ABS 2025

The 11th International Conference on
Agricultural and Biological Sciences

July 21-24, 2025 Matsue, Japan

Conference Program

Bosen Academic Research Institute

TOYO UNIVERSITY 東洋大学

The 11th International Conference on
Agricultural and Biological Sciences (ABS 2025)

CONFERENCE PROGRAM

July 21st-24th, 2025
Matsue, Japan

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Part I Conference Schedule Summary

July 21st, 2025 / Japan Standard Time (UTC+9)
Location: In front of Small Hall, Kunibiki Messe

14:00-18:00	On-site Registration

Note for registration:

* Please show us your name or paper ID for registration.

* Please pick up all the conference materials at the registration desk (Name Card, Conference Program, Lunch & Dinner Tickets, etc.).

July 22nd, 2025 / Japan Standard Time (UTC+9)
Location: Meeting Room 501, Kunibiki Messe

Opening Ceremony and Keynote Speeches are chaired by:
Prof. Emeritus Hisayoshi Hayashi, *University of Tsukuba, Japan*
Prof. Mikihisa Umehara, *Toyo University, Japan*

09:15-09:25	**Opening & Welcome Speech** ***Prof. Emeritus Hisayoshi Hayashi****, University of Tsukuba, Japan*
09:25-10:00	**Keynote Speech 1:** New Mixed Model Methodologies for Genome-Wide Association Studies in The Era of Big Data and Artificial Intelligence ***Prof. Yuan-Ming Zhang****, Huazhong Agricultural University, China*
10:00-10:25	**Group Photo** (At the entrance of Kunibiki Messe)
10:25-10:45	**Coffee Break**
10:45-11:20	**Keynote Speech 2:** Physiological Analysis of Strigolactones Using Mutant Collections in Micro-Tom ***Prof. Mikihisa Umehara****, Toyo University, Japan*
11:20-11:55	**Keynote Speech 3:** Agricultural Science and Food Education: Contributing to The Development of Healthier Human Generations ***Prof. Emeritus Hisayoshi Hayashi****, University of Tsukuba, Japan*
11:55-12:30	**Keynote Speech 4:** Applications of Large Language Models, Prompt Engineering, and AI Agents for Biology ***Prof. Dong Xu****, University of Missouri-Columbia, USA*
12:30-13:30	**Lunch Break**
13:30-17:55	**Invited & Oral Session 1:** Microbiology and Biotechnology

July 23rd, 2025 / Japan Standard Time (UTC+9) **Location: Meeting Room 501, Kunibiki Messe**	
09:00-12:10	**Invited & Oral Session 2:** Agricultural Biotechnology and Crop Improvement
12:10-13:20	**Lunch Break**
13:20-16:15	**Invited & Oral Session 3:** Soil Science and Agricultural Environmental Science
16:15-17:10	**Coffee Break and Poster Session**
17:30-20:30	**Awarding Banquet at Yuushien Garden in Daikonshima** (Please gather at the entrance of Kunibiki Messe)

July 24th, 2025 / Japan Standard Time (UTC+9)	
09:10	**Departure from Kunibiki Messe** (Please gather at the entrance of Kunibiki Messe)
09:30-10:30	**Visit Matsue Castle**
10:40-11:40	**Horikawa Sightseeing Boat Ride**
11:50-12:40	**Lunch Break**
13:00-15:00	**Matsue Vogel Park**
15:30	**Arrival at JR Matsue Station at 15:30** (Subject to no traffic delays)

Notes: Please note that the itinerary, including the order of visits and time spent at each location, is subject to change based on actual circumstances.

Part II Keynote Speeches

Keynote Speech 1: New Mixed Model Methodologies for Genome-Wide Association Studies in The Era of Big Data and Artificial Intelligence

Prof. Yuan-Ming Zhang
College of Plant Science and Technology, Huazhong Agricultural University, China

Biography: Yuan-Ming Zhang is a professor of statistical genomics at Huazhong Agricultural University (HZAU) in China. His major is quantitative genetics. He obtained his Bachelor's degree from Southwest Agricultural University in 1986, followed by his Master's degree and PhD from Nanjing Agricultural University (NAU) in 1992 and 2001 respectively. He worked on the Rongchang campus of Southwest University from 1986 to 1999 before moving to NAU, and then to HZAU in 2014. He was a postdoctoral fellow at the University of California, Riverside, from 2003 to 2005, and became an associate professor in 1995, progressing to full professor in 2002. In 2022, he was selected as one of the world's top 2% of scientists. He is an editorial board member of Heredity, BMC Genomics, Front Plant Sci (Guest), and Acta Agronomica Sinica. He is also a council member of the Chinese Society of Agri-Biotechnology, and a full member of Sigma Xi, the Scientific Research Honor Society, and the Genetics Society UK. His team has developed several software packages for identifying genes associated with complex traits. These include mrMLM, IIIVmrMLM and Fast3VmrMLM for GWAS, GCIM for QTL mapping, dQTG-seq for bulked segregant analysis, and SEA for mixed inheritance analysis. They can be downloaded for free from https://github.com/YuanmingZhang65 and https://cran.r-project.org/web/packages/. He has published over 120 articles in journals such as Mol Plant, Plant Cell, Brief Bioinform and Heredity.

