

# Emerging Trends in Managing and Using Rice Genetic Resources

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Rice genetic resources comprise traditional farmers' varieties, landraces, commercial cultivars, hybrids and other elite materials developed through plant breeding and biotechnology. They also include wild progenitors and wild relatives of rice that could be used for either agriculture or environmental benefits. These resources form the primary building blocks that provide the much needed genetic variation for all the rice improvement work undertaken by the breeders, biotechnologists and other researchers. Conservation of genetic resources is about preservation and use. For further evolution of germplasm there is a need to continue growing the resources in their natural *in situ* conditions with suitable backup through long term storage in gene banks under *ex situ* conditions. Recent advances in biotechnology and development of new molecular techniques hold promise for improving efficiency of managing the germplasm collections (stored in gene banks at high costs) by detecting duplicates and aiming possibly at true gene banks storing DNA segments/nucleotide sequences in place of seed samples, supported by more efficient computerised documentation systems. They will also promote the greater use of stored collections by more precise characterization of inventories

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at the molecular level, facilitating allelic diversification along with location of loci on genome maps responsible for the desired quantitative traits based on marker-assisted approach. Accordingly, the role of modern gene bank managers has expanded considerably and forms the focus of this paper.

Seventh meeting of the Conference of the Parties to the Convention on Biological Diversity (CBD), held in Kuala Lumpur in March 2004, emphasized the linkage between biological diversity, food (and nutrition) security and sustainable agriculture. With the International Treaty on Plant Genetic Resources for Food and Agriculture entering into force on June 29, 2004, major crops are back in the multilateral domain along with access and benefit sharing and Farmers' Rights. Bonn Guidelines on Access and Benefit Sharing provide a framework for action for developing further clarity on responsibilities and procedures related to access to germplasm. India is well placed to play a lead role in the emerging scenario because of its strong national plant germplasm system which is comparable to the best in the developed world. India's Biological Diversity Act 2002 has been enacted to meet national commitments under provisions of CBD providing access to its genetic resources under multilateral system (based on material transfer agreements) while claiming sovereign rights over them (exercised through the National Biodiversity Authority). The Protection of Plant Varieties and Farmers' Rights Act 2000 is an effective *sui generis* national legislation, patterned largely on the provisions of UPOV 1978, that protects both the breeders' and farmers' rights relevant to terms under the WTO-TRIPS agreement. Detailed information on these two legislative measures are available at the websites maintained by the Government of India.<sup>1</sup>

### **Domestication of Rice and Centres of Its Diversity**

There are two cultivated species of rice, viz., *Oryza sativa* (widely known as the Asian cultivated rice including the two ecospecies *indica* and *japonica*) and *O. glaberrima* (called the African cultivated rice). Both are diploid species with chromosome number  $2n = 24$ . The former is believed to have been domesticated in south and southeast Asia and it is widely cultivated throughout all the rice growing areas of the world. Wild rice species *O. rufipogon* (a perennial species) and *O. nivara* (an annual relative), growing naturally in several parts of India and many other adjacent areas, are considered to be its putative progenitors. The African

cultivated rice appears to have originated in tropical West Africa from the wild rice species *O. barthii* and its cultivation is almost confined to that region.

India is considered as one of the centers of origin of rice (*Oryza sativa* ssp. *indica*) and an important centre of its diversity (Ramiah, 1953; Richharia, 1960; Chang, 1976). Rice is the staple food for its large population and this crop is cultivated in almost all the Indian states under a remarkably wide range of agro-climatic conditions and ecological situations. The Jeypore tract in Orissa in particular displays striking variability in a large array of traits and growth characteristics as described in details by Richharia and Govindswami (1966) and Rao (1991). This tract has been proposed to be the likely area where indica rice was domesticated (Sharma *et al.* 1997). Traditional practices of managing and developing this vast wealth of genetic diversity by farming families within rice-based cropping systems should form an important part of the strategy for *in situ* on-farm conservation and sustainable use of rice genetic resources.

