ribulose 1,5-bisphosphate (RuBP), were speculated to be insufficient to support the increased Rubisco capacity. Therefore, we overexpressed some key enzymes for RuBP regeneration simultaneously with Rubisco to improve photosynthesis. Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) was suggested to have a control on RuBP regeneration from its antisense suppression study in tobacco. GAPDH overexpression in rice slightly increased *A* at elevated CO_2 levels, where RuBP regeneration is thought to limit *A*. Triose phosphate isomerase (TPI) has not been regarded as a key enzyme for photosynthesis because of its high capacity. However, its antisense suppression in rice decreased *A* at elevated CO_2 levels, similar to when *A* was limited by ATP supply to RuBP regeneration. TPI overexpression in rice also slightly increased *A* at elevated CO_2 levels. These results suggest that overexpression of GAPDH or TPI slightly improved RuBP regeneration. However, simultaneous overexpression of these enzymes with Rubisco did not increase *A*, indicating that the enhancement of enzyme capacities for RuBP regeneration was insufficient to support the increased Rubisco capacity and thereby improve photosynthesis. Other metabolisms such as supply of ATP and NADPH to the Calvin–Benson cycle may be necessary to be considered.

S-1-3O

Genome-Wide Analysis of Rice Panicle Development

Yiling Miao[1,*], Xinglin Du[1]

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Abstract
Rice is a vital crop feeding nearly half of the global population. Its yield is primarily determined by three main components: spikelet number per panicle, panicle number per plant, and spikelet weight. Panicle architecture strongly influences spikelet number per panicle and is shaped by the activity of the shoot apical meristem (SAM). The developmental process of the rice panicle involves transitions through several meristem types: vegetative SAM, inflorescence meristem (IM), branch meristem (BM), spikelet meristem (SM), and finally floral meristem (FM). Each meristem transition is precisely regulated by key genes. To identify critical genes governing these transitions at the whole-genome level, we conducted time-course RNA sequencing (RNA-seq) across SAM, IM, BM, SM, and FM stages. In parallel, Assay for Transposase-Accessible Chromatin using sequencing (ATAC-seq) was performed at matching time points to assess chromatin accessibility. Integrated analysis of RNA-seq and ATAC-seq data revealed six distinct groups of genes with dynamic expression patterns during panicle development. Importantly, chromatin accessibility around gene loci was closely associated with transcriptional levels, indicating that chromatin state is a prerequisite for gene expression. We also identified group-specific marker genes and transcription factor binding motifs. In summary, elucidating the gene networks and pathways in rice panicle development will enhance our understanding of the regulatory mechanisms underlying panicle traits and provide potential targets for molecular breeding.

S-1-4O

Starch metabolism contributes to the plasticity of rice plant architecture through modulating shoot gravitropism

Linzhou Huang[1]*, Wenguang Wang[2], Jiahui Jiang[1], Yonghong Wang[2], Liang Chen[1], Yin-Gang Hu[1]

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[2] State Key Laboratory of Wheat Improvement, College of Life Sciences, Shandong Agricultural University, Tai'an 271018, China

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Abstract
Rice (*Oryza sativa* L.) tiller angle is a key component for achieving ideal plant architecture and high grain yield. Studies have identified the functional links between shoot gravitropism and rice tiller angle. However, the molecular mechanism underlying rice tiller angle remains elusive. We isolated a tiller angle gene *LAZY2* (*LA2*), which encodes a novel chloroplastic protein. Lose function of *LA2* leads to defective shoot gravitropism and impaired asymmetric distribution of auxin upon gravistimulation. Histologic analysis revealed that the starch granules in gravity-sensing leaf sheath base in *la2* mutant were absent, suggesting that LA2 is involved in the starch metabolism in amyloplasts. We demonstrated that LA2 functions in the same pathway with the starch biosynthesis enzyme OspPGM and acts upstream of *LA1* in regulating rice shoot gravitropism and tiller angle. These results established the framework of the starch-statolith-dependent rice tiller angle regulatory pathway that links tiller angle, starch-statolith-dependent gravity perception, LA1-mediated asymmetric distribution of auxin, and rice shoot gravitropism. In addition, we also identified a potential upstream regulator (URL1) of *LA2* through Y1H analysis. Transgenic analysis showed that overexpression of *URL1* could enlarge rice tiller angle, suggesting that *LA2* is inhibited by URL1. Collectively, our research demonstrated that starch metabolism contributes to the plasticity of rice plant architecture through shaping moderate tiller angle and modulating shoot gravitropism.

S-1-5O

The role of tomato SNARE proteins in regulation growth and development and response to low temperature stress

Jianing Li, Nai'er Chen, Xiyao Wang, Jiangning Wang, Wenxin Zhang, Mingzhe Zhang, Wuliang Shi, Chengguo Jia, Bin Li*
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Abstract
The endomembrane system of eukaryotic cells mediates intracellular material exchange through vesicular transport, driven by soluble N-ethylmaleimide-sensitive factor attachment protein receptors (SNAREs). In plants, SNAREs are critical for cell division and expansion as well as responses to environmental cues by mediating vesicle fusion. In this study, we identified tomato SNARE protein family members and selected *SlSYP121* for functional characterization based on its distinctive expression pattern. Transgenic tomato lines overexpressing *SlSYP121* exhibited reduced leaf margin serration and significantly shorter trichomes on both stems and leaves, indicating that *SlSYP121* functions as a negative regulator of trichome elongation. Integrated transcriptomic and metabolomic analyses indicated that *SlSYP121* mediates vesicular transport and cell morphogenesis through hormone signaling networks and cytoskeletal dynamics, thereby contributing to trichome development and leaf margin serration. Yeast two-hybrid (Y2H) and luciferase complementation assays (LCA) demonstrated interactions between SlSYP121 and SlSNAP33.2/SlSNAP30, with all three proteins localized to the plasma membrane. Collectively, these findings suggest that *SlSYP121* participates in vesicular transport to regulate the CUC-PIN1-auxin pathway and cytoskeletal dynamics, coordinating with hormone signaling to modulate tomato leaf morphology and trichome development.

Keywords: Tomato; SNARE; Leaf margin serration; Trichomes; Hormones; Cytoskeleton

S-1-6O

Molecular regulation of symbiotic nodulation through interactions between the legume and *Rhizobium*

Yasuyuki Kawaharada[1,2] *

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[2] Department of Biosciences, Faculty of Agriculture, Iwate University, Morioka, Iwate 020-8550, Japan

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Abstract
Mutualistic interactions between plants and microbes are established through highly coordinated molecular communications. Leguminous plants engage in a unique symbiosis with soil bacteria such as *Rhizobium*, leading to the formation of specialized root organs known as nodules. Within these nodules, *Rhizobium* converts atmospheric nitrogen into biologically available ammonia, which benefits the host plant, while the plant provides photosynthetically derived carbon compounds in return.
During the establishment of nodule symbiosis, multiple direct molecular interactions occur between the two partners. The initial symbiotic signaling is triggered when host-derived flavonoids are recognized by the rhizobial transcriptional factor NodD, inducing the synthesis and secretion of Nod factors. These Nod factors are perceived by the plant LysM receptor-like kinases (LysM-RLKs) NFR1 and NFR5, initiating downstream signaling events. Another LysM-RLK, EPR3, recognizes bacterial exopolysaccharides to further regulate infection and symbiotic progression. In addition, rhizobial type III effector proteins, delivered via the type III secretion system into host cells, modulate host signaling both positively and negatively during nodule development.
In this presentation, I will discuss these molecular interactions and their regulatory mechanisms, with a focus on our recent findings.

S-2-1K

Improving Drought Resistance in Bread Wheat

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Abstract
Wheat is an important food crop in the world. Drought is one of the most serious threat for wheat production. This presentation will introduce wheat production in wheat, main biotic and abiotic stresses for wheat production in China, some experiences on investigating wheat drought tolerance in wheat, dwarf genes for wheat improvements, and the progress in wheat germplasm innovation, and tests of wheat lines in different ecological regions.

S-2-2O

Improving Salt Stress Resistance in Alfalfa: Integrating Genomic Insights with Breeding Strategies

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Abstract

Development of salt tolerant alfalfa cultivars has a significant value to reclaiming saline areas and increasing forage production for animal feed. The objectives of this study were to identify key traits and understand various mechanisms of alfalfa in response to salt stress, and to develop novel cultivars. A series of experiments have been carried out over last decade using Synchrotron beam lines, transcriptome analysis, salt lab tests, and field trials. Salt-tolerant populations showed greater germination percentage and seed vigor at 16 dS m^{-1} E.C. In field and salt lab studies, salt tolerant populations out-performed the check cultivars, under a high salinity. Salt tolerant selection increased alfalfa leaf protein concentration, and reduced ion accumulation in leaf tissues. In root tissue, salt tolerant populations maintained greater number of differently expressed genes (DEGs) during the first 27 h of salt stress, while the number of DEGs decreased for a susceptible population. We developed KASP assay for the SNPs linked to the highly expressed genes. Our results showed that recurrent selection has accumulated certain salt resistant related favorable alleles in the alfalfa breeding populations. Taken together, salt tolerance in alfalfa is a complex trait, and morphological, genomic, and physiological indicators have been developed for future breeding use.

