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A cell type transcriptional atlas database for rice



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Short Abstract: We have constructed a transcriptional atlas database for rice using cells isolated by laser microdissection to facilitate the comparison of data between differing cell types. This database backs a web application that offers a variety of views to browse the data and analyze it within the context of biological pathways.

Long Abstract:

The processes of multicellular organisms are based upon the interaction between a variety of distinct cell types. To fully understand these processes from a biological standpoint, it is necessary to be able to view data with cellular resolution, recognizing the varied contributions of different cell types.

To facilitate this type of research in rice (*Oryza sativa*), we have produced a cellular atlas, an exhaustive collection of cellular expression profiles obtained from a single source. By following a protocol that allows for normalization across cell type datasets, we have created a resource that enables comparison between cell types to a degree that would not be possible with an atlas assembled from multiple sources with differing experimental conditions and materials. Our approach has aided us in identifying cell “signatures”, patterns of expression unique to a particular cell type; patterns of common expression between cell types, such as “housekeeping genes”; as well as hierarchies and networks of cells.

In order to derive an accurate and useful transcriptional atlas, we used the following methodology: (1). Laser-capture microdissection (LM) was used to isolate cells of interest. This technique suited our purposes because it allows any cell target to be harvested from any plant that can be seen through microscopy, with no need for any cell-specific information. (2). RNA was isolated from these cells and treated with two rounds of linear amplification. The amplified RNA was then used as a probe on a spotted 2-slide 70-mer whole genome array along with a Common Reference probe labeled with an alternate dye.

(3) Because the cell type samples differed sharply in intensity from the Common Reference (due to real biological difference), we derived a custom iterative loess method to normalize gene expression data.(4). Finally, the datasets were validated using quantitative PCR and comparisons with published data regarding the cellular location of particular transcripts.

Our experimental data is stored in an Oracle 9i database, along with a wealth of data on the oligos used, rice genes and biological pathways significant to rice. In addition to housing this data, the database serves as the back end to a web application (<http://plantgenomics.biology.yale.edu/riceatlas/>) for browsing and working with the rice atlas. The web application uses J2EE technology and runs on an Apache/Tomcat 5.0 server. A variety of custom forms and widgets were created to enhance the user's ability to interact with the database. Data can be browsed by cell type, by gene or oligo, and also based upon data quality or expression level. Cellular data can also be viewed within the context of known biological pathways, an important capability when analyzing how varied cell types interact. A variety of statistical tests can also be performed upon the data, both at the level of individual genes or oligos and at the pathway level. Currently implemented are T-Test and one-way ANOVA at the gene level and Fisher's Exact Test and Global Test at the pathway level. The results of user searches and statistical analyses can be exported to a file in the CSV format for handling by data mining scripts and tools such as Excel. The web application also provides detailed information about our research including images of the cell types themselves and extensive annotation information for the oligos and genes that were used. In the near future, we will incorporate VitaPad, a Java application for visualizing biological pathways, as an applet, to enable the mapping of rice atlas data to user-configurable pathway diagrams.

We hope that the rice atlas database and its overlying web application will become useful resources not only for the study of cellular processes in *Oryza sativa*, but also to increase the understanding of how cellular types interact in all multicellular organisms.