Aforementioned, diversity at the genetic level within cultivars, landraces and closely related wild forms of rice is crucial for providing resilience against biotic, abiotic and climatic stresses. Accordingly, germplasm representing the diversity observed in cultivated and wild forms is collected by the breeders to access and make use of the desired traits. Gene banks further enrich such collections through planned explorations and store the collected seed samples under medium and long term storage after duly processing them. This kind of *ex situ* conservation of germplasm collections in gene banks also provides reliable backup to on-farm *in situ* conservation against unforeseen calamities while ensuring at the same time easy and instant availability of these materials to plant breeders and other researchers whenever needed. Nearly 200,000 seed samples of cultivated and wild rice forms have already been kept under long term storage in national and international gene banks (See Table 1 for information on major collections).

## Rice Genetic Resources

Major components of rice genetic resources are:

- Vast genetic diversity available in the cultivated Asian and African rices, developed and conserved by farming families over the past ten millennia or even more.

**Table 1: Some Major Ex Situ Collections of Rice Genetic Resources**

Gene Bank / Organisation	No. of Accessions Stored under Long Term Storage	Remarks
Indian National Gene Bank, National Bureau of Plant Genetic Resources, New Delhi.	66,858	Includes nearly 700 samples of wild rice forms.
International Rice Gene Bank, Genetic Resources Center, IRRI, CGIAR, Philippines.	96,261	Includes 4,370 samples of wild rice forms. In addition, over 10,000 samples are under processing.
National Plant Germplasm System, USDA-ARS, USA.	21,292	Includes 382 samples of wild rice forms.

- Twenty-two wild species of rice still growing and evolving in Asia, Africa, Australia, and the Americas. Only six of them are closely related to the cultigens. See Tables 2 and 3 for further information.
- Eleven other genera in the tribe *Oryzaceae* are distantly related to rice and some of their species, such as *Porteresia coarctata* having tolerance to saline conditions, are being investigated for their value in rice breeding, through the application of biotechnology.

### Role of the Gene Bank Manager/Curator

Gene banks are *ex situ* biodiversity reservoirs and sources of alleles for sustainable genetic enhancement of plant crops. Collecting plant germplasm along with passport information, through carefully planned explorations and exchange, is an important activity of the Gene Bank manager. Collections of plant breeders and relevant organizations are also pooled at the national level. Seed samples collected from the farmers along with related information are held in-trust with the expectation that these will be eventually returned to them in due course in the form of improved new varieties recognizing Farmers' Rights (for getting their varieties protected and for planting as well as non-labeled-marketing of seeds, also their products, harvested by them from their crop and also claiming compensation where due).

The collected seed samples are tested for their viability and health and then given an identity/accession numbers. This is followed by phenotypic and biochemical characterization and also some preliminary agronomic assessment along with resistance screening against pests and diseases. Seed or propagule regeneration and multiplication of

**Table 2: Taxonomic Relationships in Rice (*Oryza* species) 2 Cultivated and 22 wild species**

Species	Chromosome No. (2n)	Genome
<i>O. barthii</i>	24	AA
<i>O. glumaepatula</i>	24	AA
<i>O. longistaminata</i>	24	AA
<i>O. meridionalis</i>	24	AA
<i>O. nivara</i>	24	AA
<i>O. rufipogon</i>	24	AA
<i>O. glaberrima</i> ——— Cultivated	24	AA
<i>O. sativa</i> ————— Cultivated	24	AA
<i>O. alta</i>	48	CCDD
<i>O. eichingeri</i>	24, 48	CC
<i>O. grandiglumis</i>	48	CCDD
<i>O. latifolia</i>	48	CCDD
<i>O. minuta</i>	48	BBCC
<i>O. officinalis</i>	24, 48	CC
<i>O. punctata</i>	24, 48	BB, BBCC
<i>O. rhizomatis</i>	24	CC
<i>O. australiensis</i>	24	EE
<i>O. brachyantha</i>	24	FF
<i>O. granulata</i>	24	GG
<i>O. meyeriana</i>	24	GG
<i>O. neocaledonica</i>	24	GG
<i>O. longiglumis</i>	48	HHJJ
<i>O. ridleyi</i>	48	HHJJ
<i>O. schlechteri</i>	48	HHKK

