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1. Applications for two academic positions at IPSR will be closing soon!
Two academic positions starting in April 2026 are currently recruited at IPSR at Full Professor and Tenure-Track Assistant Professor levels. For details in Japanese and English visit the respective institute website:

Full Professor in the Group of Plant-Microbe Interactions
https://www.rib.okayama-u.ac.jp/recruit/20250724-post1_j/
https://www.rib.okayama-u.ac.jp/english/recruit/20250724-post1_en/

Tenure-track Assistant Professor in the Group of Plant Immune Design
https://www.rib.okayama-u.ac.jp/recruit/20250724-post2_j/
https://www.rib.okayama-u.ac.jp/english/recruit/20250724-post2_en/

Deadline for both applications is 22-September, 2025

2. Call for Joint Research Projects under the Alliance of Plant Research Centers (Platinum Scheme)
The Alliance of Plant Research Centers (five centers: Tsukuba-Plant Innovation Research Center, University of Tsukuba; Arid Land Research Center, Tottori University; Institute of Plant Science and Resources, Okayama University; Tropical Biosphere Research Center, University of the Ryukyus; and Osaka Metropolitan University, Botanical Gardens) was established to strengthen the collaboration among plant research centers in Japan. The Alliance Platinum scheme, which allows for cross-sectional collaborative research among multiple centers, will be continued in the next fiscal year 2026. The project call for proposals has been opened in September, with approximately two to three cross-proposals being expected/promoted at each center. Details on the "Alliance Platinum Scheme" carried out at IPSR are now available from the institute website:
https://www.rib.okayama-u.ac.jp/collaboration/plant-science-core-alliance/platinum

3. Introduction of Orbitrap Exploris GC-MS
In continuation of introductions that feature new instruments installed at Okayama University as part of the J-PEAKS program, we are now able to announce the installation of the Orbitrap Exploris 30K GC-MS system from Thermo Fisher Scientific at Kurashiki IPSR campus. This machine is replacing the former Agilent 240 GC-MS

system, purchased and serving in the institute since 2013. Here, only the main purpose and capabilities of the new Exploris GC-MS are highlighted, while interested users are encouraged to contact us directly for further details and conditions of collaborative use at IPSR.

In general, GC coupled detection systems are used for direct analysis of small molecule that is predetermined by necessity of separation of analytes on capillary GC columns. As an example, we often use our GC-MS for analysis of volatile compounds emitted from plants, after subjecting them to biotic stresses, such as herbivore attack. To this end, we have developed efficient methods for trapping of volatiles from headspace of rice on various sorbents, such as Porapak Q or GL Science Monotrap devices, as well as we have established the extraction method for collection of volatiles from rice tissues. Although we mostly use rice, in principle, volatiles can be analyzed from widest range of plants, pending the identification of specific compounds in each species. In comparison to Agilent 240 GC-MS, the new Exploris system facilitates the identification of unknown metabolites by providing the Compound Discoverer software and ability to determine accurate (high resolution) mass of analyzed molecules and their fragments. For quantification of known metabolites, Trace Finder software can be used after establishment of custom methods based on the information derived from the authentic standards.

Although it was mentioned above that GC is mainly used for direct analysis of small molecules(volatiles), derivatization of larger molecules by specific reagents allows quantification of larger non-volatile metabolites, such as amino acids, organic acids, and sugars on GC-MS. We routinely use derivatization of primary metabolite extracts from plants with MSTFA reagent to produce trimethylsilylated (TMS) derivatives, and run them on GC-MS. MSTFA derivatization is applicable to various

functional groups in chemical compounds, such as −COOH, −OH, −NH, and −SH groups.
In our hands, disaccharides are typically the size limit of this analytical method, thus allowing determination of disaccharides, such as sucrose and maltose, but excluding trisaccharides and higher structures, from various plant extracts.
With introduction of the new J-PEAKS instruments, we hope to develop at Okayama University as many as possible interesting collaborative research projects, especially in the area of plant science and related fields, with Japanese researches.

