

No just seed repositories: a more pro-active role for gene banks

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Gene bank curators have interest in the conservation of plant genetic resources because of the potential uses of this germplasm. Gene banks are biodiversity reservoirs and sources of alleles for sustainable genetic enhancement of plant crops. Efforts have been made to collect landraces, cultivars that were becoming obsolete, genetic stocks, and in some cases wild species important for crop improvement (FAO 1996a). Ex-situ collections were assembled, followed by phenotypic and biochemical characterization. Well-endowed gene banks also conducted agronomic assessment after field testing or resistance screening against pests and diseases (Stalker and Chapman 1989). Seed or propagule regeneration and multiplication became a routine activity in many gene banks (Breese 1989), despite the costs involved in maintaining a large germplasm collection.

Gene banks and sustainable crop improvement

The operations of a modern gene bank are not restricted to collection, characterization, regeneration and documentation (FAO 1996b). Breeding gains rely on access to useful genetic variation in the respective crop gene pools. If genes available in wild species are to be put into a usable breeding form, it is important that the long-term research agenda includes development of advanced gene pool stocks (Ortiz, 2002).

In recent years, some gene banks have made significant investments in studies to determine the extent of genetic diversity, because this knowledge enables proper germplasm organization and development of improved parents and new cultivars. In this way, gene bank curators can maximize the utilization of wild and cultivated gene pools in crop breeding.

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 documentation has 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 search for specific sites where specific genes may be found.

Of course, the time and resources spent on germplasm characterization depend on the program objectives, financial support, available data on genetic diversity (and pedigree information), and knowledge and importance of the traits being investigated. Descriptor lists have been developed for most crop species by the International Plant Genetic Resources Institute (IPGRI, formerly IBPGR) in collaboration with researchers from other organizations worldwide. Analysis of variation in germplasm collections provides an added value for gene banks that make this research investment. Well-documented analysis of the number and types of useful polymorphism allow gene bank curators to offer specific accessions with the desired characteristics to research geneticists or applied plant breeders, who can then select material tailored to their objectives.

International conservation and enhancement of plant genetic resources in the CGIAR

The CGIAR aims to help improve food security and reduce poverty in the developing world by promoting sustainable agricultural development based on environmentally sound management of natural resources. The IARCs of the CGIAR preserve crop genetic resources, particularly from developing countries, and are also brokers for international germplasm exchange, providing free access to their collections (CGIAR 1999). Indeed, the CGIAR policy on plant genetic resources is based on the unrestricted availability of germplasm held in IARC gene banks. IARCs use material transfer agreements (MTAs) to facilitate the utilization of designated genetic materials and to protect them from claims about intellectual property rights. Annually, over 100,000 accessions held in CGIAR gene banks are distributed worldwide.

The CGIAR centers focus on genetic resources conservation and delivery of improved germplasm. The conservation of genetic resources of important food crops for the long-term benefit of humanity has been the most important goal of biodiversity research in the CGIAR. CGIAR crop improvement programs not only rescue and preserve endangered crop biodiversity, but also enhance crop gene pools. Furthermore, multidisciplinary teams (crop protection, agronomy, plant physiology) have identified valuable new traits conferring resistance to biological and environmental stresses. The identification of new traits allows the development of a more stable, diversified germplasm with improved disease and pest resistance, stress tolerance, quality, and productivity. New traits are incorporated into breeding pools that are shared with partners in the national research systems in each country. In recent years IARC researchers are introducing and applying new

This approach is a logical progression from conservation-management-utilization of genetic resources to a broader approach, using new tools (and wider partnerships with national research systems) to exploit the genes available in different crop gene pools. The CGIAR centers also provide technical backstopping to regional and international crop networks, which facilitate the sharing of information and genetic resources (especially improved breeding material developed by IARCs and their partners) among network members.

In situ and on farm conservation of plant genetic resources

Gene banks should promote in-situ conservation to maintain the genetic integrity of plant populations in their natural sites (Ortiz 1999). Likewise, gene banks should support on-farm management and improvement of plant genetic resources (FAO 1996b). This evolutionary conservation approach also allows continuing natural selection in diverse environments, and has low direct costs (IPGRI 1993). It also increases people's control over their genetic resources.