Source: Lu Bao-Rong, *et al.* (2002).

recalcitrant crops is also a routine activity despite the costs involved in maintaining *in vitro* collection. They are grown in the field for seed multiplication along with characterization, based on approved descriptors, and documentation and multiplication. The resulting information is pooled in the national database network. Appropriate catalogues are prepared and shared with *bona fide* users (breeders and researchers). Both the aforementioned legislations make suitable distinction among Indian nationals, non-resident Indians and foreigners. Information on nodal authorities for signing Material Transfer Agreements, based on prior informed consent and mutually agreed terms, is available on the above mentioned websites.

For the medium term storage, seed samples are checked for seed health and viability, dried to around 5 per cent moisture content and then packaged in paper bags or laminated aluminum foils or other suitable containers before storing them at 5° C and 35 to 40 per cent RH. For the long term storage, the seed samples (containing around 3

**Table 3: Description of the Putative Wild Progenitors of Cultivated Asian Rice (*Oryza sativa*) and Cultivated African Rice (*Oryza glaberrima*)**

Description	Asian Rice		African Rice	
	Domesticated in South and Southeast Asia		Tropical West Africa	
Characteristics	<i>Oryza rufipogon</i>	<i>Oryza nivara</i>	<i>Oryza barthii</i>	
Habit	Perennial, tufted, and scrambling grass with nodal tillering; plant height variable (1-5 m) depending on the depth of water; panicles open.	Annual, short to intermediate height (usually <2 m) grass; panicles usually compact, rarely open.	Annual and erect to semi-erect grass; leaves with short ligule (<13 mm); panicles compact to open, rarely having secondary branching.	
Chromosome Number	2n=2x=24		2n=2x=24	
Genome	AA		AA	
Distribution	Asia (Australia, Bangladesh, China, India, Indonesia, Laos, Malaysia, Myanmar, Nepal, Papua New Guinea, Philippines, Sri Lanka, Thailand, and Vietnam)	Asia (Bangladesh, Cambodia, China, India, Laos, Malaysia, Myanmar, Nepal, Sri Lanka, Thailand, and Vietnam)	Africa (Benin, Botswana, Burkina Faso, Cameroon, Central Africa Republic, Chad, Côte d'Ivoire, Ethiopia, The Gambia, Ghana, Guinea, Mali, Mauritania, Namibia, Niger, Nigeria, Senegal, Sierra Leone, Sudan, Tanzania, and Zambia)	
Habitat	Found in open ditches, swampy grassland, at the edges of lakes, and in or at the margins of rice fields. Grows in clay/loam soil and black soil.	Found in swampy areas, at edge of pond and tanks, beside streams, in ditches, in or around rice fields. Grows in shallow water up to 0.3 m, in seasonally dry and open habitats.	Found in savanna. Grows in deep water, seasonally flooded land, stagnant water, and slowly flowing water or pools; prefers clay or black cotton soils. Found in open habitats.	

Source: Lu Bao-Rong, *et al.* (2002).

to 4 thousand seeds each), sealed in laminated aluminum foils, are stored at (-) 20°C in specially designed modules. Seed viability is checked at regular intervals and the samples showing more than permissible reduction in viability are sent for regeneration to the designated sites that take due care for the samples' genetic integrity. Relevant gene bank standards are also strictly adhered to.

Adequate capacity for taxonomic identification and quarantine inspection are essential requirements for such facilities. Gene banks are also equipped with modern computerized database with specialized software to suit the requirements including networking.