S-2-3O

Viruses hijack salivary proteins of insect vectors to achieve transmission and pathogenesis in plant hosts

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Abstract

Salivary effectors from piercing-sucking insects are well-established modulators of plant defense responses, yet their roles in facilitating viral transmission remain largely unexplored. This study reveals how two rice viruses hijack salivary proteins of two leafhopper species to enable viral transmission through mechanisms of plant immunity suppression. In *Nephotettix cincticeps* vector, the salivary vitellogenin (NcVg) associates with exosomal GTPase Rab5 (NcRab5) for secretion from salivary glands. Rice dwarf virus (RDV) infection upregulates NcVg expression and promotes its packaging into exosomes for delivery into rice phloem. The secreted NcVg protein suppresses H_2O_2 burst in rice through interaction with rice glutathione S-transferase F12, a key enzyme in glutathione-dependent oxidation pathways. This suppression facilitates leafhopper feeding and viral transmission. Similarly, in *Recilia dorsalis* vector, salivary glyceraldehyde-3-phosphate dehydrogenase (RdGAPDH) is loaded into exosomes and delivered into rice phloem during feeding. Rice gall dwarf virus (RGDV) infection enhances both the accumulation and exosomal release of RdGAPDH. The released RdGAPDH scavenges H_2O_2 through its reactive sulfhydryl groups, thereby suppressing plant oxidative bursts and promoting insect feeding and viral transmission. Notably, rice plants counter potential RdGAPDH overoxidation-induced cytotoxicity by employing glutathione to mediate S-glutathionylation of oxidized RdGAPDH, thus maintaining cellular homeostasis. Salivary GAPDHs from other hemipteran vectors similarly function in suppressing plant H_2O_2 bursts, indicating a conserved mechanism across insect vectors. These findings reveal that plant viruses exploit insect salivary proteins to manipulate plant defense, thereby creating favorable conditions for sustained insect feeding and efficient viral transmission, providing insights into the tripartite interactions among plants, insect, and viruses.

S-2-4O

SlNAC12, A Key Regulator of Salt Stress Tolerance and Leaf Senescence in Tomato

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Abstract

Soil salinization is a major environmental stressor limiting tomato growth and productivity. NAC transcription factors are key regulators of plant stress responses and developmental processes. This study functionally characterizes a novel NAC member, SlNAC12, in tomato. SlNAC12 localized to the nucleus and displayed weak transcriptional activity. Its expression was induced by salt stress and leaf senescence. Overexpression of *SlNAC12* resulted in growth inhibition under normal conditions but conferred enhanced salinity tolerance, as evidenced by improved growth parameters under salt stress. Transgenic lines exhibited reduced Na^+/K^+ ratio, elevated antioxidant enzyme activities, decreased ROS accumulation, and increased flavonoid content. Yeast one-hybrid assays confirmed that SlNAC12 directly binds to the promoter of SlF3'H, a key flavonoid biosynthetic gene. Furthermore, *SlNAC12* overexpression delayed leaf senescence, associated with suppressed expression of chlorophyll degradation and senescence-associated genes. A SlNAC12-interacting protein, SlLBD37, was identified, whose overexpression caused growth defects and delayed leaf senescence and flowering. Our results demonstrate that SlNAC12 positively regulates salt tolerance and delays leaf senescence, providing crucial insights for breeding improved tomato varieties.

S-2-5O

The continuing journey into exploring the role of barriers in plant survival

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Abstract
Plant ultrastructural barriers have played an essential role in plant evolutionary history ever since they colonized the land about 500 million years ago. Thus, the resilience mechanisms to both abiotic and biotic stresses in our modern day crop plants also often rely on these barriers as the site of first defense. This talk will summarize our various studies which examined and characterized various barriers from wax crystals to cuticular cell waxes to the epidermal cell wall/middle lamella, to xylem pits. A range of plants were assessed including canola (*Brassica napus*), *Arabidopsis* and mutants, potato (*Solanum tuberosum*), corn (*Zea mays*), onion (*Allium fistulosum*), winter wheat (*Triticum aestivum*) and the indigenous plant to Japan, *Keiskea japonica*.

S-2-6O

Analyzing Heat Resilience in Interspecific Chickpea: A Genetic and Phenotypic Approach for Breeding

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Abstract
Developing heat-resilient chickpea cultivars is essential for sustainable food production under climate change. This research investigates the physiological and genetic basis of heat tolerance in an interspecific chickpea population to accelerate breeding for climate resilience. We evaluated 200 inbred lines derived from crosses between an elite kabuli cultivar and wild *Cicer reticulatum* accessions using controlled heatwave simulations during flowering (35°C/29°C). Selected tolerant and sensitive lines were further tested under more severe conditions (40°C/25°C). Yield stability was influenced by both the developmental stage exposed to heat stress (flowering vs. podding) and nighttime recovery temperatures. Heat-tolerant lines maintained productivity, while elite checks and sensitive lines experienced major yield losses. Detailed physiological characterization was performed on four selected lines (three tolerant and one sensitive). Most flower loss (~90%) occurred after pollination, with the sensitive line exhibiting poor pollen viability and structural defects. Analyses of photosynthetic efficiency, pigment levels, osmoprotectants, membrane stability, and antioxidants revealed distinct heat mitigation strategies among tolerant lines. Genome-wide association linked yield-related traits under heat stress to regions on chromosome 4, including a promising SNP in a sugar transporter gene for marker-assisted selection. This work provides mechanistic insights and practical tools for developing heat-resilient chickpea cultivars for sustainable agriculture.

YS-1-1O

Reduction of off - flavours in flaxseed proteins using adsorbent resins during protein extraction

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Abstract

The goal of this study was to investigate the use of adsorbent resins (Amberlite XAD-16N, Sepabeads SP-207, and Diaion HP-20) during the extraction of flaxseed proteins, specifically to reduce off-flavours, including both volatile (VOCs) and non-volatile organic compounds (non-VOCs). These compounds can negatively affect the use and acceptance of flaxseed proteins by causing bitterness, astringency, and off-aromas and flavours. To analyze VOCs, Headspace solid-phase microextraction-gas chromatography-mass spectrometry (HS-SPME-GC-MS) was performed on flaxseed meal, untreated protein isolate (control), and resin-treated protein isolates. The VOC profile of the meal was mainly composed of hydrocarbons, whereas the flaxseed proteins also contained aldehydes, ketones, and alcohols. Results showed that Amberlite XAD-16N and Diaion HP-20 were more effective in lowering the total peak areas of VOCs. Proton nuclear magnetic resonance (1H—NMR) was used to assess non-VOCs in the samples, revealing that resin treatments significantly reduced sinapine content, while reductions in phenolics such as gallic and chlorogenic acids varied depending on the resin used. Cyanogenic glucoside levels were also significantly reduced. The functional properties of the resin-treated protein isolates were tested and did not show substantial changes compared to the control. Results from this study suggest that the use of adsorbent resins could be a promising strategy to mitigate off-flavours and improve the acceptance and applications of flaxseed proteins.

YS-1-2O

Exploring the Impact of Canopy Architecture on Drought and Heat Stress Resilience in Spring Wheat (*Triticum aestivum* L.)

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Abstract
Wheat (*Triticum aestivum* L.) is one of the major field crops in Canada, particularly in the Canadian Prairies. Although future demand for wheat is expected to increase by 2050, wheat production may decline due to the increasing frequency and severity of climate extremes, such as droughts and heatwaves. Canopy architecture plays a vital role in stress avoidance, as well as being important for achieving high yields. Erectophile wheat canopies generally produce a higher yield than planophile wheat canopies. This research aims to identify different wheat canopy architectures and related traits that enhance yield under high temperatures, drought, and combined drought and heat stress conditions. This study was conducted in a unique system of 12 field-established, environmentally controlled high tunnels (9 m x 15m each) in a randomized complete block design. Four selected wheat genotypes with contrast canopy architectures were grown in each tunnel and subjected to four treatments, including control (ambient air temperature [AT] with 90% field capacity), drought (AT with 25% field capacity), heat (AT +12 °C with 90% field capacity), and combined drought and heat stress (AT +12 °C with 25% field capacity) at the pre-anthesis stage. Canopy architecture (CA) was graded using the UPOV (International Union for the Protection of New Varieties of Plants) visual scoring scale, and grain yield was recorded. Promising physiological traits related to different canopy architectures under stress will be presented. Identifying traits associated with CA under stress is the first step toward developing high-yield, drought- and heat-tolerant crops.

YS-1-3O

Mining genomic regions associated with stomatal traits and their candidate genes in bread wheat through genome-wide association study (GWAS)

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Abstract
Stomata is a common feature of the leaf surface of plants and serve as vital conduits for the exchange of gases (primarily CO_2 and water vapor) between plants and the external environment. In this study, a comprehensive genome analysis was conducted by integrating genome-wide association study (GWAS) and genome prediction to identify the genomic regions and candidate genes of stomatal traits associated with drought resistance and water-saving properties in a panel of 184 diverse bread wheat genotypes. There were significant variations on stomatal traits in the wheat panel across different environmental conditions. GWAS was conducted with the genotypic data from the wheat 660 K single-nucleotide polymorphism (SNP) chip, and the stomatal traits conducted across three environments during two growing seasons. The final GWAS identified 112 candidate QTLs that exhibited at least two significant marker-trait associations. Subsequent analysis identified 53 key candidate genes, including 13 bHLH transcription factor, 2 MADS-box transcription factors, and 4 mitogen-activated protein kinase genes, which may be strongly associated with stomatal traits. The application of Bayesian ridge regression for genomic prediction yielded an accuracy rate exceeding 60% for all four stomatal traits in both SNP matrices, with stomatal width achieving a rate in excess of 70%. Additionally, three Kompetitive allele-specific PCR markers were developed and validated, representing a significant advancement in marker-assisted prediction. Overall, these results will contribute to a more comprehensive understanding of wheat stomatal traits and provide a valuable reference for germplasm screening and innovation in wheat germplasm with novel stomatal traits.

