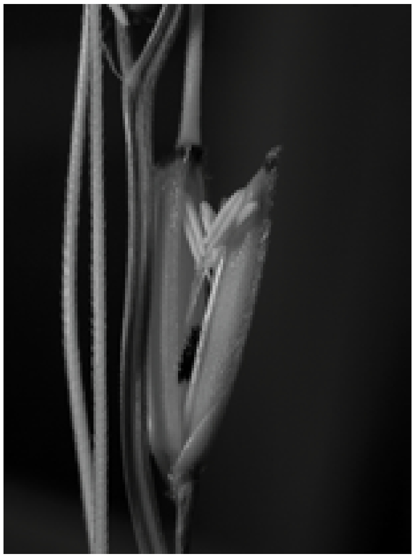
productivity and production, and reducing poverty for poor rice producers and consumers.

As well as possessing an excellent capacity to produce genetic resources, IRRI is a leader in the identification of important rice traits. This expertise is combined with an extensive collaborative research network that evaluates the behavior of newly found traits in diverse environments and under a range of biotic stresses (such as pests and diseases) and abiotic stresses (such as drought and problem soils). IRRI occupies a key position as a center for collaboration among and between both developed and developing countries. As such, the Institute is in a unique position to undertake this program's important information generation and dissemination tasks on behalf of publicly funded rice researchers and the poor rice farmers and consumers they serve.

Program 1 comprises 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 led 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, which are also freely available to any interested party—including farmers. 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

In 2006, IRRI developed and verified a novel high-throughput technique for genetic fingerprinting, which will ultimately allow tens of thousands of accessions to be characterized. The molecular characterization of the International Rice Genebank (IRG) mini-core collection of 1,536 accessions was partly completed, and will continue in 2007. The Generation Challenge Program (GCP) composite rice collection of 2,757 lines was also genotyped and the population structure determined. This knowledge will facilitate the identification of important genes by the application of association genetics, and hence will allow better use of conserved germplasm accessions for breeding and research.

The Institute's Grain Quality, Nutrition, and Postharvest Center characterized rice cooking quality in the mini-core collection (comprising cultivated and traditional varieties, and wild rice species) referred to above, which included representatives of each germplasm class of rice. We also characterized grain quality in 50 varieties of black rice. Specifically, the 1,536 mini-core accessions were characterized for amylose content, gelatinization temperature, a simple sequence repeat (SSR) marker located on an amylose gene, and a single nucleotide polymorphism on the *starch synthase IIa* gene (which contributes to gelatinization temperature). The black rice varieties were tested for all possible traits of physical, chemical, and nutritional quality, and for trait-specific and other SSR loci. We found that the mini-core samples were not diverse geographically or in terms of cooking quality. They were heavily skewed toward high amylose and high gelatinization temperature. We found evidence for an additional gelatinization-temperature haplotype, but more research is needed to confirm this. If there is another, this means that there are now five known haplotypes—linked genetic loci—that define gelatinization temperature. We also found two polymorphisms in the amylose gene and rare combinations of genes not found in domesticated rice that confer broader-than-usual quality traits (the range of gelatinization temperatures, for example, was 51–85 degrees Celsius versus the usual 60–75 degrees Celsius seen in most domesticated rice varieties). Starch structure in some accessions indicates the starch was synthesized by a combination of genes not usually found. This work offers a better understanding and better documentation of characteristics of the rice held in the genebank. It also gives breeders insight into quality traits for breeding and will help them add new traits to domesticated rice.

To better use and conserve wild relatives, we authenticated the taxonomic identification of 50% of the accessions of wild *Oryza* species held in the IRG. The newly obtained molecular, morphological, chromosomal, and biosystematic data have significantly improved the overall classification of wild rice.

General IRG maintenance continued, with all incoming samples processed, subsamples of all accessions placed in long-term storage and in safety backup, and viability tests on 12,000 samples, and multiplication of 5,000 accessions done.

Two key outputs in 2006 supported the genetic resource systems of IRRI's national partners. First, the establishment in 2006 (to be completed in 2007) of a rice biodiversity network provides a mechanism for global rationalization of efforts to conserve rice genetic resources and will enhance germplasm conservation and use around the world. Second, the improvement of the Lao PDR rice genebank will improve conservation and use of Lao germplasm as well as lower the cost and boost the efficiency of the national rice genetic resource system in Lao PDR. Samples of all remaining Lao accessions conserved in IRRI were restored to the Lao genebank for duplicate conservation there.