The gene bank manager/curator acts as the trusted link between the seed providers and users of the germplasm collections. He arranges maintenance of national active germplasm collections for important crops at suitable sites in partnership with capable institutes/organizations encouraging easy access to users through field visits.

### **Adding Value to Germplasm Collections**

A proper documentation system is the key to effective utilization of a gene bank's resources. Faster and more reliable computers allow researchers to manage and analyze data more easily, and publish catalogues and reports. Gene bank characterization and documentation have been also significantly enhanced with advances in information technology, geographical information systems (GIS) and DNA marker technology. Computerized documentation systems, and information provided by GIS or from DNA assessment of variation, can help plant explorers in searching for specific sites where specific desirable genes may be found. Well-documented analysis of the number and types of useful polymorphism allows gene bank curators to offer specific accessions with the desired characteristics to research geneticists or plant breeders, who can then select material tailored to their needs (IPGRI, 2002; De Vincente, 2004).

### ***In situ* On-Farm Conservation of Genetic Resources**

Gene banks should promote *in situ* conservation to maintain the genetic integrity of plant populations in their natural sites promoting their evolutionary development. Likewise, gene banks should support on-farm management and improvement of plant genetic resources in partnership with the farmers. This evolutionary conservation approach also continuing natural selection in diverse environments, and has

low direct costs. It also increases people's control over their genetic resources. Rational *in situ* conservation can help in supporting the co-evolutionary dynamics between crops and wild relatives, and the pathogen populations of each species.

### **Accession Duplicates and Safety Duplication of the Collections**

Duplicated accessions within a collection must be identified to avoid waste of costs and capacity. Probable duplicates can be identified on the basis of passport data, but additional assessment/confirmation is needed using descriptor lists in the field and biochemical or DNA marker testing in the laboratory. It is considered important to provide for safety duplication for the main germplasm holding at another suitable site to safeguard against unforeseen calamities and accidental losses.

### **Core Collections Concept**

Some gene banks have large and diffuse germplasm collections, which are often ineffectively managed and seldom accessed by plant breeders. Assessment of genetic diversity in these collections helps in developing core collections that help in improving both the management and also the utilization of the collection. Core collections are subsets of the main collection, comprising selective accessions that represent most of the genetic variability contained in the entire collection. The main collection can be stratified into groups (subsets) sharing common characteristics according to taxonomy, geographic or ecological origin, and descriptors, followed by sampling within these groups. A core subset provides in a way an entry point to the entire collection for accelerating the utilization of germplasm and should not be looked upon as a substitute of the latter.

### **Advent of Biotechnology Molecular Techniques**

Agricultural biotechnology has recently emerged as a priority research area in India with the expectation that it may help in developing novel, value added products and useful tools. It holds the potential to increase and stabilize food production, reduce the dependency on chemicals, and lower the cost of raw materials, all in an environmentally friendly manner (See Table 4 for relevant information). Major research topics include:

- Mapping and sequencing of agriculturally important plant/animal/microbial genomes to elucidate gene function and regulation with a view to facilitating desired genetic modifications.

**Table 4: Agriculture and Biotechnology Application**

Period	Notable Developments
Around 10,000 BC	Beginnings of agriculture. Civilisations, harvesting from natural biological resources, begin domesticating crop plants and animals while practising selection of desirable plant materials for propagation and animals for breeding.
Late 19th Century	Discovery of the principles of inheritance by Gregor Mendel in 1865 and subsequent rediscovery around 1900, laying the foundation for classical breeding methods.
1930s	Development of commercial hybrid maize.
1940s to 1960s	Application of induced polyploidy, mutagenesis, tissue culture and plant regeneration. Discovery of transformation and transduction. Double helix model by Watson and Crick in 1953 for the structure of DNA.
1970s	Advent of gene transfer through recombinant DNA techniques. Use of embryo rescue and protoplast fusion in plant breeding and artificial insemination in animal reproduction.
1980s	Tissue culture for mass propagation in plants and embryo transfer in animal production.
1990s	Genetic fingerprinting of a wide range of organisms. First field trials of genetically engineered plant varieties in 1990 followed by the first commercial release in 1992. Genetically engineered vaccines and hormones and cloning of animals.
Around 2000 onward	Bioinformatics, genomics extending to proteomics and metabolomics

Source: The State of Food and Agriculture. FAO, 2004.

