



(L-R) Paul Sanchez, a graduate student from Japan; Rod Wing, the rice genome project leader; and Hye Ran Kim, leader of the Sequencing and R&D Center, Arizona Genomics Institute (AGI), examine wild rice growing in a new greenhouse on the UA campus.

Revelations of Rice

Decoding the rice genome

by Daniel Stolte

The complete genetic code of the rice plant was deciphered by researchers at The University of Arizona's plant sciences department and UA's BIO5 Institute and other members of an international consortium. The genome sequence is published in *Nature* in August 2005.

The UA research team was led by Rod Wing, who has a key role in BIO5's Genome Structure and Function Consortium. Wing's group developed the framework for and contributed significantly to the International Rice Genome Sequencing Project (IRGSP).

"Rice is the most important food crop in the world, feeding half the population," said Wing, a professor in the department of plant sciences at the UA College of Agriculture and Life Sciences. "Demand is expected to double in 50 years, so we need to learn all we can about rice. The genetic sequence is the beginning of that."

Plant scientists will use the new knowledge to improve rice varieties. For example, they can now exactly pin down genes linked to desirable properties such as crop yield, drought tolerance and pest resistance. An important goal is to place newly identified, advantageous genes into regional rice varieties that are adapted to certain regions and growth conditions.

Rice is the first crop plant whose genome has been fully mapped and sequenced. The published data represent what scientists call a finished sequence: it reveals a comprehensive picture of the DNA codes and positions of all the genes in the

rice genome. At the same time, it is one of the most accurate and complete genome sequences obtained from a higher (i.e. multicellular) organism. The finished sequence reveals that the 12 chromosomes of the rice plant hold some 37,500 genes. A chromosome is a compact bundle consisting of a long, thread-like DNA molecule wrapped tightly around special packaging proteins to allow for storage in a cell's nucleus. The rice genome contains about 7,500 more genes than the human genome.

Wing's group developed the basic framework for the sequencing project and sequenced the short arms of chromosomes 3 and 10. Wing compares the rice genome, with its 12 chromosomes, to a book with 12 chapters, written in an alien language.

"Before we could start deciphering the book, we had to take all the pages out and make about a thousand photocopies of each, to make sure we had enough genetic material for the sequencing," Wing said. He and his co-workers then put the pages in the correct order, thereby establishing a physical map of the rice genome, which formed the basis for the actual sequencing process.

The software used to build the map for the U.S. rice sequencing collaboration was developed by Carol Soderlund, a member of BIO5's Quantitative Biology Consortium. "Our computer program identified each page, decided where it belongs and assigned it a page number," Soderlund explained.

With the physical map in place, different chromosomes were assigned to the partner institutions, which then started deciphering the genetic code, letter by letter and page by page.

The next step is to make sense of what is written in the genetic code of the rice genome, a process geneticists call functional characterization.

“Now that we know where all the genes are, we try to associate them with certain traits,” Wing explained. The accurate, map-based sequence has already led to the identification of genes that confer agronomically important traits such as yield and demand of light during growth.

The new information will be used to improve existing rice varieties and develop new ones. In addition, the rice genome sequence and map will serve as a reference for other cereal crops such as corn, barley and wheat. Because cereals evolved from a common wild grass ancestor, they share much of their genetic information.

“By sequencing rice we sequenced all the other cereals to a certain extent,” Wing said. “Many of the shared genes are in similar positions on the respective chromosomes, so when we assign a function to a given gene in rice, it is very likely that the corresponding gene in another cereal has the same or a similar function.”

The partnering institutions finished the rice genome sequencing project, officially launched in 1998, well ahead of the scheduled completion date of 2008. DNA sequence was published in public databases as soon as it was obtained. The project was led by Japan and included sequencing labs in the United States, China, France, Taiwan, India, Thailand, Korea, Brazil and the United Kingdom. In the United States, The University of Arizona collaborated with Cold Spring Harbor Laboratory

The new information will be used to improve existing rice varieties and develop new ones. In addition, the rice genome sequence and map will serve as a reference for other cereal crops such as corn, barley and wheat.

in Cold Spring Harbor, New York; Washington University in St. Louis; Clemson University in Clemson, South Carolina; The Institute for Genomic Research (TIGR) in Rockville, Maryland; and Rutgers, The State University of New Jersey.

Wing, an internationally recognized plant scientist whose work involves unraveling the genetic codes of agricultural crops like corn, rice, cotton,

soybean and tomato, brought his research programs and his reputation to the department of plant sciences within UA's College of Agriculture and Life Sciences in 2002. UA's BIO5 Institute, then named Institute for Biomedical Science and Biotechnology, helped fund the move.

“I came to The University of Arizona to be part of one of the top plant science departments in the country,” Wing said. “BIO5 offers a unique opportunity for my group to collaborate in an interdisciplinary environment with leading faculty at UA to help solve important problems in agriculture and human health using state-of-the-art, cross-cutting technology.”

Carol Soderlund is an internationally recognized scientist in computational genomics. She heads the Arizona Genomics Computational Laboratory (AGCoL) and holds a research associate professorship at the BIO5 Institute and in the department of plant sciences at the College of Agriculture and Life Sciences. Soderlund's computer program had been used to build the physical map of every large genome that has been sequenced to completion, including the human genome.

Researchers in BIO5's Genome Structure and Function Consortium and Quantitative Biology Consortium integrate laboratory experiments and computational methods into large-scale efforts to understand how organisms transform their genetic information into body structures and metabolic functions. The deciphering of the rice genome is an example of basic and translational research pursued at BIO5: improving crop plants to feed a growing population and maintaining a livable environment.

The National Plant Genome Initiative coordinated the United States portion of the project. The U.S. Department of Agriculture's Cooperative State Research, Education and Extension Service, the National Science Foundation, the Department of Energy and the Rockefeller Foundation provided support for the work. ✨

CONTACT

Rod Wing
520-626-9601
rwing@ag.arizona.edu



Rod Wing inspects rice plants in the greenhouse.