Abstract: Genome-wide association study (GWAS) is a key gene mining method and has played a significant role in the genetic dissection of complex traits in animals, plants, and humans. However, it still has shortcomings in both theory and application. The genome-wide scanning framework of existing methods does not take advantage of the AI era. Methods based on allele substitution effect (α) have low power to detect dominant, overdominant, rare, and small-α QTNs. There are almost no feasible methods available to detect QTN-by-environment (QEI) and QTN-by-QTN (QQI) interactions. These result in some important loci and trait heritability being missed. To address these issues, we have established a compressed variance component mixed model and a 3VmrMLM method. In this model, all possible effects are considered and all possible polygenic genetic backgrounds are controlled. The model is then used for genome-wide scanning to identify potential QTNs, QEIs, and QQIs. Some of these are then identified as significant QTNs, QEIs, and QQIs using machine learning. This is our two-stage method with a genome-wide scanning plus machine learning framework. This simple model can be used to detect QTNs, QEIs, and QQIs uniformly. Genetic dissection and breeding by design for polygenic traits remain substantial challenges, and its calculation speed still needs to be improved, particularly in the era of big data and AI. Thus, we have integrated advanced statistical and computer technologies with 3VmrMLM to propose Fast3VmrMLM for identifying abundant and key genes for polygenic traits. The advantages of this approach are as follows. In the 18K rice dataset containing ~3 million SNPs, more dominant, small-effect and rare QTNs were identified; 211 known genes and 384 candidate genes for 14 traits were detected; and each trait took 3.30 h to analyze. Furthermore, the SNP

marker expanded to include bin/gene haplotypes, lncRNA types, and structural variations, making mQTL detection possible. In the maize NC II breeding population containing over 30 million markers, 26 known genes and 24 candidate genes were found to be associated with seven yield-related traits. These QTNs were then used to predict excellent hybrid combinations. More importantly, a genetic network for rice yield-related traits was constructed using all the known and candidate genes. The key genes in this network were identified and a breeding strategy utilizing these key genes was proposed. The software packages IIIVmrMLM and Fast3VmrMLM can be downloaded for free from https://github.com/YuanmingZhang65. Additionally, the new methods for QEI and QQI detection in big data were introduced briefly.

Keynote Speech 2: Physiological Analysis of Strigolactones Using Mutant Collections in Micro-Tom

Prof. Mikihisa Umehara
Department of Biological Resources, Graduate School of Life Sciences, Toyo University, Japan

Biography: Mikihisa Umehara is a Professor of Department of Biological Resources and Graduate School of Life Sciences, Toyo University, Japan. His major is plant physiology and plant biotechnology. He graduated from the University of Tsukuba in 1997, finished a doctor's course at the Graduate School of Biological Sciences, the University of Tsukuba in 2004, and obtained Ph.D. in Science. He worked on onion breeding in Department of Biotechnology, Fukuoka Agricultural Research Center from 2004 to 2007. He joined RIKEN Plant Science Center as a special postdoctoral researcher in 2007 and worked on a class of plant hormones, strigolactones. In 2011, he moved to Toyo University as an associate professor, and became a full professor in 2015.

Abstract: Shoot branching is an important trait in both agriculture and horticulture, as the number of axillary buds directly influences crop yield and seed production. Strigolactones (SLs) are a class of plant hormones that inhibit shoot branching in plants. In SL biosynthesis, carlactone, a biosynthetic precursor of SLs, is synthesized from β-carotene through sequential reactions catalyzed by the β-carotene isomerase DWARF27 (D27) and carotenoid cleavage dioxygenases 7 and 8 (CCD7 and CCD8). Carlactone is then converted to carlatonoic acid (CLA) via oxidation by cytochrome P450 encoded by the CYP711A gene family. CLA is further metabolized into various types of SLs. To date, more than 30 canonical and non-canonical SLs have been identified from various plants. However, the specific bioactive SLs for shoot branching inhibition remain unidentified. In our previous research, we collected SL biosynthesis mutants in the tomato cultivar Micro-Tom to evaluate the roles of SLs in tomato, but SL signaling mutants were not available. Bioactive SLs are perceived by DWARF14 (D14), a member of the α/β-fold hydrolase superfamily. Since bioactive phytohormones tend to accumulate in signaling mutants, we hypothesized that SLs involved in shoot branching inhibition might be enriched in sld14 mutants. Therefore, we generated sld14 mutants in Micro-Tom by genome editing. Our analysis revealed that 16-hydroxymethyl carlactonoate (16-HO-MeCLA) significantly accumulated in the nodes of the mutants compared to the wild type. We also found that CYP722A is

associated with the 16-hydroxylation of CLA. 16-HO-MeCLA or the metabolites may serve as bioactive SLs. To further elucidate the physiological roles of 16-HO-MeCLA, we plan to investigate the function of the CYP722A gene.

