



IPGRI

IPGRI Handbooks for Genebanks No. 6

A guide to **effective management** of germplasm collections

J.M.M. Engels and L. Visser (editors)



WAGENINGENUR



SGRP



FAO is the largest specialised agency in the United Nations system and the lead agency for agriculture, forestry, fisheries and rural development. An intergovernmental organization, FAO has 180 Member Nations plus a member organization, the European Community. Since its inception in 1945, FAO has worked to alleviate poverty and hunger by promoting agricultural development, improved nutrition and the pursuit of food security—the access of all people at all times to the food they need for an active and healthy life.

A guide to
effective management
of germplasm collections

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The International Plant Genetic Resources Institute (IPGRI) is an independent international scientific organization that seeks to advance the conservation and use of plant genetic diversity for the well-being of present and future generations. It is one of 16 Future Harvest Centres supported by the Consultative Group on International Agricultural Research (CGIAR), an association of public and private members who support efforts to mobilize cutting-edge science to reduce hunger and poverty, improve human nutrition and health, and protect the environment. IPGRI has its headquarters in Maccarese, near Rome, Italy, with offices in more than 20 other countries worldwide. The Institute operates through three programmes: (1) the Plant Genetic Resources Programme, (2) the CGIAR Genetic Resources Support Programme and (3) the International Network for the Improvement of Banana and Plantain (INIBAP). IPGRI also convenes the System-wide Genetic Resources Programme (SGRP).

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FOREWORD

The global successes of plant breeding can be traced back to the early 1960s and largely resulted from increased use of landraces in breeding programmes. The establishment of large, crop-genepool-specific germplasm collections significantly assisted in this. These collections were based on donations from existing breeding collections and on targeted collecting efforts. One of the most significant biological consequences of this progress in agriculture was the steady replacement of locally adapted, diverse traditional landraces grown by farmers over long periods of time. This situation led to a more systematic, globally coordinated approach to collecting threatened germplasm and to the development of concepts for effective, long-term conservation of useful plant genetic resources. These concepts were based on monitoring storage and viability of seeds in genebanks, predominantly cereal grains, on the assumption that plant breeders and other researchers frequently use the germplasm and that strong linkage between conservation and utilization efforts would develop.

Conservation activities have increased manifold over the past two decades. These have encompassed not only threatened crops and their wild relatives in genebanks but also increasing attention has been paid to conservation and management of genetic resources in their natural or traditional environments. The role of humans has been recognized as integral to such conservation efforts. The result has been greater participation of stakeholder groups in planning and implementation of conservation and use of plant germplasm. Moreover, improved seed storage techniques have been developed over recent decades, including *in vitro* methods and cryopreservation. In addition, many new genebanks have been established since the 1960s.

Developments in molecular genetics over the past ten years have had a dramatic impact on plant breeding. These developments are also set to revolutionize genetic resource conservation. The future impact of genomics and bioinformatics can be expected to have an even greater effect. In addition to these technological developments, the political arena has also undergone significant changes, especially since the early nineties when the Convention on Biological Diversity was concluded. During this period the notion of ownership and access to biodiversity completely changed as a result of two developments. The first was a shift from a common heritage principle to one of national sovereignty over genetic resources, which resulted in emphasis on bilateral exchange. The second development was based on changing concepts of property rights. Increasing application of patents to protect innovations

(including identification of genes and the production of new crop varieties) has had profound effects on willingness to share genetic resources freely.

These developments had little immediate impact on the concepts and strategies characterizing routine genebank operations. There was however increasing pressure on genebanks to improve cost efficiency and be more effective. Reduced budgets and paucity of adequately trained staff led to a thorough revision of the predominating genebank management approach. This entailed a revision of concepts and recognition of opportunities for increasing cooperation at regional and international levels. A direct outcome of this was a workshop held in Wageningen, The Netherlands, in 1999 to discuss possibilities for improvement. The contributors included representatives from the System-wide Genetic Resources Programme of the Consultative Group on International Agricultural Research, the Food and Agricultural Organization of the United Nations, the Centre for Genetic Resources, The Netherlands and the Genetic Resources Science and Technology Group of the International Plant Genetic Resources Institute.

The initiative to bring experts together to discuss the consequences of changes in the roles and responsibilities of genebanks led to this publication. It is hoped that the ideas put forward lead to a more critical, balanced and creative approach towards genebank operations on the part of genebank curators worldwide. It is also hoped that decisions concerning concepts and strategies that have been or will be made at the institutional and national level on the conservation and use of plant genetic resources will be made easier by this publication. Genebank staff are encouraged to share their experiences through all means of communication. The reader is kindly invited to provide IPGRI with any comments or suggestions on the current text that would contribute to more effective and efficient conservation and thereby assist in the generation of a solid knowledge base for genebank management.

Rome, 2002

Geoffrey Hawtin
Director General IPGRI

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During the Wageningen workshop the participants decided to have the entire guide written by a limited number of authors rather than produce a series of authored chapters. Consequently, arrangements were made with Dr Trevor Williams to produce a first draft based on the inputs provided by the participants. From this the authors developed a more detailed version. Contributions were made by Ruaraidh Sackville Hamilton, Jan Engels and Theo van Hintum (Chapters 4 and 6), Bonwoo Koo and Melinda Smale (Chapter 7), Emile Frison, Martine Mitteau, Suzanne Sharrock and Bert Visser (Chapter 8), Ehsan Dulloo and Jan Engels (Appendix 2), Ruaraidh Sackville Hamilton (Appendix 3), Theo van Hintum and Bert Visser (Appendix 4) and Suzanne Sharrock and Emile Frison (Appendix 5). These contributions are duly acknowledged. The participants in the Wageningen workshop are listed in Appendix 1. All were important in the production of this publication and are acknowledged. The subsequent review process of the manuscript has led to further improvements of the text and the inputs of the following persons are acknowledged: Murthi Anishetty, Stefano Diulgheroff, Allan Stoner, Suketoshi Taba and Karling Tao. Special thanks are given to Emile Frison and Ramanatha Rao for their in-depth comments and suggestions on the draft, and to Jonathan Robinson for his editorial input. We wish to thank the Centre for Genetic Resources, The Netherlands for organizing the workshop. We also thank the Food and Agricultural Organization of the United Nations and the System-wide Genetic Resources Programme of the Consultative Group on International Agricultural Research for their financial support for the production of this publication.

A NOTE TO READERS

IPGRI's Handbooks for Genebanks are intended to provide practical information to genebank curators and others working in genebanks. To facilitate their use their binding allows them to be kept open on a desk or bench, while the wide margins and 'Notes' pages provide space for readers to make notes or annotate the text.

The Editors welcome feedback from readers on the content and format of the handbook for possible future revisions.

PARTNERS IN THIS PUBLICATION

The Centre for Genetic Resources, the Netherlands (CGN)

The Centre for Genetic Resources, the Netherlands (CGN) holds the national mandate to conserve and to promote the utilisation of plant, animal and forest genetic resources in the Netherlands. It maintains genebanks of 20 horticultural and arable crops, as well as five farm animal species, and a large number of in vivo seed reservoirs of forest tree species. CGN's mission is to contribute to innovative genebank management. In addition, CGN is responsible for contributions to in situ management of genetic resources in the Netherlands and abroad.

Furthermore, CGN carries out plant variety research, in particular for applications for plant breeder's rights on varieties of arable crops and ornamentals, and for variety lists of the Netherlands and of the European Union.

CGN is an independent unit for Statutory Research tasks within Wageningen University and Research Centre. It reports directly to the Ministry of Agriculture, Nature Management and Fisheries.

The System-wide Genetic Resources Programme (SGRP)

The **System-wide Genetic Resources Programme (SGRP)** joins the genetic resources programmes and activities of the Future Harvest Centres in a partnership whose goal is to maximize collaboration, particularly in five thematic areas. The thematic areas - policy, public awareness and representation, information, knowledge and technology, and capacity-building - relate to issues or fields of work that are critical to the success of genetic resources efforts. The SGRP contributes to the global effort to conserve agricultural, forestry and aquatic genetic resources and promotes their use in ways that are consistent with the Convention on Biological Diversity. IPGRI is the Convening Centre for SGRP. The Inter-Centre Working Group on Genetic Resources (ICWG-GR), which includes representatives from the Centres and the Food and Agriculture Organization of the United Nations, is the Steering Committee.

The Food and Agriculture Organization of the United Nations (FAO)

FAO is the largest specialised agency in the United Nations system and the lead agency for agriculture, forestry, fisheries and rural development. An intergovernmental organization, FAO has 180 Member Nations plus a member organization, the European Community. Since its inception in 1945, FAO has worked to alleviate poverty and hunger by promoting agricultural development, improved nutrition and the pursuit of food security—the access of all people at all times to the food they need for an active and healthy life.

1. Introduction

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1. INTRODUCTION

Bert Visser and

Jan Engels

1.1 Rationale

Ex situ germplasm collections have increased enormously in number and size over the last three to four decades as a result of global efforts to conserve plant genetic resources for food and agriculture (PGRFA). These collections are maintained under widely differing conditions, depending on national and international policy frameworks, institutional environments, available expertise, facilities and budgets, and on the extent of national and international collaboration. In addition, the various types of germplasm that constitute these collections require different management regimes. The importance of maintaining the highest standards in management of collections cannot be over emphasized given the sheer numbers of accessions contained in the global ex situ collections. In 1996 these totaled ca. 6 million (FAO, 1998).

The conservation and utilization of plant genetic resources (PGR) is in continuous evolution. Early in the twentieth century the emergence of science-based plant breeding resulted in large collections of germplasm being made. This genetic diversity was readily at hand to be used in plant breeding programmes. Substantial germplasm collections were created, including those of the Vavilov Institute in St Petersburg (VIR) and the Institute of Plant Genetics and Crop Plant Research (IPK) in Gatersleben, as well as those of the Consultative Group on International Agricultural Research (CGIAR). In the 1950s and 1960s genetic erosion was identified as a growing threat to the genetic diversity in food crops and their wild relatives. This threat, which also led to the creation of the International Board for Plant Genetic Resources (IBPGR), represented an important reason to collect plant genetic resources. It resulted in initiatives for

systematic conservation of plant germplasm to ensure adequate and representative diversity for future use. Some of these collections are currently used in plant breeding, but others have become conservation collections for which there are at best only weak linkages with crop improvement programmes.

The large numbers of samples collected in rescue operations during the second half of the last century led in many cases to major backlogs in regeneration and characterization of the conserved germplasm. An assessment by FAO, reported in the State of the World Report on Plant Genetic Resources for Food and Agriculture in 1998 (FAO, 1998) noted numerous constraints to efficient genebank management. For instance, at that time over 65% of the globally conserved collections needed regenerating and many national programmes were experiencing difficulties in regenerating their materials (FAO, 1998). A report by IPGRI in 1998 documented the existing management constraints for the collections of the International Agricultural Research Centres (IARCs) of the Consultative Group on International Agricultural Research (CGIAR). These collections form the basis for breeding many of the world's staple crops (SGRP, 1996; 1997).

The question of how to determine which germplasm (at the species and accession level) qualifies for maintenance in genebank collections is receiving increasing attention. In particular this is due to the ever rising costs of maintenance and regeneration and the subsequent possibilities for genetic erosion occurring in a genebank when proper management is lacking. Genebank 'economics' is an implicit dimension of any genebank's management and operation. Authorities that fund genebanks increasingly request improved accounting of operations. Genebank economics does not only represent an external factor in terms of allocating budgets to specific genebank operations but more importantly relates to internal decision-making on expenditure.

The management of germplasm collections has often evolved without good planning. Furthermore, local conditions for germplasm management differ enormously and many different management approaches have emerged, leading to a range of experiences. Some management aspects have been increasingly recognized as crucial to sustainable maintenance and optimal utilization of high-quality germplasm. These aspects have received substantial attention reflected in the voluminous literature about them. However, other aspects have been largely neglected. These include quality control schemes, the distinction between the management of germplasm collections for conservation and for

utilization, economics of conservation and integrated attempts at genebank management that account for effects of measures of one aspect (e.g. promotion of use) on other aspects (depletion of stocks; higher regeneration load). In addition, the relationship between a genebank's mandate and its specific conservation objectives has received very little attention to date. Most importantly, the linkages between ex situ and in situ conservation have not been adequately considered.

Attempts to respond to the above challenges through the provision of appropriate strategies have been limited until now. This document attempts to fill the gap and to provide genebank managers and other stakeholders with useful information on issues of germplasm collection management to help solve problems that are regularly confronted. It also represents an attempt to incorporate up-to-date technical developments into aspects of germplasm collection management.

1.2 Objective of this handbook

The objective of this publication is to provide the reader with ideas, options and considerations to assist in developing coherent and effective genebank management strategies. In particular, important elements of management at both the genebank and the collection level are analyzed, options for more efficient and cost-effective management are discussed, and genetic and economic implications are inferred. This will hopefully lead to rationalization of genebank operations under a range of economic conditions, taking account of various government policies and other important factors. It is hoped that this information, together with examples based on how different genebanks have resolved particular management problems, will help the reader to make informed decisions on appropriate germplasm management strategies.

This handbook is not intended to represent another blueprint for germplasm collection management. Blueprints run the risk of being counterproductive since they are based on conditions that are seldom met with in real life. Genebank management requires creative and adaptive decision-making tailored to operating conditions that are specific yet continuously changing.

1.3 Explanation of contents: The Roadmap

Following this introductory chapter we will analyze the context in which genebank management takes place. Consideration will be given to the policy environment, the relationships between

genebanks and national PGR programmes, governance of genebanks, including stakeholder participation in planning and decision-making, and the relationship between ex situ and in situ conservation within a country. This analysis should encourage the reader to reflect on the conditions under which a genebank operates, since these largely determine appropriate management strategies and determine which objectives are realistic.

The third chapter presents an elaboration of genebank objectives in relation to international agreements and makes a clear distinction between conservation and utilization. The discussion on genebank objectives also takes into account the impacts of available budget and infrastructure and options for collaboration with various third parties to help reach goals.

The fourth chapter focuses on biological parameters that influence genebank management, including breeding system (sexual, vegetative, inbreeding or outbreeding) and seed storage characteristics of particular germplasm, conservation and utilization concepts, relationships with breeders' collections, and the need for quality control. In this chapter some new concepts and strategies for the management of germplasm are presented that could form the basis for rationalizing collections.

The fifth chapter comprises a discussion on routine genebank operations and practices and the implications for maintaining genetic integrity and monitoring genebank economy. It deals with all routine aspects of germplasm management from collection and incorporation until distribution to users.

Chapter 6 is concerned with options for rationalizing germplasm collection and genebank management from conservation and utilization perspectives. The economics of genebank operations are discussed in Chapter 7. Chapter 8 poses the question of how responsibilities can be shared among organizations.

1.4 Target audiences

This handbook is aimed at the PGR community as a whole, but particularly at genebank staff. Although substantial differences in current capacity and experience in genebank management exist, the authors have assumed that essentially all stakeholders can benefit from some of the considerations and select useful information for particular conditions. While the PGR community is regarded as the prime target group for this publication, it is expected that policy-makers may take advantage of the analytical

framework provided and obtain a better insight into the intricacies of genebank management. In particular, it is hoped that the handbook will contribute to a better understanding of the consequences of implementation of existing and future PGR policies, as well as of the consequences of budget restrictions and constraints on the sustainability and efficiency of long-term conservation activities. It is further hoped that the publication will contribute to strengthening the role of genebanks in promoting germplasm use.