- Studying genetic control along with biochemical/molecular basis of metabolic pathways, growth and development to assist in developing new products with novel food, pharmaceutical, and industrial uses.
- Understanding the molecular basis of interactions of plants and animals with their physical and biological environments to improve genetic adaptation to stress environments.
- Strengthening food safety assurance methodologies including rapid tests for identifying chemical and biological contaminants in food and water.

### Genetic markers and DNA banking

Molecular markers are descriptors that offer reproducible results for characterizing genotypes. Applied plant genomics also improves the understanding of crop gene pools. This gene pools concept has been enlarged by including transgenes and “native” gene pools. Molecular

markers and gene sequencing are important tools for gene bank management, particularly because they can be used to estimate genetic relationships within a germplasm collection (IPGRI, 2003). Unique materials can be preserved or collection gaps identified with the aid of DNA markers, which can be used to properly assess genetic diversity (IRRI, 2002; Hamilton, 2004). Moreover, DNA markers provide an alternative means of monitoring and facilitating the introgression of genes from wild species into cultivated gene pools.

Sequencing of crop genomes has opened new frontiers in biodiversity conservation and genetic enhancement (Yu, 2002). Advances in gene isolation and sequencing in plant species offer the possibility that within a few years, gene bank curators could replace their large cold stores of seeds with crop DNA sequences, which will be electronically stored and easily accessed by users.

This characterization of plant genomes will create true gene banks, which should possess a large and accessible gene inventory of today's non-characterized crop gene pools (Richards, 2004). Of course, seed banks of comprehensively investigated stocks should remain because geneticists and plant breeders — the main users of gene banks — will need this germplasm for their work.

Finding new genes adds value to traditional agricultural products. Genetic resources available in gene banks are still the best source for an easy gene discovery. This work will be facilitated by gene databases assembled with the aid of applied plant genomics, which can also accelerate the utilization of available genes through transformation or meiotic-based breeding methods.

### **Genetic and Molecular Mapping of the Rice Genome**

A fairly detailed genetic map of rice has been developed covering all the 12 linkage groups contributing to our understanding of the structure, function and evolution of the rice genome. The linkage map contains valuable information for the rice breeders showing the relative locations of specific genes along the chromosome. Any inherited physical or molecular characteristic that differs among individuals and is easily detectable is a potential genetic marker. Markers can be expressed DNA regions (genes) or DNA segments that have no known coding function but whose inheritance pattern can be followed. DNA sequence differences are especially useful markers because they are plentiful and easy to characterize precisely. Markers must be polymorphic to be useful in

mapping; that is, alternative forms (alleles) must exist among individuals so that they are detectable among different members in the mapping population. Table 5 provides more information on additional desirable characteristics of molecular-genetic markers. The plant genomic effort is challenging since the range of plant genome size is very large extending from approximately the same size as the genome of many small animals to more than five times as large as the human genome. While the construction of detailed gene-linkage maps of complex genomes facilitates the localization of genes to specific regions on chromosomes, more precise allocation of specific genes requires cloning of high-molecular-weight DNA if it is to be done efficiently (De Vincente, 2004). Subsequently, information contained in the gene map and the molecular map needs to be verified and integrated.

