F.S.T project- biological resources for Arabidopsis

Project coordinator: Sandrine Balzergue

Groups involved:
1. BioInformatic groups led by Alain Lecharny
2. GAP Laboratory / G.Pelletier (INRA-Versailles)
3. Collaborations with RhoBio (Evry) and LE GENOSCOPE (Evry)

Objectives and assessment of the project
The objective of this project was to develop a biological and bioinformatic resource making it possible to obtain data of genomic sequences which flank the ADN-T of the mutants affected in genes of selected sequences and thus to facilitate their identifications. These genomic labels are also named FST for "Flanking Sequence Tag". This project based on a first biological resource: a collection of mutants of T-DNA insertion of Arabidopsis thaliana generated by the INRA-GAP of Versailles, composed of 55 000 primary transforming plants and managed by a data base: AGROBACT+

A protocol of FST production (for Flanking Tag Sequence), based on "gene-walking" (Devic et al.. 1997), was optimized for a large scale of an amplification and a systematic sequencing (Balzergue S, Dubreucq B et al.. 2001).

All these genomic data are managed in the data base FLAGdb/FST
(now FLAGdb++)
developed by the Bioinformatique team of INRA-URGV
(Samson F et al.. Nucleic AcidsRes. 2002 Jan).

Produced sequences F.S.T, as well as the lines ADN-T which their correspond, are accessible for the international scientific community via the Web site http://urgv.evry.inra.fr/FLAGdb.

To date, 41313 F.S.T were generated and put in public access. A deposit of approximately 30 000 FST in the EMBL web site was also carried out. Moreover, 2025 lines ADN-T were distributed within French laboratories (19 articles published) and 2716 distributed to international laboratories (3 articles published). A statistical study on 9000 F.S.T also could inform us on the mechanism of integration of the ADN-T in the genome of A. thaliana.
The requests for T-DNA lines corresponding to your favorite FST possible and are described in the pages "Ask for line" of the Web sites above. For more information: Poster_FST

The people of the production line team of the FST to the INRA-URGV were as follows:

From top to bottom and left to right:

S. Durand, A. Avon, A. Freydier, S. Chauvin, M. Boutillon, M. Daty et V. Sourice. (and also: F. Catonnet, S. Pateyron, F. Le-Boulaire, P. Libeau, S. Villatoux, D. Capitolin ..
References

T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites.
EMBO Reports. 2002 Dec. 3(12):1152-1157.
PMID:12446565

FLAGdb/FST: a database of mapped flanking insertion sites (FSTs) of Arabidopsis thaliana T-DNA transformants.
PMID: 11752264

Improved PCR-walking for large-scale isolation of plant T-DNA borders.
PMID: 11252785