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2. CONTEXT OF GENE BANK MANAGEMENT

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2.1 Policy framework

Continuity in the policy environment

External policies increasingly influence genebank objectives and operations, but such influences per se are nothing new. The establishment of genebanks was, by definition, based on decisions of external stakeholders, from both breeding institutes and government agencies. In this context, assigning germplasm stocks in plant breeding institutes as PGRFA collections for conservation has always been based on the conscious decisions of breeding programme managers. These stakeholders held views on the role of the genebank that translated into genebank objectives and policies. Therefore, it can be surmised that policies have always shaped genebank operations. The policy framework has however changed substantially in several aspects recently such that there exists growing awareness of the potential value of PGRFA. Moreover, the impact of developments in biotechnology, and the emergence of novel regulations and legislation concerning access and benefit-sharing, based on the Convention on Biological Diversity (CBD) and the International Treaty (IT) on PGRFA, have affected the way in which germplasm collections are managed.

Centralized national genebanks emerged following policy decisions that responded to the needs of national breeding industries and the need for national food security based on viable agricultural production. Donor countries (e.g. Germany, the Nordic nations and Japan) also contributed to their emergence in some developing countries as a result of aid policies. Institutional genebanks and designated germplasm collections in breeding institutes, set aside for conservation purposes, were largely

established to safeguard continued access to potentially valuable breeding or research material after breeding programmes stopped and to cope with the threat of genetic erosion. Likewise, CGIAR collections were developed on the basis of breeders' needs for genetic diversity. The subsequent establishment of the System-wide Genetic Resources Programme symbolizes the intrinsic value of the current collections, which exceeds the current needs of CGIAR breeders (<http://www.sgrp.cgiar.org/>). Whereas such collecting activities were largely driven by the immediate potential value of the germplasm, the International Board for Plant Genetic Resources (IBPGR) was established in 1974 to coordinate global collecting activities for threatened landraces and wild relatives. The threat of genetic erosion and the potential use value were principal motives for collecting PGRFA. In addition, several countries initiated their own systematic collecting activities to safeguard their genetic resources (Pistorius, 1997).

Recent changes in the policy environment

Although plant genetic resources conservation and use has always been bound by policy considerations, there have been major changes in the policy environment. Germplasm collections in genebanks have become components of a far larger entity. They no longer merely represent a supply of materials for plant breeding and research. Genebank management is affected by developments in broader issues of biodiversity conservation, especially in the context of the CBD (UNEP, 1992). Emergence of new technologies, such as those of biotechnology (including genetic modification) and information technology, coupled with increased global recognition of the value of PGR have also influenced genebank management (Visser and Nap, 2002).

A major paradigm shift at the political level has meant a change in the concept of plant genetic resources as the 'heritage of mankind', as formulated in the former International Undertaking (IU) on PGRFA, established in 1983. The concept of national sovereignty represents a central pillar of the CBD that came into force in 1993. Since 1993 conservation of genetic resources and the regulation of access to these resources have been accepted to be the responsibility of the country under which the jurisdiction of these genetic resources comes. International exchange of germplasm can no longer be taken for granted, but is based on bilateral negotiations and agreements. The succession of the FAO IU by the IT on PGRFA is a direct consequence of the acceptance of the CBD.

The second paradigm shift has been a technical one based on the power of biotechnology and in particular of genomics, which opens new avenues for using biodiversity. Selection of traits based on phenotype and evaluation may be complemented or replaced by seeking genes directly at the DNA sequence level and indirectly using molecular markers. Important genes, once located, can be transferred into adapted germplasm using traditional breeding methods or can be isolated, cloned and subsequently incorporated into a recipient plant using methods for genetic modification (Visser, 1998; Visser and Nap, 2002).

The increasing power of information technology renders it possible to search successfully for individual characters or traits from huge amounts of data. A set of variant DNA sequences in a host plant, corresponding to a set of pathogen resistance genes, can be analyzed in a large number of accessions and can be compared with phenotypic variation in host-plant resistance. This type of information will greatly enhance the capacity of plant breeders to produce better adapted material. Once the information on gene sequences and corresponding phenotypes is available in an electronic database it becomes valuable to plant breeders wherever that host-pathogen relationship exists (Karp, 2001; Sobral, 2001).

These paradigm shifts have been accompanied by an increased realization of the needs for global food security and sustainable agricultural production and of the importance of plant genetic resources in meeting such needs.

Intellectual property rights

Intellectual property rights (IPR) bear on plant genetic resources in several ways. Plant variety protection has been enacted in numerous countries, mostly through the introduction of plant breeders' rights according to UPOV. An important feature of the UPOV agreement is that it assigns the right to market a registered variety to the breeder who developed it, but simultaneously allows the use of this variety in further breeding programmes by third parties (UPOV, 1991). The effect of UPOV is that its membership offers an incentive for breeders, but the germplasm involved, including the genebank accessions used as a source, remains available to third party breeders. With the advent of plant biotechnology, patent rights are impacting on access to and availability of genetic resources and commercial varieties. In contrast with plant breeders' rights, patent rights limit access of third parties to genes protected by a patent and potentially have a negative effect on PGRFA use.

Farmers' rights recognize the contribution of local and indigenous communities and farmers of all regions of the world to the conservation and development of PGR, but they have not been developed into a legal property rights concept. Farmers' rights however stress the importance of protection of traditional knowledge and the rights of farmers to receive due benefits and participate in decision-making (Crucible II Group, 2000).

Effects of IPR on products, incorporated into or based on genebank germplasm, affect use of PGRFA maintained in genebank collections. Decisions on the protection of traditional knowledge, in addition to institutional secrecy policies, can influence the availability of such knowledge for inclusion in genebank databases. Regulations and legislation related to access and benefit-sharing of PGRFA have been established at all levels. Hence, PGR programmes and genebank management are inherently linked to policy-making. Some of the policy developments and regulations that influence genebank management are detailed below.

International agreements may appear to contradict each other on specific details, or even sometimes on more general points. The reader should be aware that the international agreements were often negotiated from different perspectives and with different objectives, with the added complications caused by lack of coordination at the national level (Frisvold and Condon, 1998; Petit et al., 2001). For several stakeholders this situation created tension in implementing the agreements.

The impact of the Convention on Biological Diversity

Article 13 of the CBD recognizes the sovereign rights of the state over those resources that occur within national borders. In Article 9 of the CBD it is stated that "each party shall predominantly for the purpose of complementing in situ measures adopt measures for the ex situ conservation of biological diversity, preferably in the country of origin of such components". For the states that are party to this convention, this infers a legal obligation to take measures accordingly. In other words, states should at least provide conditions for genebanks to maintain genetic resources originating in the country.

Many countries take their responsibility to include not only wild relatives of crops and landraces of farmers' varieties, but also commercial cultivars developed in the country. Consequently, the scope of a genebank collection in a specific country may encompass all the genetic resources originating from that country, including commercial cultivars that are no longer marketed. Such

cultivars are generally regarded as originating from the country in which they were developed as part of a breeding programme, although this is not based on a formally agreed interpretation of the concept of country of origin.

As a logical consequence of the sovereign right over its genetic resources, Article 15 of the CBD states that “the authority to determine access to genetic resources rests with the national governments, and that access should, where granted, be on mutually agreed terms”. Finally, Article 16 of the CBD links access to technology, including biotechnology, to access to genetic resources. This operates in the sense that developing countries that provide genetic resources should be provided with access to and transfer of technology that makes use of those resources.

The CBD has resulted in national legislation that frequently hampers rather than facilitates access to PGR and, as a consequence, international exchange and international genetic resources collecting missions have become more cumbersome. There is often no clear guidance on the implementation of the CBD provisions at the genebank level. Genebank managers are advised to respect carefully existing regulations and guidelines, including Codes of Conduct, Prior Informed Consent requirements, and Material Transfer Agreements (MTA). In full consideration of the above, genebank managers are also encouraged to investigate options for international collaboration within this policy framework, where this promotes the conservation and utilization of the genebank collections and the genetic resources in the country in general (Crucible II Group, 2001).

In April 2002, the Vth Conference of the Parties, held in The Hague, the Netherlands, adopted the Bonn Guidelines on Access and Benefit-sharing. These voluntary guidelines assist the genebank manager in determining the steps to be taken to obtain access to specific genetic resources of a given country, and in identifying the necessary sources of information on current policies and the authorities to approach (see the CBD website <http://www.biodiv.org>).

The impact of the International Treaty on PGRFA

The new International Treaty on Plant Genetic Resources for Food and Agriculture, which replaces the former IU, provides, in Article 5, for the exploration, conservation and sustainable use of plant genetic resources by each contracting party, distinguishing inventories of plant genetic resources as well as ex situ and in situ conservation. Part IV of the IT (Art. 10 to 13) deals with the establishment of the Multilateral System of Access and Benefit

Sharing for all PGR of a limited number of crops that are under the management and control of the contracting parties (member states) and in the public domain. This Multilateral System forms the heart of the International Treaty. As the list of species that forms the Multilateral System includes major agricultural crops, this means that in practice a substantial number of, but certainly not all, genebank collections will be covered by the Multilateral System. For these collections that fall under the rules of the IT, access shall be provided solely for the purpose of utilization and conservation in research, breeding and training for food and agriculture. Facilitated access shall be provided pursuant to a standard MTA, which will be developed by the FAO Commission on Genetic Resources for Food and Agriculture (CGRFA). Benefit sharing will be realized through transfer of technology and capacity building, and shall include the sharing of benefits arising from commercialization. The new system will also encompass most of the genetic resources that are maintained by the CGIAR centres (Cooper, 2002).

The Multilateral System can be viewed as representing a conscious decision on the part of the contracting parties to bring some of their genetic resources back into the multilateral domain. This decision is based on the realization that this component of biodiversity is critical for global food security and sustainable agriculture, that parties mutually depend on each other's germplasm to a very large extent, and that pedigrees of newly developed varieties are complex and often include many countries of origin. For these reasons a purely bilateral system would have a considerable negative effect on the utilization of PGRFA (Raymond and Fowler, 2001).

The impact of the Global Plan of Action

The Global Plan of Action (GPA) for the Conservation and Sustainable Utilization of PGRFA of the FAO (FAO, 1996b) lists 20 priority activities in the areas of in situ conservation and development, ex situ conservation, utilization of plant genetic resources, and institutions and capacity building. The GPA represents an important guide and reference for setting priorities at both the national and genebank level as well as at the regional network level. The genebank manager is advised to revisit this plan regularly and evaluate genebank programmes against the GPA, in particular priorities 5–8, which directly deal with ex situ conservation.

The impact of the WTO TRIPS Agreement

The World Trade Organization (WTO) Agreement on Trade-Related Aspects of Intellectual Property Rights (TRIPS) was concluded in 1994 to protect and enforce IPR to promote technological innovation and the transfer and dissemination of technology (WTO, 1994). This agreement concerns copyrights, trademarks, geographical indications, industrial designs, patents, and layout-designs of integrated circuits. Article 27 of the section on patents provides an option that the members may exclude plants and animals from patentability, under the condition that protection of plant varieties and animal breeds should be provided for by patents, by an effective sui generis system or by any combination thereof (Leskien and Flitner, 1997; Louwaars, 1998; Anon, 1999). The major impact of the WTO TRIPS Agreement has been that all members are required to introduce an IPR system for plant varieties, and that it has laid an international basis for the introduction of patents in plant breeding parallel to the plant breeders' rights system. Unlike the latter, patent legislation does not include options for breeders' exemption and for the farmers' privilege, and thus may have a limiting impact on availability of genes derived from germplasm conserved in genebanks. The genebank manager should be aware that patents taken out on genes isolated from germplasm distributed from its collections would limit, to some extent, use of that germplasm by third parties, as far as concerns the genes involved. It is generally believed that gene patenting does not restrict the use of the parent genotype in conventional breeding programmes based on sexual exchange. However, no jurisprudence is yet available to sustain this notion. In addition, benefit sharing to compensate for the limitation of utilization conferred by a patent may be envisaged. Genebank managers should be aware of this option and be prepared to register such use and bring the provider and user into contact to discuss benefit-sharing arrangements (see also <http://www.kewgardens.org/> for further details). In fact, the new IT on PGRFA provides some further guidance in this respect.

National and institutional policies and regulations

With the exception of the UPOV Convention, the other international agreements have been signed and ratified by most countries. This means that these legally binding agreements (the IT is yet to be ratified by 40 states and come into force) will have to be implemented in national regulations, legislation or policies. For example, many countries have developed national genetic resources programmes as a priority activity, as proposed as a general measure in the CBD (Art. 6) and in the GPA. Such national programmes should include an assessment of national needs and

priorities, ensure adequate national capacity, involve partnerships with private enterprises, NGOs, and rural and indigenous communities, and have a formally recognized status (Spillane et al., 1999). At the international level these national programmes can effectively relate to the FAO Global System for the Conservation and Utilization of PGRFA and to other international networks. It can be expected that a formally established national programme will adequately recognize the needed status of the genebank. In addition, the objectives of conservation and sustainable use of biological diversity should be integrated in other sectoral and cross-sectoral plans, programmes and policies.

Some countries have enacted legislation in the area of biodiversity in general and genetic resources in particular, whereas other countries rely on the establishment and elaboration of policies in policy documents.

In summary, genebank managers are advised to use the GPA as a reference in determining priorities, and to study the CBD and the new IT on PGRFA to understand better the international policy environment when proposing policy elements to the respective authorities. In addition, it is important to acquire recognition of the national competent authorities for the relevance of genetic resources conservation and building a structured policy framework in which the genebank manager has a role and on which the genebank policies can be based. More information on the latter can be found in Spillane et al. (1999).

2.2 Relationship between a genebank and the national PGR programme

When genebank operations are newly integrated into the framework of a wider national PGR programme this may trigger genebank management to reconsider and redefine the genebank's role. In particular, a national programme will usually incorporate activities aimed at in situ conservation, on-farm conservation and development of genetic resources. Where this is not the case it might represent a future option. Many genebanks originate from plant breeding and research programmes and are not necessarily designed to incorporate in situ and ex situ conservation approaches.

However, genebank staff are expert in inventorying and dynamics of genetic diversity and would help greatly in in situ and on-farm conservation. This type of work also makes genebank staff aware of the needs and priorities of potential users and provides an

opportunity to design work programmes that address the most important issues and put them in their social context. On-farm conservation also indicates the value of indigenous knowledge and broader aspects of genetic resources, appreciating, for example, that there is more to a plant than mere phenotype: cultivated plants are the product of conscious selection by farmers for useful traits. In situ and on-farm conservation programmes however require expertise in social, economic and cultural aspects of agriculture in addition to skills in administration and organization.

National genetic resources programmes usually have broad mandates that affect the work of genebanks. Animal genetic resources are often included in addition to plant genetic resources. Moreover, national programmes look not only at the dynamics of genetic diversity, but also at the interactions between cultivated species and farm animals, and at the roles of plant and animal species in the general agroecological environment. In summary, integrating genebank activities into a national genetic resources programme broadens the perspective, increases genebank responsibilities and promotes more balanced and realistic priority setting (Engels and Visser, 2000).

2.3 Governance of the genebank

Status of the genebank

Proposals were made in the 1960s and 1970s to develop genebanks with mandates to take account of agroecosystems, climate zones, and centres of diversity, irrespective of national borders. These proposals materialized only in a few cases. International crop-oriented genebanks were established in several CGIAR centres, and these collections constitute a major contribution to global plant genetic resources conservation, both in terms of numbers and species. In addition, the Nordic Genebank, NGB (<http://www.ngb.se/>), and the SADC Plant Genetic Resources Centre, SPGRC (<http://www.ngb.se/sadc/>), resulted from agreements between states to conserve jointly the plant genetic resources of the Nordic nations and southern Africa respectively. Cost-efficiency has been a major consideration in setting up regional genebanks such as these.