**Table 5: Desirable Properties of Useful Molecular-Genetic Markers**

Properties	Remarks
1. Highly polymorphic	Should be variable among individuals. The degree of polymorphism detected depends on the technology used to measure it.
2. Reproducible	Reproducible in any laboratory experiment, whether within experimental events in the same laboratory or between different laboratories performing identical experiments.
3. Codominant	Depending on the type of application, the selected technology must be able to detect the marker's different forms, distinguishing between homozygotes and heterozygotes (codominant inheritance). A heterozygous individual shows simultaneously the combined genotype of the two homozygous parents.
4. Evenly distributed throughout the genome	The more distributed and dense genome coverage is, the better the assessment of polymorphism.
5. Discriminating	Should be able to detect differences between closely related individuals.
6. Not subject to environmental influences	The inference of a marker's genotype should be independent of the environment in which the individual lives or its developmental stage.
7. Neutral	The allele present at the marker locus is independent of, and has no effect on, the selection pressure exerted on the individual.
8. Inexpensive	Easy, fast and cheap in detecting across numerous individuals. If possible, the equipment should be of multipurpose use in the experiment.
9. Easy to measure	

Source: IPGRI, 2002.

Detailed information on genome maps for 34 organisms, including 8 plants (Rice, Wheat, Maize, Barley, Oat, Soybean, Tomato and Thale Cress), are now available representing both completely sequenced organisms and those for which sequencing is in progress (See NCBI Website for more information). These developments have opened new vistas in characterization and classification of gene bank holdings and detect duplicates. There are publicly as well as commercially funded efforts to sequence the rice genome. There are two publicly funded rice genomic sequence projects. One, the International Rice Genome Sequencing Project, undertaken in 1997, is a collaboration of publicly funded investigators working to sequence the *Oryza sativa specie japonica genome*. The second effort, initiated in April 2000, is the whole-genome shotgun sequencing project sponsored and funded by the Chinese Academy of Sciences; Beijing, China. This project reported a draft sequence assembly of *Oryza sativa specie indica* in the April 5, 2002 issue of Science (Yu and the Team members, 2002).

The first commercial effort, by Monsanto, resulted in a database of genomic sequence that has been shared with the International Rice Genome Sequencing Project members. The second commercial effort, collaboration between Myriad Genetics and Syngenta, used the whole-genome shotgun method. However, a press release in January 2001 noting the completion of the "rice genome map" by this project notwithstanding, little genomic sequence has been deposited into the public domain.

### **Candidate Genes Identification and Transfer**

A major goal of plant genome research is to develop and implement strategies for the isolation of genes for desirable agronomic traits such as disease resistance. To begin with, there is need to isolate individual rice chromosomes and to make chromosome-specific gene libraries (one of each of the 12 chromosomes). After the completion of this work, it would be relatively easy to clone the different resistance-conferring genes from domestic as well as wild rice species (IRRI, 2002). The bacterial blight of rice is an attractive system for studies on disease resistance because both the host and pathogen are amenable to molecular genetics.

Although remarkable progress has been made in resistance breeding without the knowledge of what resistance genes do, isolation of a plant disease resistance gene may ultimately lead to novel and environmentally safe methods of disease control. The relatively small genome, large

fraction of low copy DNA and transformability of rice makes this crop a model monocot for such studies. Hence, yield losses due to stress environment can be avoided by developing rice varieties disease resistant (against viral, fungal and bacterial related diseases), and insect tolerant (against different insect pests). The gene coding for many of these traits are present in different wild rice species. It would be very important to locate and characterize these genes by screening germplasm collections systematically, first by physical mapping and then by cloning.

Gene Bank accessions with high frequency of important heritable traits need to be identified and subjected to Restriction Fragment Length Polymorphism (RFLP) mapping techniques to further define the locations of specific genes. It will be desirable to develop methods to identify genetically controlled characteristics, such as grain quality, and develop probes to expedite gene transfer among varieties. Construction of a rice library containing short tandem repeat sequences will be required, along with precise information on verified correlations between workable markers, for targeting the transfer of marker-assisted Quantitative Trait Loci (QTL).

