

A scientific milestone: mapping of rice genome

By Frank Gaglioti
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The publication of the near complete map of the rice genome in the August 11 issue of *Nature* will enhance the ability of agricultural science to produce new crop strains that not only increase productivity but expand the range of growing conditions. It will also offer insights into the evolutionary history of one of the most important cereal crops, which has played a prominent part in the historical development of mankind.

The mapping project was a major international endeavour conducted by scientists working in 32 institutes in 10 countries over eight years. The genome is the sum total of all genetic information to be found in the DNA of a species. The scientists divided the rice genome into small pieces, which were then copied for sequencing. The research was completed three years ahead of time and the data is now freely available on the Internet.

Rice is the first cereal crop and only the second plant to have its genome mapped. Takuji Sasaki, vice president of the National Institute of Agrobiological Sciences in Japan and head scientist of the International Rice Genome Sequencing Project, described the completed genome as the “gold standard”. “Now we can get the most fundamental information about the inheritance of rice plants,” he said.

The variety of rice used was the temperate subspecies *Oryza sativa japonica* mostly grown in Japan, Korea and the United States. Because growing rice requires large amounts of water and fertile soils, breeding programs could now develop new varieties and extend the range of conditions in which rice can be successfully grown. Rod Wing of the University of Arizona explained: “The accurate, map-based sequence has already led to the identification of genes that confer important traits such as yield and demand for light during growth.”

This is vital research as it is estimated that by 2025 as many as 4.6 billion people will depend on rice for their survival. Rice is the main cereal crop in Asia, currently feeding two billion people. In 2000, about 40 percent of the Earth’s population, mostly those in populous less developed countries, depended on rice as their major energy source.

Rice was chosen for sequencing because it has the smallest genome of all the cereal crops. The genomes of mammals are about the same size as each other, but those of plants vary widely. The corn genome is double that of rice while wheat is 41 times larger.

The rice genome was found to contain 37,544 genes and 389 million base pairs, the fundamental chemical unit of genetic information. Robin Buell from Institute for Genomic Research in the US explained that the results provided “the Rosetta stone for crop genomes”. Scientists will be able to use the completed rice genome as a template for their work with the other cereals, such as wheat and maize.

The actual rice genes—the portions of the base-pair sequence that produce different proteins involved in cellular functions—were identified by comparison with thale cress *Arabidopsis thaliana*, a member of the mustard family. The thale cress genome was completed in 2001 and is one-third the size of rice.

According to W. Richard McCombie, a US scientist from Cold Spring Harbor Laboratory, rice has many repetitive sequences whose role is unknown. The initial comparison with *Arabidopsis* discovered that 90 percent of its proteins are to be found in rice but that rice shared only 71 percent of its proteins with thale cress. The result suggests that rice has many distinctive genes that are probably found in other cereals.

“By sequencing rice we sequenced all the other cereals to a certain extent,” McCombie explained. “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.”

Scientists are finely tuning their sequencing of rice, completing sections more difficult to access and starting to assess the internal organisation of the genome, including how genes are turned on and off and the interaction between different products of the genes. The sequence will enable an analysis of single nucleotide polymorphisms—minute genetic variations between different rice varieties that explain

characteristics such as drought tolerance.

Although the publication of the rice genome represents an important gain for science, the enormous potential will, under capitalism, take a back seat to corporate profit. The rice genome project was partly funded by two giant transnational agricultural companies, Monsanto from the US and Syngenta AG from Switzerland.

These companies have already taken out patents on sections of the rice genome. Dr. Richard Jefferson from the Canberra based non-profit research institute CAMBIA told the Australian Broadcasting Corporation (ABC) last month, “Both Monsanto and Syngenta and many others have filed very, very substantial numbers of patents.” As a result, researchers have to negotiate with the transnationals in order to work with important sections of the genome.

There are also legitimate concerns that corporations like Monsanto and Syngenta are pushing for the use of genetically modified crops without adequate research into their impact on consumers or the environment—particularly in the long-term.

In May, the British-based *Independent* newspaper published secret research carried out by Monsanto which showed that rats fed on genetically modified corn “MON 863” developed abnormalities in their internal organs and blood. Dr Vyvyan Howard, a senior lecturer at Liverpool University, called for the release of the study, saying it gave “prima facie cause for concern”. Monsanto dismissed the results as “meaningless and due to chance” but has not made the full study public.

Monsanto and Syngenta have both produced genetically-modified crops resistant to the herbicide glyphosate (Roundup). The Monsanto varieties are called “Roundup Ready” and enable farmers to apply the herbicide to eliminate weeds without poisoning their crop. Their extensive use has led to the indiscriminant use of the herbicide—an estimated 30,000 tonnes in 2002—and to the development of glyphosate-resistant weeds that pose a potential environmental disaster.

Despite the potential of its abuse by the giant agricultural transnationals, the mapping of the genome represents an important scientific breakthrough. The rice genome could provide a more precise and scientific approach to the development of cereal crops that previously would have taken years, decades or even centuries. The development of human civilisation is intimately bound up with the domestication of cereals.

About 10,000 years ago, mankind made the transition to agriculture-based economies involving the domestication of animals and plants. The process first occurred in the Middle East, then spread to Europe. Similar independent developments occurred in Africa, Asia and the New World.

The prehistoric diet came to be dominated by one cereal crop in each area—rice in tropical Asia, wheat in Europe and temperate Asia, sorghum and millet in Africa and maize in the Americas.

Prehistoric man would first have gathered wild rice in poorly drained areas where the grain occurred naturally. Eventually, through a process of selection, plants with larger panicles and heavier grains were preferred. Later humans learnt to sow and cultivate the crop themselves.

Some of the oldest evidence for rice farming was found in He-mu-du in Chekiang in China’s Yangtze basin in 1973. Carbonised rice kernels and rice straw, along with implements such as bone spades and hoe blades were dated at over 7,000 years old.

In order to produce consistent crops, the farmers had to develop water control, farm implements, draft animals, weed and pest control, fertilisation, seed selection and harvesting and storage techniques. The process of innovation, however, was extremely slow. Only gradually, in large part through trial and error, was it possible to establish agriculture involving large-scale irrigation and to select better rice varieties.

The result was the production of numerous varieties with an enormous range of characteristics. The Chinese geneticist Te-Tzu Chang has estimated that before scientifically-improved varieties were introduced that 100,000 different types of rice were grown across Asia.

Following the development of genetics in the twentieth century, the haphazard and intuitive approach of earlier periods was replaced by scientific farming, including hybridisation, selection and testing of improved rice varieties. Yield increases of 15 to 30 percent were achieved with the introduction of genetic material from various wild rice strains.

If the appropriate precautions were taken, the mapping of the rice genome opens up the possibility for scientific research that would vastly improve the available varieties of rice for the benefit both of mankind and the environment.

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