Keynote Speech 3: Agricultural Science and Food Education: Contributing to the Development of Healthier Human Generations

Prof. Emeritus Hisayoshi Hayashi
University of Tsukuba, Japan

Biography: Dr. Hisayoshi Hayashi graduated from University of Tsukuba in 1980. After working as an extension officer in Nagano Prefecture for one year, he moved to Chushin Agricultural Experiment Station, where he worked in the field crop cultivation department for six years. He then moved to University of Tsukuba, where he served as a professor at the Laboratory of Crop Production Systems and the Laboratory of Crop Science, before being appointed professor emeritus at University of Tsukuba in April 2023. He is a former president of the Japanese Society of Farm Work Research and a fellow of Japan Association of International Commission of Agricultural and Biosystems Engineering. Since April 2023, he has been leading training programs for extension workers, researchers, and government officials in developing countries as a training advisor at Japan International Cooperation Agency Tsukuba Center (JICA Tsukuba).

Abstract: The primary goal of the educational activities of universities is to provide specialized education for the development of human resources in the relevant field. On the other hand, in recent years, universities are also required to contribute to society. Agricultural science is an academic discipline that plays an important role in the agricultural industry, and its scope is extremely diverse. It is also a field related to food, which is directly related to human survival. With the modernization of society, roles have become increasingly divided, and people live by eating food without understanding how it is produced. As the world population exceeds 10 billion in the 21st century, and hunger is difficult to solve, it is necessary to develop food education that will develop all people to understand food production.

Keynote Speech 4: Applications of Large Language Models, Prompt Engineering, and AI Agents for Biology

Prof. Dong Xu

Department of EECS and C.S. Bond Life Sciences Center, University of Missouri-Columbia, USA

Biography: Dong Xu is Curators' Distinguished Professor in the Department of Electrical Engineering and Computer Science, with appointments in the Christopher S. Bond Life Sciences Center and the Informatics Institute at the University of Missouri-Columbia. He obtained his Ph.D. from the University of Illinois, Urbana-Champaign in 1995 and did two years of postdoctoral work at the US National Cancer Institute. He was a Staff Scientist at Oak Ridge National Laboratory until 2003 before joining the University of Missouri, where he served as Department Chair of Computer Science during 2007-2016. Over the past 30 years, he has conducted research in many areas of computational biology and bioinformatics, including single-cell data analysis, protein structure prediction and modeling, protein post-translational modifications, protein localization prediction, computational systems biology, biological information systems, and bioinformatics applications in human, microbes, and plants. His research since 2012 has focused on the interface between bioinformatics and deep learning. He has published more than 500 papers with more than 28,000 citations and an H-index of 89 according to Google Scholar. He was elected to the rank of American Association for the Advancement of Science (AAAS) Fellow in 2015 and American Institute for Medical and Biological Engineering (AIMBE) Fellow in 2020.

Abstract: Large language models (LLMs), trained on massive datasets, are opening new frontiers in biology, especially when combined with prompt-based learning, retrieval-augmented generation (RAG), and AI agents. This presentation showcases our work leveraging these tools across multiple biological domains, such as plant science. We developed RAG and prompt refinement techniques to improve gene relationship prediction. We built AI agents for protein annotation and Fatplants (https://fatplants.net), our database of plant lipid-related genes and metabolism. In protein modeling, we introduced S-PLM, a contrastive learning-based, 3D structure-aware protein language model that enhances sequence-based predictions. Prompting protein language models further boosted tasks like signal peptide and targeting signal prediction. We also applied prompt-based learning to large single-cell RNA-seq models, improving several single-cell analysis tasks. In addition, we developed scPlantAnnotate, a plant-specific large single-cell RNA-seq model, for plant cell type annotation that significantly outperforms current reference-based methods across four plant species. Our findings demonstrate the transformative potential of LLMs and AI agents in advancing biological research.

Part III Oral Presentations

General Guidelines

- **All presentation times are shown in Japan Standard Time (UTC+9).**
- Duration for Invited Oral Presentation: 20 minutes of presentation, including 3-5 minutes of Q&A.
- Duration for Regular Oral Presentation: 15 minutes of presentation, including 2-3 minutes of Q&A.
- All presenters are requested to reach the Session Room prior to the scheduled time and complete their presentation on time.
- Presenters should prepare Power Point or PDF Files for Presentation with Paper ID (**ABS****) marked on the last page.
- A signed and stamped presentation certificate will be issued after the presentation.