Many countries have established a centralized national genebank. The strong point of a national centralized genebank is that it brings together expertise and investment in a single facility. The weak point is that it may be linked to one or a few breeding institutes or university departments rather than to the user community at large. Centralized genebanks tend to have a well-defined status and

mandate, since they invariably fall under the auspices of central government.

In some countries genetic resources management has been fully decentralized and, in general, strongly linked with users (e.g. the UK). Whereas this may promote utilization of the collections, and keep specific expertise close at hand, it is often difficult to secure adequate and sustainable funding and the status of the genebank and its collections might not be certain. Also, long-term conservation objectives and short-term breeding objectives may not be compatible and may interfere with effective conservation.

As an alternative, some countries (e.g. USA, India, China, Brazil, Kenya) established well-organized networks with a central coordinating base collection facility and decentralized active collections. This strategy sought to combine the strong points of the centralized and decentralized approaches but required a more complex organization.

Several motives resulted in a particular national organization of genetic resources management, be it centralized or decentralized, and these motives bear on genebank management.

- The CBD stresses national responsibility and sovereignty, and in practice promotes national solutions.
- A strategic consideration is that a national set-up guarantees access to the resources maintained and control over their quality, and constitutes a potential contribution to international networks based on in-kind contribution.
- A 'biological' motive for a national organization is that national genetic resources are likely to be better adapted to local agroecosystems.

In summary, it is most important that whatever the nature of a genebank, it should have a recognized status within the national research system in order to secure long-term funding and provide long-term security for the maintenance of the collections. Securing such status should be a major priority for every genebank manager.

Funding conservation

In most countries ex situ conservation of genetic resources has been a public responsibility. This does not however preclude private and civil sector involvement. For instance, private industry and NGOs might be involved in germplasm evaluation and NGOs can be partners in collecting and maintaining valuable germplasm in farmers' fields. Civil society has recently shown an interest in

participating in policy discussions on agrobiodiversity conservation. There are clear indications that this sector wishes to be informed and to participate actively whenever it can make a valid contribution. Similarly, private industry has participated in various efforts to conserve and utilize genetic resources (e.g. the LAMP project for regeneration of maize in Latin America).

As a consequence of the generally accepted public responsibility for genetic resource conservation, the public sector provides much of the funding for genebank operations, at least for national genebanks. The responsible authorities vary among countries according to past history and the status of the genebank in the research and development system. A germplasm collection in a university will usually be the responsibility of the ministry of science, whereas that in a breeding station is likely to come under the ministry of agriculture.

Ministries often directly support genebanks that are not part of larger research organizations. Genebanks that are part of a larger organization, including national agricultural research institutes, plant breeding institutes and universities, often receive their core funding through that organization as a component of the overall budget. In some cases genebanks have been given a 'protected status' within a larger institute for reasons of national public responsibility. Special status reduces the requirement for a genebank to compete for funds with other bodies that may in some cases work counter to germplasm conservation. The collections maintained by the CGIAR are to a large extent funded through public donor organization funding linked to aid and development.

Genebank managers need not only to focus on core funding and their relationships with representatives of funding agencies, but also to seek additional support for the genebank to develop and sustain its operations. Additional funding can take the form of research projects supported by organizations such as the Global Environment Facility and the EU. Bilateral donor organizations and charities also fund genebank projects, particularly if there are components addressing issues of rural development, food security or poverty alleviation. Research programmes at the national or international level and nature conservation organizations, especially if focused on in situ conservation, can also become partners in genebank programmes. Private plant breeding companies can also participate in evaluation and fund collecting missions for crops and their wild relatives that are important for their breeding programmes.

Stakeholder involvement

Independent genebanks are likely to be governed by a board of trustees, the composition of which will typically be decided by a ministry and might be restricted in representing the various genebank stakeholders. Even if no board exists, it remains important for a genebank to have the equivalent of a steering committee, whether a formal board or an advisory committee, or alternatively to be advised directly by a national programme committee. This also holds true for genebanks or collections that are part of a larger institution. Their activities are seldom regarded as being core by many host institutes. A board or advisory committee can function in two ways. It can bring together all potential stakeholders in genebank activities and it may provide the genebank with a network that can help strengthen the genebank's position.

National plant genetic resources committees have been established in many countries and provide a major forum for debate, planning and review of PGRFA conservation and utilization. The involvement of such committees in programming genebank activities and the backing provided by such committees represents a major force for strengthening the genebanks (Spillane et al., 1999).

Involvement of representatives from the various stakeholder groups may promote optimal use of genebank collections. Increased use in turn helps to secure a genebank's position. Furthermore, it may facilitate establishment of collaborative partnerships. Stakeholders from public, private and civil sectors should be represented to optimize priority setting and programme development.

2.4 Complementary conservation approaches (*in situ* and *ex situ*)

Genebank collections generally result from *ex situ* conservation strategies, which should ideally be complemented by *in situ* conservation. Such a complementary approach is necessary, as *ex situ* collections will never include entire genepools and *in situ* germplasm continues to adapt to changing environments. Diversity maintained *in situ* is often much less accessible than that in *ex situ* collections and its long-term conservation less secure. It is in the interest of genebanks to link with or participate in *in situ* conservation initiatives, since they facilitate priority setting of the genebank and widen the scope and expertise of the genebank staff. *In situ* conservation mostly concerns germplasm present in farmers' fields (Engels, 2001).

Barriers that have arisen among various conservation approaches and stakeholders are gradually disappearing and there is a growing realization that increased exchange of ideas and enhanced collaboration among stakeholders brings benefits (see for example Christinck et al., 2000). A continuum becomes apparent in conservation strategies if and when genebanks become involved in on-farm management of diversity. When this occurs, organizations involved with on-farm management usually include *ex situ* approaches that complement community development efforts. A continuum has also developed in the objectives of stakeholders. On-farm management of agrobiodiversity is now accepted by the formal sector as being intrinsically linked with development goals and with long-term conservation of local genetic resources that are valued by the informal sector. Stakeholders from different backgrounds have begun to exchange experiences and collaborate, and consequently programmes involving formal and informal sector organizations have emerged (see e.g. <http://www.cbdcprogramme.org> and <http://www.ipgri.cgiar.org/system/page.asp?theme=1>). Organizations involved in on-farm management have realized the need to increase impact by enlarging the scale of their operations, whereas organizations involved in *ex situ* conservation appreciate the importance of locally adapted germplasm (Engels and Visser, 2000).

Locally maintained germplasm in farmers' fields can be kept in a genebank as a security measure, to be reintroduced if lost. While this handbook emphasizes the importance of *ex situ* conservation, *in situ* conservation is important for numerous reasons, including that:

- Not all plant genetic resources can be stored *ex situ*. Underutilized and neglected crops are poorly represented in genebank collections.
- Germplasm maintained *in situ* continues to adapt to changes in the environment including those caused by biotic and abiotic stresses.
- Support for the improvement of locally maintained and adapted plant genetic resources complements private and public investments in breeding staple crops and other valuable crops for which markets exist or for which government support is provided.
- Support for *in situ* maintenance allows for the introduction of valuable traits from formal varieties into locally managed germplasm, whereas continuous development of local germplasm makes this a more valuable resource for formal sector breeding.

- Support for the *in situ* maintenance of plant genetic resources substantially contributes to local community empowerment; it makes communities more self secure for food and income.

Authorities responsible for managing national parks and nature reserves may contribute to strengthening *in situ* conservation of wild relatives in species-rich habitats. In general, management of protected areas is often not focused on the conservation of genetic diversity and much more needs to be done to extract as much information as possible that could benefit conservation efforts.

In conclusion, it is in the interest of genebanks to link with or participate in *in situ* conservation as it facilitates priority setting and widens the scope and expertise of the genebank staff. *In situ* conservation mostly concerns plant genetic resources found in farmers' fields.

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3. SETTING OBJECTIVES FOR GENE BANKS

*Bert Visser and
Jan Engels*

Depending on circumstance, a genebank might have been given a national mandate by its government. If not, a first step should be to work towards formulation of a mandate, irrespective of its scope. Subsequently, it is important to examine critically the precise objectives of the genebank and to identify the constraints under which the genebank operates. Having developed clear objectives it will be possible to establish detailed annual workplans against which performance can be regularly assessed and practices modified.

A logical framework represents a suitable format for developing workplans. Such a framework details programme background, long-term objectives, expected outputs, approaches taken to achieve outputs, criteria and milestones by which to evaluate progress, and the financial means, human resources, facilities and consumables needed to carry out the programme successfully.

Genebank objectives should be reviewed regularly and modified in response to changes in societal needs, utilization, user groups, budgets, funding agencies and donor policies. In general, it should be recognized that PGR programmes, of which genebanks are an important element, operate in the wider context of PGR management (in situ and on-farm management, as well as civil efforts), and often complement genebank operations. Genebank activities should fit in this wider framework. Genebank scope is influenced by the importance of national heritage and sovereignty over PGR and the nature of the user groups. New user groups of genebank germplasm, including the organic farming sector and local farming communities in the South, are becoming increasingly important. Society also

requires more sustainable agricultural production approaches and improved food security. This is occurring while genebank budgets have shrunk and policies have restricted access to germplasm. This has required genebanks to review their objectives regularly to be able to formulate realistic workplans and generate required outputs.

It is recognized that current IPGRI/FAO genebank standards are adequate and represent the best practice for genebanks. However, strict adherence to these standards in countries with limited facilities should be avoided as the standards were designed for an ideal situation that seldom exists. Genebank managers have to interpret these standards and modify them according to local conditions without jeopardizing the long-term safety of the collections. It is recommended that each genebank retain a complete set of the standards it follows and where needed a justification for them.

3.1 Implementing international and national policy frameworks

Scope of mandate and origin of diversity

An important issue regarding scope of a genebank collection is whether it should be confined to germplasm from the country in which the genebank is located or whether the mandate should be extended to accommodate the needs of its user groups. If the latter, the next decision to take would be to define geographical region or limits of the crop gene pool that should be covered. Decisions such as these are unlikely to be taken internally, but will be made by the funding agency. The CBD (Article 8) promotes the first option, but plant breeding and collaborative research programmes may require decision-makers to favour the second option. Situations have developed where both options have been chosen. For example, the NGB and the SPGRC have opted for a strategy of conserving regional genetic resources. Many older genebanks, such as the VIR, IPK and the National Germplasm Resources Laboratory (USA), but also including the much younger CGN, have opted for broader coverage of genetic diversity to support breeding and research¹. In all instances, the collections comprise germplasm that can be used in agricultural production and breeding in the respective countries and for the requirements of a wider user community. Coverage of a collection will largely be determined by the size of the budget. Thus, some mandates require a genebank to cover all crops that play a role in national agriculture, but in other cases priorities have to be set.

¹ For more detailed information see the websites of CGN (<http://www.cgn.wageningen-ur.nl/pgr/>), NGB (<http://www.ngb.se/>), SPGRC (<http://www.ngb.se/sadc/>), the Vavilov Institute (<http://vir.nw.ru/>), IPK (www.ipk-gatersleben.de), GRIN (<http://www.ars-grin.gov>)

In view of the above, it is important that a genebank manager is provided with clear guidance on the scope of the collections maintained. This will have to be sought from the competent authorities if not specified in the mandate of the genebank.

User groups

Composition of any germplasm collection will largely be determined by the characteristics of the intended user groups. Many genebanks in developed countries have been established to provide germplasm for plant breeding and research, both in the public and private sectors. In developing countries the establishment of collections has more often been based on collecting farmers' varieties to safeguard traditional diversity. Increasingly, farmers' communities, NGOs and extension services have been recognized as having a major influence on maintenance of genetic diversity on farm and improvement of farmers' varieties. For such purposes, genebank collections may also serve to back up genetic diversity maintained in the field and genebank accessions can be used in genetic enhancement and reintroduction of germplasm into farmers' fields (for an overview see Almekinders and De Boef, 2000).

Types of germplasm

Decisions on a genebank's mandate and its potential users directly influence which germplasm is collected and included in a genebank:

- When private breeders form a major user group, the focus of a collection might be on acquiring accessions with useful traits, such as those for resistances. Accessions could include wild relatives and farmers' varieties from other regions.
- When farmers' communities constitute a major user group it is important to acquire and maintain varieties adapted to the agroecosystems and farming systems. The focus then shifts from accessions with useful individual traits to varieties that represent overall added value.
- When the genebank mandate specifies maintenance of traditional diversity in the country, collection of older landraces, to conserve national bio-cultural heritage, is a clear responsibility of the genebank.

Naturally, some genebanks will have to supply accessions to a range of user groups, requiring sufficient coverage of each type of germplasm. However, if cultivars are maintained by the breeding industry, because they represent potential commercial value, or if farmers' varieties are widely maintained by farming communities as

preferred for their agronomic traits, it seems not to make much sense to give priority to such varieties in a genebank collection.

In general terms, the following categories could be used to guide germplasm inclusion in a genebank (Ramanatha Rao, personal communication):

- Accessions with known traits.
- Accessions representing a wide range of genetic diversity.
- Wild relatives of bred crops.
- Obsolete landraces.
- Landraces that are commonly used as parents (locally adapted agronomic background) for developing new cultivars.
- Threatened landraces.

Services provided to the user

Services provided by a genebank to its users vary widely, but provision of passport information on the accessions is a minimum requirement. If a genebank is to promote use of its collection, it should strive to provide additional information on the accessions, including characterization and evaluation data. A strong correlation exists between the extent of information available on a given accession and the interest taken in the accession by a potential user. The information might be provided in written form or electronically through the Internet, and selection of accessions might be made either by the curator or directly by the user. Databases are becoming linked to an ever greater extent, allowing selection of accessions from a single database that might be managed at different locations and by different genebanks (international crop databases). The SINGER, GRIN and in the near future the EURISCO databases provide information on the CGIAR Centres' collections, the USA holdings and European genebanks respectively.

An additional and related service concerns establishment of core collections from a genebank collection at an institutional or international level. Core collections should help users to search for useful germplasm in a representative subset of the collection. This initial search can be complemented later with more detailed analysis of germplasm related to that identified during the first search. Such a two-tiered approach optimizes the probability and cost-effectiveness of locating useful accessions. Furthermore, the following activities can be undertaken as specific services to users upon request or in collaboration with users:

- Searching for and acquiring requested genetic resources from foreign collections.
- Carrying out collecting expeditions for potentially high-value germplasm.
- Arranging specific subsets of collections for evaluation.
- Base broadening (or genetic enhancement) and pre-breeding.
- Providing seed in larger quantities.
- Providing DNA of accessions.
- Publication of a newsletter.

All genebank activities, including those listed above, require financial resources and will inevitably be restricted in their availability. Genebank funding bodies may impose restrictions on activities according to their own mandates and perspectives. Provision of specific services by a genebank can however also attract additional funds.

3.2 What to conserve?

Numerous factors govern the nature of the genetic resources that can be conserved in a genebank. Some are prescriptive, including policy requirements, others relate to priority setting by the curator and there are inevitable biological constraints related to differences among species and propagation.

Policy requirements

Genebank policy is usually determined by the funding agency, which is often a government ministry. Genebank managers nonetheless have a responsibility to provide information to a range of individuals and agencies to keep them abreast of developments in conservation science and practice and changing priorities. Policy often determines the origin and type of germplasm to be conserved and the principal users.

Institutional arrangements

Genebanks that are closely associated with breeding or research institutes are often major suppliers of their germplasm. Such relationships can confer mutual advantages since evaluation data obtained by a breeding institute can be easily made available to an allied genebank, and in turn, promote the germplasm use. As a consequence, such collections are often used intensively. It is important, however, that managers of such genebanks should be alert to short-term interests of an associated research institute that might conflict with the long-term responsibilities of the genebank. For example, termination of a crop-breeding programme should not result in neglect or termination of a genebank collection. In this

context, it is important to establish the nature of any inter-institutional relationships carefully so as not to jeopardize the security of the genebank. Furthermore, the nature of such relationships is likely to have direct bearing on budget allocations. In some instances genebanks have developed as a side-activity of an institute. In some countries the management of genebank collections may be highly decentralized, and closely linked to a research or breeding institute for particular crops. Such genebank collections may be more prone to neglect in the longer-term unless the government has taken explicit responsibility for continued maintenance of such decentralized collections.

