PERSPECTIVES: THE RICE GENOME

The Cereal of the World's Poor Takes Center Stage

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The milestone publication in this week's *Science* of not one, but two, draft genome sequences of rice (*Oryza sativa*) brings the cereal crop of the world's poor to center stage (*1*, *2*). Just 16 months ago, the science community caught its first glimpse of the completed genome sequence of *Arabidopsis thaliana*, an economically insignificant but "research-friendly" weed related to the cabbage and mustard family (*3*). Only 64 days later, Celera and the International Human Genome Sequencing Consortium published draft sequences of the human genome itself (*4*, *5*).

We believe that the scientific community will conclude that sequencing of the genomes of two rice subspecies will be the first sequencing project to yield tangible results for humankind from the standpoints of food security and combating malnutrition. The draft sequence of the *indica* rice subspecies by the Beijing Genomics Institute (BGI) (*1*) and of the *japonica* subspecies by Syngenta (*2*) will have a global impact on human health. These drafts will be combined with a complete rice genome sequence being compiled by the public International Rice Genome Sequencing Project (IRGSP) coordinated by the Japan Rice Genome Program. The IRGSP sequence is expected to be published later this year. The BGI and Syngenta draft sequences do not diminish the value of IRGSP's public sequencing effort. Indeed, all three versions contribute to the completion of a truly accurate rice genome road map that will be invaluable to plant biologists and agricultural scientists. The highly accurate IRGSP sequence will serve as the gold standard for all future investigations of genetic variation in crops (see the Perspectives by Ronald and Leung on page 58, and by Bennetzen on page 60).

If a single plant species were to be voted the most popular by scientists and laymen alike, it would be *Oryza sativa* (*6*). Rice, the world's most important cereal crop for human consumption, is the food staple of more than 3 billion people, many of them desperately poor (see the figure). In addition, rice—like *Arabidopsis*—is a model experimental plant; it has a much smaller genome than those of other cereals, and has a high degree of colinearity with the genomes of wheat, barley, and maize. The blending of the complete *Arabidopsis* and rice genome sequences will forever change the way we approach plant biology research. The new genetic knowledge and tools derived from these sequences will help scientists to address intractable problems that limit crop productivity in the developing world. Syngenta reports that 90% of the rice genes on a microchip can be used to probe gene expression in maize—just one example of the value of rice sequence information for elucidating the biology of other important crops.

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IRRI, CIMMYT, and the other 14 Future Harvest Centers of the Consultative Group on International Agricultural Research (CGIAR) welcome the public and private efforts to sequence the rice genome. CGIAR relies on the sharing of genetic information and seed stocks to develop technology and products for the developing world.

The sequencing of the rice genome will benefit many other plant genomics initiatives that rely upon publicly available genome sequence data. During a May 2001 meeting at CIMMYT, experts developed strategies to promote the application of genomics research to the improvement of cereal crops. This initiative is now part of the U.S. Agency for International Development's effort to assist the agricultural sciences in developing countries. In addition, the U.S. Congress is considering proposals to support a cereal genomics program that will champion collaboration among U.S. universities and the CGIAR centers. Also, CGIAR is actively implementing a new collaborative research model called "challenge programs," which target CGIAR goals of regional or global significance that require partnerships among a wide range of institutions. Genomics has the potential to address many different aspects of crop research, including genetic diversity and productivity improvement. In addition, genomics research will help us to understand how plants tolerate abiotic stresses, such as drought or salinity, and biotic stresses, such as disease or predation by insects. CIMMYT, IRRI, and other CGIAR centers are actively engaged in these efforts.

Recognizing the immense value of genomics research to crop improvement, IRRI, in collaboration with its partners in national agricultural systems that conduct and disseminate research, is preparing to take advantage of this treasure trove (*7*). IRRI advocates broad collaborations in rice research (*8*) that embrace innovations by both the public and private sectors, with emphasis on the need to provide the best science to serve the poor. IRRI is pursuing a public research platform through an International Rice Functional Genomics Working Group (*8*). The public availability of the rice sequences published in this issue will boost this commitment.

The continuing challenge is to broaden the developing world's access to information and technology. We must provide not only finished products but also the technologies that will enable a new generation of researchers in developing countries to solve their food production problems.

Providing affordable and nutritious food must be an integral part of any development program that aims to improve the lives of the poor (see the Perspective by Serageldin on page 54). In today's volatile world, we believe that collaborative research in the public and private sectors across developed and developing countries will contribute to reducing international tensions. We congratulate BGI and Syngenta on their milestone contribution to science and to humankind.

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