

The publication in August 2005 of the finalized sequence of the rice genome has presented scientists with the opportunity to delve further than ever before into the rice plant's genetic secrets.

Through these activities, IRRI continues to foster public access to rice genetic information. As well as possessing an excellent capacity to produce genetic resources, the Institute has the expertise necessary for identifying important traits and an extensive collaborative research network for evaluating the behavior of newly found traits in diverse environments and under a

range of biotic stresses (such as disease) and abiotic stresses (such as drought or problem soils). In this light, IRRI is in a unique position to undertake this important task on behalf of publicly funded rice researchers, and of the poor rice farmers and consumers they serve.

There are two projects. One deals with all aspects of maintaining the germplasm and the other seeks to understand the functioning of the rice genome.



PROJECT 1

Germplasm conservation, characterization, documentation, and exchange

Since its foundation almost 50 years ago, IRRI has been at the forefront of international efforts to collect and conserve the genetic resources of rice. The world's largest rice germplasm collection is held in trust in the International Rice Genebank at IRRI (along with a collection of biofertilizer germplasm, including Azolla, blue-green algae, and nitrogen-fixing bacteria). Plant breeders and researchers worldwide use these genetic resources to develop new rice varieties. The germplasm held in the genebank has also allowed the re-establishment of traditional rice varieties thought lost and even the restoration of an entire rice industry—such as in the case of Cambodia, where agriculture was devastated after years of warfare and civil strife. Effective use of germplasm requires characterization (Output 1), evaluation (Output 2), and access to information (Output 3).



Output 1: Rice and biofertilizer genetic resources conserved and characterized

Ensuring the long-term preservation of the collections in the IRG is an ongoing commitment. In 2005, IRRI continued the safety duplication of the IRG

collection, sending samples of almost 6,000 accessions to the National Center for Genetic Resources Preservation (NCGRP) in Fort Collins, Colorado, USA. These samples are not accessed or distributed from NCGRP but are held as a black-box safety duplication in case

of a catastrophe at IRRI. Some 2,500 new accessions were added to the IRG in 2005. Three thousand cultivated and 550 wild accessions underwent seed replenishment. IRRI tested the viability of more than 19,000 accessions in the active collection and more than 17,000 accessions in the base collection. The total number of accessions at the end of 2005 was 108,706, of which the core collection, a subset of samples representing the range of rice varieties and ecosystems, was about 10%. Location information was updated, corrected, and validated for 63,386 accessions from 69 countries. Location names were validated and geographic coordinates assigned. Rejuvenation, characterization, and viability monitoring continue as core activities.

A set of Generation Challenge Program partners—IRRI, Centro Internacional de Agricultura Tropical (CIAT), Africa Rice Center (WARDA), Cornell University, Chinese Academy of Agricultural Sciences, Centre de coopération internationale en recherche agronomique pour le développement (CIRAD), and Empresa Brasileira de Pesquisa Agropecuária (EMBRAPA)—is now collaborating to determine patterns of alleles (versions of a gene) or genetic fingerprints, using DNA markers (a marker is a segment of DNA linked to an allele that controls an important trait and can easily be detected in the lab) distributed across the genome for previously identified accessions showing diverse reactions to drought stress. This will be one of the largest sets of rice accessions characterized to this level for determining population structure. In 2005, we obtained fingerprinting data on more than 1,500 rice accessions. Genotyping on the remaining accessions continues.

By studying molecular variation at the sites of genes identified as being

involved in drought response and other important traits, we will go on to identify sources of new alleles for plant breeding. This work employs EcoTILLING, an application of TILLING (Targeting Induced Local Lesions IN Genomes) designed to detect small variations in gene sequences in natural populations. In 2005, we characterized more than 400 cultivated accessions and nearly 100 wild accessions. Rare allele types were detected at several candidate gene loci. We identified several promising DNA markers that may allow marker-assisted breeding (which involves linking a desired gene with a marker) for salinity tolerance. Accessions showing good tolerance will be used in breeding programs to produce new varieties that will have an important benefit for farmers in saline areas.

In line with IRRI's growing focus on nutritionally enriched rice, we have begun work to identify micronutrient-dense rice varieties, and are currently examining some 1,400 accessions whose micronutrient (iron and zinc) content will be measured.