YS-1-4O

Transcriptomic Analysis Reveals a Regulatory Network and significance of VcWOXs During Adventitious Root Formation in Blueberry

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Abstract

Adventitious rooting (AR) underpins clonal propagation of blueberry, yet its regulatory circuitry remains poorly resolved. Here, stage-resolved transcriptomics across four morpho-developmental phases of juvenile stem AR reveals extensive transcriptional reprogramming and a rapid adjustment of cytokinin homeostasis to a range permissive for AR initiation. We cataloged 26 differentially expressed VcWOX genes, several exhibiting hormone-responsive expression. Among them, VcWOX11 functions as a positive regulator that promotes AR primordium formation and enhances lateral root development; promoter–reporter assays (WOX11pro::GUS and WOX11pro::GFP) localize its activity to root domains associated with initiation sites. DAP-seq identifies ERF109 as a direct downstream target of VcWOX11, and functional analyses demonstrate that ERF109 suppresses blueberry lateral root development; yeast one-hybrid and dual-luciferase assays validate VcWOX11 binding and transcriptional control of the ERF109 promoter. Furthermore, yeast two-hybrid and BiFC assays show that VcWOX11 physically interacts with pik-1, implicating a protein partner in WOX11-mediated signaling. Together, these findings establish a mechanistic framework for AR morphogenesis in blueberry and nominate a WOX11–ERF109 axis—modulated by cytokinin dynamics and reinforced by the WOX11–pik-1 interaction—as a core module linking hormonal cues to root organogenesis.

YS-1-5O

N^6-methyladenosine RNA modification regulates transcriptional and metabolic responses in wheat to drought stress

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Abstract
N^6-methyladenosine (m^6A) is the most prevalent and functionally significant chemical modification on mRNA, extensively involved in plant responses to abiotic stress. However, the specific role of m^6A modification in the response of wheat to drought remains unclear. This study analyzed the m^6A modification profiles of drought-tolerant (L1773) and drought-sensitive (L98) wheat varieties under drought stress. Our results reveal significant differences in m^6A modifications between the two wheat varieties. Compared with normal water control, L1773 exhibited global hypermethylation under drought stress, while L98 showed no difference. Gene Ontology (GO) term enrichment analysis showed that drought-induced m^6A-modified genes were primarily involved in RNA processing, stress response, and physiological metabolism. GSEA enrichment analysis indicated that the difference in drought tolerance between L1773 and L98 may be related to photosynthesis, energy metabolism, and the activation of antioxidant systems under drought stress. Interestingly, metabolomics analysis revealed that L98 suffered metabolic activation under drought stress, which may be associated with more severe damage levels. Additionally, this study built a joint network of m^6A epitranscriptome and metabolome, elucidating the mechanisms of transcriptional and metabolic responses associated with m^6A modification in wheat under drought stress, and identified key drought-tolerant genes. Silencing key drought-tolerant genes (*TaNAC154-7A*, *TaAP2-2A*) resulted in reduced drought tolerance in wheat seedlings. In general, our findings reveal wheat's response to drought stress across multiple levels—including m^6A modification, gene expression, and metabolite levels—and deepen our understanding of the m^6A regulatory mechanisms during drought stress in wheat.

S-4-1K

Inhibitory mechanisms of proline utilization in yeast: A step toward proline-free wine

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Abstract

The yeast *Saccharomyces cerevisiae* plays a central role in alcoholic fermentation, influencing both ethanol yield and the aroma and flavor of beverages. The quality of wine and beer therefore depends strongly on the metabolic characteristics of the yeast used. Proline is the predominant amino acid in grape must and wort and represents a potentially significant nitrogen source; however, conventional *S. cerevisiae* strains cannot efficiently utilize proline under fermentative conditions. To address this limitation, we constructed a proline-auxotrophic yeast strain and analyzed the molecular mechanism underlying proline non-utilization. We found that arginine inhibits proline utilization by triggering endocytosis of the proline transporter Put4. Genetic screening revealed that the arginine transporter Can1 mediates this inhibition. Interestingly, the arginine uptake activity of Can1 was not required, and Can1 directly activated the protein kinase A (PKA) signaling cascade without elevating cAMP levels, through binding to its catalytic subunits (Tpk1/2/3). These findings demonstrate that Can1 functions as a transceptor integrating nutrient sensing and metabolic regulation. Furthermore, using the Phaff Yeast Culture Collection (UC Davis), we screened over 1,300 wild yeast strains and discovered isolates capable of utilizing proline and performing efficient wine fermentation. Fermentation trials with these strains yielded a novel wine with distinct aromatic and sensory properties. Our findings provide mechanistic insight into amino acid sensing and highlight the potential of wild yeast biodiversity for developing innovative fermentation technologies.

S-4-2O

Value addition on the agriculture products towards sustainable food and feed supply

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Abstract
Since the Industrial Revolution, the world population has been exponentially growing. Currently world population exceeds 8.2 billion, and is predicted to grow to over 9.7 billion by 2050. This growth has pressured natural environment through deforestation, soil erosion, greenhouse gas emission, and resulting climate change. The pressure surpasses the degrees nature can absorb, threatening coordination of ecosystem. This situation refrains our direction in food supply from simple expansion of agriculture to more sustainable, renewable food supply practice. They include new breeds, new practice of cultivation, effective water usage, and more. In my research program, we study the utilization of neglected food/feed sources, especially to generate proteins from underutilized Saskatchewan agriculture products. We have worked on utilization of insects, microbes, and enzymes to address the value recovery from underutilized agriculture products and byproducts. The topics include rearing insects as feed using oilseed meals and crop straw, fermentation of legume starch to increase protein ratio (single cell protein), modification of legume proteins using enzymes and microbes, and beyond.

S-4-3O

Theanine Derived from Tea Leaves Modulates Monoamine Metabolism: A Single-Hair Analysis

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Abstract

Chronic psychological stress is a major contributor to mental health disorders, including depression. L-Theanine (LT), an amino acid abundant in tea leaves, is known for its umami taste and relaxation effects, yet its detailed mechanisms in the brain remain unclear. This study aimed to elucidate the neurochemical basis of LT's relaxing effects by analyzing monoamine metabolism in both brain tissue and single hairs from mice administered LT. Imaging mass spectrometry (IMS) was used to visualize changes in catecholamines (L-DOPA, dopamine, and norepinephrine) and stress-related metabolites (γ-aminobutyric acid and others). LT administration suppressed stress-induced alterations in catecholamine metabolism in the brain, suggesting a protective effect against depression-like symptoms. Notably, similar metabolic trends were observed in single-hair (fur) IMS using stress-related biomarkers newly identified through omics analysis, indicating that hair can serve as a reliable reflection of brain neurochemical status.

Our findings demonstrate that tea-leaf-derived LT modulates monoamine metabolism both centrally and peripherally[1]. Moreover, the results highlight the potential of hair IMS as a non-invasive diagnostic tool for evaluating stress and mental health conditions. This integrative approach provides a foundation for linking dietary components to neurochemical regulation and emotional well-being.

1. Taira, S., et al., *Theanine modulation of monoamine metabolism visualized by derivatized imaging mass spectrometry.* Scientific Reports, 2025. **15**(1): p. 23075.

S-4-4O

Creation of potato leaf samples under indoor conditions and using biostimulant for nutrient sensing development based on machine learning

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Abstract

Potato is an open-field crop planted in Canada exclusively during the summer season. This presentation describes a trial to grow potatoes indoor for research purposes during the winter season by focusing on controlling light and temperature conditions. Potato Plantlets and mini tubers were grown under different light conditions and with the use of biostimulant to find optimum conditions for the biggest possible biomass growth. Also, a control group was grown inside a greenhouse to compare the influence of using LED light on growing potatoes. In the indoor chamber, the plants were exposed to different phosphorous fertilization rates to try to induce deficiency in their leaves so that a phosphorus sensing model that relies on leaf spectral data can take advantage of a wide range of phosphorous concentration data. The results showed that indoor planting was successful in maintaining good conditions of the crops until they were harvested. Also, the variable light and biostimulant application appeared to have influence on the status of the plant in terms of their shoot and root sizes by the end of season.

S-4-5O

Deciphering human transport systems for micronutrients and bioactives from foods

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Abstract
Micronutrients and bioactives, though required in trace amounts, are essential for cellular functions across all organisms. Many of these compounds—including D-amino acids, vitamins, polyols, and phytosterols—are derived from plants. While their impact on health and disease has gained substantial attention, the mechanisms and dynamics of their absorption remain largely unexplored. Major challenges include the lack of a state-of-the-art strategy for transporter identification, the "3C" characteristics of transporters (Competition, Coordination, and Compensation) in physiological contexts, and the technical difficulties in detecting trace-level compounds. Our research focuses on the identification and characterization of human transporters for micronutrients and bioactives. By using cell-free transport methodology, we have characterized transporters for vitamins and polyols. Recently, we developed a unique multi-hierarchical approach to investigate transport systems for micronutrients under physiological conditions. As a paradigm, we identified transport systems for D-amino acids, which serve as biomarkers for kidney function and inflammatory response. Our study sheds light on the significant of transport mechanisms for micronutrients and bioactives and establish a comprehensive framework for analyzing nutrient dynamics, particularly for investigating multiple transport systems operating under physiological and multifactorial conditions.

