CATdb: a public access to Arabidopsis transcriptome data from the URGV-CATMA platform

Séverine Gagnot1, Jean-Philippe Tamby2, Marie-Laure Martin-Magniette1,3, Frédérique Bitton1, Ludivine Taconnat1, Sandrine Balzergue1, Sébastien Aubourg1, Jean-Pierre Renou1, Alain Lecharny1,4 and Véronique Brunaud1,*

1Unité de Recherche en Génomique Végétale (URGV) - UMR INRA 1165-CNRS 8114-UEVE, 2 Rue Gaston Crémieux, 91057 Evry Cedex, 2Laboratoire de Biologie Cellulaire - Institut J.P. Bourgin - INRA Centre de Versailles-Gif, Route de Saint Cyr (RD 10), 78026 Versailles Cedex, France, 3Unité de Mathématiques et Informatique Appliquées (MIA) - UMR 518 AgroParisTech-INRA, 16 Rue Claude Bernard, 75231 Paris Cedex and 4Université Paris-Sud, Institut de Biotechnologie des Plantes (IBP) - UMR CNRS UPS Bâtiment 630, 91405 Orsay Cedex, France

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ABSTRACT

CATdb is a free resource available at http://urgv.evry.inra.fr/CATdb that provides public access to a large collection of transcriptome data for Arabidopsis thaliana produced by a single Complete Arabidopsis Transcriptome Micro Array (CATMA) platform. CATMA probes consist of gene-specific sequence tags (GSTs) of 150–500 bp. The v2 version of CATMA contains 24,576 GST probes representing most of the predicted A. thaliana genes, and 615 probes tiling the chloroplastic and mitochondrial genomes. Data in CATdb are entirely processed with the same standardized protocol, from microarray printing to data analyses. CATdb contains the results of 53 projects including 1724 hybridized samples distributed between 13 different organs, 49 different developmental conditions, 45 mutants and 63 environmental conditions. All the data contained in CATdb can be downloaded from the web site and subsets of data can be sorted out and displayed either by keywords, by experiments, genes or lists of genes up to 100. CATdb gives an easy access to the complete description of experiments with a picture of the experiment design.

INTRODUCTION

Transcriptome characterization by microarray technologies is a powerful tool for functional analysis of genes. The primary purpose of most of the experiments was finding candidate genes for further experimental work. Nevertheless, with the accumulation of data, a complementary usage of the transcriptome resource is the integration of large sets of data to infer, for instance, gene regulatory networks. Several databases dedicated to microarray data exist and can be distributed in three general classes (i) public repositories including ArrayExpress, Gene Expression Omnibus (GEO) and The Center for Information Biology Gene Expression Database (CIBEX) (1–3); (ii) general databases oriented toward tools for the analyses and displaying of different types of arrays, like Genevestigator or the Stanford Microarray Database (SMD) (4,5) and (iii) specific databases dedicated to a species like The Arabidopsis Information Resource, or the expression browser (eFP) from the Bio-Array Resource for Arabidopsis Functional Genomics, or specific to a life kingdom like the Plant Expression Database (PLEXdb) (6–8). Despite considerable and valuable efforts done to define and apply the Minimal Information About Microarray Experiment (MIAME) (9) recommendations, a recent survey of the data in public repositories indicated that data submission and quality are troublesome for integrating current microarray data (10). The diversity of transcriptome data and methods to analyse them is one of the problems for the occasional users. We have developed CATdb to manage the microarray data resource generated by the URGV transcriptome platform (http://www.versailles.inra.fr/urgv) and allow an easy access to the data by the community of biologists. We took advantage of the unique origin of the URGV-CATMA data to concentrate our effort on the quality of the data and to systematically collect a global view of each project with the details of the experiment design. Thus, CATdb provides an easy

*To whom correspondence should be addressed. Tel: +33 1 60 87 45 14; Fax: +33 1 60 87 45 49; Email: brunaud@evry.inra.fr

The authors wish it to be known that, in their opinion, the first two authors should be regarded as joint First Authors.

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access to a large and growing set of microarrays named CATMA (Complete Arabidopsis Transcriptome Micro Array) (11). All the RNA samples are sent by collaborators at the URGV then checked for quality control, labelled and hybridized following normalized protocols. The scanning is performed with common settings and a unique normalization followed by a statistical analysis procedure is applied to each experiment as described subsequently.

