

# New tool probes function of rice genes

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A new tool for investigating the rice genome has been developed by researchers at UC Davis led by Pamela Ronald, professor of plant pathology. The inexpensive, publicly-available rice DNA microarray covers nearly all the 45,000 genes in the rice genome. Details are published this week in the open-access journal *PLoS ONE*.

In higher organisms, such as humans or rice plants, each cell type express different genes at different times. Scientists have developed high-throughput methods to examine these gene expression profiles using "DNA Microarrays," thousands of fragments of DNA fixed to a glass slide. DNA microarrays can be used to figure out which genes are important for responding to a stimulus or tolerating stresses.

Ronald and her colleagues used the new rice microarray to investigate gene expression changes when plants are grown in the light versus the dark. They then combined this gene expression data with biochemical pathway data to correctly predict the function of genes whose role was previously unknown. The newly identified genes carry out light-related biochemical processes such as photosynthesis and photorespiration.

The methods and array developed in this paper will aid researchers in identifying the function of the 45,000 rice genes, only a few of which have so far been characterized, Ronald said. The group also has developed a web-based program that allows the user to compare gene expression profiles across multiple rice microarray platforms, which will further accelerate this research.

Citation: Jung K-H, Dardick C, Bartley LE, Cao P, Phetsom J, et al. (2008) Refinement of Light-Responsive Transcript Lists Using Rice Oligonucleotide Arrays: Evaluation of Gene-Redundancy. PLoS ONE 3(10): e3337. doi:10.1371/journal.pone.0003337  
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