Goal

Plants differ in various ways from animals and have inherent capabilities that animals do not have, such as plant-hormone-mediated regulation, responses to various environmental stresses, light regulation, and high-efficient totipotency.

Our research group is studying functions of plant genes using various mutants (T-DNA/transposon insertional mutants and enhancer-tagged mutants) of Arabidopsis thaliana. This group is interested in plant genes involved in environmental stress responses and tolerance, plant hormone responses, seed development and germination. This group aims to understand complex systems that are involved in the regulation of gene expression and cellular signal transduction in response to environmental stimuli in higher plants. It also contributes to collection of useful resources for basic biology and biotechnology through these research and development.

Activities

1. Analysis of plant genes by using insertional mutant and enhance-tagged mutant
2. Development of reduction-of-function-type transgenetic plants by using RNAi and antisense technology
3. Analysis of plant genes involves in response to plant hommores, seed development and germination

Members

Chief Scientist, Director of Gene Discovery Research Group
Kazuo SHINOZAKI, Ph. D. (1989. 4 ~ )

Senior Research Scientists
Motoaki SEKI, Ph. D. (1998. 4 ~ )  Takuya ITO, Ph. D. (2000. 4 ~ )

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Takeshi KATAGIRI, Ph. D. (2001. 10 ~ )

Special Postdoctral Researches

Contract Researchers
Yoshiteru NOUTOSHI, Ph.D. (2000.4 ~ 2004.12)

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Ms. Yoko OONO (2003. 4 ~ )  Mr. Fuminori TAKAHASHI (2004.4 ~ )

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Akihiro MATSUI, Ph. D. (2005.10 ~ )

Trainees

Mr. Masaki NAKAMURA (2005.4 ~ )

Supporting staffs (from Science Service)

Ms. Kumiko OZAWA (2003.4 ~ )

Transformation of Arabidopsis with Agrobacterium tumefaciens.

Nakano Subculture of Arabidopsis T87 cultured cells.

Selection of plant materials in Arabidopsis.

Etoh, Katagiri, Saito, Takahashi, Ohnuki, Yoshida, Matsuo
Ito, Nakamura, Umezawa, Mizukado, Fujita
Kobayashi, Shodai, Shinozaki, Urano, Ozawa
Specific aim

I. Analysis of plant genes by using insertional mutants and enhancer-tagged mutants.
Using transposon-tagged or T-DNA-tagged Arabidopsis mutants with knock-out genes, we analyzed functions of various plant genes. We observed phenotypic changes of the mutants and analyzed the function of disrupted genes.

II. Development of reduction-of-function-type transgenic plants by using RNAi and antisense technology.
We tested various introns in the hairpin region of hairpin-loop RNAi constructs to improve the efficiency of gene silencing. Using RNAi (RNA interference) and antisense transgenics technology, we analyzed functions of plant genes involved in gene expression and signal transduction in Arabidopsis plant.
III. Analysis of plant genes involved in responses to plant hormone, seed development and germination.

We are interested in plant genes involved in environmental stress responses and tolerance, plant hormone responses, seed development and germination. We used these mutants and transgenic plants to analyze complex systems involved in the regulation of gene expression and cellular signal transduction in response to environmental stimuli in higher plant, we used various mutants and transgenic Arabidopsis plants.

![Arabidopsis functional genomics](image)

Figure 3. In systematic analysis of Arabidopsis genome functions, it is important to collect both full-length cDNAs and tagged mutants. We have collected 18,000 full-length cDNAs from Arabidopsis, 70,000 T-DNA tagging mutant lines and Ds tagging lines and deposited to RIKEN Bioresource Center for the distribution of the resources for plant scientists.

**Publications**

Original Papers (*Peer reviewed Journal)

1. Abe H., Urao T., Ito T., Seki M., Shinozaki K. and Yamaguchi-Shinozaki K.: Arabidopsis AtMYC2 (bHLH) and AtMYB2 (MYB) function as transcriptional activators in abscisic acid signaling. Plant Cell, 15, 63-78 (2003). *


Reviews


Oral Presentations


33. Toyoda T., Konagaya A., Matsui M. and Shinozaki K: Bioinformatics for genome phenome analyses plants, URGV-RIKEN Genome Sciences Center meeting, May 7-8, Evry France (2004).


38. Hirayama T., Nishimura N., Yoshida T., Murayama M., Hayashi S., Kuromori T., Asami T. and


47. Shinozaki K. and Yamaguchi-Shinozaki K.: Global analysis of gene networks involved in abiotic


Improve Plant Production under Drought Stress, Sep 24-28, Rome, Italy.