S-4-6O

Advances in Precision Quality Control Technologies for Seafood: Insights from Shellfish Studies

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Abstract
With growing global seafood demand, ensuring quality and safety is crucial. Advanced technologies like hyperspectral imaging, electronic sensing, and AI analytics now enable accurate, non-destructive, real-time quality assessment. This study focuses on Pacific oysters (*Crassostrea gigas*), where shell morphology varies with aquaculture environment and directly impacts vitality. We combined 3D morphometrics with biochemical analyses (ATP-related compounds, pH) to evaluate oyster vitality during -1°C storage. Results showed 70.0% classification accuracy between round and flat shells using 3D techniques. Round oysters maintained higher vitality, with AEC values stable at 50%-60%, while flat oysters declined from 59.19% to 39.98%. AEC correlated with water content, demonstrating 3D morphometrics' potential for non-destructive, real-time supply chain classification. This presentation highlights how integrated biochemical, microbiological, and physicochemical approaches enhance precision monitoring in shellfish, providing valuable strategies for optimizing seafood quality control across processing and distribution systems.

Keywords: seafood, shellfish, precision quality control, biochemical analyses, AI

YS-2-1O

Modification of the substrate specificity of *Lactococcus lactis* prolidase by rational design

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Abstract

Aminopeptidase P (APP) and prolidase are homologous enzymes that cleave peptide bonds adjacent to proline residues, yet they exhibit significant differences in substrate specificity. Prolidase exclusively hydrolyzes dipeptides, whereas APP is capable of processing longer peptides. We determined the crystal structures of *Lactococcus lactis* APP (*Ll*APP) and prolidase (*Ll*Prol) and hypothesize that *Ll*Prol discriminates against longer peptides through an arginine residue (Arg40) located on an N-terminal loop near the C-terminal catalytic histidine residues (His204 and His303). In *Ll*prol, Arg40 interacts with the carboxyl terminus of dipeptides to promote substrate binding, while its side chain sterically hinders the entry of longer peptides. Based on this speculation, this study aimed to engineer *Ll*prol via rational mutagenesis to broaden its substrate specificity. Four strategies were employed: (1) introducing a distal arginine residue to stabilize the binding of longer peptides, (2) loosening dimer interactions by disrupting hydrogen bonds, and (3) swap the N-terminal domain of *Ll*prol and *Ll*APP. *Ll*prol mutants targeting the dimer interface, such as prolidase Δ101 and D78R/Δ101/R293S mutants, exhibited reduced but detectable activity toward a tripeptide substrate while maintaining dipeptidase activity. Preliminary analysis of domain-swapped mutants suggests that some variants show activity toward both di- and tripeptides, reaffirming the catalytic role of C-terminal histidine residues. These findings underscore the challenges of modifying substrate specificity without compromising catalytic efficiency and suggest that targeted engineering of domain interfaces and substrate-binding regions is a promising strategy for expanding the functionality of proline-specific peptidases.

YS-2-2O

Deubiquitinase ZmUBP5 is essential for maize kernel development

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Abstract
Ubiquitination and deubiquitination are critical post-translational modifications in eukaryotes, playing essential roles in various aspects of plant growth and development. However, their involvement in maize kernel development remains largely unexplored. In this study, we characterized a novel maize kernel mutant (*ubp5-ems#1*) induced by ethyl methanesulfonate, which exhibited a smaller size, arrested embryo, smaller endosperm, and pigment deficiencies. Through bulked segregant analysis, we identified a stop-gained mutation in the *ZmUBP5* gene as the cause of these phenotypic abnormalities. This was further validated by allelic confirmation and CRISPR/Cas9 knockout. ZmUBP5, identified as a ubiquitin-specific protease with deubiquitinase (DUB) activity, was localized to the nucleus, and the stop-gained mutation disrupted these functions. Protein interaction and degradation assays revealed that ZmUBP5 interacts with and may deubiquitinate ZmEMB140. The stop-gained mutations in *ZmEMB140* resulted in smaller kernels with reduced embryo and endosperm size, as well as lethal seedlings. ZmEMB140 is likely a spliceosome-associated factor, interacting with six other proteins involved in pre-mRNA processing. Overall, this study underscores the critical roles of the DUB ZmUBP5 and its potential substrate ZmEMB140 in maize kernel development.

YS-2-3O

Elucidating the molecular mechanism of auxinic herbicides, dicamba and picloram in *Arabidopsis thaliana*

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Abstract

Synthetic auxins such as 2,4-D, dicamba, picloram are widely used as herbicides in the crop field. They are selective herbicides, only kill the dicotyledonous plants but not monocotyledonous plants. However, the mechanism of selective herbicide action of these synthetic auxins remains unclear. Previous study on 2,4-D demonstrated that its selective herbicidal action may be linked to the cytoskeletal component, actin. 2,4-D treatment has been shown to selectively depolymerize the actin cytoskeleton followed by cell division arrest in dicotyledonous plants. Further it was demonstrated that 2,4-D-induced actin depolymerization is regulated by Rop-interactive CRIB motif-containing (RIC) family protein. In the present study, we tried to understand whether a similar or different mechanism determines the selective herbicidal activity of picloram and dicamba. Similar to 2,4-D, exogenous application of dicamba and picloram in Arabidopsis resulted in depolymerization of actin. Next, we focused on understanding the mechanism of dicamba-and picloram-induced actin cytoskeleton depolymerization. The cellular dynamics of actin cytoskeleton are regulated by RIC and actin depolymerization factor (ADF) protein families. RIC family mainly regulates actin polymerization. On the other hand, ADF family functions in the cleavage and depolymerization of F-actin. Dicamba and picloram did not alter the RIC gene expression, and *ric2*, *ric4* mutant showed a wild-type like response to dicamba and picloram, indicating that dicamba and picloram -mediated actin depolymerization is not RIC-dependent. On the other hand, both *ADF8* and *ADF11* expressions were altered by dicamba and picloram as observed by quantitative PCR and GUS assay using promoter-GUS lines. Taken together, these results suggest that although actin is a common target for auxinic herbicides, 2,4-D and dicamba/picloram use distinct molecular regulatory pathways.

YS-2-4O

Genetic and molecular basis of ABA response in wheat seedlings shared with mature-stage drought tolerance revealed by integrated GWAS and transcriptomics

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Abstract
Drought stress is a major constraint to wheat production, yet the relationship between early-stage abscisic acid (ABA) response and mature-stage drought tolerance remains poorly understood. Here, we evaluated 173 diverse wheat accessions for seedling biomass traits under exogenous ABA treatment and grain weight under field drought conditions. Seedling fresh weight indices under 15 μM ABA showed significant variation among genotypes and were positively correlated with thousand-grain weight (TGW) under drought, suggesting that ABA induced seedling responses partially reflect mature-stage drought tolerance. A 660K SNP array-based genome-wide association study (GWAS) identified multiple loci for seedling ABA response indices (LFW, RFW, TFW) and TGW under drought, with several genomic regions co-localized across traits. Haplotype analysis further highlighted a subset of candidate genes with shared effects on both ABA response and drought tolerance. Transcriptome profiling of an ABA-tolerant cultivar (JM47) and an ABA-sensitive cultivar (ZM366) revealed distinct regulatory patterns: JM47 preferentially activated pathways related to phenylpropanoid metabolism, MAPK signaling, trehalose biosynthesis, and hormone crosstalk (ABA-JA/ET), while ZM366 maintained growth-associated processes such as photosynthesis and cell wall biosynthesis with limited stress defense activation. Weighted gene co-expression network analysis (WGCNA) identified a key root-associated module enriched in ABA and stress-responsive genes, including hub genes overlapping with GWAS candidates such as *WRKY24*, *ERF4*, and *GID1*. Collectively, these results demonstrate that seedling ABA sensitivity shares a genetic and molecular basis with drought tolerance at maturity, and provide candidate loci and regulatory networks for improving wheat adaptation to water deficit.

YS-2-5O

Genome-wide association study of novel genetic loci for cadmium accumulation and germplasm screening for low-cadmium accumulation in common wheat (*Triticum aestivum* L.)

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Abstract

Cadmium (Cd) contamination in wheat farmland is increasing at an alarming rate, posing threats to food security and public health. Breeding and utilizing wheat varieties characterized by low Cd accumulation levels constitute an effective strategy in the battle against wheat Cd contamination. The adoption of molecular marker-assisted approaches can greatly expedite the selection and enhancement of wheat varieties with low Cd accumulation. Nonetheless, research concerning genes associated with wheat cadmium accumulation remains scarce. In this study, a high-density 660K SNP array was employed for conducting genome-wide association studies (GWASs) on the grain Cd concentration (GCdC), bioconcentration factor (BCF) and translocation factor (TF) in 175 wheat germplasms. The findings revealed 401 significant SNPs identified across three diverse environments. Linkage disequilibrium analysis revealed 30 core quantitative trait locus (QTLs)capable of reliably modulating wheat Cd accumulation phenotypes. Through gene annotation, transcriptomics, and gene molecular features, four candidate genes (TraesCS7B02G000200, TraesCS4A02G035900, TraesCS4A02G040900, TraesCS5D02G564000) were identified as potential constituents of the biological process of wheat Cd accumulation. Furthermore, in this study 6 wheat germplasms exhibiting low grain Cd accumulation were isolated, and two Kompetitive Allele Specific PCR (KASP) markers conducive to breeding selection were developed. These findings provide valuable genetic resources for cultivating wheat with low Cd accumulation and establish a foundation for understanding the molecular mechanisms underlying low Cd accumulation in wheat. The candidate genes and KASP markers elucidated in this research have potential for effective employmentuse in genetic enhancement and marker-assisted selection in the breeding of wheat with low Cd accumulation.

