PROJECT 1

Germplasm conservation, characterization, documentation, and exchange

Since its foundation, 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. Effective use requires characterization (Output 1), evaluation (Output 2), and information access (Output 3).

Output 1: Rice and biofertilizer genetic resources conserved and characterized

Ensuring the long-term preservation of the collections in the International Rice Genebank (IRG) is an ongoing commitment. During 2004, samples of more than 13,000 accessions were sent to the National Center for Genetic Resources Preservation (NCGRP) in Fort Collins, Colorado, USA. These samples bring the safety duplication of the IRG collection up to date. They are not accessed or distributed from NCGRP but are held as a black-box safety duplication in case of a catastrophe at IRRI. It remains only to continue this duplication with newly processed accessions. Some 5,000 new accessions were added to the base collection in 2004 and 3,000 accessions underwent seed rejuvenation. The total number of accessions at the end of 2004 was 106,865, of which the core collection, a subset of samples representing the range of rice varieties and ecosystems, was about 10%. Rejuvenation, characterization, and viability monitoring continue as core activities.

A bank of freeze-dried leaf tissue samples has been established for the core collection of 11,000 cultivated (*Oryza sativa*) rice varieties and 1,500 non-*sativa* accessions. Of these, DNA was extracted and stored from 2,000 and 700, respectively. This DNA is being used for molecular characterization to ensure wide sample coverage of the collection, to understand the phylogenetic structure of the collection, and ultimately to locate novel alleles (versions

of genes) affecting important traits for plant breeding.

A collection of more than 3,000 accessions showing diverse reactions to drought stress has been identified from the IRG core collection and by nominations from partners in the Generation Challenge Program. The partners—IRRI, Centro Internacional de Agricultura Tropical (CIAT), Africa Rice Center (WARDA), Cornell University, Chinese Academy of Agricultural Sciences, and Empresa Brasileira de Pesquisa Agropecuária (EMBRAPA)—are collaborating to determine patterns of alleles or genetic fingerprints, using markers distributed across the genome for these accessions. This will be one of the largest sets of rice accessions characterized to this level for determining population structure.

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. In 2004, new equipment allowed us to undertake EcoTILLING, an application of TILLING (Targeting Induced Local Lesions IN Genomes) designed to detect small variations in gene sequences in natural populations. Using this method, we discovered variants of two genes involved in the regulation of drought response. Short DNA sequences (primers) have been developed for 48 candidate genes for stress tolerance and quality, and we expect to discover novel variants of these genes in the same way.

Some 200 accessions with excellent grain quality are being screened 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.

Work has continued on pinning down the identity of 4,453 wild rice accessions using both molecular and morphological techniques. Some of the accessions were found to have been misidentified. The work in 2004 involved tissue sampling (2,812 accessions), determining chromosome numbers (1,345), DNA extraction (943), field characterization (380), and inter- and intraspecific hybridization.

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 the most visible features of IRRI's collaboration with the national agricultural research and extension systems (NARES) and other international centers. In 2004, we assembled and distributed more than 300 "nursery" sets to 28 countries. Also, we sent 400 outstanding INGER lines to requestors in seven countries. Four irrigated lowland varieties are showing promise in East Timor.

The system of germplasm exchange through INGER was reviewed during the year, as a result of which the NARES' roles have been broadened with regard to prioritization of requests, in-country multiplication of germplasm, and charging arrangements. This will increase the efficiency of the overall system.

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

A major strategy of the International Rice Information System (IRIS) 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. Activities in 2004 focused on the

International Rice Genebank Collection Information System (IRGCIS): combining various tables to consolidate all available knowledge on each germplasm. One benefit has been discovering gaps and inconsistencies in the data. These are now being addressed. The work was slowed by technical problems in making the wide range of data accessible through the system's information portal, which is based on the generic International Crop Information System (ICIS).

Location data on IRG accessions are being reviewed and reorganized to provide comprehensive and accurate site information for use in research, management, and decision making. The bulk of this work was done in 2004 and the data management system will be launched in the first quarter of 2005.

Improvements were made to the way in which we describe plant phenotypes in IRIS. With more precise definitions, we can compare different lines more exactly. The initial work was done on IR64 rice mutants (Project 2, Output 4) and this will be extended to general crop types.

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