Oral Presentation Guidelines

Devices Provided by the Conference Organizer:

- Laptops (with MS-Office & Adobe Reader) & Projectors & Screen
- Laser Sticks
- Microphones
- Please send us the PowerPoint once it is ready and have the PPT back up in a U-disk. For presenters who do not send the PowerPoint, please save it in the laptop of the corresponding session 15 min in advance. Kindly tell the Session Chair (before the start of your session) that you are present.

Best Oral Presentation Selection Procedure

ONE best presentation will be selected from EACH session based on the following criteria:

- ✓ Research Quality
- ✓ PowerPoint Design
- ✓ Presentation Performance
- ✓ Effective Communications
- ✓ Presentation Language

Selection Procedure

- An assessment sheet (see picture) will be delivered to listeners before the session starts.
- When the session finishes, each listener is required to fill out the sheet (he/she can vote for two excellent presentations) and give it to the Session Chair.
- The Session Chair will count the votes and select the best oral presentation with the most votes. If there is a tie, the Session Chair will make the final decision.
- Invited presentations do not participate in the best oral presentation selection.

Best Oral Presentations Award

The Best Oral Presenter from each session will be awarded an official certificate at the Awarding Banquet and a complimentary registration to the ABS 2026.

Sample of Assessment Sheet

Oral Presentation Assessment

Dear participants,

After carefully listening to the presentations of this session, please kindly recommend two excellent Oral Presentations with reference to the following evaluation criteria. Invited presentations do not participate in the best oral presentation selection.

The Session Chair will count the votes from each presentation and select ONE Best Oral Presentation in this session. If there is a tie, the Session Chair will make the final decision.

The winner will be announced on the official website after the conference.

You can refer to the following criteria for best oral selection:

Items	Assessment
Content	Right, Logical, Original, Well-Structured
Language	Standard, Clear, Fluent, Natural
Performance	Spirited Appearance, Dress Appropriately, Behaves Naturally
PowerPoint	Layout, Structure, Typeset, Animation, Multimedia
Reaction	Build a Good Atmosphere, Speech Time Control Properly

Please write down the paper ID and give reasons for your recommendation:

Paper ID	Reasons

Evaluated by:__________________
Paper ID: _____________________

Note: Please fill it out and give it to the Session Chair or assistant so that the Best Oral Presentation can be selected.

Invited & Oral Session 1: Microbiology and Biotechnology

Time: 13:30-17:55, July 22nd, 2025 **Location: Meeting Room 501, Kunibiki Messe**
Session Chairs:
13:30-15:25 Prof. Fufeng Liu, Tianjin University of Science & Technology
15:50-17:55 Prof. Huawen Fu, National Tsing Hua University

13:30-13:50	**ABS4716 (Invited)**	**Combining genes from different yeast species in a non-GMO way through interspecific hybridization** *Prof. Matthias Sipiczki, University of Debrecen, Hungary*
13:50-14:10	**ABS4725 (Invited)**	**Immobilization of sucrose isomerase and its application in the production of isomaltulose** *Prof. Fufeng Liu, Tianjin University of Science & Technology, China*
14:10-14:25	**ABS4739**	**Rational design and high-throughput screening of D-allulose 3-epimerase** *Dr. Hui-Min Qin, Tianjin University of Science & Technology, China*
14:25-14:40	**ABS4726**	**Research on pathogen detection technology based on CRISPR/Cas biosensing systems** *Dr. Lijuan Yin, Tianjin University of Science & Technology, China*
14:40-14:55	**ABS4683**	**Unravelling the stress tolerance mechanisms of *lacticaseibacillus paracasei* zhang - insights into the viable but non-culturable state** *Ms. Ran Gao, Inner Mongolia Agricultural University, China*
14:55-15:10	**ABS4685**	**Screening of entomopathogenic fungi to effective whitefly nymph management: Enzymatic activity and secondary metabolites analysis using FTIR** *Ms. Sudarat Pimkhonburee, Suranaree University of Technology, Thailand*
15:10-15:25	**ABS4752**	**Microbial activity and community characteristics of organic and conventional farmland** *Ms. Youngmi Lee, National Institute of Agricultural Science, Rural Development Administration, South Korea*
15:25-15:50		**Coffee Break**
15:50-16:10	**ABS4719 (Invited)**	**Helicobacter pylori neutrophil-activating protein: From a virulence factor to a potential therapeutic target** *Prof. Huawen Fu, National Tsing Hua University*
16:10-16:30	**ABS4730 (Invited)**	**Integrated strategies for evaluating natural products in hyperuricemia and gout management: from uricosuric effects to anti-inflammatory effects** *Assoc. Prof. Ting Wu, Huazhong Agricultural University, China*