### **Cost of Genetic Resources Conservation**

The danger of excessive reliance by farmers and breeders on a narrowing genetic base was dramatically revealed by the widespread infestation of US hybrid corn (having cytoplasm male sterility) with southern corn leaf blight in the early 1970s. This incidence renewed worldwide effort to expand the amount of agricultural biodiversity conserved *ex situ* in gene banks for use in crop breeding. Over six million samples of seed and other propagules are now stored in about 1300 gene banks worldwide at enormous costs. Modern biotechnologies, providing new and less costly ways of screening crop samples for useful traits, have increased the usefulness of genebanks to breeders.

The storage costs of seed samples at IRRI and ICARDA gene banks (average around US\$0.47 per accession per year for crops kept at both locations) are comparatively low because of the cheap labour and electricity costs, whereas these costs are higher at ICRISAT (US\$1.32 per accession), where electricity is expensive (Koo *et al.*, 2003). Conservation cost, including both recurrent and non-recurrent components, per accession per year in the Indian National Gene Bank varies around US\$ 0.77 (Singh and Saxena, 2004). Long term conservation cost (including periodic viability testing and regeneration costs) of wild rice at IRRI is

about US\$68.76 per accession and that of chickpeas at ICRISAT comes to nearly US\$15.48 per accession, respectively) because of the higher costs of repeated regeneration (See: Koo *et al.*, 2003). conserving *in vitro* costs US\$11.98 per accession per year. As a rule, wild and weedy varieties, cross-pollinating crops, and vegetatively propagated crops, that are relatively expensive to regenerate, are more costly to conserve over the long term. Distribution costs are substantially higher than the conservation cost in present-value terms because of the more frequent viability testing and the additional regeneration costs associated with medium-term storage.

### **Multilateral Trade and Environment Agreements**

Release of genetically modified organisms (GMOs) and genetically engineered crop varieties ushered in a new era of highly contested developments relevant to safeguarding the environment and also the centres of origin and diversity of crop plants. The genetic use restriction technology (GURT) sought to enable the multinational seed companies to develop such high yielding varieties of self-pollinated crops like wheat that would prevent the farmers from using the seed of their own crop for sowing in the following season. The government of India responded promptly by banning the import of such products in India.

Provisions under Trade-Related Intellectual Property Rights (TRIPS) Agreement of the World Trade Organization (WTO) made it obligatory for the member countries in 1995 to protect plant breeders' rights by enacting suitable national legislation for this purpose or through an effective *sui generis* system of plant variety protection. India's Protection of Plant Varieties and Farmers' Rights Act 2000 sought to meet this obligation.

Entry into force of the Convention on Biological Diversity (CBD) on 29th December, 1993 was another significant event since this Convention recognized for the first time the sovereign rights of nation states over their natural biological resources and also on setting terms of access to them based on prior informed consent ensuring equitable and fair sharing of benefits. This replaced the earlier notion adopted by the FAO (Through the Commission on Plant Genetic Resources), viz., that plant genetic resources were the common heritage of humankind. Cartagena Protocol on Biosafety was subsequently adopted by the CBD to regulate the movement of GMOs and pursue related matters. India is actively participating in the follow-up negotiations

including the precautionary principle and polluter to pay provisions. India has enacted Biodiversity Act 2002 responding to obligations under the CBD.

Issues concerning agricultural biodiversity in general, and plant genetic resources (PGR) in particular, have attracted priority attention in the agenda of successive meetings of the Conference of Parties to CBD. Two items related to PGR were referred to the FAO for perusal, viz., the status of designated germplasm collections held in International Gene Banks under the CGIAR system and the decision regarding germplasm collections made/transferred prior to the CBD. The FAO-CPGR responded by suitably revising the content of the International Understanding on PGR in harmony with provisions of the CBD. These prolonged negotiations led to the International Treaty on PGR that entered into force on 29th June 2004 bringing the genetic resources of 35 food crops and 29 forages back into the public domain for common access through multilateral system to ensure food and nutrition security.

There is some apparent overlapping and even inconsistency in the provisions of the aforementioned two legislations and it is expected that the implementation rules being framed for them would take care to reconcile them.