YS-2-6O

Tapping the flax gene pool: from domestication traits to hybridization barriers

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Abstract
Cultivated flax (*Linum usitatissimum*) has a narrow genetic base due to its long domestication history, limiting genetic improvement and reducing its resilience to biotic and abiotic stresses. Expanding cultivated flax genetic base requires exploring into its wild relatives, but obstacles arise at multiple levels, from reproductive isolation to undesirable genetic drag. This study examines both ends of this spectrum to better define and address the barriers limiting the use of wild diversity. Within the primary gene pool, *L. bienne*, the wild progenitor of cultivated flax, readily crosses and provides valuable alleles such as resistance to pasmo disease. However, the use of *L. bienne* also introduces unfavorable domestication traits such as boll dehiscence. To investigate its genetic basis, nine interspecific populations totaling 314 advanced lines were developed from reciprocal crosses between the cultivar CDC Bethune and nine diverse *L. bienne* accessions. Field evaluations for boll dehiscence and pasmo resistance were conducted at two locations over three years. Both GWAS and QTL mapping consistently identified a major locus on chromosome 3 associated with dehiscence. Crosses with the species from the secondary and tertiary gene pools, such as *L. grandiflorum* and *L. decumbens* revealed both pre- and post-zygotic barriers, including arrested pollen tube growth and potential embryo abortion. The use of distant species for genetic improvement may require additional steps, such as embryo rescue and/or bridge crosses. Together, these findings provide a framework for systematically harnessing wild diversity to broaden the genetic base of cultivated flax.

YS-2-7O

Correlation Study Between Canopy Temperature (CT) and Wheat Yield and Quality Based on Infrared Imaging Camera

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Abstract
As an important physiological indicator, wheat canopy temperature (CT) can be observed after flowering in an attempt to predict wheat yield and quality. However, the relationship between CT and wheat yield and quality is not clear. In this study, the CT, photosynthetic rate (Pn), filling rate, wheat yield, and wheat quality of 68 wheat lines were measured, in an attempt to establish a connection between CT and yield and quality and accelerate the selection of new varieties. This experiment used an infrared imaging camera to measure the CT of wheat materials planted in the field in 2022. Twenty materials with significant temperature differences were selected for planting in 2023. By comparing the temperature trends in 2022 and 2023, it is believed that materials 4 and 13 were cold-type materials, while materials 3 and 11 were warm-type materials. The main grain filling period of cold-type materials occurs in the middle and late stages of the grain filling period and the Pn and the thousand-grain weights of cold-type materials were higher than those of warm-type materials. Similarly, under continuous rainy conditions, cold-type materials had a higher protein and wet gluten contents, while warm-type materials had higher sedimentation values and shorter formation times.

YS-2-8O

Robust and affordable root phenotyping approaches for early-stage wheat growth

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Abstract
Root System Architecture (RSA), which represents the spatial configuration of roots in soil, is a primary basis for resilience and productivity. Traditionally used pots often constrain root growth and complicate phenotyping for roots. Existing rhizotron technologies are costly, and large-scale use is difficult. Two robust and affordable approaches, rhizobox and rhizocylinder, were tested to phenotype roots in wheat. Rhizobox reuses a square petriplate, and the rhizocylinder uses plastishield to improve conventional root assessment. Root scans from the rhizobox, conducted weekly post-germination, revealed consistent traits: diameter, volume, and surface area. The rhizobox technique showed promise for phenotyping within a few days of germination. However, the rhizobox can only hold limited soil, and uses very little water (8-14 g/rhizobox) during the first week post-germination. Besides, maintaining consistent seedlings was found to be challenging, and root elongation was restricted in deep-rooting grass species like wheat. This situation led to the search for newer vertical platforms capable of mimicking real root growth conditions. “Rhizocylinder” validated that root length at 100% field capacity significantly differed between contrasting drought-responsive varieties. Significant biomass differences were observed in both platforms. Overall, this study using the “Rhizocylinder” platform highlighted the potential of drought-tolerant varieties to grow longer and larger roots during the first few weeks of germination in control conditions. Volume and surface area were reinforced as important RSA traits. The applied workflow demonstrated that the new platform can be an effective, scalable, and imaging-compatible option for early-stage holistic root analysis, with a lowered risk of root loss.

YS-2-9O

Novel QTLs/genes affecting single stem elasticity, stem strength, and three lodging indices in bread wheat (*Triticum aestivum* L.) identified by genome-wide association analysis

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Abstract
Lodging is a complex trait and has implications for wheat grain quality and yield, stem-associated traits are crucial for lodging resistance. Understanding the genetic basis of lodging-associated traits, especially single stem elasticity (SSE), stem strength (SS), and lodging index, is essential for developing effective strategies to enhance lodging resistance in wheat. In this study, 10 lodging-associated traits of 238 diverse wheat varieties were investigated across three diverse growing seasons. The ANOVA revealed significant variations on all traits among wheat genotypes and across three growing seasons. There were significant correlations between SSE, SS, three lodging indices (LI 1, LI 2, LI 3) and stem morphological traits. A total of 126 key candidate quantitative trait loci regions containing at least two marker-trait associations were identified using genome-wide association analysis. By integrating multiple analytical approaches, 84 key candidate genes were screened, including genes encoding enzymes related to stem cell wall synthesis, photosynthesis, hormone synthesis, and root development, which may play an important role in lodging resistance. By using Bayesian ridge regression for genome prediction, the prediction accuracy increased as the number of significant SNPs increased, and high prediction accuracy can also be achieved using only a few top-ranking SNPs. In summary, the results of this study would provide valuable insights for understanding lodging resistance in wheat and its genetic mechanism.

P01

Which fertilization component enhances cold tolerance in highly cold tolerant rice varieties "Tohoku PL1-3", "Ouu PL4,5"? - Estimation of fertilization process using anther morphology-

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Abstract
Cold stress in rice causes significant yield losses, breeding for cold tolerant cultivars is essential for stable production. In Japan, highly cold-tolerant cultivars such as "Tohoku PL1," "Tohoku PL2," "Tohoku PL3," "Tohoku PL4," "Ouu PL4," and "Ouu PL5" have been bred (Endo2013), but the factors enhancing their cold tolerance remain unclear. In this experiment, we focused on the processes of fertilization, which suffer the most from low temperatures. In 2024 and 2025, these varieties and "Hitomebore", "Sasanishiki" are grown in totally 4 temperature conditions (natural temperature and 3 cold conditions：18.5℃, 18.0℃, 17.5℃, cold water irrigation) from panicle initiation to heading. Before flowering, specific spikelets were collected. The process from pollen formation to pollination under low temperature conditions was observed based on ① number of microspores, ② number of mature pollen grains, and ③ pollen fertilization efficiency (Satake and Shibata1992). These were estimated based on ① anther length in natural condition, ②reduction rate in anther length under low temperatures, and ③ sterility under low temperatures divided by anther length under low temperatures (Shimono 2018). Sterility are above 90% in most cultivars in natural temperature. In 17.5℃, "Tohoku PL1-3","OuuPL4,5" showed high sterility (72.1% - 94.4%) compared to "Hitomebore (57.6%)". In these cultivars, different components enhanced cold tolerance: in "Tohoku PL1," increased microspore number and mature pollen number contributed to improved cold tolerance, while in "Tohoku PL2" and "Tohoku PL4", increased pollen fertilization efficiency enhanced cold tolerance.

P02

Genotypic variation in phenotypic plasticity of 23 rice accessions: Both root and shoot responses to low planting density

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Abstract
Crops including rice respond to environmental variations not only in their aboveground parts (leaf and stem), but also in the belowground system (root) to attain higher productivity while adapting to a changing climate. Very limited information is available for root response to environments in terms of genotypic variation in relation with aboveground response. To gain knowledge on the association between these parameters, we evaluated the response of 23 rice accessions under normal planting density (NPD: 22.2 plants m^{-2}) and low planting density (LPD: 11.1 plants m^{-2}) in Iwate, Japan (39°42′ N, 141° 8′ E), the relative response of shoot and root biomass between NPD and LPD was used as an indicator to evaluate the phenotypic plasticity of the genotypes. The LPD was adopted to simulate an environment rich in CO_2 as each plant has more access to CO_2 relatively to NPD. Measurements of biomass showed that LPD significantly stimulate the shoot and root biomass production ($P < 0.001$) and the extent vary according to genotypes ($P < 0.001$). Similarly, the phenotypic plasticity of the shoot biomass differs among the genotypes ($P < 0.05$) with XI GU ZAO and C8005 exhibiting superior plasticity while the genotypic difference in the root biomass plasticity was also significant ($P < 0.01$), Kaluheenati and Keiboba were more responsive in term of root plasticity. Correlation analysis between aboveground and belowground biomass plasticity revealed no significant association ($r = 0.17$ ns) between the two parameters, suggesting that shoot and root biomass phenotypic plasticity respond independently under LPD.

P03

Nighttime-heating exposure at above ground and below ground; which is more influential on rice yield?