16:30-16:50	**ABS4692** **(Invited)**	**Real time capacitance variation monitoring due to cell-drug reactions using single and multi-well array ECIS impedance biosensor in NIH/3T3 cells** *Prof. Moongyu Jang, Hallym University, South Korea*
16:50-17:10	**ABS4636** **(Invited)**	**Summer-ready moths: innovations in bamboo borer breeding practices** *Assoc. Prof. Manaporn Manaboon, Chiang Mai University, Thailand*
17:10-17:25	**ABS4609**	**Identification of plastic-degrading bacteria in the human gut** *Prof. Sukkyoo Lee, Daegu Gyeongbuk Institute of Science and Technology, South Korea*
17:25-17:40	**ABS4780**	**Development of a photoinduced nuclear translocation thiophene-based fluorescent drug to increase anticancer efficiency of doxorubicin** *Mr. Dat Thanh Dinh, National Chung Hsing University*
17:40-17:55	**ABS4762**	**Assessing the conservation and enhancement value of revegetated strips on arthropod assemblages in a pasture landscape** *Dr. Peter O'Donnell, Kongju National University, South Korea*

Video Presentations

Video presentations are listed on https://www.academicconf.com/video?confname=abs2025

ABS4773	**How microfluidics shape light in scarab beetle** *Dr. Danica Pavlović, Institute of Physics Serbia, Serbia*
ABS4770	**Evaluation of amaranth bioactive compounds with hypoglycemic effect in murine in vivo models and human pilot phase** *Dr. Leslie Becerril Serna, University of Valle de Atemajac, Mexico*

Invited & Oral Session 2: Agricultural Biotechnology and Crop Improvement

Time: 09:00-12:10, July 23rd, 2025 **Location: Meeting Room 501, Kunibiki Messe**

Session Chairs:

09:00-10:35 Prof. Yuan-Ming Zhang, Huazhong Agricultural University, China
10:50-12:10 Dr. Jariya Roddee, Suranaree University of Technology, Thailand

09:00-09:20	**ABS4711 (Invited)**	**Waste mushroom fungi beds as source of good biostimulants which gives solution for rice yielding and grain quality problems under high temperature stress** *Prof. Kimiko Itoh, Niigata University, Japan*
09:20-09:35	**ABS4687**	**Advancing multi-technology approaches for selection of rice varieties resistant to feeding by brown planthopper (*Nilaparvata lugens*)** *Dr. Jariya Roddee, Suranaree University of Technology, Thailand*
09:35-09:50	**ABS4649**	**The effect of biological treatment of soybean in organic farming on production and quality parameters** *Assoc. Prof. Petr Konvalina, University of South Bohemia, Czech Republic*
09:50-10:05	**ABS4686**	**Stomata on bracts and petals as possible mediators in the ant-pollinator conflict of interest of *Vachellia cornigera* (Leguminosae)** *Dr. Sandra Luz Gómez-Acevedo, Universidad Nacional Autónoma de México, Mexico*
10:05-10:20	**ABS4697**	**^{15}N-Isotope labelling of cover crop and nitrogen recovery by subsequently grown cabbage, komatsuna, and lettuce: hairy vetch vs. oats** *Dr. Khin Thawda Win, National Agriculture and Food Research Organization, Japan*
10:20-10:35	**ABS4696**	**Development and evaluation for the low-carbon precise pneumatic servo plug tray seeding machine** *Prof. Hao-Ting Lin, National Chung Hsing University*
10:35-10:50		**Coffee Break**
10:50-11:10	**ABS4652 (Invited)**	**The resistance mechanism of different ecotype bananas to fusarium wilt of banana** *Prof. Sijun Zheng, Yunnan Academy of Agricultural Sciences, Alliance of Bioversity and CIAT, China*
11:10-11:25	**ABS4688**	**Early detection of cotton verticillium wilt based on generative adversarial networks and hyperspectral imaging technology** *Dr. Fei Tan, Shihezi University, China*
11:25-11:40	**ABS4755**	**Genome-wide association studies and multi-omics analysis unravel genetic architecture of heterosis and identify its candidate genes in maize NCII population** *Dr. Ying Chen, Huazhong Agricultural University, China*

11:40-11:55	**ABS4761**	**The genetic basis of heterosis for yield-related traits in rice** *Dr. Miaomiao Zhao, Huazhong Agricultural University, China*
11:55-12:10	**ABS4641**	**Response of growth and physiological characteristics and root soil reinforcement of *artemisia ordosica* to erosion damage in central and western Inner Mongolia** *Ms. Xin Zhang, Senior Engineer, Institute of Water Resources for Pastoral Area Ministry of Water Resources, China*

Invited & Oral Session 3: Soil Science and Agricultural Environmental Science

Time: 13:20-16:15, July 23rd, 2025 **Location: Meeting Room 501, Kunibiki Messe**

Session Chairs:

13:20-15:00 Prof. Seong Kyun Kim, Daegu Gyeongbuk Institute of Science and Technology, South Korea