Many genebanks operate independently of user institutes. Although superficially attractive, a major risk is associated with loose contacts with users. This can mean limited access to crop expertise and necessary facilities for regeneration and characterization of the collections. Unfortunately, feedback from evaluators to the genebank is generally poor and should be accorded higher priority. This could be done through arranging evaluation programmes with independent major users to follow-up on obligations accepted under MTAs.

In some cases a genebank's main objective is solely long-term conservation of germplasm, the responsibility for short-term use being vested in other institutes. Under such conditions the risk of isolation for the genebank might be greater, and securing improved contacts with major user groups becomes crucial.

Some genebanks have a clear mandate to evaluate germplasm, whereas others are explicitly advised by funding agencies not to undertake evaluation using the core budget. Genebanks are at an advantage if close links can be maintained with users. This usually affords access to otherwise unavailable facilities and expertise. It also helps to reduce costs and simplify genebank management policy.

Historical load

Institutional history has often resulted in collections the size and content of which were determined by past decisions and programmes. This heritage is termed the historical load. Germplasm collections typically have derived partly or fully from working collections in associated institutes or from independent national institutes. It is only logical for the genebank to take full responsibility for such collections, but in practice the responsibility may represent a delicate balance between burden and opportunity. The historical load should be taken into account in formulating work programmes.

A working collection may be extensively documented and evaluated and represent a major asset, possibly unique, for the genebank that can be improved and extended.

If a collection no longer fits the priorities of a genebank an attempt should be made to house the germplasm elsewhere. This may be an attractive strategy if the inherited collection is relatively small or requires highly specialized expertise or facilities, but it is often difficult to maintain collections when the number of germplasm requests is low. Genebanks holding much larger collections are more likely to be known to users of a particular crop. Whether a genebank can exploit this option or not depends often on national policies. Alternatively, inherited working collections might be modified (see Chapter 6) to render their maintenance cost-efficient.

User requirements

A conservation mandate will often require the conservation of genetic diversity of a given crop species in general terms, regardless of specific genotypes, but user requirements should be considered before accepting responsibility for a collection. Requests for germplasm may originate from the public, private or civil sector. Users may want germplasm for breeding, for searching for specific genes, for basic research or for introduction and reintroduction material into farming systems. Whereas breeders and researchers will be interested in adaptive traits to incorporate into their breeding materials, which may be present in anything from elite lines to wild relatives, farming communities generally require adapted varieties from comparable agroecosystems. Sexual regeneration may lead to loss of a specific genotype, but conservation of the genes in other genotypes that can be used in further breeding may suffice. Moreover, it should be determined whether specific characters and traits are already contained in other accessions in the collection. Maintenance of specific genotypes is important however for direct reintroduction into a farming system. In summary, anticipated germplasm use often determines the way it is conserved: as specific genotypes or as a population in which an individual plant genotype is not fixed over generations. In all cases, genebanks play a particular role in making germplasm available that is might not be otherwise readily available (see also Greene and Morris, 2001).

In some cases a crop may be important in a dominant farming system, and thus merit *ex situ* conservation of the genetic diversity, even in the absence of an active breeding programme. In some cases a crop may no longer be cultivated in a given location but breeding programmes for the crop might exist elsewhere (e.g. flax in the Netherlands).

Most genebanks play national or regional roles or else have well-defined users. However, as a consequence of globalization and the advance of information technology, new users from distant locations increasingly approach genebanks for material. Genebank managers need to develop policies on how to provide services to such non-traditional users who are unlikely to provide anything in return.

A genebank manager has to fully appreciate the needs of current and potential users in light of a genebank's mandate and objectives. It is also necessary to consider how to adjust conservation policies to accommodate optimally for utilization. More specifically, decisions on (1) the prioritization of crop collections, depending on availability of germplasm elsewhere; (2) limiting coverage of a collection to germplasm from particular agroecological zones or geographic origins, or parts of a crop gene pool; (3) the desired balance between advanced cultivars, older cultivars, farmers' varieties, wild relatives etc. regarding their representation in a collection will need careful attention.

Geographic considerations

The mandate of a genebank may specify guidelines on restrictions to conservation obligations for germplasm from particular locations. For example, the NGB has the mandate for conserving diversity from the Nordic region only and WARDA has a specific responsibility for maintenance and development of rice germplasm for cultivation in West Africa (see for example Hijmans et al., 2000).

Phytosanitary regulations can also influence conservation policies. Given strict EU legislation on viruses, maintenance of potato germplasm in EU member states for use in the EU is an absolute requirement for breeders in the short term. From a long-term conservation perspective maintenance in the Andean region might suffice. Short-term utilization of genetic resources thus requires additional germplasm storage in Europe. A comparable example is provided by the need for intermediate plant quarantine in third countries that can result in generating germplasm collections. For instance, for quarantine reasons, Barbados hosts a collection of cacao germplasm for further distribution, closely linked to the global cacao germplasm collection maintained at the University of the West Indies in Trinidad and Tobago (Eskes et al., 1998).

The distribution of many underutilized crops is often restricted to a certain region (Chweya and Eyzaguirre, 1999). The genebanks in such a region are specifically responsible for the conservation of such crops since these are unlikely to be conserved extensively

elsewhere. Such a responsibility follows from the CBD, which states in Art. 8 that each country should take measures to conserve its own biodiversity.

Geographical location

Climate may have a significant influence on the success of genebank operations. The regeneration of germplasm originating from vastly different ecosystems may pose problems, generate additional costs and result in major genetic bottlenecks if at all successful. Transfer of germplasm from short-day to long-day conditions may easily promote undesirable effects. The regeneration of genetically heterogeneous wild relatives under different climatic conditions may also prove problematic (Brown et al., 1997). The results of several studies on genetic erosion of barley in genebank stocks, as a result of genetic drift and shift, indicate this (Parzies et al., 2000). In theory, genetic shift can be avoided by regeneration in the area of origin, but this is often logistically complex or impossible for a host of reasons. Therefore, biological effects may pose constraints on building global germplasm collections for important cultivated crops to the same extent as policy considerations do. For this reason germplasm maintenance in the country of origin or in the same agroecological zone should be seriously considered as a viable alternative to distant storage.

Budget and infrastructure

In most cases the overriding limitations to implementation of genebank operations in general, and genebank collections in particular, result from budget and infrastructure limitations. Whenever these factors are limiting it is necessary to prioritize conservation objectives.

Budget limitations represent the major justification for explicit proactive collection management policies and strategies designed to limit collection sizes. It is usually possible to estimate costs for regeneration of particular numbers of accessions. Since each genebank will have to regenerate not only newly introduced germplasm accessions, but also near-depleted accessions and where viability has dropped below an acceptable threshold, each genebank can only successfully maintain a limited collection, occupying a limited space. The maximum available budget for regeneration determines the capacity for regenerating existing germplasm and the introduction of new germplasm. In other words, the current size and viability of the existing collection will determine how much of the budget remains available to expand the collection. Genebank managers should determine accurate figures for each of these two categories.

Naturally, no genebank can devote its entire budget to regeneration and neglect collecting, documentation, information services, seed management, viability testing, distribution and evaluation of the collections. Nevertheless, many genebanks hardly follow optimum regeneration protocols and regeneration is often overlooked, even at the planning stage. Regeneration is also an activity that attracts little funding from donors and hence plans must be made for it well in advance if the investments made in establishing collections are to be protected.

No specific figure can be suggested for regeneration costs, in contrast to other genebank operations. However, determining the fraction of the budget available for regeneration is paramount during priority setting. To add to this complexity, regeneration cannot be treated separately from other activities. For example, a large number of new accessions will affect total costs, including regeneration. A better documentation and information system will enhance demand, contribute to the exhaustion of stocks and require a larger part of the regeneration budget to be spent on currently maintained accessions, limiting the chance for expanding the collection. Increased spending on evaluation will have a similar, albeit slower, effect on increasing germplasm requests and eventually accelerating exhaustion of stocks.

Prioritization may also result in a relatively high percentage of the total available budget being spent on a limited number of crop collections in a genebank, preferably those representing a higher percentage of unique accessions, or those of more interest to users.

As an example, CGN has committed itself to spend not more than 50% of its total available core budget from the Ministry of Agriculture on regeneration. In addition, it spends 80% of its core budget on only eight priority collections out of a total of over 20, regardless of the type of activity. Those priority collections have been selected on the basis of user demand, representativeness and availability of the germplasm in collections elsewhere.

A major consideration is whether germplasm can be effectively stored as seed, or whether only more expensive and less reliable storage methods have to be considered, such as *in vitro* conservation, cryopreservation and field genebanks. It is naturally advisable to restrict the number of crop collections that produce recalcitrant seeds or can only be propagated vegetatively to a level that is affordable to the genebank and is likely to be sustainable in the long run. Where this tends to be in contradiction with a country's obligation to conserve its own germplasm, options for international

collaboration and regional sharing of responsibilities may represent a solution.

Finally, infrastructure and expertise may influence collection size and crop prioritization. Storage of the germplasm of some crops requires greenhouses, in vitro maintenance or cryopreservation facilities and expertise. In general, all base collections of species that can be conserved as seed should be stored under optimal conditions, preferably at -18°C. However, seeds of some crops will remain viable for many years even at +4°C if and when their moisture content is sufficiently low and seeds are hermetically sealed in special containers, such as aluminium foil bags (Walters and Engels, 1998).

Collecting strategies

Two factors contribute to the development of collecting strategies given that collecting will only make sense if sufficient and good-quality regeneration and storage facilities are available. The quantitative factor was described in the section on budget and infrastructure. The total available budget for regeneration minus the costs for regenerating already introduced accessions will determine the options for incorporating new accessions, and collecting strategies should take this annual maximum capacity into account.

In a qualitative sense, the GPA provides guidance under priority Activity 7. It states that long-term objectives should include collecting threatened germplasm and associated information and collecting material for which there is an anticipated use. An intermediate objective is that the material might fill gaps in the genetic diversity of existing collections. For this purpose, the results of past collections need to be assessed for diversity, using either geographical (GIS), molecular and/or morphological techniques (for details see Ferguson et al., 1998; Van Treuren, 2001). Not all diversity maintained on farm or existing under natural conditions is under threat of being lost, and its collection should therefore be low priority. Moreover, genebanks should carefully draw up inventories specifying germplasm that has already been acquired by other genebanks and is freely accessible. Only in exceptional cases is repeated collection of germplasm at the original site justified over regeneration of already collected germplasm.

In general, collecting expeditions should focus on non-staple crops, or staple crops with very limited distribution areas, given the very large ex situ collections of global staple crops that have already been established. Policy frameworks impact on collecting strategies, in particular on international collecting missions. The

CBD states the right of contracting parties to require prior informed consent before providing access to genetic resources and an obligation to respect the knowledge of indigenous communities regarding conservation and sustainable use. It may not be easy to identify the appropriate government authority that should facilitate access, although the recently adopted Bonn Guidelines of the CBD require identification of Competent National Authorities. The FAO International Code of Conduct for Plant Germplasm Collecting and Transfer, concluded in 1993, proposes procedures to request and/or issue licences for collecting missions, provides guidelines for collectors themselves, and extends responsibilities and obligations to the sponsors of missions, the curators of genebanks, and the users of genetic material. It calls for the participation of farmers and local institutions in collecting missions and proposes that users of germplasm share the benefits derived from the use of plant genetic resources with the host country and its farmers. The recently drafted Bonn Guidelines on Access to Genetic Resources and Fair and Equitable Sharing of the Benefits Arising out of their Utilization (Section IV), as well as the new IT on PGRFA (Art. 12), provide further guidance for the steps to be taken for collecting germplasm.

Genebanks are strongly advised not to embark on international collecting missions without consent from the competent national authorities of the country where the collecting mission is planned to take place. Even while collecting within the country of the genebank, appropriate clearances will need to be obtained, sometimes from local communities. In addition, knowledge of local relationships is essential to identify the right persons or platforms to provide the prior informed consent when access to on-farm diversity is desired. Local partners who are respected by local communities will often be instrumental in obtaining prior informed consent from the proper persons and groups.

3.3 Setting objectives to promote utilization

The ultimate objective in managing a germplasm collection is to encourage use of accessions to promote food security and sustainable agricultural production. Major uses include breeding (Dudnik et al., 2001), but alternative uses may include reintroduction of diversity in situ and support to community-based development projects focused on use of PGR. Investments in characterization, evaluation and documentation generally increase utilization and thus need the utmost attention.

Scientific research also relies on availability of genebank accessions. An often understated or little considered use has been, and will continue to be, the supply of materials for studies on species biology, crop evolution and for assessing patterns of diversity. Developments in molecular biology and diagnostics have facilitated novel approaches. The results of such studies benefit the curators in management, since they greatly increase the knowledge about the collection structure and allow for informed decisions in priority setting for maintenance. Also, continued conservation of genetic diversity will contribute to advances in biotechnology-related aspects of crop improvement.

Whereas conservation for future use is the bottom line for all genebanks, short-term use is of immediate importance, and requirements are more easily anticipated in the short term. However, not all diversity will be used to the same extent, if used at all, but future needs nonetheless make conservation necessary. Similarly, differences in efforts to promote utilization of germplasm may be justifiable, both among and within collections. Depending on local farming systems and markets for high-value products of plant breeding programmes, some collections may be actively used in plant breeding and others may come to represent solely conservation collections without strong linkage to crop improvement.

Conservation

Optimal conservation of germplasm hinges on the reasons for conservation. Depending on storage costs, availability of the germplasm, availability of alternative accessions and other factors, genebank curators might decide in favour of long-term, medium-term or even short-term storage. Details of this will be provided in Chapter 4.

Definition of the user

Decisions on distributing germplasm are determined by user status (legal status and nationality) and intended use. It may sometimes be necessary to make germplasm accessions available only to organized groups—communities, universities, companies etc.—to optimize the cost-effectiveness. Single users may not be able to use germplasm effectively because of lack of adequate access to necessary facilities, expertise and user networks.

The Multilateral System of the IT on PGRFA requires that all contributing parties facilitate access to the designated germplasm. In many cases this will mean that no distinction should be made based on nationality, as long as the requesting party operates under the coverage of the IT and its Multilateral System. Access includes

associated information, unless availability of such information is restricted (<http://www.fao.org>). The CBD requires the intention to provide access to genetic resources under mutually agreed terms for those collections not covered by the IT on PGRFA. In turn, genebanks have to respect the FAO Code of Conduct for Collecting, and only provide germplasm to users under the terms of this Code, the IT on PGRFA, and the CBD provisions.

It is often necessary to use an MTA (as required in the Multilateral System of the IT) to guarantee that all germplasm provided to a specific party remains available to any other party, and that no patents can be obtained on the germplasm without prior informed consent. This does not represent an active restriction of access according to use on the part of the genebank, but is a provision to protect access for other users against patents infringing free access.

Access to crop germplasm not covered by the Multilateral System depends solely on national policies. However, it should still be in agreement with the general text of the IT on PGRFA and the CBD, in particular the (voluntary) Bonn Guidelines on Access to Genetic Resources and Fair and Equitable Sharing of the Benefits Arising out of their Utilization. The IT on PGRFA requests that each party develop policy and legal measures that promote the sustainable use of PGR (Art. 6). The CBD requires that parties shall “endeavour to create conditions to facilitate access to genetic resources for environmentally sound uses” (Art. 15).