**CATMA MICROARRAYS**

CATMA is a generic *Arabidopsis thaliana* microarray developed by a European consortium (12). The design of the probes for CATMA microarrays is different from the design of both the *A. thaliana* Agilent arrays (Palo Alto, CA, USA) and the ATH1 Affymetrix GeneChips (Santa Clara, CA, USA) (13) that use respectively oligonucleotide probes of 60 mers and sets of oligo-nucleotides of 25 mers. CATMA probes consist of gene-specific sequence tags (GSTs) of 150–500 bp that have been designed with SPADS (Specific Primers & Amplicons Design Software) (14). Tagged genes come from both the EuGene software prediction (15) and the annotation from The Institute for Genomic Research (TIGR).

The v2 version of CATMA contains 24,576 GST probes representing ~85% of the predicted genes, 615 probes tiling the chloroplastic and mitochondrial genomes (v2.1) and 44 probes of non-protein coding genes (v2.2). A thorough benchmark study established the CATMA array as a mature alternative to the Affymetrix and Agilent platforms (16). The CATMA GSTs are also the basic materials in the AGRIKOLA (Arabidopsis Genomic RNAi Knock-out Line Analysis) European project focusing on the large-scale systematic RNAi silencing of *Arabidopsis* genes (http://www.agrikola.org/).

**DATABASE CHARACTERISTICS AND CONTENTS**

Primarily, CATdb was based on the schema and objects used in the ArrayExpress database (17). Then, the ArrayExpress schema has been adapted to our platform to include some new features. The main differences are: (i) the systematic addition of a figure describing the design of an experiment in standardized format, (ii) the possibility to manage a supplementary step with the pooling of samples or extracts and (iii) the storage of the statistical analyses using technical replicates (see the Data Analysis section).

The complete description of the experiments is submitted via a private web interface that helps to respect the MIAME instructions. CATdb generates the SOFT (Simple Omnibus Format in Text) format developed by the GEO repository (Gene Expression Omnibus, http://www.ncbi.nlm.nih.gov/geo/). Data from the 1724 hybridizations in CATdb are also available either at GEO or at ArrayExpress. In the description of each project or experiment, there is the corresponding access number in GEO or ArrayExpress with a link to their respective web pages.

All the data submissions and analyses are performed in our laboratory, so the development of CATdb has been oriented by the visual approaches used by biologists at URGV, like using colours to encode the data values, to facilitate the analyses and comparisons of the data.

The increasing number of research projects involving CATMA microarrays shows that the CATMA arrays are an important tool for biologists. CATdb gives a public access to all the data produced by the URGV-CATMA platform even those that have not been published after one year. CATdb contains 46 projects with 1724 hybridizations corresponding to 627 different samples. The samples of these projects concern 13 types of organs: cells (73 samples), protoplasts (10), roots (116), hypocotyls (24), stems (18), leaves (129), flowers (36), pollen (2), siliques (4), seeds (17), whole aerial plants (43), plantlets (39) or whole plants (116). These samples are distributed between 49 different developmental conditions, 31 developmental stages, 45 mutants and 63 different abiotic/biotic stresses or treatments.

**DATA ACCESS**

CATdb is a free web resource available at the following address: http://urgv.evry.inra.fr/CATdb. There are four different possibilities to select a subset of data. First, a list of all the available projects is displayed by default. A limited list may be obtained by querying the database by keywords. These keywords are searched for in both the description of the projects, i.e. coordinator name, experiment type, environmental or treatment factor, mutant name and the description of the samples, i.e. plant species, organs, treatments and type of arrays. Second, an experiment name may be selected in the project table giving access to the entire description of the corresponding experiment including a picture of the experiment design (Figure 1A). The swap column gives access to all the results of hybridizations organized by dye-swap for the selected experiment. Normalized log₂ intensities, log₂-ratios and Bonferroni P-values are given for each probe (Figure 1B). As this table is rather large, only the probes with statistically significant differential expression for a dye-swap are displayed on the screen. Nevertheless, the complete table may be downloaded as a tabulated text file. Third, from either a gene or a probe accession, one may obtain signal intensities and Bonferroni P-value for all the dye-swaps processed in all the projects (Figure 2). Furthermore, data may be sorted by project, organ or any statistics. For each probe, the associated features, i.e. sequence, quality of PCR results and if applicable, the tagged gene with functional annotation, are given. Fourth, from a list of genes or probe accessions, one obtains a table containing, for each selected probe, the log₂-ratios for all the projects (Figure 3). The coloured display of the differential expression allows the comparison of the data for a list of up to 100 genes.