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Abstract
Rising night-time temperatures (HNT) associated with climate change are increasingly recognized as a critical constraint to rice productivity. Here, we examined separately effects of exposure to HNT of aboveground and belowground. A greenhouse experiment was conducted at Iwate University (39◦42′ N, 141◦ 8′ E) (2025) using two rice genotypes, '*Hitomebore', Japanese cultivar,* and '*Shoni', Bangladesh cultivar*, to assess responses of root and shoot traits to HNT. 4 treatments done, only root-zone heating (CH), only above-ground heating (HC), combined heating (HH), and not heating of control (CC), each applied during whole growth stages. Root and shoot parameters were measured at maturity. Night-time heating significantly reduced total biomass and yield in both rice cultivars. Heating applied only to the shoot zone (HC) caused a noticeable decline in biomass for both cultivars. Yield reduction was most pronounced under HC for 'Hitomebore' (40%), whereas for 'Shoni', the highest reduction (37%) occurred under combined heating (HH). In 'Shoni', the decline in yield was primarily associated with reduced biomass, while in 'Hitomebore', yield loss resulted from reductions in both biomass and harvest index. Overall, shoot-zone heating had a greater negative effect on yield, with cultivar differences reflecting variations in biomass production and harvest index.

P04

Potential roles of lipid transport family protein in the cold stress response of *Arabidopsis thaliana*

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Abstract
The cold stress response in plants is a multifaceted process involving substantial changes in gene and protein expression. We previously demonstrated that overexpressing GNOM, an ADP-ribosylation factor guanine nucleotide exchange factor (ARF-GEF) essential for endomembrane trafficking and development, enhances cold tolerance in plants. To further understand how the protein trafficking regulator GNOM modulates cold stress response, we performed a comparative proteomic analysis using Col-0, GNOM overexpression line (GNOM ^{OE}) and GNOM loss of function (*gnom*$^{B/E}$) line. A total of 2705 proteins were identified, with 50 proteins showing significantly higher relative abundance in cold-resistant GNOM ^{OE}. Gene Ontology analysis of these differentially expressed proteins (DEPs) indicated a strong overrepresentation of proteins involved in lipid transport. Focusing on several candidate lipid transfer proteins identified in the proteome, we performed root growth screening of their respective T-DNA insertion mutants following cold treatment and recovery. Notably, mutants for Polyketide Cyclase (PKC) and ABCG12 exhibited significantly faster primary root recovery and produced more lateral roots during the cold and recovery periods compared to the wild-type. Taken together, our findings suggest that Polyketide Cyclase and ABCG12 act as positive regulators in the plant's cold stress response and may function downstream of GNOM-regulated membrane trafficking. Future studies will focus on characterizing the transcriptional and translational control of these key proteins under cold stress.

P05

Regulation of Efferocytosis as a Key Mechanism in the Anti-Atherosclerotic Effects of Resveratrol

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Abstract
Atherosclerosis is a chronic inflammatory disorder characterized by defective efferocytosis, resulting in the accumulation of apoptotic cells within vascular lesions. Resveratrol, a grape-derived polyphenol, has been reported to mitigate plaque progression, yet its molecular targets remain incompletely defined. Here, we profiled transcriptomic changes in human THP-1-derived macrophages treated with resveratrol and a representative inflammatory inducer, lipopolysaccharide, identifying 977 upregulated and 555 downregulated genes. Functional enrichment revealed suppression of cytokine signaling, leukocyte chemotaxis, and extracellular-matrix interaction pathways, accompanied by a shift toward a resolution-associated, efferocytic macrophage phenotype. By classifying macrophage subpopulations within public single-cell RNA-seq data from human atherosclerotic plaques and performing differential expression analysis among symptomatic and asymptomatic, we identified Cysteine-rich protein 1 (*CRIP1*) as an overlapping candidate gene when integrated with our *in vitro* transcriptomic dataset. Mechanistically, CRIP1, a zinc-binding protein, drives epithelial-mesenchymal transition, suppresses apoptosis, and facilitates tumor cell migration. Collectively, these findings identify *CRIP1* as a potential mediator of resveratrol-induced inflammation resolution and provide molecular insight into its atheroprotective mechanism.

P06

Bradyrhizobium ottawaense Type III Secretion System mediated Compatible and Incompatible Nodulation in *Vigna* species

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Abstract

Legume- rhizobium interaction result in nitrogen fixing symbiosis, forming specialized organ root nodules. The collaboration progresses through multiple interactions from rhizobial attachments and infection to nodule development- driven by precise molecular signaling and symbiotic gene networks determining compatibility and efficiency of nitrogen fixation. The rhizobial Type III Secretion System (T3SS) is a key determinant regulating symbiotic nodulation by delivering Type III effector (T3E) proteins into host plant cells. Depending on the host varieties, these T3Es either promote infection and nodule organogenesis or restrict nodulation by triggering innate immunity. However, the functions of individual T3Es in *Bradyrhizobium ottawaense* remains unclear. This research aimed to elucidate the role of T3SS and specific T3Es of *B. ottawaense* SG09 during symbiosis with diverse *Vigna* species. 26 *Vigna* species were inoculated with SG09 and its T3SS-deficient mutant (*Δrhcj*), and according to nodulation phenotypes and number they were classified as T3SS-compatible, -incompatible or independent. Ten *Vigna* species were identified SG09 T3SS-compatible. To identify responsible effectors behind the compatibility, single and double mutants of T3E *nopE1* and *nopE2* in SG09 were analyzed, revealing that both NopE1 and NopE2 contribute positively to nodulation in some species. In contrast, seven *Vigna* species showed SG09 T3SS-incompatible nodulation. Notably, in one incompatible species, *V. unguiculata* cv. Blackeye pea, the infection system was regulated independently of T3SS, and no infection threads were observed in both SG09 and the *Δrhcj* mutant compared to *B. elkanii* USDA61. These results demonstrate that the T3SS of *B. ottawaense* SG09 governs host dependent compatibility and incompatibility in *Vigna* species, however, doesn't determine the infection process in non-permissive ones.

P07

Indole-3-butyric Acid (IBA) functions as an independent hormone to regulate the lateral root developmental process in *Arabidopsis thaliana*

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Abstract

Auxin is an essential plant hormone that affects almost all aspects of plant growth and development. Although plants synthesize two forms of auxins, Indole-3- acetic acid (IAA), and Indole-3-butyric acid (IBA), it is believed that IBA is a precursor of IAA and functions only through conversion to IAA. In the present study, we challenged this idea. Using physiological, genetic and cellular analyses, we demonstrate that IBA can function independently of IAA. The concentrations of IAA and IBA that caused 50% inhibition of root growth showed differential responses for lateral root emergence. IBA application consistently produced more lateral roots than IAA. Furthermore, IBA concentration that does not inhibit root growth still stimulates the lateral root production, suggesting that lateral root organogenesis may use distinct response pathways for IBA and IAA. To confirm this, we used auxin transport mutant *aux1-7*, and auxin signaling mutant *axr-1-3*, both of which show strong resistance to IAA for both primary root elongation and lateral root emergence. Interestingly, although both the mutants show strong resistance to IBA for primary root elongation, their lateral root emergence displays wild-type-like sensitivity, confirming that IBA functions independent of canonical auxin response pathway to regulate lateral root organogenesis. Additionally, *ibr* mutants, which are defective in genes involved in the conversion of IBA to IAA, also respond to IBA for lateral root emergence but not for primary root elongation. These results suggest that IBA-IAA conversion may be tissue- specific. The alteration in the signal ratio observed in the IAA marker lines DII-VENUS, and R2D2 in presence of exogenous IAA and IBA confirmed that the IBA-IAA conversion in lateral forming zone is minimal. Taken together, these results suggest that for lateral root organogenesis, IBA functions independent of its conversion to IAA and uses a distinct regulatory pathway.

P08

Elucidating the response mechanism of tomato roots to cold stress response

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Abstract
Plants endure various stresses while growing. For instance, low-temperature stress possesses a significant threat, inhibiting growth and potentially causing death, particularly in chilling-sensitive crops like the agronomically important tomato. One of the major regulatory pathways that contribute to cold stress response in flowering plants is linked to C-repeat binding factor (CBF) gene family. Although CBF family is widely conserved in the flowering plants, their cold tolerance relates to the specific characteristics of the CBF genes and their regulatory networks within each species. Chilling-sensitive tomato has CBF genes but exhibits a reduced "CBF regulon". This study focused on understanding the molecular basis of tomato chilling sensitivity using roots as a model, as roots respond immediately to cold stress and influence whole-plant development. Compared to Arabidopsis, tomato roots are more sensitive to cold stress both at 10°C and 4°C. Expression analysis of tomato CBF genes *CBF1* and *CBF2* revealed no change at 4°C compared with 23°C in root, stem and leaf, suggesting that tomato cold stress response is mediated by a CBF-independent pathway. To further understand the mechanism of cold response in tomato, we focused on hormones. The quantification of hormones using LC-MS/MS revealed that under cold stress IAA is increased in the root, while ABA is increased in leaf. Both the hormones' levels were unaltered in stem. Taken together, our results suggest that the cold stress response in tomato is regulated by a tissue specific novel mechanism, where IAA and ABA play crucial roles. Future studies will aim to identify the components of these response pathways.

