

## UC Riverside geneticists to study how plants adapt to a changing environment

March 23 2011



Photo shows Jason Stajich (left) and Susan Wessler before a Solexa/Illumina HiSeq2000 instrument at UC Riverside that they and their colleagues will use to sequence the genomes and measure the gene expression of several rice varieties. Credit: UCR Strategic Communications.

Transposable elements (TEs) – DNA sequences that move from one location in the genome to another – are abundant in plants and animals, evolve rapidly and promote the evolution of the genome. What role they play in how plants generate the diversity needed to adapt to a changing climate is the focus of a study at the University of California, Riverside being funded by a nearly \$4.8 million five-year National Science Foundation grant.

Susan R. Wessler, the principal investigator on the grant and a distinguished professor of genetics, and Jason Stajich, a co-principal investigator and an assistant professor of plant pathology and microbiology, will focus their attention on the rice plant, which serves as



an excellent model due to its small and fully sequenced <u>genome</u> that can be easily transformed with foreign DNA.

"We will attempt to understand the impact of a rapidly amplifying TE – one that is increasing the number of its copies at a high rate – on generating diversity in rice," Wessler said. "We will analyze how *mPing*, the high copy TE, rapidly diversifies the genome of rice, a largely self-pollinating organism, and, in doing so, alters rice's ability to respond to a changing environment. By doing so, we will document for the first time the global impact of a TE burst in any organism."

Wessler explained that rice, which has one of the most stable genomes and is the most important source of calories for humans globally, is paradoxically host to the most active TE characterized in any eukaryote.

"This fortunate set of circumstances will allow us to sequence rice cultivars related to each other and also do a survey of global changes in <u>gene expression</u>, associated with responses to stresses like drought, floods and disease, across these rice cultivars," she said.

Wessler and her team will use a "transposon tagging system," a useful tool in genomics that allows researchers to track a mobile TE as it moves around the rice genome and inserts itself into or near a gene to abolish or alter the gene's expression or function.

"In the transposon tagging system, we mutagenize the plants with TEs, then identify plants with interesting traits," Wessler said. "By simply using TEs as a hook you can see where the TE is located, and chances are you will find it sitting in the gene that has led to that trait."

She explained that rice is a rare example of an organism in nature where a TE – *mPing* in rice's case – is fast increasing its copy number. This TE started moving in the last 50-100 years and could stop moving in the next



50 years or so.

"Thus far, only in rice do we see a TE increasing its copy number at an incredibly high rate," she said. "This TE is going under the radar of the genome immunity system of the plant, meaning the plant is not detecting the TE's movement. In this project we hope to understand how a TE is able to avoid a host's immunity. By studying many generations of rice plants, we may be able to find plants in which the host plant has recognized the active TE and turned its activity off."

The study has important implications in how organisms cope with so many TEs in their genome. In some cases, specific TE insertions affect traits and the plants show, for example, increased resistance to stress. The research team will examine the impact of TEs on gene expression by comparing strains of rice with high and low copy numbers and their progeny from a genetic cross. This work requires high throughput sequencing technologies and substantial computational resources to evaluate and map the effects to precise regions of the genome.

The grant to Wessler and her team also has a strong outreach component in which the researchers will generate resources for the scientific community for tracking TE movement and understanding how traits are determined by the insertion of a TE in a gene.

The team will also channel outreach activities through The Dynamic Genome Courses of Wessler at UCR in which an interdisciplinary team of scientists will integrate research output from the project into undergraduate and high school classes.

Wessler and Stajich will be joined in the research project by Thomas Brutnell from Boyce Thompson Institute, Ithaca, NY; and Qi Sun from Cornell University, NY. The team will use a Solexa/Illumina HiSeq2000 instrument in the UCR Institute for Integrative Genome Biology (IIGB)



genomics core to sequence the genomes and measure the gene expression of several <u>rice</u> varieties with variation in TE copy number, and the IIGB bioinformatics computer cluster to perform computational analyses of the sequence data.

## Provided by University of California - Riverside

Citation: UC Riverside geneticists to study how plants adapt to a changing environment (2011, March 23) retrieved 23 April 2024 from <u>https://phys.org/news/2011-03-uc-riverside-geneticists-environment.html</u>

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