Japan

http://www.arabidopsis.org/portals/masc/countries/Japan.jsp
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In Japan, ongoing programs for *Arabidopsis* functional genomics are mainly found at RIKEN (www.riken.go.jp/engn/index.html) and Kazusa DNA Research Institute (www.kazusa.or.jp/eng/index.html). Other programs are supported by the CREST program of the Japan Science & Technology Corporation, the Program of Promotion of Basic Research Activities for Innovative Biosciences (BRAIN), the NEDO project, and Grants-in-Aid for Science from the Ministry of Education, Science, Culture and Sports (MEXT).

RIKEN

- RIKEN groups involved in *Arabidopsis* functional genomics include the Plant Functional Genomics Research Group (PFGRG), the Plant Science Center (PSC) and the BioResource Center (BRC). In 2005, the PSC (Director: Kazuo Shinozaki) started a new project entitled "Understanding metabolic systems for plant productivity" to integrate metabolomics with transcriptomics. The Metabolomics Research Group (Group Director: Kazuki Saito) was established at the PSC (http://prime.psc.riken.jp/) in 2005, while the PFGRG (Group Director Minami Matsui) joined PSC in April 2006.
- PFGRG in the RIKEN PSC (http://pfgweb.gsc.riken.go.jp/index.html) PIs are Kazuo Shinozaki, Minami Matsui and Motoaki Seki; projects include: (1) A collection of full-length cDNAs, (2) A collection and phenotype analysis of *Ds*-tagged lines, Activation tagging lines, and *Arabidopsis* and rice Full-length-cDNA-overexpressing (FOX) *Arabidopsis* transgenic lines, (3) Transcriptome analysis of genes expression in response to both abiotic and biotic stress using tiling array, (4) Homozygous *Ds*-insertional lines in gene-coding regions, (5) Reverse proteomics for functional analysis of *in vitro* expressed proteins using the wheat germ cell-free protein synthesis system in collaboration with a group at Ehime University (Yaeta Endo, Principal Investigator & Motoaki Seki).
- Since 2004, PSC has contributed to AtGenExpress (Yukihisa Shimada and Shigeo Yoshida) (www.arabidopsis.org/info/expression/ATGenExpress.jsp). PSC is now collecting large-scale transcriptome and metabolome data (Yukihisa Shimada and Kazuki Saito) to develop the integrated database.
- The RIKEN BRC is supported by the National BioResource Project and distributes plant materials developed in Japan. More than 23,000 plant materials including RAFL clones, *Ds*-tagged lines and Activation (T-DNA)-tagged lines (see below for more information) have been provided to approximately 920 laboratories located in 36 countries. Homozygous seeds of Ds-tagged mutants are under preparation, and some of them are publicly available now. Masatomo Kobayashi (kobayasi@rtc.riken.jp) is in charge of distributing *Arabidopsis* resources at the BRC (www.brc.riken.jp/lab/epd/Eng/).
- The PFGRG and Genome Exploration Research Group of the RIKEN Genome Sciences Center and the Experimental Plant Division of the BRC produced the *Arabidopsis* DNABookTM containing 1,069 RIKEN *Arabidopsis* Full-Length (RAFL) cDNAs for transcription factors (http://pfgweb.gsc.riken.jp/DNA-Book/).

Kazusa DNA Research Institute

- At the Kazusa DNA Research Institute (Satoshi Tabata) ongoing projects include a collection of T-DNA tagged lines and *Arabidopsis* and *Lotus japonicas* ESTs. A major project is the genomic sequencing of *Lotus japonicas* and tomato.
- *Arabidopsis* T87 cultured cells have been transformed with RAFL cDNAs and other cDNAs for metabolic profiling of primary and secondary metabolites (Daisuke Shibata).
- New websites include KaPPA-View: Integration of transcriptome and metabolome data in plant metabolic pathways (Dr. Toshiaki Tokimatsu), and KATANA, Kazusa Annotation Abstract: Integration of major database sites of *Arabidopsis* genome annotation (Dr. Kentaro Yano).

Other Arabidopsis functional genomics activities

Several groups at other centers and universities are also involved in *Arabidopsis* functional genomics.

