

Shinozaki Research Collaborative Group

Plant Science Center, Gene Discovery Research Group

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Chief Scientist, Director of Gene Discovery Research Group

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 transgenic plants by using RNAi and antisense technology
3. Analysis of plant genes involves in response to plant hormones, seed development and germination

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Transformation of Arabidopsis with
Agrobacterium tumefaciens.



Selection of plant materials in Arabidopsis.



Nakano Subculture of Arabidopsis T87 cultured cells.

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.

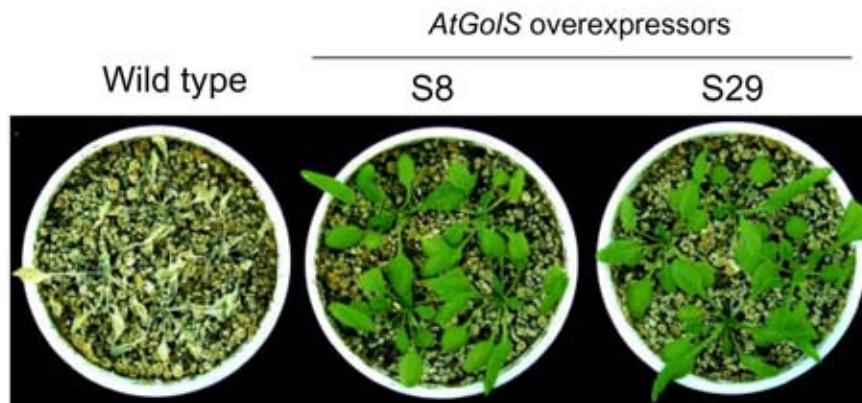


Figure 1. Drought tolerance of transgenic Arabidopsis plants that overexpress galactinol synthase (AtGolS).

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.

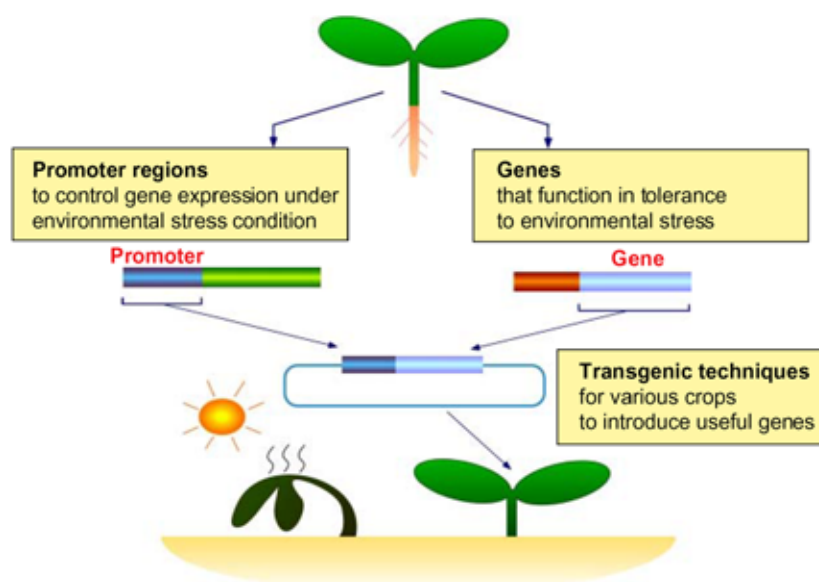


Figure 2. Strategies to develop transgenic tolerance to environmental stress in plants. Combination of genes involved in stress response is important for molecular breeding of drought, salinity and cold stress tolerance.

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.