### **The Way Ahead: New Role of Gene Bank Managers/Curators**

It is paradoxical that the countries, that are considered the centers of origin and diversity of major food crops including rice, happen to be lagging behind in development as may be observed among the Group of 17 Biodiversity Diverse countries spread across the globe. This is so when these countries have unmatched reservoirs of naturally occurring plant genetic resources and many of them have also developed large gene banks. A common constraint appears to be lower application of recent advances in biotechnology and molecular biology for want of access and adequate funding. There is indeed a large scope for technical cooperation and technology transfer at regional and international levels (See: IPGRI, 2002; Raney and Pingali, 2004).

A noteworthy development in this context is the beginning of a positive dialogue in recent years between the enthusiastic supporters of biodiversity conservation movement and the advocates of sustainable development opening up vast avenues of meaningful interactions and moving forward. Indian economy is essentially agro-based and, hence, sustainable development in India is inseparably linked to sustainable

agriculture pointing out the urgency of taking up more comprehensive strategies and programmes of diversifying agriculture (Rana, 2004). The crop improvement projects, underway in different agro-ecosystems and varying agroclimatic conditions, will have to play a key role in achieving this objective and they will have to draw more and more from the germplasm collections held in gene banks employing new biotechnology and molecular techniques.

Following this approach, the gene bank managers will henceforth be required to cater to the needs of biotechnologists and molecular biologists in addition to breeders and other researchers (De Vincente, 2004). They will also be required to solicit active involvement of specialists in these fields for accelerating the characterization of germplasm collections, screening against molecular markers for disease resistance and QTL, and identification, isolation, cloning and transfer of candidate genes in rice and other major crops (SGRP, 1999; IPGRI, 2002; Richards, 2004; Hamilton, 2004; IRRI, 2004). Development of reliable databases, updated through new information technology, will facilitate access of relevant data to all *bona fide* users (IPGRI, 2003, Dhillon *et al.* 2004).

A fast emerging role for the gene bank managers and PGR workers relates to IPR issues and the development of workable Material Transfer Agreements (and also their implementation through active follow up actions) vis-a vis the implementation of the provisions of various genetic resources-related agreements and international treaties. Additional responsibilities will include registration of elite genetic stocks/developed germplasm and storing referral seed samples of all the varieties released for commercial cultivation. Introduction of genetically engineered crop varieties and GMOs will also demand more compelling attention. Considering that the seed samples along with passport information were obtained from the farmers of different parts of the country in trust, the gene bank manager/curator has the obligation towards promoting Farmers' Rights to their resources, knowledge, technology choices and production systems as protected under the Protection of Plant Varieties and Farmers' Rights Act 2000.

India is a Contracting Party to many international treaties related to biodiversity, environment and trade that have apparently conflicting provisions and require harmonization (Bragdon, 2004). In addition, there are two recently enacted national legislations with direct bearing upon access to genetic resources and benefit sharing implications. These

aspects require not only the effective coordination at the highest level among different national nodal points with overlapping responsibilities but also convergence of policy decisions of relevant Union Ministries and State Governments.

Costs are steadily rising for collecting germplasm samples, growing them for seed multiplication, characterizing and documenting them, processing seeds for storage, packaging and storing them for long term, monitoring their viability and regenerating them when due. Estimated costs vary across gene banks from less than 1 to over 15 US\$ per accession per year (See: Koo *et al.*, 2003). Since conservation, characterization, documentation of plant genetic resources and their supply to all *bona fide* users is a national responsibility for the NBPGR, there is need for committing funds for this purpose on a long term basis and making appropriate budgetary allocation, both at the national and state levels.

Developing and acquiring new biotechnology tools and molecular biology techniques are costly propositions for the developing countries and also require additional infrastructure and capacity building. Scope and feasibility of regional and multilateral technical cooperation, provided under terms of various biodiversity-related international agreements/conventions, need to be explored with greater urgency to assist the desired technology transfer and also capacity building in developing countries.

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