P09

Identification of novel cadmium uptake transporters in *Arabidopsis thaliana*

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Abstract

Cadmium (Cd) is a heavy metal that is produced annually by industrial activities worldwide in the amount of about 13,000 tons. It is known to be highly mobile, to cause adverse effects on soil, water, and the plants and animals that use them, and to have a very long half-life of 10 to 30 years. In recent years, phytoremediation, a method of removing heavy metals from soil using plants, has been gaining attention. However, successful application of this technique requires plants that can efficiently absorb and accumulate heavy metals and detoxify them. The efflux transporters of Cd in several plant species have been identified, while the uptake transporters of Cd have been limited to Nramp family protein. In this study, we focused on the ABC (ATP Binding Cassette) protein family, particularly ABCG transporter proteins, which are known to localize cell membrane and transport multiple metals, as candidates for novel Cd uptake transporters. Here, we suggest that ABCG14 is involved in Cd uptake in *Arabidopsis thaliana*. Knockdown of ABCG14 resulted in significant resistance to Cd-induced root growth. To further understand whether Cd regulates *ABCG14* at transcriptional level, we performed the expression analyses of the gene under Cd treatment. Quantitative RT-PCR result revealed that the expression of *ABCG14* is altered by Cd. Taken together, these results suggest that *ABCG14* is transcriptionally regulated by Cd and may function as a potential novel uptake carrier of Cd in the *Arabidopsis* roots.

P10

Control of seed dormancy using iron-powder coating in rice

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Abstract

Control of seed dormancy of crops is important to increase productivity in agriculture. However, physiological mechanism of seed dormancy remains unclear. We found that coating the seed-surface with a mixture of iron powder and gypsum can delay the germination speed in rice, and affect seed dormancy (Enya et al., 2024). Here, we examined the causal factors of this effect from the physical effects of coating per se or the composition of the coating material. To evaluate the effects of coating materials on seed dormancy, germination test (25°C) was conducted using five treatments: 1. Non seed-coated control without any materials, 2. Seed coated by a mixture of iron powder and gypsum, physically sealed from outside, 3. Material of iron powder, 4. Material of gypsum powder, 5. Material of both iron and gypsum powder. Rice seeds with different dormancy conditions were used, highly kept dormancy seeds (kept -30°C after harvest 2024) and less dormancy seed (kept 4°C after harvest) of two cultivars, less dormancy "Hitomebore" and high dormancy "Akitakomachi". Dormancy level: 'Akitakomachi' kept -30°C (AK-30), followed by 'Hitomebore' kept at -30°C (HB-30), and 'Akitakomachi' kept at 4°C (AK+4), and least dormancy level is 'Hitomebore' kept at 4°C (HB+4). Experiments were repeated four times. We found based on 4 independent experiments that the effects of iron-powder coating on seed dormancy was attributed to the physical coating effect, coating layer isolated from outside, rather than the materials per se.

P11

Effect of soil inoculation on rice productivity under different soil and water conditions

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Abstract

Attractive option for sustainable agriculture with reducing chemical fertilizers is a use of natural soil microbiome. The present series study aimed to find effective soil microbiome on rice productivity. In 2024, we successfully screened three candidate microbiomes from the candidate 14 microbiome origin from different location in Japan. In this study in 2025, we tested the reliability of the three microbiomes tested at three different soil and water conditions under natural field environments. The experiment was conducted at Iwate University, Morioka, Japan (39°42′ N, 141° 8′ E) using 4L pot at 6 conditions (2 water regimes x 3 different soil, sterile (2 Andosol and 1 Gray lowland soil)). Inoculation of microbiome on rice seedling of ‘Hitomebore’ was conducted using three microbiomes from three soils x 2 (sterile or non-sterile) during the nursery period of 3 weeks: ID3 (Ebetsu, Hokkaido, Japan), and ID14 and ID17(Ishigaki, Okinawa, Japan) and each Negative Control (NC) of sterilized by heat (110°C for 15 min ×2). Each microbiome of the soil was mixed with nursery soil at a 1:9 ratio. No fertilizer was added. At maturity, dry weight, panicle weight, culm length, panicle length, and panicle number were measured. In ID3 microbiome, in 5 out of 6 conditions (excluding flooding Gray lowland soil), shoot and panicle dry weight was increased by 10 ~ 41% and 8 ~ 60% compared to each NC, respectively. On the other hand, in ID14 microbiome, only 2 out of 6 conditions, and ID17 microbiome, only 3 out of 6 conditions, shoot dry weight was increased consistent effect. These results suggest that soil microbiome of ID3 (Ebetsu, Hokkaido, Japan) mostly enhanced rice growth and yield over the water management and soil type.

P12

Yield potential of a BNI elite wheat line under cool climate

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Abstract
Wheat (*Triticum aestivum*) requires a large amount of nitrogen fertilizer to achieve high yield and grain quality. But 50~70% of applied nitrogen fertilizer is not up took by crops and runs off outside as nitrate. Leaching is one of the main causes of groundwater pollution. Use of nitrification inhibitors is a method to decrease nitrogen leaching. Recently wheat line processing Biological Nitrification Inhibitor treats (BNI treats) have attracted attention. Generally, BNI-elite wheat line secretes BNIs from root system and inhibits enzyme activity of nitrifiers, as a result nitrogen leaching is decreased. However, some paper reports that this treat depends on environmental conditions, and we can't know whether BNI treats can always contribute to yields or not. This study examined the effects of cultivating Munal (parent line) and BNI-Munal under pot and field conditions in Morioka City, Iwate Prefecture. In the 2024 greenhouse experiment, leached nitrate amount was slightly reduced in BNI-Munal compared to parental line, but the positive effect on yields was minimal. In the 2025 field experiment, there was no difference in yields between the two lines under no-nitrogen condition. Under nitrogen-supplemented conditions, the parental line yielded higher than BNI-Munal. On the other hand, we confirm BNI-Munal has significant Stay-green treats and seed pre-harvest sprouting resistance treats. These results indicate that we should focus on utilizing new BNI-derived lines suitable for cultivation trial sites, whilst also investigating whether other beneficial traits are attributable to BNI characteristics.

P13

Analysis of the dorsal-ventral axis formation in rice embryos as a model for monocots

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Abstract

The arrangement of organs in the embryos of dicots and monocots exhibits significant differences. In dicots, the shoot apical meristem (SAM) is located between the two cotyledons. In monocots, SAM is located on the lateral side of the cotyledon, defining the dorsal-ventral axis of embryo as SAM on the ventral side and the cotyledon on the dorsal side. In the monocot embryo, a cotyledon located on the dorsal side absorbs nutrients from the adjacent endosperm as energy source for initial growth, supporting the germination of shoot residing on the ventral side. Therefore, the dorsal-ventral axis characterizes monocots embryos both morphologically and functionally. However, the mechanism of the dorsal-ventral axis formation remains unclear. To elucidate the mechanism of dorsal-ventral axis formation in monocot embryos, I analyzed a rice mutant which showed aberrant dorsal-ventral axis formation. Transcriptome analysis of mutant and wild-type embryos revealed that the expression levels of two *PIN g*enes were decreased in the mutant. One of them, *OsPIN2,* showed localized expression at the dorsal side in wild-type embryos. This suggests that, unlike dicots embryo, auxin is transported asymmetrically between the dorsal and ventral side in rice embryo. In mutant embryos, *OsPIN2* was expressed ubiquitously, and abnormal expression of auxin-response reporter genes was observed. These findings suggest that localized auxin response, mediated by the polar auxin transport on the dorsal side, is crucial for proper establishment of dorsal-ventral axis in monocot embryos.

P14

Development of High-Value-Added Products from Sanriku Sea Cucumbers Based on Their Biochemical Characteristics

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Abstract

This study aimed to clarify the distinctive quality characteristics of Sanriku (Iwate)-origin dried sea cucumbers (*Apostichopus armata*) through biochemical, volatile, and sensory analyses. Thin Layer Chromatography analysis confirmed the presence of saponins in all tested samples, with Sanriku specimens exhibiting slightly lower Rf values, suggesting the presence of more polar and stable saponin structures. CNH elemental analysis showed higher nitrogen and carbon contents and lower C/N ratios in Sanriku samples, indicating greater protein density and potential nutritional value. GC-IMS analysis revealed a rich and stable volatile profile characterized by alcohols and esters, reflecting good aroma retention even after rehydration and suggesting superior oxidation resistance during processing. In sensory evaluations of smoked products, participants preferred richer flavors such as “Chinese-style special sauce” and stronger aroma intensity (sliced form), highlighting the importance of aroma balance in enhancing product appeal. These findings indicate that Sanriku sea cucumbers maintain both chemical and sensory advantages derived from their marine environment and gentle processing conditions. Overall, the results demonstrate that Sanriku sea cucumbers possess favorable compositional and sensory characteristics—such as high protein content, structural stability, and natural aroma retention—providing a scientific basis for product quality improvement, regional brand development, and further utilization in high-value marine food production. It is suggested that the flavor characteristics and the contents of bioactive (health-promoting) compounds in sea cucumber products vary depending on the freshness of raw materials and the processing methods.

P15

Temporal Variation of GABA Levels in Tomatoes During Ripening in Mori Town, Hokkaido

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Mori Town, located in the southern part of Hokkaido in Japan, is a region rich in natural resources, stretching across the foothills of Mount Komagatake. The area thrives in agriculture, forestry, and fisheries, taking advantage of its favorable environment. In particular, the volcanic ash soil formed by volcanic activity is rich in minerals and organic matter, providing optimal conditions for crop cultivation. This study aims to visualize and semi-quantitatively analyze the distribution of amino acids in tomato flesh grown around Mount Komagatake in Mori Town using Imaging Mass Spectrometry (IMS), based on the degree of ripeness. In this study, we compared the distribution and relative amount of amino amino acids of tomatoes harvested on the day of harvest with tomatoes harvested 4 and 8 days later. The goal is to determine whether there are visual differences in amino acids distribution over time. As representative data, IMS results showed that glutamate, a key umami-related amino acid, was mainly localized in the outer pericarp and remained relatively constant during ripening. In contrast, γ-aminobutyric acid (GABA) gradually decreased after harvest, particularly in the pericarp and vascular tissues, suggesting that the conversion of GABA to intermediates in the TCA cycle may be enhanced under postharvest metabolic stress. Therefore, this study revealed the relationship between tomato ripeness and amino acids content by IMS.

