

PublisherInfo		
PublisherName	:	BioMed Central
PublisherLocation	:	London
PublisherImprintName	:	BioMed Central

Arabidopsis insertional mutant database

ArticleInfo		
ArticleID	:	4823
ArticleDOI	:	10.1186/gb-spotlight-20030801-02
ArticleCitationID	:	spotlight-20030801-02
ArticleSequenceNumber	:	175
ArticleCategory	:	Research news
ArticleFirstPage	:	1
ArticleLastPage	:	2
ArticleHistory	:	RegistrationDate : 2003-8-1 OnlineDate : 2003-8-1
ArticleCopyright	:	BioMed Central Ltd2003
ArticleGrants	:	
ArticleContext	:	130594411

To date, the only report of a [genome-wide collection of disruption mutants](#) is for the unicellular budding yeast *Saccharomyces cerevisiae*. Such a collection of mutants enables the functional analysis of the full gene complement of an organism, but the creation of a similar collection for eukaryotes has been hampered by the efficiency of homologous recombination. In the August 1 [Science](#), José M. Alonso and colleagues at [The Salk Institute of Biological Studies](#) report the generation of a genome-wide, sequence-indexed *Arabidopsis thaliana* insertion mutant collection. Using their mutant database, the authors identified a new family of proteins involved in the ethylene pathway (*Science* 2003, **301**:653-657).

Alonso *et al.* used selected *Agrobacterium* [transferred DNA](#) (T-DNA) to generate about 150,000 transformed *A. thaliana* plants. The genomic location of each integration event was mapped - identifying 88,122 T-DNA/genome junction sequences, and confirming the generation of mutation in 21,799 of the 29,454 annotated genes. The preferences and frequencies of T-DNA integration on an individual chromosome level, within specific genetic elements (e.g., UTRs), and on a gene expression basis were all investigated.

The authors then screened their collection for genes responsive to treatment with ethylene - a plant hormone involved in disease resistance and fruit ripening. Using this approach, they were able to isolate mutant plants for a new family of ethylene response DNA binding factors.

"One of the most significant findings revealed through analysis of genomes of multicellular organisms is the large number of genes for which no function is known or can be predicted. An essential tool for the functional analysis of these completely sequenced genomes is the ability to create loss-of-function mutations for all of the genes," conclude the authors.

References

1. Large-scale analysis of the yeast genome by transposon tagging and gene disruption
2. *Science*, [<http://www.sciencemag.org>]
3. The Salk Institute of Biological Studies, [<http://www.salk.edu>]
4. Melcher U: T-DNA Transformation in *Molecular Genetics*, 1998-2000, p. 4373., [<http://opbs.okstate.edu/~melcher/MG/MGW4/MG4373.html>]