

# THE INTERNATIONAL RICE GENOME SEQUENCING PROJECT: A Case Study

C. Robin Buell



Peter Beyer/University of Freiburg

Golden and regular white rice.

*What started as a Japanese research project evolved into an international research venture that delivered a key tool for advancing a second “green revolution.” By involving researchers and resources from many countries, the International Rice Genome Sequencing Project (IRGSP) in 2005 produced a “map” of rice’s genetic makeup. This map will enable breeders to accelerate their breeding programs and develop more hearty rice varieties, and farmers to improve their growing methods and extend their growing seasons. Also, scientists have been able to utilize the complete rice genome to further their studies on other cereals.*

*C. Robin Buell is an associate investigator with the Institute for Genomic Research and was a participant in the IRGSP.*

**A**n ancient Chinese proverb states that “precious things are not pearls and jade but the five grains, of which rice is the finest.” Indeed, based on daily worldwide consumption, rice is more precious than pearls: Some 50 percent of the inhabitants of the planet consume rice every day. For a large percentage of these people, rice is the major, and possibly the only, caloric source.

Being able to provide sufficient and nutrient-rich

rice is essential to meet the needs of the world’s population. While conventional plant breeding has significantly increased rice output, international collaborative efforts have resulted in a better understanding of the rice genome that promises the development of rice varieties with even greater yields and disease resistance.

## A SECOND GREEN REVOLUTION

Over the past 40 to 50 years, scientists were able to make major improvements in the yield, pest resistance, and nutritional content of rice as well as of other crops. They achieved these results through the implementation of conventional breeding involving genetic crosses between varieties of plants and selection by the breeder for the most desirable progeny. This phase of improvements in agricultural output was termed the Green Revolution, and Norman Borlaug, a key geneticist, was awarded the Nobel Peace Prize in 1970 for his achievements in enhancing agricultural production.

However, in the 21st century, the growing worldwide population, coupled with reduced acreage for agricultural production, will present serious challenges to the world’s ability to feed itself. Thus, a second “green revolution” is needed.



IRGSP participants; the author is third from the left in the front row.

One tool now in use that can advance this second green revolution is genomics, which involves understanding the genes within an organism and how they function in the growth and development of the organism. The science of genomics took a major step forward about 10 years ago when researchers at the Institute for Genomic Research in the United States were able to determine the complete sequence (a map of the genetic makeup) of a free-living microorganism, *Haemophilus influenzae*, a bacterium that causes the flu. The techniques developed at the institute are now widely used to determine the genetic makeup in all types of organisms, including animals, plants, and fungi.

### THE RICE GENOME PROJECT

In the early 1990s, Japanese scientists began research on sequencing the rice genome. In 1998, in an effort to accelerate this work and utilize international expertise, a group of scientists from several countries, led by Japanese researchers, initiated the International Rice Genome Sequencing Project. With funding from many countries—including Japan, China, Korea, Thailand, India, France, Brazil, and the United States—and from Taiwan, hundreds of scientists from around the world contributed to sequencing the rice genome. The international collaboration enabled the division of labor and distribution of costs among the participants. It also allowed participating countries to have a defined stake in the project and get recognition for completing a part of or an entire chromosome. The project was completed in December 2004, and the results were published in August 2005.

The IRGSP was able to identify in excess of 37,000 genes in the rice genome, more than the number of genes

in the human genome. Analysis of other rice genome sequences with the IRGSP sequence resulted in the identification of more than 80,000 new genetic markers—genes that produce a recognizable trait—that will enable breeders to accelerate their breeding programs and develop more hearty rice varieties.

Even before the IRGSP had completed its task, the project's investigators were making their findings publicly available to scientists around the world for use in a broad range of plant biology research. One finding was the critical gene involved in controlling flowering time in rice. Day length—the hours of daylight versus darkness that change throughout the seasons—controls when a plant such as rice flowers and consequently when it sets seed. By identifying the mechanism of flowering time, scientists can now attempt to develop rice varieties that flower earlier in the planting season, thus expanding the growing season for farmers.

### BROADER IMPLICATIONS

Although rice has a substantial role in worldwide agriculture, it has another role for scientists. It is well known that primates such as humans and chimpanzees have similar genes and genomes. The same relationship occurs with rice and its close relatives—cereals such as wheat, maize, barley, oats, sorghum, and millet. For technical and financial reasons, a complete genome sequence is available only for rice. But with the close relationship between the cereals, scientists who work on other cereals have been able to utilize the rice genome to further their studies. Indeed, researchers were able to use the rice genome sequence to identify a key barley gene involved in resistance to a fungal pathogen responsible for a disease known as powdery mildew.

The benefits of the rice genome project are clear:

- As new crop and hardier crop species are developed, and as the understanding of basic plant biology accelerates, countries will be better positioned to meet the needs of a growing population in the 21st century.
- The IRGSP's collaborative format demonstrates the scientific leaps that can be accomplished when experts from around the world have access to each other's research.
- The IRGSP has shown that state-of-the-art scientific endeavors do not have to involve only highly developed countries, and that collaborative international efforts can serve to enable less developed nations to acquire cutting-edge technologies.
- The IRGSP experience will likely yield new efforts with stronger collaborative features. This has already begun

with the International Rice Functional Genomics Consortium—a collaboration among international scientists to expand understanding of rice’s 37,000+ gene functions so as to meet increasing production needs.

### **PUBLIC-PRIVATE PARTNERSHIPS**

Clearly, completing the mission of the IRGSP was a challenge, and there were bumps in the road. The largest issue that the IRGSP had to address involved the parallel efforts to sequence the rice genome by Monsanto and Syngenta, two large, international agribusinesses, and the Beijing Genomics Institute, a research center in China. The IRGSP subsequently collaborated with Syngenta and Monsanto, establishing a highly productive public-private partnership. This partnership incorporated private sector data into the public research results.

The benefits have far outweighed any challenges. In addition to providing an invaluable resource for the world’s scientists and farmers, the successful completion of the IRGSP demonstrates that international scientific collaborations are productive and serve purposes greater than their initial goals. Certainly for other large scientific endeavors, international collaborative efforts should be considered as a viable strategy. ■

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