

INBIOSIS SEMINAR SERIES 22



METABOLOMICS-BASED FUNCTIONAL GENOMICS AND SYSTEMS BIOLOGY IN PLANTS

By
PROF. DR. KAZUKI SAITO
RIKEN Plant Science Center, Japan

5 NOVEMBER 2012 (Monday)
8:30 am - 11:00 am

INBIOSIS Seminar Hall
UKM, Bangi



TENTATIVE PROGRAMME

8:30 am – 9:00 am
Registration

9:00 am – 10:30 am
Introduction & Welcome Speech
Seminar: Metabolomics-based Functional Genomics &
Systems Biology in Plants

10:30 am – 11:00 am
Conclusion, Q&A and Wrap-up



SPEAKER

**PROF. DR.
KAZUKI SAITO**

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Group Director of Metabolomic Function Research Group
RIKEN Plant Science Center
Professor of Graduate School of Pharmaceutical Sciences
Chiba University, Japan

Kazuki Saito obtained his PhD for bio-organic chemistry/biochemistry from the University of Tokyo in 1982. He has been appointed as a full professor at the Graduate School of Pharmaceutical Sciences, Chiba University, Japan, since 1995 until now. Since April, 2005, he has been additionally appointed as a group director at RIKEN Plant Science Center to direct Metabolomic Function Research Group. He also holds the post of Deputy Director of RIKEN Plant Science Center. He was awarded several prominent prizes such as The Prize for Science and Technology (Research Category) by the Minister of Education, Culture, Sports, Science and Technology, Japan, and The Award for Distinguished Research from Japanese Society for Plant Cell and Molecular Biology. He was also selected as one of ASPB TOP AUTHORS in 2010. His research interest is metabolome-based functional genomics, biochemistry, molecular biology and biotechnology of primary and secondary metabolism in plants.

ABSTRACT

METABOLOMICS-BASED FUNCTIONAL GENOMICS AND SYSTEMS BIOLOGY IN PLANTS

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Metabolomics plays a major role in systems biology, functional genomics and biotechnology in plants (1). At the hypothesis generation phase, systems biology plays an important role for prediction of gene-to-metabolite relations in a model plant *Arabidopsis thaliana*. A metabolomic database of *A. thaliana*, AtMetExpress, was developed as a systems biology tool. AtMetExpress Development was designed to be compatible with AtGenExpress to allow the efficient elucidation of metabolite-transcript networks during tissue development. AtMetExpress 20 Ecotypes is representing metabolic diversity of 20 natural variation of *A. thaliana*. Detailed analysis of co-regulation frameworks of genes and metabolites in the pathways of flavonoid and lipid revealed the functions of novel genes and metabolites. Metabolomics developed in *Arabidopsis* is further applicable to crops and medicinal plants to decipher their genes' functions and evaluate the traits of biotech crops. An excellent coverage of chemical diversity of our metabolomics platform was suitably applied to the study metabolite quantitative loci (QTL) analysis in rice. The technology was further applied to identify genes involved in the biosynthesis of specialized (secondary) metabolites, e.g., saponins and alkaloids, in medicinal plants. The crucial roles of metabolomics in plant systems biology and application to crop biotechnology will be discussed.

Reference

1. Saito, K., Matsuda, F. (2010) Metabolomics for functional genomics, systems biology, and biotechnology. *Annu. Rev. Plant Biol.* **61**: 463-489

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By Prof. Dr. Kazuki Saito (Riken Plant Science Center, Japan)

Date: 5 November 2012

Researcher Student Others : _____

Name : (Prof. / Dr. / Mr. / Ms.) _____

Institution : _____

Address : _____

Tel No. : _____

Email : _____

Attendance confirmation should be made no later than **31 October 2012 (Wed)** and sent to:

Institute of Systems Biology
Universiti Kebangsaan Malaysia
43600 UKM Bangi or
faxed to **03 8921 3398**

Registration Fee: RM 50

Method of Payment: Cash upon registration

As places are limited, early registration is recommended

Enquires

For more information please contact:

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