Genebanks should require that their clients meet conditions for use of germplasm. Genebank managers are encouraged to review these requirements and consider whether they are in agreement with the conditions of the IT and the CBD. They are also strongly advised to take decisions in consultation with national authorities, once identified.

Characterization and evaluation

Germplasm use can be promoted best through better characterization and evaluation. This can be done by the genebank or by third parties in the private, public or civil sector. Characterization can generally be carried out alongside regeneration, but evaluation requires greater financial inputs, more technical expertise, special facilities and detailed knowledge of users' needs. Therefore, only few genebanks can carry out major evaluation programmes under their own direction using core funding. However, several viable alternatives to manage evaluation have proven to be effective, especially when based on partnership with other genebanks.

Firstly, genebanks might secure additional funding from government or private sources to carry out an evaluation programme on one or more specific traits in a given crop for which the genebank possesses significant genetic diversity. This is essential for genebanks that cannot finance the work from their core budget. Secondly, genebanks may cooperate at the national, regional or international level and share tasks in an evaluation programme, each genebank evaluating a common set of accessions composed of germplasm maintained by the collaborating genebanks for one or more specific traits. The advantages of such cooperation are cost savings and access to evaluation data on the genebank's own collection and on collections from other genebanks. Thirdly, genebanks may collaborate with a single user or a group of users to promote the evaluation of traits of interest. The genebank will normally make a substantial amount of germplasm available, may be involved in or responsible for inspection and measurements of the targeted traits and will take care of documentation of the results. The advantage to the users is that they have direct access to data on specific accessions. Another advantage is that users may decide to share the results obtained in a multilateral evaluation programme in the period before they are made more widely available to third parties. Each of these approaches may require contracts to be signed by contributing parties.

Documentation and information management

Documentation is essential in good genebank management to allow efficient and effective use of germplasm. Characterization and evaluation data are of little use if they are not adequately documented and incorporated into an information system that can facilitate access to the data.

There are many genebank documentation systems. Systems are generally defined by the locally available resources (hardware, network, software and knowledge) and the requirements (data volume, data type, number and type of users and intended use). Simple systems consisting of written notes have their uses, but as the number of users and accessions increases, and as requirements become more demanding, computers become essential. This inevitably requires database management software (DBMS), genebank software applications, and the Internet.

Sophisticated systems generally contain three types of data: passport data, which provide the identity (name, origin, etc.); evaluation and characterization data, which describe the phenotype of the accessions; and management data concerning the storage

location, amount and quality of the seed, distribution, etc. Management systems should allow easy access to the data. The systems should be secure and the data protected from inadvertent and unauthorized modification or loss. The systems should however be flexible and allow easy data input, conversion and querying. Systems for genebank documentation management are generally based on commercial DBMSs such as MS Access, Oracle or FoxPro. The more complex the system, the greater its capacity, but also the higher the level of expertise needed to maintain it. Access to expert knowledge, also in the case of relatively simple stand-alone applications (such as pcGRIN), is essential especially as information exchange is very important in documentation and genebank coordination. The establishment of an Internet site to allow global access to genebank information is a highly recommended means to promote utilization of the material and collaboration. The site can include information on conservation policies and access conditions, alongside information on the germplasm.

Genebank documentation is often low quality, incomplete and unreliable. This is particularly true of evaluation data. Currently, interpretation of most data is difficult without support from the curator. This reduces the value of the information from being an aid to selection to a mere description of the properties of the material. Getting the data in the best possible format to ease user access requires expert input and can be expensive.

Security measures have to be instituted to protect information on germplasm against damage and loss and ensure smooth functioning, easy access and unrestricted availability. The appointment of a specialist information manager responsible for information and web site management brings benefits.

International crop databases

Common databases have been developed for several crops at several institutes. This has been done by either establishing a novel database in which the data from individual collections and databases have been collected, or by building a virtual database that offers a single entry point and provides access to information managed elsewhere. Most international databases have been established on a crop basis, e.g. the International Beta Database, the Inter-genebank Potato Database (Huamán et al., 2000) and the many ECP/GR databases such as the European Brassica database (Boukema et al., 1997). There are also institutional databases such as SINGER that provides access to collection data of the CGIAR institutes (<http://singer.cgiar.org>).

World Information and Early Warning System on Plant Genetic Resources (WIEWS)

The World Information and Early Warning System on Plant Genetic Resources, WIEWS², is an international database containing metadata on PGRFA holdings of more than 1500 national, regional and international collections. It was established by FAO as a worldwide dynamic mechanism to foster information exchange among countries and as an instrument for the periodic assessment of the state of the world's PGRFA. This was done in line with Articles 7.1 (e) and (f) of the IU on PGRFA and following the recommendations of the Commission on PGRFA (CGRFA).

WIEWS currently serves a growing community of data users and providers through a multilanguage (Arabic, English, French and Spanish) web-based facility for information searching, report generating and remote updating. Additional information stored under WIEWS includes country reports submitted to the FAO IV International Technical Conference on PGRFA and reports on the state of implementation of the GPA for the Conservation and Sustainable Use of PGRFA.

In conclusion, one of the major advantages of international databases is that they offer users ready access to information on germplasm, irrespective of the genebank source. They promote the utilization of genetic resources, particularly when diversity is distributed among a large number of genebanks. Genebank managers are encouraged to consider whether they are in the position to provide crop collection data maintained by their institute to such international databases, and to contribute to establishment of such databases.

Structuring collections

Some collections have become very big, and for some crops numerous genebanks maintain collections. To facilitate the use of such collections, Frankel (1984) suggested the establishment of core collections. A core collection can be defined as a collection of limited size with minimum similarity among its entries. It should represent maximum genetic diversity of a large collection, a crop, or group of crop-related species. A core collection will always be substantially smaller than the collection(s) from which it derives. It may help in acquiring knowledge on the distribution of genetic diversity in the collection, identification of gaps and priorities, and the potential use value of incorporated germplasm in various environments, as well as apportioning responsibility among collection holders.

² <http://apps3.fao.org/wiews>

The GPA (FAO, 1996) recommends core collection development as one of the priority activities. Procedures to establish a core collection have been described in an IPGRI Technical Bulletin (Van Hintum et al., 2000).

Other structured subsets of collections need not necessarily aim at representing maximum diversity in the entire collection of the crop, but may focus on maximum representation of the diversity for specific traits, e.g. certain resistances, and thus serve the needs of specific user groups.

Several genebanks, including that at ICRISAT (Ramanatha Rao, personal communication, 2002) have gained experience on changing the composition of 'proactive' subsets of collections based on specific traits, or geographic regions, to promote use of collections.

Base broadening and pre-breeding

Base broadening and pre-breeding narrow the gap between raw germplasm and commercial crop genotypes and thereby promote the use of genebank collections. Plant breeders and other users are often hesitant about using material directly from a genebank as it is often too unadapted to be of immediate use for crossing with elite lines. Base broadening and pre-breeding are often aimed at combining various sources of interesting genetic material into a single population, sometimes followed by light mass selection under suitable stress conditions. Base broadening can usually be more easily carried out by genebanks than pre-breeding. It aims at increasing the genetic diversity available for utilization by combining potentially useful features of several genotypes in a single population, thereby allowing for new genotypes to be developed for incorporation into breeding programmes (Cooper et al., 2000).

Increased use of genebank collections through base broadening and pre-breeding requires good communication between users and suppliers of the germplasm. However, only a small amount of the total human and financial resources allocated to plant breeding by public and private breeding programmes is directed towards pre-breeding and base broadening.

Other user requirements

Researchers and breeders generally only need small quantities of seeds from genebanks. Civil sector clients and farming communities may have little capacity to multiply seeds by themselves and require larger quantities for evaluation and introduction. Their information needs also differ. Researchers and

breeders may be interested in specific traits and in detailed knowledge about the traits, including information on molecular and biochemical details, whereas farmers will be more interested in agronomic properties. The ability to interpret and analyze standard information varies and users might need support. Germplasm is increasingly being requested for genomic analysis and gene isolation. DNA can be isolated from accessions in genebanks and can, possibly for a fee, be provided to clients similarly as for the germplasm itself.

3.4 Budget and infrastructural arrangements

Constraints

Many genebanks face serious financial constraints. This may be the result of a failure to appreciate their relevance and their costs of operation. It can also result from poor financial management. Genebanks have to cope with the challenge of enlarging their collections when funds might be diminishing. If genebank growth is not carefully monitored problems will inevitably emerge. In particular, the establishment and increase in size of collections should only follow from careful analysis of the long-term maintenance costs. Poor management of a collection will result in genetic erosion and can jeopardize the entire collection.

Two factors deserve specific attention in estimating the long-term maintenance costs of a collection. Firstly, distribution of materials will eventually result in exhaustion of the stocks in the active collection. This necessitates close monitoring of distribution and knowledge of remaining stocks. It should be possible to project patterns of future use to be able to plan investments needed to maintain the active collection. Secondly, viability of accessions in the base collection needs regular monitoring. When the viability of the stock in the base collection falls below an established threshold (in the Genebank Standards 85% of the initial germination), the accession needs to be regenerated. Much of this information can be gained from experience and has been documented. IPGRI is currently in the process of designing an expert system to assist genebank managers in exerting more effective control over their collections.

Estimations of future use and likely viability of the germplasm in germplasm collections should provide an insight into maintenance costs. In turn this should contribute to better financial management. Promoting germplasm use is not simply a matter maintaining stocks. Funds should be sufficient to establish and maintain a good

documentation system, to provide information to potential users and to allow further studies on the germplasm, autonomously or in close collaboration with third parties (Engels, 2002).

Genebank managers may consider setting aside a proportion of their core budget for such additional essential activities to avoid degeneration of the collection. The costs will differ among genebanks and can be very high. For instance, CGN limits spending on collection maintenance from its core budget to 50%.

Outsourcing activities

Genebanks sometimes carry out tasks that might be done better and cheaper by others. Examples of this include collecting, viability testing, documentation and supplying information. Programming, web site development and maintenance and molecular characterization of germplasm also fit into this category. If a competitive market for such services exists, it might be cheaper to outsource the work and maintain or improve the quality of the service. Options will depend heavily on the institutional setting of a genebank and the external expertise available. Genebanks might join forces in outsourcing or share tasks among themselves.

Funding opportunities

Most genebanks receive core funding from a public source, often a government ministry. However, budget allocations for genebank activities are not always simple, especially if a genebank operates in the framework of a larger institute. Furthermore, whereas core funding may be received from a public source, this is likely to be on a short-term basis. Long-term funding is usually less certain. Many genebanks have reported decreasing budgets (Clark et al., 1997) and despite the long-term nature of their work, genebanks are in a similar position to many research institutes regarding decreasing funding. It has often become essential for genebanks to search for supplementary funding.

Genebanks can successfully compete for research funds, particularly in specialist areas such as germplasm analysis, genetic enhancement and development of information systems. Generally, such attempts will be more successful if done in collaboration with others. Alternatively, donor organizations do fund activities that strengthen in situ and on-farm management of plant genetic resources, and genebanks can be partners in such initiatives. An example of a database of European funding opportunities for development-oriented projects maintained by IPGRI can be found at <http://www.ipgri.cgiar.org/regions/europe/home.htm>.

Plant breeders in particular and the biotechnology industry often fund specific activities, such as those listed in Section 3.1, additional to the services usually provided by genebanks. Such agreements are often made on an ad hoc basis; a genebank must reach a conclusion as to whether it can meet such requirements given the increased flow of funds.

Finally, some genebank activities, in particular evaluation but also regeneration and characterization, can be funded or sponsored by users through direct involvement. Users might make facilities and expertise available to carry out the tasks. Such collaborative efforts usually depend on the presence of active breeding programmes. For example, in France such collaboration has been institutionalized and is a fundamental feature of the organization of plant genetic resources conservation and utilization. Specific discounts and cost exemptions for plant quarantine, viability testing etc. are also possible and require negotiating with the competent authorities.

Additional sources of income

Charging fees for distributing germplasm has been contemplated on various occasions and by a number of genebanks. These can be based on full costs of collecting, regeneration, characterization, storing and distribution, or solely on the costs of processing the request. Naturally this would represent increased income for the genebank. A strategy involving fees fits in with current thinking that users should pay for services and even that free service seldom equates with good quality. Charging fees could deter potential users from requesting more material than could be realistically used and from asking for the same accessions repeatedly. However, charging fees is not always straightforward:

- Charging fees may deter users from contributing funds to project activities or collaboration with the genebank, in order to compensate for their increased costs.
- For those resources covered by the Multilateral System of the IT, only handling fees are allowed, thus reducing the potential income that can be generated through tariffs.
- Exceptions will have to be made for sample requests from other genebanks, parties in the country of origin, users with scarce resources, partner organizations, etc., again decreasing the potential added income.
- Setting fees requires introduction of an administration system that will absorb part of the extra income.
- Users may seek other genebanks that offer identical or similar germplasm without charge or that charge lower fees.

- The introduction of high, full-cost based fees might interfere with the objectives and obligations to promote the use of genetic resources.

These complications have prompted IPGRI to suggest the following policy.

IPGRI encourages genebanks to find ways of promoting the use of genetic diversity. Even small handling charges could be counterproductive and possibly discourage requests from potential users. For many countries, the difficulty of obtaining foreign exchange, even for small handling fees, could restrict requests for material from a genebank. The cost and effort required to set up a system for recovering handling costs could easily outweigh any benefits derived from it. However, it is understood that charges may need to be levied when large quantities of germplasm are requested that would entail substantial multiplication and shipping costs.

In considering the possible introduction of handling charges, IPGRI believes that special attention should be given to the possibility of:

- Not applying handling charges to requests from developing countries.
- Not applying handling charges for germplasm exchanges with other genebanks (reciprocal free-exchange agreements are often more appropriate).
- Waiving handling charges for institutions, including private companies, that agree to make their own germplasm (genetic stocks, advanced lines, etc.) available to the genebank (Hoekstra et al., 2001).

IPGRI also encourages the idea of genebanks becoming self-sustaining. For example, in the case of the International Coconut Genebank, the partners have been urged to generate income through additional activities ranging from marketing of produce to seed nut sales (Ramanatha Rao, personal communication, 2002).

Additional funding might be generated through offering extra services, not on a project basis resulting in extra funding but on a transaction basis resulting in ad hoc income. The criterion for selecting such services should be that genebanks and users regard them as extra services, additional to those normally provided. Their costs might be covered by the user or by third parties, but at a competitive price reflecting the quality of service. For example, the provision of DNA samples, in particular when already available through regular genebank operations, might suit tariff-based

transactions. Moreover, information services and analysis or facilitation of sample requests from foreign genebanks might justify charges being set. In general, this issue seems to merit more attention from the genebank community.

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4. CONSIDERATIONS FOR IMPROVED CONSERVATION AND UTILIZATION CONCEPTS AND STRATEGIES

*Ruaraidh Sackville Hamilton,
Jan Engels and
Theo van Hintum*

Whereas organizing and effectively running a genebank depends largely on the economic, social and legal background of its establishment and its continuing support, it is also necessary that sound scientific methods be employed that account for the differences among species. The biological nature of the crop species gene pools affect sampling, conservation and utilization. In many cases species-specific practices have to be developed. A single set of scientific standards cannot be used to cover all species.

In general there are two distinct objectives for germplasm conservation. The first involves material conserved for the long-term, with the aim of preserving the genetic information in the accessions, and the second concerns material currently in use or about to be used.