The total number of accessions at the end of 2006 was 108,955, 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.

Output 2: Rice germplasm exchanged and evaluated internationally

In 2006, 18 new nurseries—14 ecosystem-based and four stress-oriented—were assembled for the International Network for the Genetic Evaluation of Rice (INGER). These were distributed to 30 countries. Outstanding materials from these nurseries were identified, used in national breeding and testing programs, and subsequently either released as varieties or used to develop new varieties with better characteristics for farmers' use. Twelve regular nurseries and four special nursery sets were also composed and dispatched to 38 countries. The IRG sent a record high of nearly 50,000 seed packets in response to 225 requests from 32 countries. Combined with nearly 45,000 seed packets distributed by INGER and other IRRI organizational units (12,000 packets sent by INGER in response to 164 seed requests from 38 countries; 33,000 packets sent by both INGER and other IRRI organizational units to INGER partners and other breeding collaborators), total distribution of germplasm reached a record high of nearly 95,000 seed packets in 2006.

The 2006 users of the breeding lines from 2003-05 INGER nurseries are NARES breeders in Bangladesh, China, DPR Korea, Egypt, India, Iran, Italy, Japan, Malaysia, Myanmar, Nepal, Pakistan, Philippines, Republic of Korea, Sri Lanka, Sudan, Surinam, Thailand, Turkey, and Vietnam, with 758 breeding lines used as parents in hybridization; 879 breeding lines used in further yield evaluation; 242 breeding lines from 2003-05 INGER nurseries screened for resistance to insect pests and diseases and evaluated for salinity and cold tolerance; and 600 breeding lines from 2003-05 INGER nurseries conserved in gene banks. NARES breeders in the countries listed above are using the germplasm developed in 2003-05 in characterization and evaluation research in the search for new traits or adaptation, and in local breeding programs to increase the diversity of local gene pools for subsequent testing by the national testing authorities and ultimate release to, and use by, farmers.

The Genetic Resources Center, Crop Research Informatics Laboratory, Seed Health Unit, and Plant Breeding, Genetics, and Biotechnology Division worked together assiduously to prepare IRRI for implementation of the International Treaty on Plant Genetic Resources for Food and Agriculture. A historic agreement, signed between IRRI and the Governing Body of the Treaty on 16 October 2006, required IRRI to change its procedures for germplasm exchange by 14 January 2007, in particular to conform to the requirements of a new Standard Material Transfer Agreement (SMTA). This involved an extensive exercise to classify the status of all IRRI's germplasm under the Treaty, record this information in the International Rice Information System (IRIS), develop new software in IRIS to process seed requests, create an SMTA for each seed request, and create a new Web site to publish data associated with each SMTA. IRRI was the only international agricultural research center able to immediately comply with the Treaty by the 14 January 2007 deadline and therefore to continue germplasm exchange without interruption, and IRRI's system has been demonstrated at international meetings as a model for others to follow.

The role of intellectual property rights (IPR) in international agricultural research—in germplasm exchange, for example—is growing rapidly, and it is vital that NARES breeders and germplasm specialists increase their awareness in this area. In 2006, IRRI provided two half-day training courses (one at IRRI headquarters, one in India) and one 5-day training course (in Myanmar) in IPR issues associated with genetic resources.

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

To improve management of information in the IRG, a genetic resource information management module for the International Crop Information System (ICIS) was completed and deployed as part of IRIS. The resultant integration and joint publication of genetic resource and crop improvement information will benefit genetic resource specialists and plant breeders working with rice and other crops, ultimately allowing accelerated development of new, improved varieties that exploit novel alleles from genetic resource collections.

The development of an ICIS module for molecular characterization of germplasm will benefit biologists and genetic resource specialists working on biodiversity analysis, functional genomics, and allele mining. The module integrates molecular characterization from different projects with phenotypic evaluation of germplasm used to identify novel alleles from rice accessions. This information resource will allow the development of improved rice cultivars with enhanced traits conferring resistance or adaptation to intractable environments. In 2006, the core data model and database were completed. Software development and data encoding are continuing within the context of the GCP and within various other collaborative projects.

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