- Gene Regulation Reseach Group of Research Institute of Genome-based Biofactory in AIST (http://unit.aist.go.jp/rigb/gf-gre/index.html)is systematically analyzing function of transcription factors using dominant repressors (CRES-T system) (Masaru Ohme-Takagi, National Institute of Advanced Industrial Science & Technology in Tsukuba).
- Genome-wide analysis of the two-component system is performed in Nagoya University (Takeshi Mizuno).
- A database on metabolites, KNApSacK, is available from NAIST (Shigehiko Kanaya).

***Arabidopsis* genomics tools and resources**

- Plant Functional Genomics Research Group in The RIKEN PSC (PIs of the PFGRG are Minami Matsui, Kazuo Shinozaki and Motoaki Seki) (http://pfgweb.gsc.riken.go.jp/index.html)
    1. A collection of full-length cDNAs (RAFL clones: Motoaki Seki) (http://rarge.gsc.riken.go.jp/)
    2. A collection and phenotype analysis of *Ds*-tagged lines (Takashi Kuromori), (http://rarge.gsc.riken.go.jp/)
    3. A collection and phenotype analysis of activation tagging lines (Minami Matsui), (http://amber.gsc.riken.jp/act/top.php)
    4. A collection and phenotype analysis of Arabidopsis full-length-cDNA-overexpressing (FOX) Arabidopsis transgenic lines (Takanari Ichikawa)
    5. A collection and phenotype analysis of rice FOX Arabidopsis transgenic lines (Minami Matsui)
    6. Structural proteomics of plant regulatory proteins with novel structures in collaboration with the GSC Protein Research Group (PI: Dr. Shigeyuki Yokoyama) (http://protein.gsc.riken.go.jp/Research/index_at.html)
    7. Transcriptome analysis using tiling arrays and 454 sequencing (Motoaki Seki and Tetsuro Toyoda)
    8. Homozygous *Ds*-insertional lines in gene-coding regions (Takashi Kuromori, Fumiyoshi Myouga) (http://pfgweb.gsc.riken.go.jp/pjAcds.html)
    9. Reverse proteomics for functional analysis of *in vitro* expressed proteins using the wheat germ cell-free protein synthesis system in collaboration with a group at Ehime University (Yaeta Endo, Principal Investigator & Motoaki Seki) (www.ehime-u.ac.jp/English/faculties/cell.html)
    10. A collection of large-scale-transcriptome data using the Affymetrix GeneChip as part of the AtGenExpress project. The data, consisting mainly of phytohormone responses, has been provided from the AtGenExpress JAPAN web site (http://pfg.psc.riken.jp/AtGenExpress/index.html) as well as from TAIR (http://www.arabidopsis.org/info/expression/ATGenExpress.jsp).
    11. Based on the data of AtGenExpress, correlations in gene expression patterns were analyzed in a genome-wide scale. A web-based system to show co-expressed genes has been provided as “Cluster Cutting” (http://prime.psc.riken.jp/?action=agetree_index).

- RIKEN Plant Science Center (www.psc.riken.go.jp/indexE.html)
- RIKEN Genome Sciences Center (www.gsc.riken.jp/indexE.html)
- Kazusa DNA Research Institute (www.kazusa.or.jp/eng/index.html)
- RIKEN BioResource Center (www.brc.riken.jp/lab/epd/Eng/)
- KaPPA-View (http://kpv.kazusa.or.jp/kappa-view/)
- KATANA (Kazusa Annotation Abstract: www.kazusa.or.jp/katana/)
- KNApSacK (http://kanaya.aist-nara.ac.jp/KNApSAcK/)
- PRIMe; The Metabolomics database at the PSC (http://prime.psc.riken.jp/)
- AtGenExpressJAPAN (http://pfg.psc.riken.jp/AtGenExpress/index.html)
- ATTED (http://www.atted.bio.titech.ac.jp/)

Major funding sources for Arabidopsis functional genomics

- CREST of Japan Science and Technology Corporation (www.jst.go.jp/EN/)
- Program of Promotion of Basic Research Activities for Innovative Biosciences (www.brain.go.jp/welcome-e.html)
- NEDO (www.nedo.go.jp/english/activities/1_sangyo/1/pro-sangi2e.html)
- Grants-in-Aid for Science from the Ministry of Education, Science, Culture and Sports (MEXT) (www.jsps.go.jp/english/e-grants/grants.html)