

Researchers Create an Epic Genetic Atlas of Rice

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(PhysOrg.com) -- Yale researchers have published a cellular atlas of genetic activity in rice, documenting with unprecedented detail how and when genes are turned off and on within cells of a living organism.

The staggering amount of data collected during <u>the five-year project</u>, published online in the journal *Nature Genetics*, chronicles the molecular differences and similarities among 40 cell types essential to the life cycle of one of the world's most important crops.

"All crops will benefit from knowledge and tools derived from the rice atlas," said Timothy Nelson, professor of molecular, cellular & developmental biology and senior author of the study.

For instance, scientists hope to find networks of genes responsible for photosynthesis and those that could lead to production of food and biomass for uses such as alternate energy, he said.

The atlas is composed of cell-specific transcriptomes—huge datasets that document the relative activity of each of rice's 30,000 genes for a particular cell type. The collection of 40 transcriptomes released in this study permit the comparison of any gene's activity among each of 40 cell types, including different stages of the development of roots, shoots and embryos. Eventually, the Yale team hopes to add another 40 different cell types to the data, which are available on the web to researchers around the world.



"The atlas provides a unique resource to the research community—comprehensive data on the gene-by-gene contribution of the cell types that cooperate to make tissues, organs, and the entire body function," Nelson said. "The comprehensiveness of the atlas is a technical achievement—some important cell types were extremely difficult to sample in sufficient quantity."

Among its immediate applications, the data allow researchers to distinguish which genes are activated in key cell types at certain stages of development, providing clues to their roles in building the body. Also, scientists were able to identify genes with critical "housekeeping" functions that are essential at all times in all cell types.

"This cellular atlas is a deep resource that can be mined for cellular information on any gene or biological process," Nelson said. The Plant Genome Research Program of the National Science Foundation funded the work. Other members of the Yale team were: Yuling Jiao, S. Lori Tausta, Neeru Gandotra, Ning Sun, Tie Liu, Nicole K. Clay, Teresa Ceserani, Meiqin Chen, Ligeng Ma, Matthew Holford, Huiyong Zhang, Hongyu Zhao and Xing-Wang Deng.

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Provided by Yale University

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