All the public data contained in CATdb can be downloaded from an anonymous FTP (File Transfer Protocol) site (ftp://urgv.evry.inra.fr/CATdb). Users who
have subscribed to the CATdb e-mailing list receive news about updates and new tools.

DATA ANALYSIS

Statistic methods were developed under the software R (R Development Core Team, http://www.R-project.org) in collaboration with the group ‘Statistics and Genome’ at UMR AgroParisTech/INRA MIA 518 and are available in the R package ‘Anapuce’ on their web site (http://www.inapg.fr/ens_rech/maths/outil_A.html). For each CATMA array, the raw data include the logarithm of median feature pixel intensity at wavelengths 635 nm (red) and 532 nm (green), no background is subtracted. A normalization per array is performed to remove systematic biases. First, spots that are considered badly formed features are excluded. Then, a global intensity-dependent normalization is performed using the lowess procedures (18) to correct the dye bias. Finally, for each block, the log-ratio median calculated over the values for the entire block is subtracted from each individual log-ratio value to correct effects on each block, as well as print-tip, washing and/or drying effects. At the end of the normalization step, a normalized log-ratio, which is equivalent to an expression difference (in log base 2) between the two samples co-hybridized on the same array,
is given for each spot. It is equal to the raw log-ratio minus
the lower correction minus the block correction. A nor-
malized logarithm intensity for each sample is also
calculated. It is done according to the within-array
correction proposed by Yang and Thorne (19), which is
a redistribution of the correction calculated for the log2-
ratio normalization on each channel.

To determine differentially expressed genes from a
dye-swap, a paired t-test is performed on the log 2-ratios.
Since the number of observations per spot equals two, it
is inadequate for calculating a specific variance. For this
reason, it is assumed that the variance of the log 2-ratios
is the same for all spots. This solution has the main
advantage to calculate an estimator over a large number
of data, leading to a robust estimation of the variance
and to a gain in the power of the test. Nevertheless,
this solution should be applied with some precautions
since some spots display an extreme specific variance
(too small or too large) and prevent that the assumption
of common variance is verified. Indeed spots with a too
small specific variance decrease wrongly the estimate of
the common variance and hence it could lead to increase
the number of false positives, and spot with a too large
variance increase wrongly the estimate of the common
variance and hence it could lead to decrease the test
power. For the above reasons, spots with extreme specific
variance are excluded from the statistical analysis.

The spots that are excluded are those with a ‘specific
variance/common variance’ ratio smaller than the ‘alpha-
quantile of a chi-squared distribution of one degree
of liberty’ or greater than the ‘1-alpha-quantile of a
chi-squared distribution of one degree of liberty’ with
alpha equal to 0.0001. This rule stems from a direct
application of Cochran’s theorem. The raw P-values
are adjusted by the Bonferroni method, which controls the
Family Wise Error Rate (FWER) (20). When the
Bonferroni P-value is lower than 0.05, the spot is declared
differentially expressed. Spots with a missing P-value are
spots with an extreme variance or genes for which one
observation only is available. That is, when for one of
the two arrays, the spot corresponding to the gene was a badly
formed feature.

DATA QUALITY

Information on the CATMA probes and the correspond-
ing genes is available in CATdb. This includes probe
sequences and their estimated specificity, amplification
efficiency, localization within genes (intron, exon) or
between genes. All these annotations are graphically
displayed in the genome database FLAGdb++ (21) and
there are direct links from probes and genes in CATdb
toward the probe loci in FLAGdb+++. To validate
transcriptome data, the biologist relies on quantitative
RT-PCR applied to a set of genes exhibiting differential
expression between two experimental situations. On the
CATMA resource, quantitative RT-PCRs were done on
more than 200 genes and CATMA results have been
confirmed in more than 90% of the validations. The
details of RT-PCR from tested genes are described in the
publications associated to the different research projects
using CATMA arrays. A list of these publications is
available on the CATdb web site.
FUTURE PLANS

Based on the number of not yet public data, 4336 hybridized samples, stored in CATDb, the number of public projects is expected to double in the coming year. Updating data depends on the submission date of a project. As in most public repositories, data cannot be maintained under the private status more than one year and any data are publicly released after this period of time or before on the authors’ request.

CATMA is an ongoing project and new array designs will be released soon including 7189 new GSTs (collaboration with CATMA members) tagging the remaining annotated genes and different paralogues belonging to a gene family. Furthermore, probes for small RNA genes were designed by URGV in collaboration with O. Voinnet and L. Navarro (IBMP Strasbourg) and will be included in a future version. CATDb developments needed by the new designs are done in parallel.

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