Large-scale international collecting efforts, many of which were supported by the IBPGR during the late 1970s and 1980s, focused primarily on the world's major food crops. These included cereals, some legumes and a few root and tuber crops. Many of these crops produce 'orthodox' seeds, which can tolerate desiccation and exposure to low temperatures without loss of viability. A convenient procedure was thus worked out for conserving them by reducing moisture content of seeds to approximately 5% and storing them at a temperature of -18°C (IBPGR, 1985). Continued research aimed at optimizing conditions for seed storage led to the adoption of a two-tiered conservation strategy:

- Long-term conservation of 'base collections' of adequately dried seeds usually stored at -18°C in hermetically closed containers.
- Short-term storage of 'active collections' under relatively less stringent conditions: at $+5^{\circ}\text{C}$ and a controlled air humidity of $\pm 35\% \text{RH}$.

These procedures and conditions were widely adopted as the conventional method for ex situ conservation of orthodox seeds in facilities termed seed genebanks. Unfortunately, adoption frequently took place without determining the best procedures for the genebank under its given conditions, e.g. infrastructure and energy supply, the need to conserve non-orthodox seed species, lack of adequately trained personnel, intensity of collaboration with users of germplasm and a very fast changing environment of information technology and intellectual property rights. The current chapter is written in this context.

The limitations of conventional seed storage procedures and the historical context in which the early ex situ collections of plant germplasm were established resulted in a relative over-representation of orthodox seed-producing food crops in the world's major genebanks. Alternative methods were needed for conserving vegetatively propagated crops for which seed conservation is not appropriate, e.g. potato, cassava and banana. Hence, the establishment of field genebanks—collections of plants maintained as living specimens—was given due attention and later also the development of in vitro collections in which germplasm is conserved as tissue culture in glass or plastic containers.

4.1 Biological parameters

In order to be able to manage germplasm effectively in a genebank some basic information is required. This includes information on flowering biology and seed production, mating systems, patterns of genetic diversity and methods of maintaining population integrity through suitable cultivation methods. Some physiological traits also have to be understood including seed dormancy, germination and storability; or in the case of vegetative materials, growth behaviour in tissue culture under in vitro conditions. Some of this information exists and some needs to be generated. It is generally advisable to conduct a comprehensive literature search before determining details of the management procedures for species for which information on optimal conservation conditions is unavailable.

Some major issues related to conservation methodology and utilization of PGR determined by species biology are given below in the form of questions:

(i) If seeds are produced, which of their features have to be taken into account in conservation? Does the target species produce orthodox seeds that can be conserved using standard cool, dry conditions? Does the species produce intermediate or recalcitrant seeds? Does it have to be maintained clonally? If the target species does not produce seeds, how is it to be conserved?

(ii) What is the extent of genetic variation that exists between and within samples and accessions, i.e. populations, mixtures, pure lines or clones? How can regeneration be carried out to reduce impact of genetic shift and drift?

(iii) If the target species is sexually reproduced, what is the nature of the mating system? What is the extent of self-pollination? What is the degree of outcrossing, and how does it affect genebank operations? Under which conditions and to what extent is pollen contamination a problem? The latter can only be determined by knowledge of nearby feral, wild and experimental populations of compatible species. Decisions need to be made on whether isolation is necessary for regeneration.

(iv) What is known about fecundity, i.e. how many seeds are produced compared with the number sown? Can seed production be optimized to match expected demand?

(v) What is known about seed longevity at species and individual accession level under particular storage conditions? What is the optimum seed moisture content for extending longevity under the given storage conditions? How big should seed lots of a given accession be to allow adequate testing to be done?

(vi) How much is known about the genetic variation in longevity within and between accessions? How can the viability monitoring be tailored to particular accessions? Do pathogen infections affect longevity?

(vii) How large are the seeds and how many are needed per lot for regeneration and distribution? What volume of seed is needed per accession in order to represent the genetic variation adequately? What are the most appropriate storage containers and should subsamples of accessions be stored to facilitate their management?

(viii) If material is to be stored vegetatively what is the conservation purpose? Is it for clonal selection and use, to be kept in a field genebank or in vitro collection, or is it managed for propagation, as is the case for some multipurpose trees? How many accessions or provenances can be maintained and what are the requirements for land area and laboratory facilities?

(ix) If material is clonal and in vitro culture is used as a means of conservation or disease eradication, is the technology to be used linked to rapid multiplication facilities? Is it part of a complementary conservation strategy, i.e. linked to the management of diversity in a field genebank or material stored as seed?

4.2 Conservation concepts and structuring of collections

A good knowledge of species biology will determine appropriate conservation methods and clarify genebank requirements. In this section we will briefly describe the traditional conservation concept, largely based on management of orthodox seed germplasm in base and active collections. This will be followed by descriptions of new approaches and strategies that have been tried in many genebanks in developing and developed countries. At the end of the section the issue of structuring collections is briefly described.

Current conservation concepts and strategies

A more systematic approach to the management of germplasm collections followed establishment of IBPGR in 1974. This was a response to successes in modern plant breeding in the sixties and early seventies that were associated with serious losses of genetic diversity, particularly of landraces, in crops like rice and wheat. The global collecting effort for those threatened landraces needed to be coordinated. With the help of a panel of experts, IBPGR proposed an approach for the conservation of orthodox seed collections and conservation of the germplasm in base collections. The material was also maintained at higher temperatures for use in active collections.

A base collection essentially comprises accessions in long-term storage that are only used for regeneration. Such regeneration is kept to the absolute minimum and storage is done under optimal conditions to maximize viability. Active collections comprise the same accessions, but they are kept under less stringent storage conditions and are more easily accessible. This material might need to be more frequently grown out for characterization and evaluation and is made available for distribution to users. When accessions in

the active collection show noticeable genetic change they are replaced with material regenerated from the base collection. The active collection can be held under less rigid conservation conditions because the base collection is large enough to cope with long-term storage and regeneration.

Although much of this work has been validated, refinements are needed according to local circumstance, the precise objectives of the genebank, the existing infrastructure, available human resources and the extent of financial resources. Some specific reasons for a critical assessment of the traditional concepts and revision of the accepted practices include the following:

- The costs of refrigeration can be too high in many parts of the world and facilities are prone to technical problems.
- Many genebanks try to maintain active collections that are too large and often under-used.
- Results of research on seed drying, especially on very low moisture contents, led to extended viability of some species at higher than normal storage temperatures.
- Many genebanks have gained considerable experience using their germplasm and have been able to design more effective storage procedures.
- *In vitro* conservation systems were developed slowly due to the limited applicability of procedures among species, and costs involved, especially for routine operations. This situation has changed significantly during the last decade.
- Financial resources for genebank operations have not kept pace with the increased running costs and budgets have often decreased.

Vegetatively propagated species and those with recalcitrant seeds have been treated similarly to species that can be propagated by orthodox seeds, although the concepts were not designed for such materials. When stored *ex situ* in field genebanks these species are prone to biotic and abiotic stresses. This type of maintenance can only be considered viable in the short to medium term. Such storage therefore constitutes an active collection. Storage *in vitro* allows establishment and regeneration of a base collection (tissues in cryopreservation), an active collection (tissues under conditions allowing slow growth), or a working collection (tissues in *in vitro* culture with no special treatment). In most cases *in vitro* collections complement the germplasm maintained in field genebanks, as the latter do not provide sufficient security for safe conservation. However, germplasm in field genebanks is easily accessible and is used for characterization and multiplication as well as for

conservation. Where no seed collections or in vitro collections are maintained, and genetic diversity is solely maintained ex situ in field genebanks, a distinction between base and active collections is meaningless.

For these reasons, new standards and procedures have been developed at different genebanks. In this section an attempt is made to consolidate these experiences and propose new strategies and procedures for management of collections for conservation and utilization.

Revised conservation concepts and strategies

This section discusses the most effective procedures for long-term conservation of germplasm maintained by a genebank. In order to facilitate a proper understanding of these procedures, definitions of the different types of collections are presented before proceeding with the description of the procedures. It should be noted that the 'ideal' situation is being described and that it seldom, if ever, exists. It is therefore best to work towards the ideal situation without jeopardizing the overall operation of the genebank.

The **base** collection is a set of accessions, each of which should be (1) distinct, (2) in terms of genetic integrity as close as possible to the original sample, (3) preserved for the long-term future, and (4) unavailable for distribution.

The **active** collection comprises accessions available for multiplication and distribution for use.

A **security backup** collection comprises accessions of the base or active collection deposited at a different location to that of the base or active collection for safety purposes.

An **archive** collection consists of germplasm accessions that are stored but not actively maintained. A genebank has relinquished responsibility for conserving or distributing these accessions.

Standards for storage conditions, sample sizes, monitoring sample quantity, viability, and thresholds for regeneration are further described in Chapter 5 and are summarized in Appendix 2.

Long-term conservation

In a collection maintained for long-term conservation accessions should be handled carefully to ensure minimum loss of genetic integrity. The collection type that comprises those accessions is termed the 'base collection' and consists of the 'most original

sample', the 'security backup'. These components are described in detail below.

- A 'most original sample' (MOS) should be identified that is genetically as close as possible to the original population that it is intended to represent. The MOS may be a subsample of the original seed lot. Alternatively, if the original seed lot requires initial regeneration before storage, the MOS may be a seed sample from the first regeneration cycle. The regeneration should follow the best possible protocol for maintaining genetic integrity and to produce high-quality seed.
- The MOS should be prepared and stored in the best possible conditions for safe long-term survival.
- Seed from the MOS should never be distributed for use (see FAO/IPGRI (1994) and Sackville Hamilton and Chorlton (1997)).
- One subsample (the 'primary MOS') should be stored in the genebank responsible for its conservation.
- The number of seeds in the primary MOS (see Sackville Hamilton and Chorlton (1997)) should be the sum of:
 - The seed required to regenerate the MOS. This is at least the minimum amount of seed that represents the genetic diversity of the original sample, and at least the minimum amount needed to produce the required number of seeds of the next generation, whichever is the larger of these two minima. Calculations must allow for germination rates of < 100%, and must include an additional amount as a safety factor. These seeds should be left untouched until they begin to lose viability.
 - The seed required for routine viability testing, to detect loss of viability and therefore determine when the MOS must be regenerated.
 - The seed required for regenerating germplasm for distribution. Allowance must be made for possibly several regeneration cycles, to ensure that sufficient seed will remain untouched until the MOS begins to lose viability.

The three categories of seed in the primary MOS can be kept in a single container or in several containers, at the discretion of the curator, provided they are all kept under the same optimal conditions.

- For additional security, a second smaller subsample (the 'secondary MOS') should be sent to a distant genebank as a security backup. This is maintained under black-box conditions at least as stringent as those used for the primary MOS. The second genebank will be contracted to store the secondary

MOS under the best possible conditions, but beyond that will have no rights or responsibilities for maintenance or distribution of the secondary MOS.

- The secondary MOS should never be recalled, except in the event of unforeseen disasters that result in the loss of the primary MOS.
- The secondary MOS should contain just enough material to regenerate the MOS (with safety factor built in as above; see Sackville Hamilton and Chorlton (1997))
- A viability monitoring routine should be established to ensure that the MOS is regenerated before it loses viability. If it is decided to store the active collection separately from the MOS, it will usually be appropriate to conduct viability tests only on the active collection, at least early in the life of the MOS. If the active collection is stored under less optimal conditions, then viability in the active collection will drop before it does in the MOS. When that stage is reached, separate viability tests will be needed on the MOS itself.
- When it begins to lose viability, the MOS should then be regenerated using most appropriate protocol for maintaining genetic integrity and producing high-quality seed.
- Following regeneration of the MOS, a sample of the seed produced should be set aside as the next MOS and conserved in the same way, including replacement of the subsample held at a second genebank as a security backup.

Note that the MOS is not necessarily maintained as a physically distinct entity. The important feature is that some seed of the original sample should never be distributed, but should be set aside for conservation. This may be most easily achieved by keeping seed for distribution physically separate from the MOS, but there is no absolute requirement to do so. If it is administratively easier and economically more efficient, a genebank may opt to maintain one sample of each accession for both conservation and utilization.

In the case of species producing orthodox seeds, the seed kept in long-term storage for conservation is termed the 'base collection' of the genebank. This is not to be confused with nationally or internationally designated 'base collections' founded on a different concept.

Security backup

In the same way as a duplicates of the conservation (base) collection of one genebank should be sent for safe storage to a second genebank, so the genebank should provide black-box security backup facilities for base collections stored elsewhere.

Storage conditions should be the same as or better than those for the duplicate base collections, i.e. optimal for long-term storage, and normally would be the same as for the local base collection.

Beyond providing the best possible storage conditions, a local genebank holding a security backup collection takes no further responsibility for ensuring the accessions remain viable. Preparation of seed (drying, cleaning, packing) for storage is the responsibility of the genebank holding the duplicate base collection. The local genebank should never use, regenerate or distribute germplasm from the security backup. The germplasm should never be touched, except to be (a) returned on request to the responsible genebank (an exceptional eventuality in the case of a disaster occurring at the primary genebank), or (b) replaced, at the request of the responsible genebank, with newly regenerated germplasm. There is no need for any documentation beyond simply recording what is held.

Archive

In certain cases a genebank may choose to store other germplasm accessions at low cost that do not represent a base collection (possibly only applicable to seed storage) while relinquishing responsibility for conservation or distribution, i.e. to 'archive' germplasm accessions for (opportunistic) reasons of eventuality only (see below).

As it is likely that some accessions that could be included in the archive collection occur in the security backup, it is logical that they can physically remain there. When accessions actually form an archive they should be maintained under optimal conditions for long-term survival, but with no further investment in monitoring or maintaining viability and genetic integrity. Unlike the security backup, archived germplasm is not duplicated when it is the responsibility of other genebanks.

Reasons for adding germplasm to the archive collection include the following:

- Black-box conservation of experimental lines that could be bound by IPR (actual, pending or potential). As with accessions in the security backup collection, the genebank holding the accessions will never regenerate or distribute such accessions, but will return them on request to the IP-holder.
- When a collection has had to be disbanded, for instance for lack of funding. If the accessions from that collection lie outside the genebank's mandate, the genebank may still choose to rescue

them to prevent their complete disappearance. Ideally, another genebank should be identified with a relevant mandate so that they will be archived only temporarily.

- Following a reassessment of the genebank's mandate, a curator decides that some accessions are not within its mandate or are no longer needed in the collection. Rather than discarding them altogether they are archived. Ideally, another genebank should be located with a mandate relevant to the accessions so that they are archived only temporarily.
- Following a reassessment of its objectives and constraints, a curator decides that the size of the base collection must be reduced by eliminating accessions that are within its mandate. In the case of rationalization, the genebank might be forced to decrease the size of its base collections. This could lead to removal of duplicate accessions and accessions whose traits overlap significantly with those of others. Rather than discard the accessions altogether, a curator might archive them. If circumstances subsequently change (e.g. funding levels increase, erroneous decisions are discovered in the rationalization process leading to the cessation of maintenance of accessions), the curator can later bring the accessions back into the conservation collection. These accessions must be comprehensively documented.

Structuring collections

A genebank manager might want to organize collections in such a way that they facilitate their conservation and utilization. It might be necessary to organize a collection in a specific way in cases where the collection is large or where the genebank has entered into a collaborative arrangement with other genebanks.

An example for the latter case is the proposed arrangement between genebanks that participate in the European Cooperative Programme for Crop Genetic Resources Networks (ECP/GR). Each genebank is being asked to identify the genetically unique accessions being maintained and to accept a long-term responsibility to conserve these accessions and to share them freely and readily with the other genebanks. These so-called national collections together constitute the dispersed 'European base collection'. If fully implemented, it could lead to a significant reduction in the total number of accessions that the genebanks hold collectively compared with the current situation where numerous duplicate accessions are kept by various genebanks.

Examples of establishing a core collection of all accessions maintained of a given species or crop are less frequent but do exist. CIP has created a type of a core collection from the potato germplasm collection. This strategy aims to reduce drastically the number of accessions maintained in its field genebank and those duplicated for safety reasons in its *in vitro* collection. Substantial reduction in costs has resulted. For details see Box 1.