15:00-16:15 Prof. Ashfaque Ahmed, University of Dhaka, Bangladesh

13:20-13:40	**ABS4784 (Invited)**	**Mangrove forests in the context of food security and climate change** *Prof. Ashfaque Ahmed, University of Dhaka, Bangladesh*
13:40-14:00	**ABS4758 (Invited)**	**Water-efficient artificial phytoextraction technology for the remediation of heavy metal contaminated soil** *Prof. Seong Kyun Kim, Daegu Gyeongbuk Institute of Science and Technology, South Korea*
14:00-14:15	**ABS4674**	**Potential of sophorolipids as promising surfactants for environmental remediation** *Ms. Glen Lelyn Quan, Saraya Co., Ltd., Japan*
14:15-14:30	**ABS4747**	**Effects of no-tillage on soil bulk density under major soil types in China** *Prof. Lifeng Hu, The Open University of China, China*
14:30-14:45	**ABS4734**	**Unmanned aerial vehicle spray plantation to steep slide slopes** *Assoc. Prof. Pei-Chi Shao, Chang Jung Christian University*
14:45-15:00	**ABS4655**	**Overview of landslide ecosystem with super-thick material in Ngasinan village** *Ms. Anastasia Neni Candra Purnamasari, Universitas Gadjah Mada, Indonesia*
15:00-15:15	**ABS4668**	**Driving factors of vegetation cover change in Beibu Gulf Urban Agglomeration** *Dr. Zhaogang Fu, Lingnan Normal University, China*
15:15-15:30	**ABS4705**	**A study on the coordination of recruiting farm volunteers through green tourism: an interview with JA Tourism & Communications** *Mr. Hiroyuki Murata, Ohara Graduate School of Accounting, Japan*
15:30-15:45	**ABS4646**	**The role of wildlife photography in conservation and scientific research: A visual approach to protecting biodiversity** *Mr. Tiago Rodrigues, Bioventura Institute, Brazil*
15:45-16:00	**ABS4777**	**Innovative foam-based approaches for treating trichloroethylene dense non-aqueous phase liquid: comparative assessment of regular and persulfate-oxidative foams** *Ms. Xuyen Thi Hong Luong, National Chung Hsing University*
16:00-16:15	**ABS4618**	**Green synthesis of ZIF-8 for selective adsorption of dyes in water purification** *Mr. Muyuan Zhai, Dalian University of Technology, China*

Part IV Poster Presentations

Poster Presentation Guidelines

Materials Provided by the Conference Organizer:

- Poster Board
- Adhesive Tapes or Clamps

Materials Provided by the Presenters:

- Home-Made Posters
- Posters Printed by Conference

Requirement for the Posters:

- Material: not limited
  Size: W1200*H2100

Poster Board

Best Poster Presentation Selection Procedure

Selection Criteria:

- Research Quality
- Presentation Skill
- Design

Samples of Stickers

Selection Procedure:

- 6-8 volunteers will be invited from the participants to serve as the judges to review the posters (Note: judges have no conflict of interest with the presenters).
- 2 red stickers and 2 green stickers will be provided to the judges. The red sticker stands for "Research Quality" with a value of 2 points; the green sticker stands for "Presentation Skill and Design" with a value of 1 point.
- Each judge will go around the poster session and give the stickers to the poster which he/she thinks is of high quality or well designed and well presented, please be noticed that the judge cannot give 2 red or 2 green stickers to the same poster (one red and one green sticker is acceptable).
- After the poster session, the conference secretary will count the points from each poster and ONE best poster presentation with more points will be selected. If there is a tie, the one with more red (Research Quality) stickers wins.

Nature of the Award

- This award consists of free registration to the ABS 2026 and a certificate.
- **TWO** outstanding poster presenters will be selected and honored with certificates during the award ceremony. The winners will be announced at the banquet and featured on the ABS 2026 official website.

List of Posters

Time: 16:15-17:10, July 23rd, 2025 **Location: Meeting Room 501, Kunibiki Messe**