Rational in-situ conservation can help preserve the co-evolutionary dynamics between crops and wild relatives, and the pathogen populations of each species (Frankel et al. 1995). Dynamic genetic interactions exist for micro-evolutionary changes in this whole host-disease system. For example, the co-evolution in a wild host and its resident pathogen population runs parallel to evolutionary changes in the pathogen population infecting crops (these changes can be a response, for example, to the introduction of new cultivars containing introgressed wild resistance genes). Likewise, pathogen biotypes from the wild alternative host can invade crops, eliciting a response reaction by wild resistance gene(s), already incorporated in improved cultivars, to the new crop pathogen population.

Duplication and germplasm repatriation

Duplicated accessions within a collection – and between gene banks – must be identified to avoid waste of capacity. Putative duplicates can be identified on the basis of passport data, but additional assessment/confirmation will be needed using descriptor lists in the field and biochemical or DNA marker testing. These duplicate accessions may need to be bulked to prevent loss of alleles in case of partial duplication. Networking will help gene banks share responsibilities, resources, and costs. For example, a national or regional gene bank with limited resources can focus on its own geographical domain, or it may agree to duplicate collections for safety purposes.

Repatriation or “import” of native germplasm available only in “foreign” collections should be an important activity for gene banks with a national or regional mandate. This activity may be followed by germplasm restoration aiming at in-situ conservation or on-farm management of these genetic resources in the locations where they were originally collected.

Core collections to enhance utilization of gene banks

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 has helped establish core collections. These core collections are subsets of large germplasm collections, containing chosen accessions that capture most of the genetic variability in the entire collection. Thus, developing a core collection improves the management and utilization of a germplasm collection.

Core collections are assembled considering a hierarchical structure of the gene pool. The entire collection can be stratified into groups sharing common characteristics according to taxonomy, geographic or ecological origin, and neutral or non-neutral descriptors, followed by sampling within these groups (Huamán et al. 1999, Ortiz et al. 1998 and references therein). Using this process core subsets can be identified. Genetic studies in selected crops have shown that common widespread and localized alleles occurring in the entire collection are contained in the core subset (Huamán et al., 2000). Only rare localized alleles may be excluded during the sampling process. The core subset often provides an entry point to the entire collection for further investigation of biodiversity or for the utilization of these resources (Ortiz et al. 1999).

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 that are becoming available through comparative analysis of plant biological repertoires (Lee 1998).

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. Unique materials can be preserved or collection gaps identified with the aid of DNA markers, which can be used to properly assess genetic diversity. Moreover, DNA markers provide an alternative means of monitoring and facilitating the introgression of genes from wild species into cultivated gene pools.

conservation and genetic enhancement (Ortiz 1998). 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 (e.g., through the Internet).

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. 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.

Globalization, genetic resources and social sciences

Most major crops originated in today's poor developing world, which still has the highest plant biodiversity. However, many gene banks in the developing world rely on external funding. International collaboration between gene banks from the North and South, and commitment from development investors to preserve and enhance crop biodiversity, should lead to a global system for the conservation of plant genetic resources.

The private seed sector, driven by the need for profit, also defends its interests, with patents and intellectual property rights. Germplasm exchange between gene banks and users is affected by this evolving environment. Gene banks should therefore focus not only on scientific and technical questions but also on research that may influence government policy-making decisions on plant biodiversity. One aim should be to determine the consequences of a multilateral system of access and benefit-sharing arising from the utilization of plant genetic resources (Lesser 1998). Policy research may provide options to compensate farmers for their past contributions to crop genetic resources. Other areas for study should focus on developing a method to evaluate the worth of a germplasm collection, or carrying out investigations to understand the links between biodiversity and socio-economic factors.

Impact assessment of plant genetic resources conservation and enhancement will improve prioritization and setting of research targets in gene bank operations. Furthermore, impact assessments that quantify a gene bank's contribution towards protecting the environment will help attract more donor funding.

Gene banks, biodiversity and development

A germplasm collection that is not fully exploited is simply a museum of plant accessions or a living herbarium. Conserving and enhancing plant biodiversity is an essential part of sustainable genetic enhancement of crops. Therefore, by promoting the broad utilization of plant genetic resources, gene banks are fulfilling their role in improving human well being. As IPGRI (1999) pointed out, improved use of plant genetic resources can help alleviate poverty, increase incomes, and create new income-earning opportunities.

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