Box 1. Eliminating duplicate clones and splitting seed accessions in the Potato Collection

Case study:

Potatoes at CIP

(Centro Internacional de la Papa, Lima, Peru)

Conservation of potato as clones in a field genebank is expensive. It is more cost effective to undertake a comprehensive assessment of duplication and make major savings by reducing the size of the collection from 15000 to 3500. Accessions stored as seed are genetically variable so it was decided to assess whether they should be split. This was found to be unnecessary.

Cultivars are maintained as clones in a field genebank, and are grown every year. The field genebank is backed up by storing tubers in cold stores, through *in vitro* culture of diverse accessions at two locations and by conventional seed conservation of fertile accessions. Botanical seed is stored dry in medium- and long-term storage in accordance with international standards for seed conservation. This approach is necessary for secure conservation, but is expensive.

It was decided to look for and eliminate duplicate clones. The search involved a sequential process of morphological characterization for preliminary identification of potential duplicates, followed by a complete morphological characterization of the potential duplicates. Electrophoretic analysis of tuber proteins and esterase isozymes in morphologically identical accessions followed (Huamán, 1994; 1998). This resulted in identification of 3500 genetically distinct cultivars in the original collection of 15000 clonal accessions. Duplicates have been eliminated.

Accessions stored as seed are relatively cheap to maintain, but significant genetic variation within accessions creates a risk of diversity loss through drift. RAPD markers have been used to test for genetic drift in the *ex situ* seed collection, and repeat collections have been made to compare levels of *ex situ* and *in situ* drift. Large changes have been detected *in situ* (Rio et al., 1997a), but no significant drift has been detected during regeneration *ex situ* (Rio et al., 1997b). It is concluded that there is no need to split accessions to reduce *ex situ* drift.

Genetic Resources Unit, CIP, Lima, Peru

For more information: <http://www.cipotato.org/projects/germplasm.htm>

Similar approaches have been considered by the South Pacific countries to ensure the conservation of the total range of genetic diversity, especially for root and tuber crops. Thus, they may be able to ensure sustainable conservation (Taylor, 2002).

Structuring collections can also serve to highlight that part of the collection that best represents specific characters or traits and not the genetic diversity of the entire core collection, e.g. resistances. Such structuring, as described above, will usually involve a virtual rather than a physical effort (van Hintum et al., 2000).

4.3 Combining conservation and utilization strategies

The focus in the previous section was on long-term conservation. In most genebanks long-term conservation is only justified and sustainable if and when the accessions are used. In order to achieve this, options are presented below that allow an optimal combination of long-term conservation with immediate or imminent utilization. Consequently, this section deals with the handling of accessions stored for research and distribution in the active collection and with the links to long-term conservation of the germplasm in the base collection.

There are numerous storage options, and the only general rule is to use the best economically viable conditions. For example:

- For species with orthodox seed storage characteristics, it is usual to keep the active collection of seed at approximately 5% seed moisture content and between 0 and 4°C. This often confers more than adequate longevity and reduces the need for regeneration to maintain viability.
- Storage at room temperature may be acceptable if use is substantial and additional regeneration is relatively cheap and effective compared with cold storage. However, the regeneration must not be allowed to interfere with effective conservation of the MOS.
- At the other extreme, it can be economically more effective to maintain the active collection in long-term storage with the base collection, since this will require operation of only one rather than two storage systems. Complicating factors include:
 - The mandates for long-term conservation and short-term utilization may rest with different institutes (as in USA and India). There may exist a centralized base collection for conservation and a distributed set of active collections

maintained more by the users. In such cases, base and active collections have to be kept physically separate.

- The genebank may already have been built with a store for long-term conservation and a store for medium- or short-term utilization. In these cases, the long-term store will often not be large enough to hold both base and active collections, requiring two physically separate collections.
- Some long-term storage facilities, including chest freezers, are logistically inappropriate for frequent and easy access. If these are chosen to house the base collection, it may not be possible to use the long-term store for the active collection.
- It may best fit local conditions not only to use the same storage facility for base and active collections but to keep them in a single container, such as a large glass jar, preferably with several subsamples to facilitate management and increase safety. The benefit of this system is that only a single set of containers is required, and consequently the procedure for monitoring quantity and quality involves only one container per accession. Special attention must be paid to procedures required to retain the MOS in this event.

The numbers of seed or other propagules representing each accession may need to be modified in accordance with the storage options and the expected level of utilization. Further guidance is given in the Regeneration Decision Guide (Sackville Hamilton and Chorlton, 1997; Rao and Engels, 1998).

4.4 Relationship between genebank and breeders' collections

It is important to realize that many of the current germplasm collections managed by genebanks are based on collections provided by plant breeders. Therefore, some information is provided on these so-called breeders' collections in order to understand better the relationships between the active collections on the one hand and breeders' collections on the other.

Plant breeders traditionally base breeding programmes on collections of carefully selected genotypes of a given crop that possess useful traits for incorporation into an adapted variety. Therefore, breeders' collections tend to be dynamic and are modified according to needs. This also means that a breeder will discard samples that are no longer useful. Off-types in a sample will be removed continuously by growing and roguing the entire collection on an annual basis. This allows only a snapshot of the genetic diversity that was present in a breeder's collection and was included in the genebank collection.

4.5 Quality management and genebank standards

Increase in the number and size of ex situ collections requires establishing international standards for genebank management. IPGRI and its predecessor IBPGR, in close cooperation with the FAO and its Commission for Genetic Resources, developed Genebank Standards (FAO/IPGRI, 1994). These standards deal predominantly with storage of seed collections, both in active and base collections, and related topics. Standards for most routine operations have however not been dealt with to any great extent.

Development of detailed international procedures and standards for routine and key genebank operations is needed to encourage increased regional and international cooperation and improve task sharing among genebanks (see also Chapter 8).

What constitutes quality management?

The quality of genebank management is judged, consciously or unconsciously, by a genebank's staff, by its funders and users and by collaborating institutions. Quality management aims to install and apply a management system that actively and explicitly guides and administers an organization in terms of standards. Such a system can be certified to ensure that agreed quality standards are adhered to and that critical steps in processes are observed and implemented.

A quality management system can be regarded as a management tool to monitor and improve processes in an organization. Such a system strives towards uniform, assured quality. The system should however be able to accommodate changes in the working environment of the organization. A well-developed quality management system results in satisfied users (and funders), lower costs following from reduced instances of production failures, quality conscious staff and improved opportunities for collaboration. Such a system requires active participation of management and staff, adequate capacity and a practical and appropriate design. Factors that hinder implementation concern half-measures rather than complete changes and lack of clarity as to why quality management is important and how it can be achieved.

Quality management in an organization requires thinking in terms of systems and processes. For a genebank this means identifying activities and steps taken in germplasm conservation and promotion of its use, and the means by which these objectives are reached, through documentation and research. It also implies a

clear set of policies that provide guidance for management. All the steps in the primary process should be documented in a 'Quality Handbook', which should be made available to all staff and be regularly updated. The handbook should contain procedures (which steps to follow, e.g. how to decide on inclusion of a new accession in the genebank) and protocols (how to carry out certain activities, e.g. how to regenerate a specific crop collection). An example of a scheme describing the primary process is presented in Figure 1.

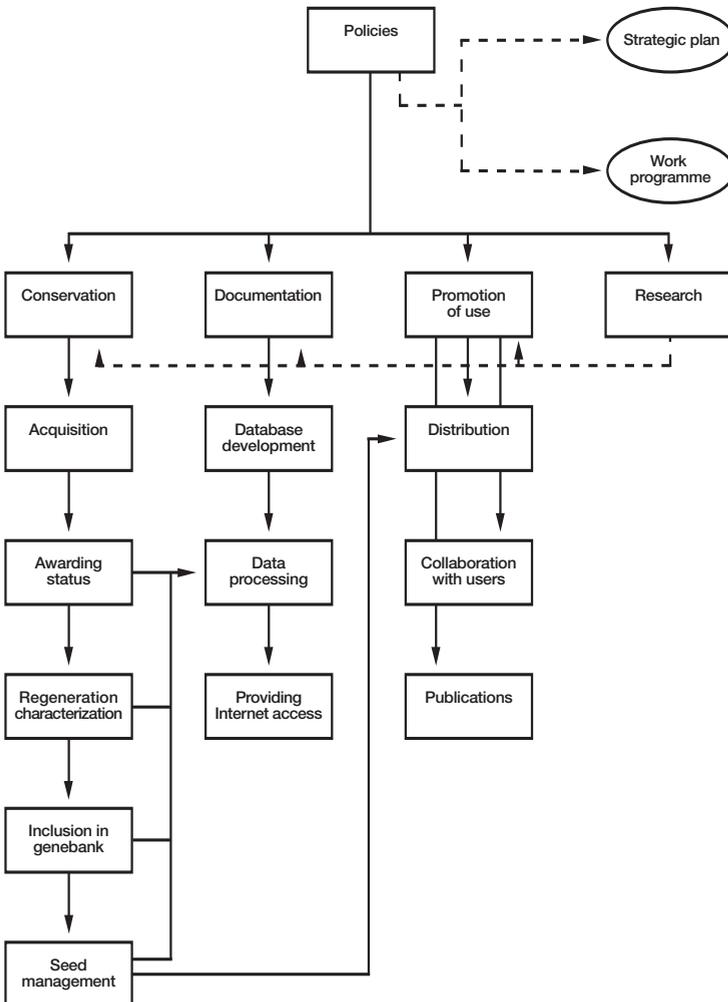


Figure 1. Flow chart showing the primary process of genebanking activities, as developed by CGN.

The most appropriate international system for quality control is based on ISO 9000³. This system is used in both the private and the public domain, and provides for the implementation of quality control procedures and standards in vastly different organizations and for a wide range of processes in industry and government organizations. Independent specialized organizations will, on request, monitor whether the quality management system of an organization (e.g. a genebank) meets the internationally agreed requirements of the ISO norm. NGB and CGN are examples of genebanks that are currently preparing for certification according to the ISO norm.

Other certification schemes have also been introduced in a number of countries but they less suited for implementation in genebanks. Examples of these are STERLAB, STERIN, GMP and GLP (good manufacturing and laboratory procedures) rules.

It should be emphasized that certification entails only a detailed description of the procedures and standards adopted by a genebank without strict regard to their quality. While it is very clear through ISO 9000 accreditation how a genebank works ('tell what you do, do what you tell, and show that you do what you tell'), agreement is lacking among collaborating genebanks on the desired quality of standards. In general, the adoption of external quality control provisions would allow easy reference to procedures, would contribute to sharing responsibilities among genebanks, and would provide the basis to formalize such collaborations and thereby contribute to more efficient and effective global conservation. In addition, adoption of quality control systems greatly improves the internal operation of genebanks. Alternatively, an independent neutral institution could be appointed that would oversee the compliance of cooperating genebanks with agreed standards. This, in turn, would provide a more solid basis for trust and cooperation, would encourage genebanks to surrender responsibility for collections taken care of by others and hence reduce duplication.

In Appendix 2 details of currently recommended genebank standards are included for easy reference.

While it has been recognized that the current IPGRI/FAO genebank standards are adequate and represent the best practice for genebanks, some people have observed rigid, non-creative compliance to these standards, whereas others regard the standards as an unachievable ideal. Genebank managers should decide carefully when interpreting these standards. Quality control

³ The International Organization for Standardization (ISO) is a global federation of national standards bodies representing more than 140 countries. ISO is a non-governmental organization established in 1947. The mission of ISO is to promote the global development of standardization and related activities with a view to facilitating international exchange of goods and services, and to developing cooperation in the spheres of intellectual, scientific, technological and economic activity. ISO's work results in international agreements that are published as International Standards. <http://www.iso.ch/iso/en/ISOOnline.frontpage>

of genebank operations is considered an important prerequisite for effective collaboration, germplasm exchange and reliable data management. An international certification system for genebanks may be considered necessary. In all cases, genebanks should produce a detailed manual of operating procedures. These procedures should describe in detail what is actually done, including the standards that are followed.

1. Introduction
2. Context of genebank management
3. Setting objectives for genebanks
4. Considerations for improved conservation and utilization concepts and strategies
- 5. Genebank management praxis**
 - 5.1 Collecting strategies**
 - 5.2 Conservation methods**
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5. GENE BANK MANAGEMENT PROCEDURES

*Jan Engels
and Bert Visser*

This chapter provides a sequential overview of routine genebank operations that affect management of collections, starting from germplasm collection through to the distribution of samples by the genebank. Wherever possible, options and alternative approaches are presented with the aim of contributing to informed decision-making by genebank managers and staff.

5.1 Collecting strategies

Sampling strategy is determined by the precise mandate of the genebank and the objectives of the collecting mission, i.e. gap filling, targeted collection of specific genotypes, or reducing loss of genetic diversity from genetic erosion. Attention is paid to aspects of geographical coverage, sample size, genetic diversity etc. A comprehensive technical guide on collecting plant genetic resources providing many practical and managerial suggestions was published by Guarino et al. (1995). Whenever possible it is advisable to include an experienced plant breeder in the collecting team, especially in the case of targeted collecting missions, to benefit from specific knowledge of the crop species and thereby ensure that breeders' needs are considered. In cases where the collecting mission focuses mainly on local or traditional crops it could be beneficial to include an ethnobotanist in the team to take care of the socio-economic aspects.

The fundamental objective of collecting plant genetic resources is to capture the maximum amount of useful genetic variation in the smallest number of samples (Marshall and Brown, 1975). The development of efficient sampling strategies depends on the extent of the information on the

type and amount of genetic variation in target taxa populations and their distribution in the target geographical region (Allard, 1970). In some cases when information is lacking on the target species and the collecting area it might be prudent to organize an exploration mission to collect such information.

The basic parameter for measuring variation in a given population is allelic richness: the number of distinct alleles at a single locus. This is usually assessed at a large number of marker loci after the sample is taken (Brown and Marshall, 1995). If several populations are to be sampled in a given area, the extent of genetic divergence (a measure for the genetic distance between populations) and the total genetic variation among the populations is important. The latter is reflected in the range and pattern of distribution of numbers of alleles per locus (Schoen and Brown, 1991). The generally accepted benchmark criterion for collecting germplasm is to ensure that at least one copy of 95% of the alleles at a frequency greater than 0.05 be included in the collected sample (Marshall and Brown, 1975). A sample of 50 individuals from each population will meet this criterion, although it is realized that such numbers may not always be feasible. Further information on basic sampling strategy (including number and location of sampling sites; number of individual plants sampled at a site; choice of individuals; and number and type of propagules per plant) can be found in Brown and Marshall (1995).

The knowledge and understanding of the genetic structure of many plant populations has increased significantly, providing a more secure base on which sampling strategies can be developed. For example, wild relatives of crops are becoming increasingly valuable to breeders as biotechnology provides tools that enhance wide-crossing. However, wild species differ from domesticated crops in many ways, for example in the distribution of the species; local abundance; inter-population migration; habitat diversity; life-history traits such as duration of the life cycle; population age structure; vegetative reproduction; fecundity; determination of flowering and seed maturation; mating system (outbreeding, self-fertilization or apomixis); pollination mode; and conspicuous polymorphisms. As a result of these differences, sampling strategies for wild species may differ substantially from those for crops (Brown and Marshall, 1995).

Collecting techniques

Collecting techniques and equipment employed will depend on the type of material to be collected, i.e. seed, pollen, vegetative propagules or whole plants. To maintain population or varietal integrity in the case of landraces, the sample should be of the type

used by the farmer. For example, seed should be collected for seed propagated crops (maize, rice), and vegetative samples for clonally propagated species (e.g. tubers for potatoes and offshoots for bananas), some of which never produce seed. Where grafting is the propagation technique used by farmers, rootstocks must be grown. However, it should be realized that for the conservation of genetic diversity per se, maintenance of population or varietal integrity is not a necessary prerequisite, and this leaves the option to maintain diversity occurring in clonally propagated species in the form of seed.