Work has continued on pinning down the identity of 4,450 wild rice accessions using both molecular and morphological techniques. Nearly 1,500 of the accessions were found to have been misidentified. In 2005, 96 accessions were completely authenticated and 141 accessions were partially authenticated.

Output 2: Rice germplasm exchanged and evaluated internationally

Exchange and dissemination of improved rice germplasm through the International Network for Genetic Evaluation of Rice (INGER) are some of the most enduring features of IRRI's collaboration with national agricultural research and extension systems (NARES) and other international

centers. Once improved germplasm is received through INGER, NARES are then able to use it in ways that best fit local needs. In 2005, we assembled and distributed 300 "nursery" sets to 30 countries (22 in Asia, three in Africa, and five in South America). In addition, INGER facilitated the seed requests of 39 countries for some 6,343 seedlots and a special rice blast nursery was sent to five sites in India for field screening. We also supplied salt-tolerant lines to eight NARES in Asia and Africa under an initiative to establish a network of salinity breeding in Asia and Africa.

As part of an ongoing review of the system of germplasm exchange through INGER, an intellectual property rights (IPR) training-workshop and technical advisory committee meeting were conducted. Issues on germplasm and information exchange were discussed in the context of recent developments on international agreements and national laws and policy on IPR and plant variety protection. The workshop was in line with the Council for Partnerships on Rice Research in Asia's goal of building the institutional capacity of NARES in germplasm management, which includes NARES variety contributions to INGER in a changing IPR environment. The meeting also provided a chance to analyze the ways in which NARES use INGER materials—information that will serve as a good database for further studies and breeding programs.

Output 3: International Rice Information System developed and used by rice breeders and researchers

A major strategy of the International Rice Information System (IRIS)—the rice implementation of the International Crop Information System (ICIS), which is a database system that provides integrated management of global informa-

tion on genetic resources and crop cultivars—is to consolidate existing IRRI germplasm-related databases, including those for genetic resources, breeding, and INGER, into a single system that can be easily searched via the Internet.

In 2005, we developed and deployed prototypes of software facilities for interoperability between IRIS and other major international biological databases based on Web-service architecture. Consequently, basic interoperability between Web-service applications and databases is now available, although entire ICIS functionality is not yet fully available for all adopted Web-service/Internet protocols.

IRRI and other crop research centers are starting to generate enormous sets of molecular data. These will need a proper database and analysis framework for optimal scientific usage and relevance. In this light, we enhanced IRIS's analysis and visualization tools

for molecular characterization of data and populated IRIS with allele-mining data integrated with associated evaluation data from a core collection.

To properly interpret germplasm characteristics, it is crucial to have a sound understanding of the local environment. This is facilitated through geographic information system (GIS)-driven analyses. In 2005, we integrated GIS capability with IRIS to enable analysis of the eco-geographical distribution of genetic diversity.

We also saw in 2005 the beta release of Java-based stand-alone and Web applications for ICIS/IRIS, which are now available for download from the ICIS Web site (www.icis.cgiar.org). The next generation of ICIS, written in



Java, will be independent of computer operating systems and will have wider bioinformatics tool integration.

Project leader

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PROJECT 2

Functional genomics

Genomics, the science of deciphering DNA sequence structure, variation, and function, is increasingly driving the discovery of plant traits that can improve crop production and, in due course, improve the livelihoods of millions of resource-poor rice farmers. Ultimately, genomics will allow researchers to discover every rice gene, the functional diversity of the various versions of these genes among the myriad rice species and varieties, and the relationship

between a rice variety's DNA sequence and its phenotype—the actual form the plant takes in the field. This knowledge will lead to new strategies for genetic improvement that will allow farmers to grow rice more efficiently and profitably.

Through the efforts of the International Rice Genome Sequencing Project and private-sector contributions, the finalized sequence of the rice genome was published in August 2005. This

progress, building on the draft sequence published in 2002, has presented scientists with the opportunity to delve further than ever before into the rice plant's genetic secrets. This recent leap forward in structural genomics—determining the sequence of the DNA and mapping the location of genes or relatively small regions of the genome that influence phenotypic traits—has laid the foundation for great advances in functional genomics—the whole-