P16

Stress Biomarkers in Mouse Fur under Low Gravity Conditions on the International Space Station (ISS)

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Abstract
The Artemis program is NASA's initiative to return humans to the moon and establish a sustainable presence there within 50 years. However, it is expected to take unknown stress under low gravity. To understand this new type of stress through objective assessment and verification, it is necessary to develop novel techniques that can replace conventional methods such as questionnaire and blood test. Our research group has chosen hair as a new biological sample. Hair contains a vast amount of molecular information that is highly sensitive to chemical and phycological influences. Because hair grows continuously, it is possible to evaluate biological changes over time by analyzing hair samples from the root to the tip. Thus, hair samples can be used to obtain daily biological information in a non-invasive manner. In this research, we analyzed the mouse's fur that raised on the ISS for 30 days under 1/6 G conditions (FLT) to identify potential space stress markers by LC-MS, using ground control mice (GC) for comparison. The fur of FLT mice (n=12) was crushed and extracted metabolites with methanol. A non-targeted analysis was performed using LC-MS to explore potential biomarkers. As a control, the same analysis was conducted on the fur of GC mice (n=12). As a result of statistical analysis, 56 compounds showed significant differences between the two groups (FLT and GC) ($p<0.05$). Especially, BCAAs, which are components of muscle, showed significant changes, indicating muscle atrophy induced by the space environment may be reflected in the fur.

P17

Administration of Vitamins (A_1, B_1, B_6) prevent a Parkinson's Disease Symptom

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Abstract

Parkinson's disease (PD) is one of the representative neurodegenerative diseases, causing motor dysfunction due to the degeneration of dopamine neurons. Currently, symptomatic treatment with L-DOPA is the mainstream approach, but long-term use poses challenges due to the development of motor complications, necessitating the development of new preventive and therapeutic strategies. Vitamins are not only essential nutrients but also play a crucial role in maintaining brain function through antioxidant and neuroprotective effects. In recent years, attention has focused on these physiological functions of vitamins, suggesting the potential for nutritional interventions in neurodegenerative diseases. This study investigated the effects of combined administration of retinol (VA_1), thiamine (VB_1), and pyridoxine (VB_6) on catecholamine metabolism in a unilateral 6-hydroxydopamine (6-OHDA)-induced PD mouse model. Each vitamin possesses distinct neuroprotective properties: promoting neuroplasticity (VA_1), supporting energy metabolism (VB_1), and enhancing dopamine synthesis (VB_6). Following PD induction, oral administration was conducted for 7 weeks, followed by an apomorphine-induced rotation test. Following administration, dopamine distribution was analyzed via imaging mass spectrometry (IMS), and neuronal changes were assessed using tyrosine hydroxylase (TH) and c-Fos staining. Results showed significantly fewer turns in the vitamin-treated group, indicating suppression of symptom progression. IMS analysis revealed a marked decrease in striatal dopamine levels in the untreated group, whereas the treated group maintained approximately 90% of baseline levels. Furthermore, the number of c-Fos-positive cells was reduced by 1.25-fold compared to the non-treated group ($p < 0.05$). These results suggest that combined vitamin administration may exert neuroprotective and functional recovery effects on PD by preserving dopamine metabolism and regulating neural activity.

P18

Analysis of the efficacy of phenethyl isothiocyanate on recovery from skeletal muscle atrophy induced by disuse

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Abstract
Skeletal muscle atrophy occurs when protein degradation exceeds synthesis during muscle inactivity, accompanied by elevated oxidative stress. We revealed that phenethyl isothiocyanate (PEITC), an antioxidant inducer, suppresses oxidative stress and muscle protein degradation in tail-suspended rats. This study examined the effects of PEITC during the recovery (reloading) period following disuse induced by tail-suspension. Four-week-old male Wistar rats were fed either a control diet or a 0.1% PEITC-supplemented diet. After 7 days of tail suspension, rats were dissected immediately (HC: control diet group, HP: PEITC diet group) or after 7 days of reloading with the control diet (RC: control diet during suspension group, RP: PEITC diet during suspension group). Skeletal muscles were collected and analyzed for weight and molecular markers of protein metabolism. Muscle weights of the soleus, plantaris, and gastrocnemius significantly increased after reloading, but PEITC intake did not further enhance this recovery. PEITC tended to upregulate the antioxidant enzyme NQO-1 and downregulate the ubiquitin ligases MuRF1 and atrogin-1, although changes were not statistically significant. Reloading markedly increased slow-type myosin heavy chain (MyHC) expression, while PEITC showed little additional effect. These results suggest that PEITC may modestly influence muscle proteolysis-related pathways but does not significantly enhance muscle mass recovery within 7 days of reloading. Further investigation of earlier recovery phases is needed to reveal the effect of PEITC on recovery of skeletal muscle after disused atrophy.

P19

Effect of two-depth split application of liquid fertilizers on rice root system architecture

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Abstract

Polymer-coated fertilizers are commonly used in rice cultivation in Japan. To reduce microplastic emissions from paddy fields while maintaining the convenience of single basal fertilization, alternative systems are needed. Deep placement of liquid and paste-type fertilizers offers a plastic-free solution for sustaining rice productivity without topdressing. We have developed a no-topdressing cultivation technique that allocates fertilizers to shallow soil layer for early growth and to deeper layer for later growth stage. In a two-depth fertilization experiment using paste fertilizer containing organic components and low-cost liquid urea, root systems increased at the deep fertilization site for both fertilizer types. However, root development patterns varied depending on the fertilizer, suggesting that nutrient diffusion and release characteristics of fertilizers influenced root distribution. Enhanced root growth in deeper layers enabled continuous nutrient uptake during the latter growth stages, resulting in yields comparable to conventional methods despite the absence of topdressing. These findings demonstrate that rice, typically a shallow-rooted crop, can be guided to develop deeper roots through strategic fertilizer placement. Deep rooting is particularly beneficial for stress avoidance under extended midseason drainage aimed at methane mitigation or during drought conditions, even when using existing cultivars. This approach contributes to sustainable rice production by reducing plastic dependency and enhancing resilience under environmental stress.

P20

Visualization of Stress Levels from a Single Strand of Hair Using IMS

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Abstract

AbstractIn modern society, various social and environmental factors cause individuals to experience chronic stress, resulting in a decline in quality of life and an increase in mood disorders. Therefore, establishing objective and quantitative methods for stress evaluation has become an important challenge. Conventional stress assessments mainly rely on subjective medical interviews or invasive procedures such as blood tests, and reliable biomarkers for stress remain limited. To address this issue, we focused on human hair as a non-invasive biological sample that continuously records physiological information over time. Since hair grows approximately 300–400 µm per day and reflects biochemical changes via capillary supply, longitudinal analysis of hair allows retrospective visualization of stress-related alterations.In this study, we aimed to develop a novel approach to visualize and quantify stress using hair. Hair samples were longitudinally sectioned with a hair cross-sectional cutting device (KATANA®), and molecular distributions were analyzed by Nano-Particle Assisted Laser Desorption/Ionization (Nano-PALDI) imaging mass spectrometry (IMS). Comprehensive omics analyses were then applied to identify potential stress-responsive biomarkers. As a result, we successfully visualized stress levels based on a newly discovered biomarker, demonstrating the feasibility of hair-based stress profiling.This study establishes a foundation for the objective and quantitative evaluation of stress and provides a promising strategy for early detection of pre-disease conditions and health prediction.

P21

Localization Analysis of Toxic Components in Higher Plants Using Imaging Mass Spectrometry (IMS)

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Abstract
Toxic secondary metabolites in higher plants play crucial roles in defense against herbivores and pathogens but occasionally cause food poisoning through misidentification of edible and poisonous species. To promote food safety and understand phytochemical localization, we visualized key plant toxins using imaging mass spectrometry (IMS). We profiled seven toxins from three taxa: aconitine, mesaconitine, and hypaconitine in aconite; lycorine, galantamine, and galanthaminone in narcissus; and colchicine in gloriosa. Leaves, stems, and roots were examined. Many targets lie at low *m/z*, and sub-tissue mapping is required. We therefore compared matrix-assisted laser desorption/ionization (MALDI) and nanoparticle-assisted laser desorption/ionization (Nano-PALDI) and selected, for each plant, the modality that delivered higher signal-to-noise in the low-mass range and finer spatial resolution. IMS succeeded across all taxa. MALDI yielded robust ion images for aconite with higher-molecular-weight alkaloids, whereas Nano-PALDI excelled for narcissus and gloriosa with lower-molecular-weight toxins. Hypaconitine in aconite, galantamine and galanthaminone in narcissus, and colchicine in gloriosa were strong, while aconitine and mesaconitine in aconite and lycorine in narcissus were weak. Patterns likely reflect ionization efficiency or content variability, motivating sampling. Toxins localized to subterranean organs: hypaconitine throughout aconite tubers; galantamine and galanthaminone in outer narcissus bulb scales; colchicine in outer gloriosa bulb scales. In a misidentification scenario, imaging distinguished narcissus leaves from garlic chives Allium tuberosum by the presence or absence of marker toxins. These findings contribute to the identification of toxic plants, the prevention of food poisoning, and a deeper understanding.

Memo