Japan

http://www.Arabidopsis.org/info/2010_projects/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 in April, 2006.
- Since 2004, PSC has contributed to AtGenExpress (Yukihisa Shimada and Shigeo Yoshida) (www.arabidopsis.org/info/expression/ATGenExpress.jsp).
- The BRC is supported by the National Bio-Resource Project and distributes plant materials developed in Japan. More than 18,000 plant materials including RAFL clones, *Ds*-tagged lines and Activation (T-DNA)-tagged lines (see below for more information) have been provided to approximately 730 laboratories located in 38 countries. Homozygous seeds of Ds-tagged mutants are under preparation, and some of them will be publicly available this year. 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.

- The Plant Gene Function Research Team of AIST (http://unit.aist.go.jp/gfrc/pgrt/) is systematically analyzing various functions of transcription factors using repressor domain (CRES-T system) (Masaru Ohme-Takagi, Agency of 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).

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)

***Arabidopsis* genomics tools and resources:**

- Plant Functional Genomics Research Group in The RIKEN PSC (PIs of the PFGRG are Minami Matsui and Kazuo Shinozaki) (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 (Miki Nakazawa), (http://amber.gsc.riken.jp/act/top.php)
    4. Full-length-cDNA-overexpressing (FOX) transgenic lines (Takanari Ichikawa)
    5. 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)
    6. Transcriptome analysis of genes expression in response to both abiotic and biotic stress using RAFL full-length cDNA microarray analysis (Motoaki Seki) (http://pfgweb.gsc.riken.go.jp/pjCdma.html)
    7. Homozygous *Ds*-insertional lines in gene-coding regions (Takashi Kuromori, Fumiyoshi Myouga) (http://pfgweb.gsc.riken.go.jp/pjAcds.html)
    8. 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)
- RIKEN Plant Science Center (www.psc.riken.go.jp/indexE.html)
- RIEKN Genome Sciences Center (www.gsc.riken.jp/indexE.html)
- Kazusa DNA Research Institute (www.kazusa.or.jp/eng/index.html)
- 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/)
- The Metabolomics database at the PSC (http://prime.psc.riken.jp/)