

UA Contributes to International Rice Genome Sequencing

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Rod Wing inspects rice plants in the greenhouse.

The University of Arizona has collaborated with an international consortium of scientists to decode the sequence of the rice genome, furthering work in improving a crop consumed by more than half the world's population. The completion of the advanced draft sequence—high-quality blueprint—of the rice genome was announced December 18 in Tokyo, Japan, the lead country in the effort, and in Washington, D.C.

Each of the ten countries participating in the project was assigned parts of the genome to sequence. Other countries collaborating in what is known as the International Rice Genome Sequencing Project (IRGSP) include Brazil, China, France, India, South Korea, Taiwan and Thailand, and the United Kingdom.

Rod Wing, a professor in the UA Department of Plant Sciences in the College of Agriculture and Life Sciences and director of the Arizona Genomics Institute, heads the Arizona team. So far, Arizona researchers have completed the entire sequence and analysis of rice chromosome 10, and a draft sequence of the “short arm” of chromosome 3. Wing, who arrived at the UA last year from Clemson University, had worked there since 1996 on the sequencing of most of chromosome 10. The Clemson group also developed a framework to sequence the rice genome, a physical map that was used by the entire IRGSP in completing the sequence.

The United States was assigned chromosomes 3, 10 and half of chromosome 11. The U.S. rice genomics program involves three collaborative groups. The ACWW includes Clemson University in South Carolina, Cold Spring Harbor Laboratory in New York, Washington University in Missouri and the University of Arizona. The Institute for Genomic Research (TIGR) and the Plant Genome Initiative at Rutgers (PGIR) are the other partners.

The milestone project involved an unprecedented world collaboration among academic, governmental and private sector entities from the ten countries. The entire genetic draft has been released for full and unrestricted public access on GenBank, a National Institutes of Health database, allowing rice improvement, comparative cereal studies and basic plant research to proceed simultaneously worldwide.

“The nice thing about rice is that it has a very compact genome,” Wing says. “It has 12 chromosomes and is considered a model plant for research in cereals.” Rice contains certain genes arranged in the same order or direction as those found in other cereal grasses, including wheat, maize, oats, barley, and sorghum.

“By decoding the complete rice genome, we’ll understand the regulatory networks involved in disease tolerance, drought tolerance and other mechanisms that will help in the breeding of rice varieties that are higher yielding, more stress tolerant and more environmentally friendly,” Wing says.

The high-quality draft sequence just released gives researchers enough to work with developing their projects. The next step for all IRGSP members, including the University of Arizona, is to “finish” the genome within the next two to three years by characterizing, annotating and identifying the functions of the individual rice genes. U.S. funding for the project was provided by the USDA, the National Science Foundation, and the United States Department of Energy. ☐



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