ABS4677	**An anti-mycobacterial drug inhibits dengue virus replication through AMPK-mediated antiviral responses** *Prof. Jin-Ching Lee, National Sun Yat-sen University*
ABS4689	**Identification of early resistance-related genes in luffa against *fusarium* wilt through transcriptome analysis** *Ms. Yu-Xuan Jiang, National Chung-Hsing University*
ABS4690	**Trait analysis and genetic structure of hybrid progeny between *hydrangea macrophylla* and *hydrangea chinensis*** *Ms. Chu-Chang Yin, National Chung-Hsing University*
ABS4691	**Genome-wide association study identifies loci associated with *fusarium oxysporum* f. sp. *luffae* Fomh16 resistance in luffa** *Ms. Yu-Chi Liu, National Chung-Hsing University*
ABS4694	**Genetic architecture and QTL tagging of flowering and fruit traits in bitter gourd using computer-assisted phenotyping** *Ms. Chi-Chen Wei, National Chung-Hsing University*
ABS4695	**Transcriptome analysis of early resistance gene expression in luffa against *fusarium* wilt caused by *fusarium oxysporum* strain FOLUST** *Mr. Che-Han Chu, National Chung-Hsing University*
ABS4701	**Comparative analysis of the plastomes of *Iris* species from Kazakhstan** *Dr. Shyryn Almerekova, Institute of Plant Biology and Biotechnology, Kazakhstan*
ABS4702	**Chloroplast genome sequencing of *lonicera* L. species from Kazakhstan: comparative and phylogenetic analyses** *Dr. Moldir Yermagambetova, Institute of Plant Biology and Biotechnology, Kazakhstan*
ABS4703	**Characterization of the plastid genomes of allium species from Kazakhstan** *Prof. Saule Abugalieva, Institute of Plant Biology and Biotechnology, Kazakhstan*
ABS4704	**Genetic exploration and genome-wide association study of leaf morphology in sweet potato germplasm from the TARI Chiayi Branch, Taiwan** *Mr. Chong-Wei Lee, National Chung-Hsing University*
ABS4706	**Cotton verticillium wilt severity detection based on hyperspectral imaging and SSFNet** *Mr. Yang Gao, Shihezi University, China*
ABS4735	**Pressure–temperature interactions affecting hydration resistance in rice paddy** *Ms. Xin-Fang Li, National Taiwan University*
ABS4736	**Innovative processing of nano-structured cellulose for Pickering emulsion stabilization** *Prof. Shih Hsin Chen, National Taiwan University*
ABS4740	**The study on the synthetic chromosomes rearrangement improving yeast β-glucan and regulatory target localization** *Dr. Peipei Han, Tianjin University of Science & Technology, China*

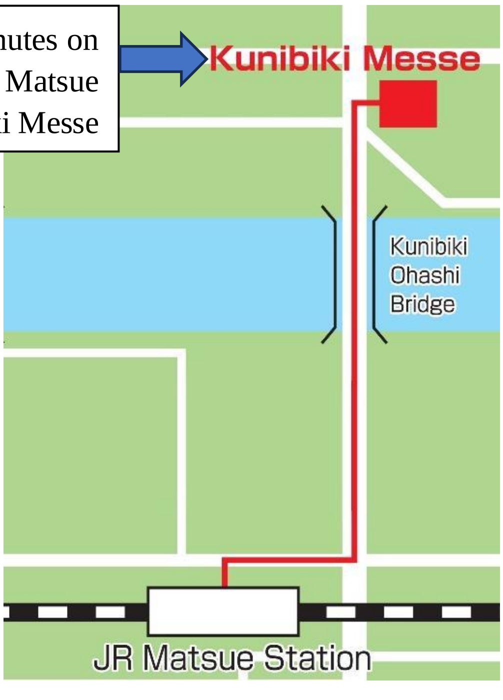
ABS4741	**Sensory evaluation of beer brewed with *NTH1* and *FKS3* gene-deleted *Saccharomyces cerevisiae*** *Prof. Yun-Chin Chung, Providence University*
ABS4754	**Development of ultrafast real-time PCR assay for identifying *Lupinus angustifolius* and *Lupinus albus*** *Dr. Ho Soo Lim, National Institute of Food and Drug Safety Evaluation, South Korea*
ABS4769	**UPLC-QTOF-MS-based metabolomic analysis of tea leaves during fermentation by *Eurotium cristatum*** *Dr. Eun-Hye Kim, Tea Industry Institute, South Korea*
ABB1344	**Design of HPK1 inhibitors for cancer immunotherapy by protein structural biology** *Dr. Su-Ying Wu, National Health Research Institutes*
ABS4783	**Effects of growing seasons on growth and yield of 12 parthenocarpic cucumber cultivars cultivated under greenhouse conditions in Thailand** *Dr. Arak Tira-umphon, Suranaree University of Technology, Thailand*
ABS4772	**Effects of *gynura procumbens* on the immune system: a scoping review of its antioxidant properties** *Dr. Fais Natasya Muhammad Faisal, Universiti Teknologi MARA Cawangan Selangor, Malaysia*

Part V Conference Venue

Kunibiki Messe
(Shimane Prefectural Convention Center)

The biggest convention center in Shimane prefecture, Kunibiki Messe, is located in the center of Matsue City. There are Exhibition Hall (4,018 sqm), Multipurpose Hall (686 sqm), International Conference Hall (510 sheets), and 19 meeting rooms.
Free Wi-Fi is available in building.

