

# 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/eng/index.html](http://www.riken.go.jp/eng/index.html)), Kazusa DNA Research Institute ([www.kazusa.or.jp/eng/index.html](http://www.kazusa.or.jp/eng/index.html)) and **National Institute of Advanced Industrial Science and Technology (AIST)** (<http://unit.aist.go.jp/rigb/gf-gre/index.html>).

1. Metabolomics study on *Arabidopsis* is carried out in several laboratories, being RIKEN Plant Science Center (Kazuki Saito) and Kazusa DNA Research Institute (Daisuke Shibata) as the major contributors. The projects supported by Japan Science and Technology, JST, are conducted to investigate metabolic regulation of plants. Several databases for *Arabidopsis* metabolomics research are available.

- PRIME; The Metabolomics database at the PSC (<http://prime.psc.riken.jp/>)
- KNApSACK (<http://kanaya.aist-nara.ac.jp/KNApSACK/>)
- KaPPA-View (<http://kpv.kazusa.or.jp/kappa-view/>)
- MassBank (<http://www.massbank.jp/index.html?lang=en>)

2. **Integrated Database Project:** By the support of the Integrated Database Project (2006-2010) by the Ministry of Education, Culture, Sports, Science and Technology: A RIKEN and Kazusa collaborative effort to integrate with databases for *Arabidopsis* 'omics research information and comparative genome DB among plants (with *Lotus japonicus*, *Eucalyptus*, *Tomato* etc.) has been established.

3. **RIKEN** groups include the Plant Science Center (PSC), the BioResource Center (BRC) and Bioinformatics And Systems Engineering division (BASE). The RIKEN PSC (<http://pfgweb.gsc.riken.go.jp/index.html>) have been carrying out the following projects;

(1) A collection of full-length cDNAs (RAFL clones, Motoaki Seki), (2) Phenotype analysis of *Ds*-tagged lines (Takashi Kuromori), and *Arabidopsis* and rice Full-length-cDNA-overexpressing (FOX) *Arabidopsis* transgenic lines (Minami Matsui), (3) Homozygous *Ds*-insertional lines in gene-coding regions (Takashi Kuromori), (4) Collection of *Ds*- or T-DNA tagged mutants for nuclear-encoded chloroplast protein genes,

(5) Collection of *Thellungiella halophila* full-length cDNAs in collaboration with a group at Tokyo University of Agriculture (Teruaki Taji), (6) Rice FOX *Arabidopsis* Mutant Database (<http://ricefox.psc.riken.jp/>) (Minami Matsui, Tetsuya Sakurai). PSC is now collecting a large-scale data of transcriptome and metabolome (Yukihisa Shimada and Kazuki Saito), to develop the integrated database ([www.arabidopsis.org/info/expression/ATGenExpress.jsp](http://www.arabidopsis.org/info/expression/ATGenExpress.jsp)).

The RIKEN BRC is supported by the National Bioresource Project and distributes plant materials developed in Japan. More than 27,000 plant materials including RAFL clones, *Ds*-tagged lines and Activation (T-DNA)-tagged lines have been provided to approximately 1,080 laboratories located in 36 countries. Homozygous seeds of *Ds*-tagged mutants are prepared and publicly available for approximately 1,800 lines now. Masatomo Kobayashi ([kobayasi@rtc.riken.jp](mailto:kobayasi@rtc.riken.jp)) is in charge of distributing *Arabidopsis* resources at the BRC ([www.brc.riken.jp/lab/epd/Eng/](http://www.brc.riken.jp/lab/epd/Eng/)).

RIKEN Bioinformatics And Systems Engineering division (BASE) (PI: Tetsuro Toyoda) (<http://www.base.riken.jp/>)

(1) Bioinformatics tools and data mining (2) *Arabidopsis* transcriptome informatics (CAGE, tiling-array) (3) Informatics platform towards genome design and metabolic engineering in *Arabidopsis* (4) Japan's national integrated database project covering *Arabidopsis* 'omics information resources PosMed (Positional Medline) for *Arabidopsis* genes is an intelligent search engine integrating genome information and literature (<http://omicspace.riken.jp/PosMed/search?objectSet=gene&species=At>)

#### 4. Kazusa DNA Research Institute

- (1) *Arabidopsis* T87 cultured cells have been transformed with RAFL cDNAs and other cDNAs for metabolic profiling of primary and secondary metabolites (Daisuke Shibata).
- (2) An open genome annotation system "Kazusa Annotation" (<http://a.kazusa.or.jp/>) is being constructed, with the aim of improving genome annotation for plants and plant-related microorganisms.

#### 5. National Institute of Advanced Industrial Science and Technology (AIST)

The Gene Regulation Research Group in AIST (Masaru Ohme-Takagi; <http://unit.aist.go.jp/rigb/gf-gre/>)

index.html) developed a novel gene silencing system using dominant repressors (CRES-T system) and is systematically analyzing function of transcription factors in *Arabidopsis* and identifying factors that would be useful for improvement of plant traits by preparing a chimeric repressor transgenic plants library.

## 6. Other *Arabidopsis* functional genomics activities

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

- A database on metabolites, KNApSack, is available from NAIST (Shigehiko Kanaya).
- A database on plant promoters, ppdb (<http://ppdb.gene.nagoya-u.ac.jp>) is available from Nagoya University (Yoshiharu Y Yamamoto and Junichi Obokata)

In 2007, a new 6-year research program on plant molecular, cellular, and developmental biology supported by a Grant-in-Aid for Scientific Research on Priority Areas from MEXT (program leader: Yasunori Machida, Nagoya University) was started. The program consists of about 40 projects including 14 core projects (13 of which are mainly on *Arabidopsis*) from 10 research institutes. It focuses on such topics as mechanism of meristem formation and organ formation, cell proliferation and differentiation during organogenesis, regulation of meristem function by local and long-distance signaling, genetic and epigenetic regulation, and search for novel signals and their receptors.

*Arabidopsis* genomics tools and resources being developed, where they are deposited, and how the community can access them:

- RIKEN Plant Science Center ([www.psc.riken.go.jp/indexE.html](http://www.psc.riken.go.jp/indexE.html))
- Kazusa DNA Research Institute ([www.kazusa.or.jp/eng/index.html](http://www.kazusa.or.jp/eng/index.html))
- RIKEN BioResource Center ([www.brc.riken.jp/lab/epd/Eng/](http://www.brc.riken.jp/lab/epd/Eng/))

- RIKEN Bioinformatics And Systems Engineering division (BASE) (<http://www.base.riken.jp/>)
- KaPPA-View (<http://kpv.kazusa.or.jp/kappa-view/>)
- KazusaAnnotation ( <http://a.kazusa.or.jp/> )
- 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/>),
- RIKEN *Arabidopsis* Genome Encyclopedia RARGE (<http://rarge.psc.riken.jp/>)
- Phenome analysis of Ds transposon tagging line (<http://rarge.gsc.riken.jp/phenome/>)

## Major funding sources for *Arabidopsis* functional genomics:

- CREST of Japan Science and Technology Corporation ([www.jst.go.jp/EN/](http://www.jst.go.jp/EN/))
- Program of Promotion of Basic Research Activities for Innovative Biosciences ([www.brain.go.jp/welcome-e.html](http://www.brain.go.jp/welcome-e.html))
- NEDO ([www.nedo.go.jp/english/activities/1\\_sangyo/1\\_pro-sangi2e.html](http://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](http://www.jsps.go.jp/english/e-grants/grants.html))