4. Reflections on the International Workshop on Genome Modification for Sustainable Crop Development
The workshop recently organized as part of the Joint Use/Research Center program at IPSR introduced three speakers, including our distinguished guest Dr. Cathie Martin from John Innes Centre (UK), Dr. Minako Sumiyoshi (Sanatech Life Science Co., Ltd.), and Dr. Yuriko Osakabe (Institute of Science Tokyo). The common theme of the first two presentations was the development of genome edited/modified crops, exemplified on tomato, while Dr. Osakabe was talking about their current advances in development of genome editing tools. In particular, development of new CRISPR/Cas systems for large genomic deletions using their TiD-X platform looks very promising for future users. On the practical side and tomato editing, while finding proper targets for editing seems very important, marketing and getting public acceptance of genome edited crops is a major issue for their practical use. While Dr. Martin successfully developed tomato with high levels of provitamin D3, which can be converted to bioactive vitamin D3 after exposure to UV, this product has not yet been commercialized. On the other hand, the introduction of genetically modified (GMO)

anthocyanin-rich purple tomato was successfully launched in US market. As an important marketing points, Dr. Martin stressed the easy access to seeds of modified plants by home users, for instance by distributing them on internet, so allowing them freely test these products and their benefits. Nevertheless, it took time from the first publication in 2008 until the actual release of their commercial product in 2023. In fact, the easy access to seeds followed the example of Sanatech Life Science that released their GABA-rich genome edited tomatoes in Japan in 2021. In their public polls, it seems that the public acceptance of genome edited products slightly increased in the last two years following the release of GABA-rich tomatoes. As GABA, anthocyanins, and vitamin D3 have indisputable health benefits, these three examples show that development and use of biofortified foods in the future is practically feasible, and scientists should not only focus on their development but also consider the ways of practical implementation of their work, for example to counteract the negative aspects of global warming, or improve nutritional quality of food products.

5. Editors article pick

In this column, we aim to bring attention to noteworthy scientific advances, not necessarily limited to plant research. Most recently, I was intrigued by the article announcing the generation of a microorganism with artificially reduced genetic code. Whilst 64 triplet codons are typically used to encode 20 canonical amino acids in all forms of life on Earth, a common model microorganism Escherichia coli with 61 codons has previously been successfully constructed. However, the question whether organisms could tolerate even deeper codon compressions remained open. The answer comes in the July's issue of Science article that introduced Syn57 E. coli strain depending on the usage of 57-codon genetic code

(55 sense codons and 2 stop codons). Such results are of particular interest as reducing the number of codons may practically allow, for example, a construction of smart virus-resistant organisms, by limiting the ability of viral cellular parasites to use their host's translation machinery for the purpose of virus replication.
For details see article at publisher website:
https://www.science.org/doi/10.1126/science.ady4368
Robertson et al. (Science 2025) Escherichia coli with a 57-codon genetic code

6. Recently released publications

Nguyen Thao, T., Mitani-Ueno, N., Urano, R., Saitoh, Y., Wang, P., Yamaji, N., Shen, J., Shinoda, W., Ma, J.F., Suga, M.
Structural insights into a citrate transporter that mediates aluminum tolerance in barley.
Proceedings of the National Academy of Sciences of the United States of America, 122(32):e2501933122 (2025)
Doi.org/10.1073/pnas.2501933122

Sakamoto, W.
Thylakostasis: Key factors in thylakoid membrane organization with emphasis on biogenesis and remodeling proteins in vascular plants.
Plant & Cell Physiology, pcaf098 (2025)
Doi.org/10.1093/pcp/pcaf098

Ma, L., Dong, B., Sun, M., Hao, R., Wang, X., Yu, H., Han, C., Muhire, A., Gachie, S.W., Li, D., Sakamoto, W., Zhang, L.
VESICLE-INDUCING PROTEIN IN PLASTIDS 1 from thylakoid-lacking Gloeobacter promotes thylakoid formation in Arabidopsis.
Plant Physiology, kiaf359 (2025)
Doi.org/10.1093/plphys/kiaf359

Sabanadzovic, S., Abergel, C., Ayllon, M.A., Botella, L., Canuti, M., Chiba, Y., Claverie, J., Coutts, R.H.A., Daghino, S., Donaire, L., Forgia, M., Hejna, O., Jia, J., Jiang, D., Kotta-Loizou, I., Krupovic, M., Lang, A.S., Legendre, M., Marzano, S.L., Mu, F., Neri, U., Nerva, L., Penzes, J., Poimala, A., Rigou, S., Sato, Y., Shamsi, W., Sutela, S., Suzuki, N., Turina, M., Urayama, S., Vainio, E.J., Xie, J., ICTV Taxonomy Summary Consortium, NA. Erratum: Summary of taxonomy changes ratified by the International Committee on Taxonomy of Viruses (ICTV) from the Fungal and Protist Viruses Subcommittee, 2025. The Journal of General Virology, 106(8):10.1099/jgv.0.002144 (2025) Doi.org/10.1099/jgv.0.002144

7. Posting request

We continuously encourage all PSSNet members to contribute information about their latest publications, meetings and seminars, staff, postdoc, and student recruitments, etc. Please send your information to [pssnet-admin@okayama-u.ac.jp] E-mail address. You can also directly publicize your information via mailing list of the PSSNet.

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