It takes only 7 minutes on foot from JR Matsue Station to Kunibiki Messe

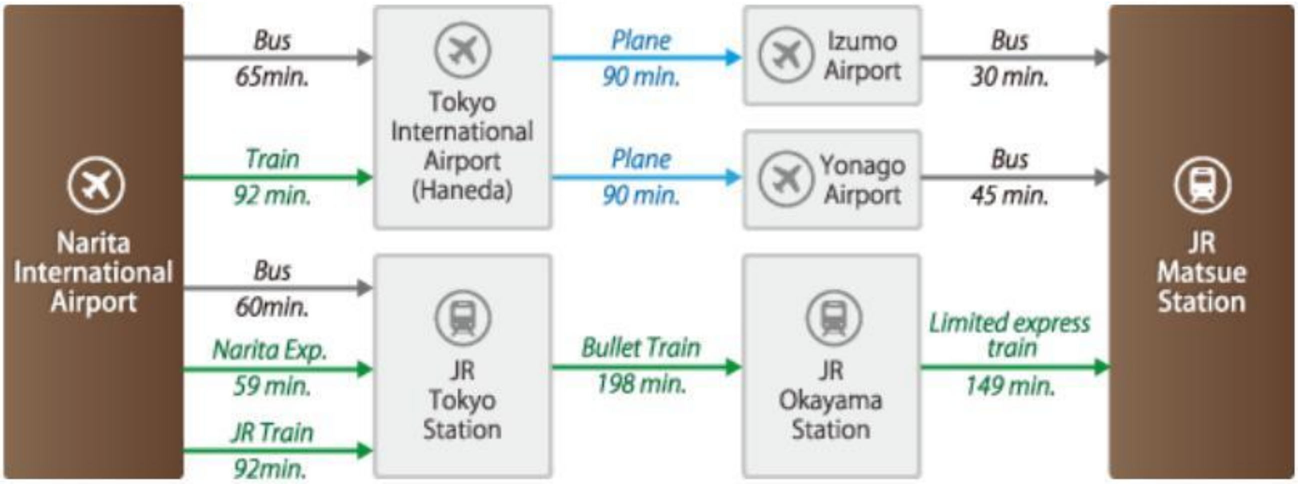


Kunibiki Messe
Address: 1-2-1 Gakuen Minami Matsue City, Shimane, JAPAN 690-0826
Tel: +81+852-24-1111
Fax: +81+852-22-9219
E-mail: kunibiki@kunibikimesse.jp

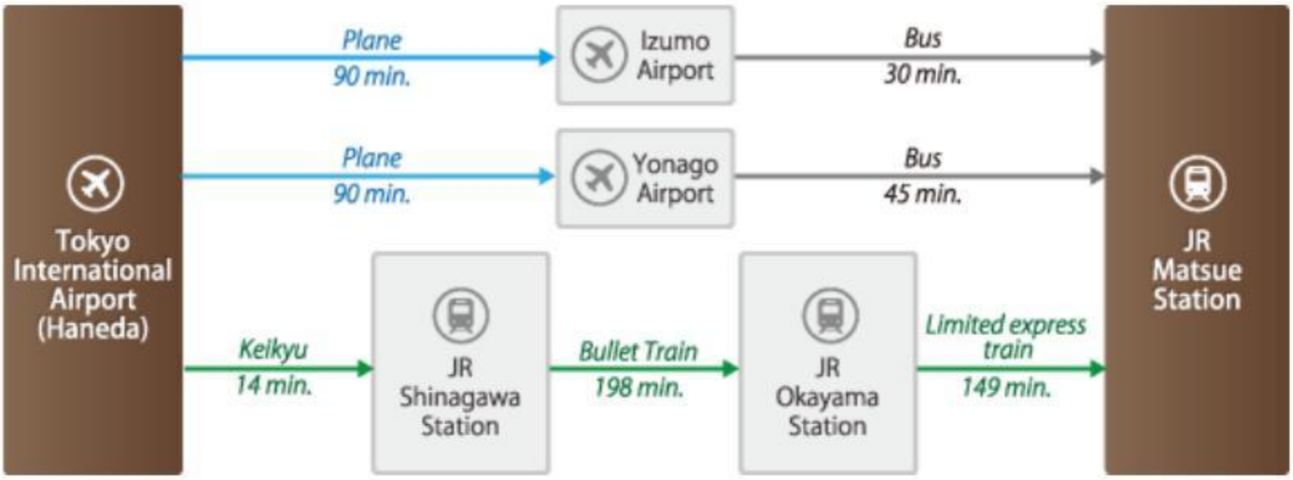
Access to JR Matsue Station:

→ Train → Bus → Plane

1. **From Narita International Airport**



2. **From Tokyo International Airport**



3. **From Kansai International Airport**

Part VI Acknowledgements

On behalf of the ABS 2025 Organizing Committee, we would like to take this opportunity to express our sincere gratitude to our participants. We would also like to express our acknowledgements to the Technical Program Committee members who have given their professional guidance and valuable advice as reviewers. For those who contribute to the success of the conference organization without listing the name below, we would love to say thanks as well.

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