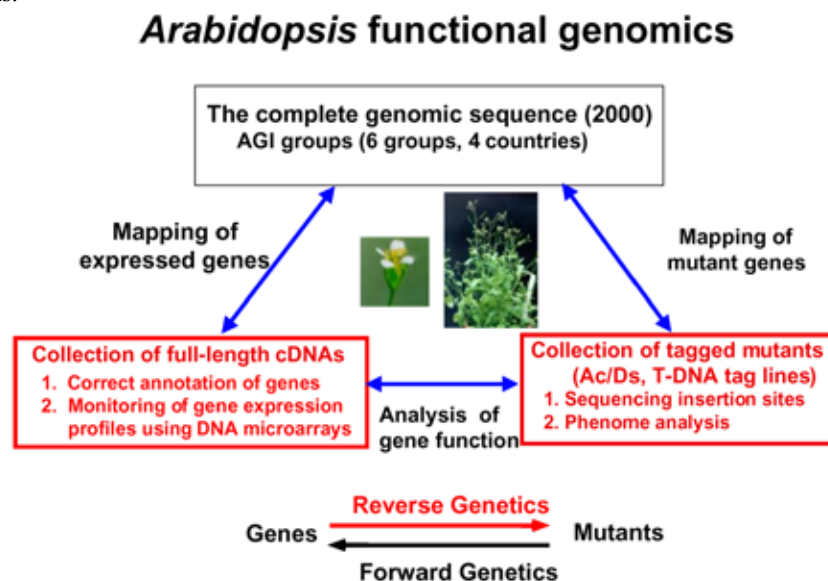


Figure 3. In systematic analysis of Arabidopsis genome functions, it is important to collect both full-length cDNAs and tagged mutants. We have collected 18,000 full-length cDNAs from Arabidopsis, 70,000 T-DNA tagging mutant lines and Ds tagging lines and deposited to RIKEN Bioresource Center for the 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). *
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6. Urano K., Yoshida Y., Nanjo T., Igarashi Y., Seki M., Sekiguchi F., Yamaguchi-Shinozaki K. and Shinozaki K.: Characterization of Arabidopsis genes involved in biosynthesis of polyamines in abiotic stress responses and developmental stages, *Plant Cell Environ.*, 26, 1917-1926 (2003).*
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8. Urano K., Yoshida Y., Nanjo T., Ito T., Yamaguchi-Shinozaki K. and Shinozaki K.: Arabidopsis stress-inducible gene for arginine decarboxylase AtADC2 is required for accumulation of putrescine in salt tolerance, *Biochem. Biophys. Res. Commun.*, 313, 369-375 (2004)*
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11. Fujita M., Fujita Y., Maruyama K., Seki M., Hiratsu K., Ohme-Takagi M., Tran L-S. P., Yamaguchi-Shinozaki K. and Shinozaki K.: A dehydration-induced NAC protein, RD26 is involved in ABA-dependent stress signaling pathway, *Plant J.* 39, 863-876 (2004).*
12. Taji T., Seki M., Satou M., Sakurai T., Kobayashi M., Ishiyama K., Narusaka Y., Narusaka M., Zhu J-K. and Shinozaki K.: Comparative genomics in salt tolerance between Arabidopsis thaliana and Arabidopsis-related halophyte, *Thellungiella halophila* using Arabidopsis microarray, *Plant Physiol.*, 135, 1697-1709 (2004) .*
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Reviews

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6. Seki M., Satou M., Sakurai T., Akiyama K., Iida K., Ishida J., Nakajima M., Enju A., Narusaka M., Fujita M., Oono Y., Kamei A., Yamaguchi-Shinozaki K. and Shinozaki K.: RIKEN Arabidopsis full-length (RAFL) cDNA and its applications for expression profiling under abiotic stress conditions, *J. Exp.Bot.*, 55, 213-223 (2004).
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Oral

Presentations

Conference (International)

1. Shinozaki K.: Global analysis of gene expression in response to cold, drought and high salinity: crosstalk in stress signaling, 2003 Gordon Conference on Temperature Stress in Plants, Ventura USA, Jan. 26-31 (2003).
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7. Motohashi R., Myouga F., Yamazaki T., Ito T., Kuromori T., Hirayama T., Seki M., Kobayashi M., Shinozaki K.: Large-scale analysis of albino and pale green mutants using *Ac/Ds* transposon system in Arabidopsis, 14th International Conference on Arabidopsis Research, Madison USA, June 20-24 (2003).
8. Shinozaki K., Yamaguchi-Shinozaki K., Seki M., Urao T., Yoshida R., Maruyama K., Imura Y., Umezawa T.: Molecular responses to drought, high salinity and cold stress: difference and crosstalk in stress signaling, The 17th International Congress on Plant Molecular Biology, Barcelona, Jun. 23-28 (2003).
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10. Shinozaki K.: Gene expression and signal transduction in osmotic stress response, National Societies (NS) and FEPS Sponsored Meetings, Nice France, Jun. 28-Jul. 3 (2003).
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22. Shinozaki K., Yamaguchi-Shinozaki K., Seki M., Osakabe Y., Yoshida R., Maruyama K., Imura Y., Taji T., Umezawa T., Oono Y. and Satoh R.: Gene networks involved in dehydration and cold stress responses, Keystone Symposia on Plant Response to Abiotic Stress, Feb 19-24, Santa Fe, USA (2004).
23. Noutoshi Y., Ito T. and Shinozaki K.: Forward and reverse genetic approaches for the analysis of ABA signaling network by using Arabidopsis Ds transposon insertion mutants, Keystone Symposia on Plant Response to Abiotic Stress, Feb 19-24, Santa Fe, USA (2004).
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27. Umezawa T., Yoshida R. and Shinozaki K.: Functional analysis of osmotic stress-activated SnRK2 protein kinases in Arabidopsis, Keystone Symposia on Plant Response to Abiotic Stress, Feb 19-24, Santa Fe, USA (2004).
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29. Shinozaki K., Seki M., Kuromori T., Motohashi R., Ichikawa T., Matsui M., Maruyama K. and Yamaguchi-Shinozaki K.: Arabidopsis functional genomics to understand gene functions

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