

University of Arizona-led group awarded \$9.9 million to develop 'super rice'

September 3 2010



"We need to figure out a way to come up with a rice variety that can grow on less land, on poorer soil and with less water and fertilizer," said Rod Wing, a University of Arizona plant science professor. Credit: Norma Jean Gargas / UANews

A University of Arizona-led consortium has been awarded \$9.9 million from the National Science Foundation to develop a deeper understanding of the wild relatives of cultivated rice with the ultimate goal of creating next-generation varieties that are better capable of withstanding drought and poorer soils and produce higher yields than current forms of domesticated rice.

The main goals are to study the genes of different wild [rice](#) species and identify genes that could be used to improve the crop.

Cereal crops - including rice - provide 60 percent of the calories and protein harvested worldwide, said UA plant scientist Rod Wing, who is director of the Arizona Genomics Institute in the College of Agriculture and Life Sciences, holder of the Bud Antle Endowed Chair for Excellence professor in the School of Plant Sciences and a member of the BIO5 Institute.

"Half of the world's population depends on rice, and that population is expected to double in 30 years," he said. "We need to figure out a way to come up with a rice variety with increased yield and capable of growing on less land, on poorer soil, with less water, and with less fertilizer."

Part of RICE 2020, an international coordinated effort in rice functional genomics, the NSF funds the undertaking of functionally characterizing the genomes of all 24 rice species, with the goal of transforming not only crop biology but evolutionary biology as well.

Using wild rice to improve rice crops

"What we're trying to do is identify and catalog all the genes found in the wild relatives of rice and analyze their functions," Wing said. "The idea is to identify genes that confer adaptations helping wild varieties cope with [extreme environments](#) and breed them into cultivated rice."

The data could be used immediately to enhance food security, Wing pointed out, by providing a "toolkit of genes" that can be used to improve crop rice.

In addition, the project has crucial implications for evolutionary biology.

"We want to really understand the evolution of the rice genus *Oryza* in great detail," Wing said. "For example, which genes are the shared ones that make a rice plant a rice plant, and which are those that account for

the differences we see between species?"

To do this, the researchers have to understand all the so-called "structural variations of the rice genome." Over the course of its 15-million year evolutionary history, genes have been gained, lost, crippled or inverted, rendering some of them non-functional while allowing others to take on new functions.

Together with collaborator Manyuan Long, a professor of genetics and evolution at the University of Chicago, Wing's team also will try to answer the question, where did new genes come from?

The highly collaborative project builds on previous accomplishments by several collaborators brought together under the International Oryza Map Alignment Project, or I-OMAP. Wing's group led an effort to determine the entire genetic sequence of the two rice species most widely used in agriculture, Asian Rice (*O. sativa*) and West African Rice (*O. glaberrima*).

Preserving wild rice populations

I-OMAP's goals include improving cereal crops as well as maintaining their diversity and ensuring their conservation in the wild.

"This line of research involves field studies," Wing said, "for example, going to the Philippines and identifying, say, a strand of the wild rice *Oryza officinalis*, so it can be set aside as a nature reserve."

Wing's group will focus on structural differences among the genomes of the 24 rice species and the role of transposable elements (pieces of DNA that, over generations, "jump" from one place in the genome to another, taking other genetic sequences with them in the process) and their impact on gene evolution.

"If we discover a gene that looks to be of interest, we can go to a population of a wild rice species and see how important it is. So we would ask, 'Is this gene present across the entire population or is it just in the specific specimen whose DNA we happened to analyze?'"

Questions like these, which are of general importance to evolutionary biology as a whole, will be addressed by Carlos Machado, a long-time collaborator of Wing's who was an assistant professor in the UA's department of ecology and evolutionary biology before joining the University of Maryland two years ago.

Another aspect of the project is being led by Michael Sanderson, a BIO5 member and professor in the department of ecology and evolutionary biology in the UA's College of Science. His research group is going to compare the genomes of domesticated rice and its wild relatives and reconstruct an evolutionary tree of the relationships of these species to each other. This will provide a framework for better understanding the evolution and function of genes in these genomes.

As a key step in this endeavor, Wing and his group are going to sequence the genome of *Oryza punctata*, which is considered one of the most primitive rice species.

"*Oryza punctata* serves as a so-called out-group species," Wing said, "A reference species to compare all the others to, so we can make evolutionary inferences about the genes we identify - is this gene evolving rapidly or slowly?"

In addition, *O. punctata* contains a number of genes that could be important to improve cultivated rice, for example genes for stress tolerance.

The domestication bottleneck

"During the domestication process, people end up selecting a couple of plants and crossing them," Wing said. "This way, one of them became the founder of all the domesticated plants. That variety was then improved over thousands of years, but it contains only a very small variety of genes that could be used for crop improvement."

Domesticated rice varieties have been selected for short stature, high yield and low shattering of the grains during harvesting.

This so-called domestication bottleneck leads to crop plants with highly desirable traits such as high yield but deficiencies in other areas such as compromised ability to fight off diseases or cope with droughts.

West African Rice, for example, is more tolerant to drought and salty soils than Asian Rice.

"The system we are developing can be utilized by evolutionary biologists around the world to address grand challenge questions in [evolutionary biology](#)," Wing said. "This would be the first of such a system in a crop plant."

The project will provide training and mentoring to postdoctoral scientists, graduate and undergraduate students and high school students with an interest in [genome](#) evolution, plant breeding and careers in academic and corporate science.

As an outreach component, the project will include a biannual Plant Science Family Night program at Ventana Vista Elementary School in Tucson, targeting K-5 students and families, with the goal of getting children and their families in the greater Tucson area excited about plants and the role plant science plays in ensuring a safe, sustainable and secure food supply for our planet.

Other collaborators in the project include Doreen Ware at Cold Spring Harbor Laboratory, Jianxin Ma at Purdue University; Detlef Weigel at the Max-Planck-Institute for Developmental Biology in Tübingen in Germany; and Olivier Panaud of the University of Perpignan in France.

Provided by University of Arizona

Citation: University of Arizona-led group awarded \$9.9 million to develop 'super rice' (2010, September 3) retrieved 19 April 2024 from <https://phys.org/news/2010-09-university-arizona-led-group-awarded-million.html>

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