Genomics: The Way of the Future

The years 2000 and 2001 have seen wildfire growth in the new scientific field of genomics, which is expected to revolutionize the breeding of future food crops.

Rice, the staple grain for half the world's population, remains at the forefront of the latest advances and, through judicious planning and participation, IRRI has consolidated its role in the tide of discovery as well as promoting access to the new science for the rice-growing world.

The high point was the announcement in January 2001 that the multinational agribusiness corporation, Syngenta, had completed the sequencing of the rice genome, and was happy to release its results to freely benefit poor farmers and consumers in the developing world.

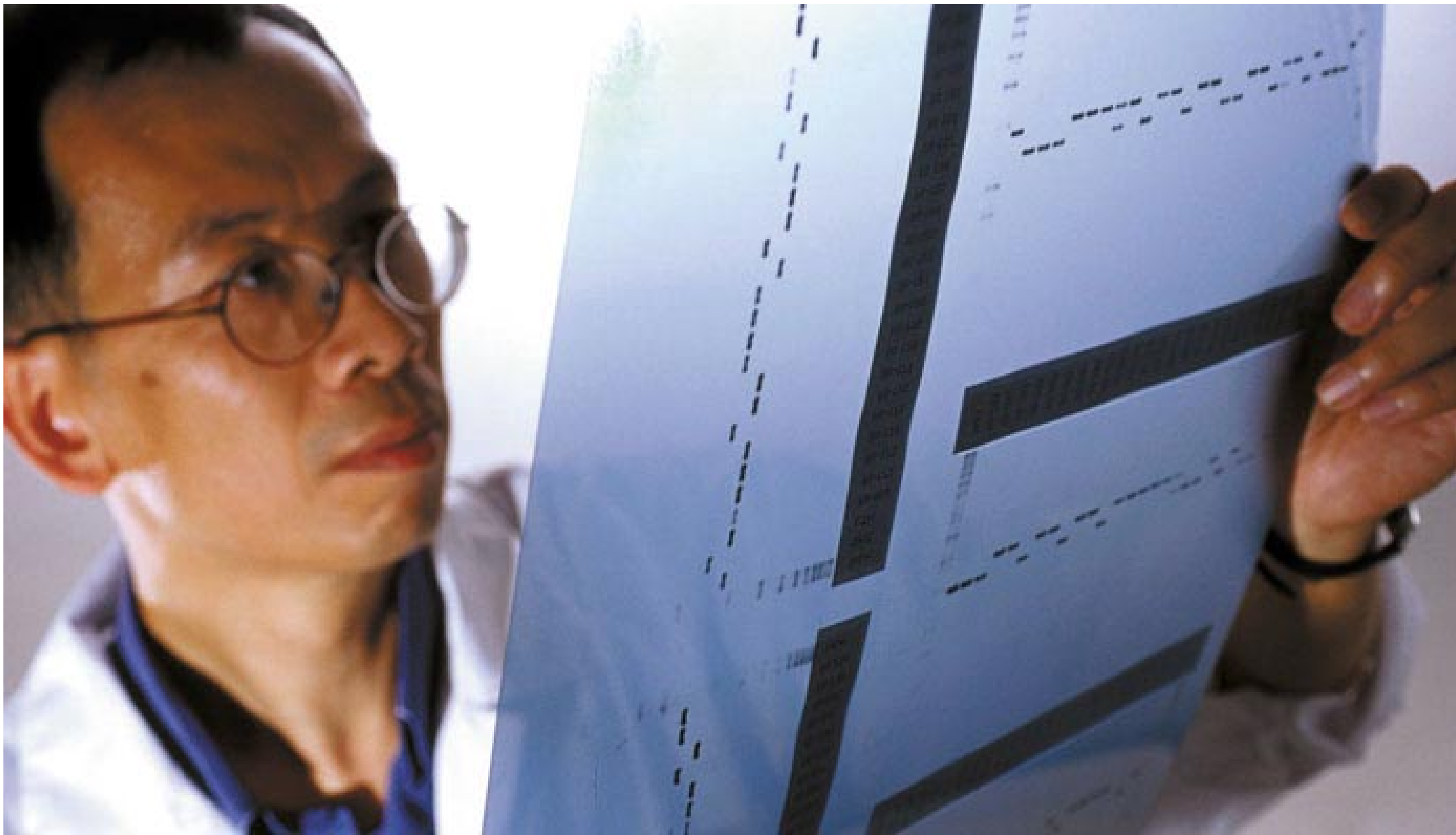
The announcement came when an international effort to sequence the genome was progressing well. This effort was expected to complete one of the largest chromosomes in early 2001. Sequencing involves the painstaking ordering of DNA sequences that encode about 50,000 genes in the rice genome. The genome of rice has 12 chromosomes consisting of 430 million base pairs of DNA. Each gene consists of about 3,000 base pairs.

Rice is the first of the world's major food crops to have its genome fully sequenced. The end result is a "map" that identifies every gene on the 12 chromosomes.

The next big step is discovering what the genes do: how they function, how their functions combine with those of other genes, and for what purpose. This is called "functional" genomics, and this is where IRRI holds a unique research position.

One way to track down the function of any one gene is to simply delete the gene from the chromosomes of a rice plant using chemical or irradiation processes, then examine the plant as it grows. By looking for what is missing, what characteristics the plant does not have, researchers are able to deduce the function of the missing gene. The plants are called "deletion mutants," and IRRI now has a collection of 18,400 of them, with different genes deleted. By the middle of 2002, the collection will have grown to about 40,000.

Dr. Hei Leung.



The Institute's functional genomics project is also developing a large collection of what are called "introgression lines," plants that carry a wide range of unique chromosome segments implanted from commercial varieties and wild rice. These will be used in the discovery of the functional diversity of the genes, and to understand the overall genetic, biochemical, and physiological systems in the rice plant.

Backed by the unique collection of rice germplasm in the International Rice Genebank, IRRI researchers are multiplying their collection of modified plants—what they call their "genetic resources"—so that mutants and introgression lines can be supplied to other institutions assisting them in the challenging task of assigning functions to all the rice genes.

According to the plant pathologist and geneticist leading the IRRI team, Dr. Hei Leung, the Institute has benefited from the rice sequencing projects of both the private and public sectors. It has been working with information as it has become available. The international consortium led by Japan is expected to finish its sequencing effort in two to three years, and this is particularly significant because of its anticipated accuracy and the fact that it will be completely open to public access.

Dr. Leung's favorite analogy for the functional genomics project is that, after the genome is fully sequenced, scientists will have a dictionary full of words, with each word representing a gene, but with no definitions giving the words meaning or purpose.

Functional genomics will help overcome disease.

The job of the IRRI team is to give a meaning to every "word," to find a function for every gene. Already, by studying the deletion mutants and introgression lines, Dr. Leung's team has identified several genes giving the plants enhanced resistance to various types of organisms that cause disease. Mutants were isolated for genetic analysis after displaying tolerance for submergence. The team has also produced plants containing small chromosome segments from wild species that confer resistance to multiple diseases and insects.

The scientists also found introgression lines and mutants that grew and yielded well in soil with too much or too little water. They studied the drought-response process in rice plants being grown under different water conditions, and identified a variety of proteins produced by the plants in the process of responding to drought and salinity stress. Such studies allow them to better understand the way rice plants respond to stress, and to find genes for use in plant breeding. For example, more than 100 genes that can help the plants defend themselves against pathogens have been found and are already being used to select better disease-resistant rice varieties.

Dr. Leung says that an exciting aspect of genomics is that tools for gene discovery are constantly being improved. He and his team hope eventually to begin using "gene chips," or "microarrays," in their search for an understanding of genetic function. This relatively new technology involves massing about 20,000 genes on one display slide. This so-called "chip" can then be used as a sensor to detect genetic messages that are turned on or off when the plants are exposed to stress.

The expression of the genes can be recorded and analyzed to give a total picture of how the plant behaves under different conditions. In this way, scientists will be able to identify hundreds or even thousands of genes that may combine and interact to achieve a particular function, such as tolerating drought, resisting disease, or producing more nutritious grains.

"This technology allows us to discover in weeks what would, in the past, have taken maybe two years of work,

looking at the genes one at a time," Dr. Leung says.

Of paramount importance in IRRI's functional genomics project are efforts to protect the interests of rice farmers and consumers from the private exercise of intellectual property rights, which could lead to increased prices or delays in the extension of benefits to the public.

To broaden access to information, IRRI has launched a database on the Internet to describe the biological characteristics of its collection of deletion mutants. Another similar database has been developed for information on stress-response genes. These will be linked to genome sequence databases to facilitate information exchange.

The Institute has also established an International Rice Functional Genomics Working Group (http://www.cgiar.org/irri/genomics/) as a first step toward developing a public research platform to accelerate gene discovery. Dr. Leung says that more than 14 research groups, including laboratories and institutions from the international rice research community, have agreed to contribute resources and expertise, and to promote the sharing of genetic stocks.

"Contributions from the IRRI team are now crucial to the success of this public research platform," he says. "We must produce tangible things, make discoveries, and develop materials to give away. Within three years, I want researchers around the world to see the benefits of working with us. We don't want to be the only player on the field, but we would like to be the preferred player because of IRRI's mission and the quality of our work."

He says that it's critical that the national agricultural research and extension systems (NARES) from rice-growing countries become involved in the working group.

"We need to make sure that this is not seen by the NARES as research beyond their reach. They must have a common place in which to work with someone they know and trust. We will make all our genetic resources and tools available to our partners."

So far, the process of unraveling the secrets of the rice genome has been a harmonious combination of public and private efforts, and Dr. Leung says he's been impressed with the readiness of private organizations to contribute.

"I think they've gradually realized that rice improvement is a longer-term process than they thought, and that there are no quick returns. They've also recognized that their benefits will accrue from better welfare for rice consumers in the developing world."

Dr. Leung believes that it will take about ten years for scientists to complete the writing of the functional genomics "dictionary." It will begin with the assignment of functions to every gene in the rice genome, but he points out that the true biological function of the genes is beyond that, and he quotes a few figures to illustrate the vastness of the job.

"There are 50,000 genes, but the function of each may vary in every rice variety because the genetic background of one is different from that of another. Just think, the International Rice Genebank has 110,000 different samples of rice germplasm."

Ultimately, plant breeders may be able to refer to a database to find precisely which genes they need to achieve specific plant characteristics. Then, using "maps" of the genome, they'll select the genes and mix them, according to their plans, and the resulting plant should be just what they're looking for. But Dr. Leung concludes that, "like words in poetry, the creative composition of genes is the essence of successful plant breeding, and it will come down to how well we can use the dictionary."