The seed of many crop species, especially tropical fruits with seed of high moisture content, cannot be stored under standard cold dry conditions generally used in genebanks. An early recognition of the problem of transporting the collected seed of tropical plants led to the development of the 'Wardian case'—in effect, a portable greenhouse—developed in the 1830s to transport plants as seedlings on deck during long sea voyages until the advent of air transport (Hepper, 1989). More recently, zygotic embryos and vegetative tissues such as budwood, shoots or apices have been sampled, treated, transported and subsequently grown under acceptable conditions at a distant location. Withers (1995) discussed in detail the application of in vitro techniques to collecting germplasm. Engelmann (1997) specified several cases in which in vitro collecting can be advantageous. These include long missions to remote areas when vegetative material or seeds may not survive; when the size and weight of seeds is a problem; when the risk of transferring pests and diseases is high (when soil particles remain on collected material); and, finally, when there are insufficient seeds to collect.

For several crops, well-established protocols, procedures and equipment for the collecting and transport of the material exist that can be adapted to other species. These include collecting budwood described for cocoa (Yidana, 1988); extraction of zygotic embryos described for coconut (Assy Bah et al., 1989); use of stem nodal cuttings for cotton and related species (Altman et al., 1990); and use of herbaceous plantlets as explants described for some forage grasses (Ruredzo, 1989). Collecting DNA-rich material such as leaves and root nodules can be done with little additional effort when specimens are collected for herbaria or genebanks. The material should be stored with a desiccant or immersed in a stabilising buffer immediately after collecting to ensure successful subsequent DNA extraction. As such, this represents a simple long-term storage method (Adams, 1997). However, it should be realized that DNA will only form a source for the introduction of individual

traits though application of methods in biotechnology. In addition, unlike seed, DNA is non-regenerable and stocks will be exhausted sooner or later. This means that storing DNA can never replace storage of living materials, whether as seed, *in vitro* tissue or cryopreserved material.

Important decisions to be made by the collector relate to the amount of seeds to collect for each accession, not only from a genetic diversity perspective but also from a genebank management perspective. If the genebank wishes to avoid the initial regeneration and instead use the collected material as the starting point for the conservation effort, a significant amount of seed is needed for each accession. This procedure is being applied by the genebank of the Royal Botanic Gardens at Kew, UK. However, it should be noted that it might be difficult to collect seeds of optimum physiological condition that a curator wants in order to ensure optimal longevity of the seed for long-term conservation. Furthermore, it will be important to monitor the collected material carefully, check its phytopathological status (see also a Section 5.8 on this aspect) and carry out characterization and possibly a preliminary evaluation of it. Only then will the genebank manager be able to make the right decisions for efficient and effective management. In practice, optimal conditions for collecting large numbers of seed are often not met.

5.2 Conservation methods

It is now widely accepted that conservation can be done on-site (*in situ*) and off-site (*ex situ*). In this section these and other conservation approaches and methods will be briefly described.

***In situ* conservation**

The CBD (UNEP, 1992), covering both wild and domesticated species, uses a complex definition for *in situ* conservation: “the conservation of ecosystems and natural habitats and the maintenance and recovery of viable populations of species in their natural surroundings and, in the case of domesticates or cultivated species, in the surroundings where they have developed their distinctive properties.” There may be substantial differences in approach for the conservation of wild species and domesticates. For example, for wild species conservation, the introgression of alien genes into populations of the target species would be avoided. In contrast, for crops, it has been argued that introgression of genes from wild species into crop populations is an evolutionary event and one advantage of *in situ* conservation and thus should be allowed to occur (Altieri and Merrick, 1987, and many others).

With the conclusion of the CBD and Agenda 21 in 1992, and with the adoption of the GPA by the participating countries in the Fourth International Technical Conference on Plant Genetic Resources (FAO, 1996), a significant impetus has been given to in situ conservation. In recent years on-farm conservation activities have become closely linked with development work, including the farmer empowerment (Jarvis and Hodgkin, 2000a).

Protected areas: Protected areas are widely regarded as instrumental for in situ conservation of wild relatives. Wild relatives of crops and domestic animals may occur beyond the influence of farming, in natural and semi-natural ecosystems and their conservation may well fit into the existing system of nature reserves. Many proposals relied on this approach (Ingram, 1984; Prescott-Allen, 1984; Prescott-Allen and Prescott-Allen, 1984; Wilcox, 1990) but, until recently, few of these proposals were funded. Currently the conservation of agrobiodiversity in protected areas is largely unplanned and this component of biodiversity is usually not specifically addressed. A feature of this form of conservation is that evolutionary processes continue to operate and that entire populations can undergo changes, and can become extinct. A disadvantage of protected area conservation is that the conserved material is not readily available for agricultural use. Also, with limited opportunity for management, little characterization and evaluation can be done on the germplasm, restricting its use as a genetic resource (Maxted, et al., 1997b).

Conservation on-farm: Farmers worldwide have been practising on-farm conservation for as long as agriculture has existed, as a necessary part of crop production. For them, the most effective management practices have been those that combined highest yields with the greatest food security. Usually, these practices are based on within- and among-species diversity, surviving in areas that are not served by modern high-input agriculture. In addition to crops, wild and weedy species occur that are associated with farming. Suggestions have been made for intervention to boost the effectiveness of this age-old process. Jarvis et al. (2000b) provided detailed suggestions and procedures for the management of these resources on-farm in the framework of traditional farming systems, that allow for continued maintenance and evolution of traditional landraces and wild and weedy species that depend on traditional agricultural practices for their survival. Potential advantages and disadvantages of conservation on-farm will need to be weighed for suitability for application to conservation, as well as for impact on farm livelihoods.

Home gardens: Home gardens are a reservoir of diversity for fruits, vegetables and small domestic livestock. Proximity to the home allows detailed selection, for example, of colour variants of most plants and animals, as well as generation of the vast morphological variation that exists in many domesticated species. Several authors (Maxted et al., 1997a; Damania, 1996; and Engels, 1995) list the conservation of plant genetic diversity in home gardens separately. As for on-farm conservation, the method is dynamic. A community of gardens may need to be included, as the intraspecific diversity within an individual garden is often limited, whereas the variation among gardens is often substantial (Engels, 2002b).

Many ideas and proposals have been put forward for in situ conservation of agrobiodiversity, ranging from 'mass reservoirs' (Simmonds, 1962; Frankel and Bennett, 1970; Frankel et al., 1995) to recommendations of ethnobotanists (Brush, 1986 and 1999; Oldfield and Alcorn, 1987; Altieri and Merrick, 1987). Others proposed to contribute to on-farm conservation by genetic base broadening through decentralized multi-site adaptation of composite populations. A good overview of lessons learned from on-farm conservation can be found in Jarvis et al. (2000b).

***Ex situ* conservation**

Seed storage: Storing genetic diversity as seed is the best researched, most widely used and most convenient method of *ex situ* conservation. Much is known about the optimum treatment of the seed of most of the major food crops. For an early review, see Harrington (1970). Requirements include adequate drying, i.e. seed moisture contents as low as 3% for oily seeds and 5% or more for starchy seeds; appropriate storage temperature (-18°C is recommended for long-term storage); and careful production of quality seed to ensure the greatest longevity (Rao and Jackson, 1996). Recent research shows that very low moisture contents could be sub-optimal and care is needed.

However, the seeds of many crop species, especially tropical shrubs and trees, will lose viability if dried (so-called 'recalcitrant' seeds). Seeds of some species can be dried to some extent but cannot survive low-temperature storage and are intermediate in storage characteristics. This category includes coffee, citrus species, rubber and others. In addition, seeds of wild relatives do not always behave similarly to the seed of domesticates, and optimal storage conditions have to be individually determined.

An IPGRI protocol to determine the precise seed storage characteristics of little researched species (Hong and Ellis, 1996) and a compendium of available data on storage behaviour of approximately 7000 species, including references to individual species, is available (Hong et al., 1996; Engels et al., 2001).

Most national genebanks now rely on cold storage facilities for seed maintenance. However, these depend on a reliable electricity supply, which can represent a problem in some countries. To overcome this problem, alternative approaches to low temperature storage have been developed, including the so-called 'ultra-dry seed' technology. Drying seeds to a moisture content as low as 1% (in the case of oily seeds) or approximately 3% (starchy seeds) and hermetic packaging allows storage for long periods at room temperature. Care must be taken to prevent over-drying of the seeds (Walters and Engels, 1998).

Some genebanks have also experimented with storing seeds in liquid nitrogen. Besides the already mentioned danger of over-drying the (orthodox) seeds, seed size is important for economic cryopreservation. Furthermore, it has been agreed that this approach might have advantages under circumstances where electricity supply is unreliable.

Pollen storage: The technique for pollen storage is comparable with that for seed storage, since pollen can be dried (less than 5% moisture content on a dry weight basis) and stored below 0°C. There is limited experience on the survival and fertilizing capacity of cryopreserved pollen more than five years old (Towill, 1985). Hoekstra (1995) using information on more than 1500 plant species failed to determine a clear correlation between the storability of pollen and of seed of the same species. Pollen might represent an interesting alternative for the long-term conservation of problematic species (IPGRI, 1996). However, pollen has a relatively short life compared with seeds (although this varies significantly among species), and viability testing can be time-consuming and uneconomical. Pollen has, therefore, been used to a limited extent in germplasm conservation (Hoekstra, 1995). Other disadvantages of pollen storage are the small amount produced by many species; the lack of transmission of organelle genomes via pollen; the loss of sex-linked genes in dioecious species; and the general inability to regenerate into plants (Hoekstra, 1995). An advantage is that pests and diseases are rarely transferred by pollen (excepting some virus diseases). This allows safe movement and exchange of germplasm as pollen.

Field genebanks: Field banks are used for the conservation of clonal crops; where seed is recalcitrant; and for crops that rarely produce seed. The rule of thumb is to use the same propagation techniques as the farmer, for example not disrupting adapted clones through genetic segregation in a seed cycle. Many temperate and tropical fruit trees fulfil one or more of these conditions, as do many commodity crops such as cocoa, rubber, oil palm, coffee, banana and coconut as well as most root and tuber crops. An example of the scale of management of field genebanks is that oil palm genetic resources in Malaysia are planted at a density of 140 palms per hectare, and the collection from Nigeria alone occupies 200 ha. Since oil palm seed cannot be stored for more than two years, and pollen only for three years, a living collection, although expensive, is currently the only practicable conservation method. Similarly, the coffee genebank in Jimma, Ethiopia contains over 1600 accessions of coffee trees from the centre of diversity of the crop.

Management may be the same as used during routine farming, and cultivation methods can be adapted to local circumstances. Conserved material can be readily characterized and evaluated and then accessed for research and use. Some natural selection may take place within and between accessions, but management is designed to prevent it. Major constraints faced by field genebanks include costs and all the natural hazards of farming, including pests and diseases, drought, flood, cyclones etc. (Engelmann and Engels, 2002).

In vitro conservation: When a conservation method is susceptible to unavoidable hazards, as with field genebanks, an alternative, complementary method should also be used. In vitro conservation involves maintenance of explants in a sterile, pathogen-free environment and is widely used for the conservation and multiplication of species that produce recalcitrant seeds, or do not produce seeds (Engelmann, 1997). Although research on in vitro techniques only started some 20 years ago the technique has been applied for multiplication, storage and, more recently, for collecting germplasm of more than 1000 species (Ashmore, 1997).

Various in vitro conservation methods are used. For short- and medium-term storage the aim is to increase the intervals between subcultures by reducing growth. This is achieved by modifying the environmental conditions, including the culture medium, to realize so-called slow-growth conservation. The most widely applied technique is temperature reduction (varying from 0–5°C for cold tolerant species to 9–18°C for tropical species) that can be combined with a decrease in light intensity or storage in the dark

(Engelmann, 1997) and adjustment of the growth medium. Alternatives to standard slow-growth conservation include modification of the gaseous environment of cultures, desiccation and encapsulation of explants. The latter is termed synthetic seed where the idea is to use somatic embryos as true seeds. Embryos encapsulated in alginate gel can be stored after partial dehydration and sown directly in vivo (Janick et al., 1993).

For small volumes, long-term storage is practicable through storage of cultures in cryopreservation at ultra-low temperature, usually by using liquid nitrogen (-196°C). At this temperature all cellular divisions and metabolic processes are virtually halted and, consequently, plant material can be stored without alteration or modification theoretically indefinitely (Engelmann, 1997).

Botanical gardens and arboreta: Botanical gardens have played a historical role in the exchange and introduction of crop genetic resources. Usually botanical garden collections consist only of one or a few individuals per species (FAO, 1998), although in recent years there has been a tendency towards the establishment of conservation units, including seed banks (Laliberté, 1997). Unfortunately, most botanical gardens have limited interest or expertise in crop genetic resources, although efforts are being made to change this (Heywood, 1998).

DNA storage: This more recently developed technique is increasing in importance. DNA from the nuclei, mitochondria and chloroplasts is now routinely extracted and stored. For the purpose of analysis, DNA is often immobilized on nitrocellulose sheets where it can be probed, including with cloned genes. With the development of PCR (polymerase chain reaction) specific oligonucleotides and genes can now be routinely amplified. DNA cloning technology has further facilitated efficient use of DNA sequences. These advances have led to the formation of an international network of DNA repositories for genomic DNA (Adams, 1997). The advantage of storing DNA is that it is efficient and simple and overcomes many physical limitations and constraints that characterize other forms of storage. The disadvantage lies in problems with subsequent gene isolation, cloning and transfer, but, most importantly, it does not allow the regeneration of live organisms (Maxted et al., 1997a; for recent updates see also www.cgn.wageningen-ur.nl/pgr/).

Complementarity of conservation strategies

Farming itself is the original method of conservation, linked directly with utilization. But farming is changing, rendering conservation of diversity at the farm superfluous given development of specialized

crop breeding. Most farmers cannot afford and would not wish to be curators of living museums of agrobiodiversity (as suggested by Wilkes, 1971). Fortunately, the wide spectrum of conservation methods can meet a wide range of conditions. With the range of genetic diversity included in conservation, security and accessibility can be balanced against feasibility and cost-efficiency. The choice of a single method of conservation will often not be enough: different and complementary methods of conservation have advantages and disadvantages. In making choices it is important to take a holistic view of the intended conservation effort and to place it in a wider context of current and potential future user groups, whenever applicable. It is also important to examine carefully the technical and human resources available as well as the administrative and political environment in which the conservation will be done in order to minimize problems (Engels, 2002a).

In choosing alternative or complementary methods of conservation, the most obvious contrast is between *in situ* and *ex situ* approaches. The dynamic processes of *in situ* conservation could be combined with the usually more secure approach of *ex situ* conservation, and improve accessibility to the germplasm. As a result of disease pressure and natural selection, continuous adaptation is likely to occur, possibly enhancing the value of on-farm populations as a source of variability for breeding for disease resistance. This potential for exploiting the evolutionary process during on-farm conservation was noted by Allard (1990) for disease resistance (of the barley-scald pathosystem). However, the rate of this adaptation is unknown, and methods of sampling or evaluation in the field have not yet been thoroughly developed to monitor this process (Maxted et al., 1997a).

Many minor but locally important crops have been neglected by collectors and *ex situ* genebanks. For these crops and their wild relatives, *in situ* (including on-farm) conservation is appropriate. Notwithstanding the advantages of continuing evolution on farm, and the substantial diversity of material that can be conserved, there will be limited access to those resources; a lack of adequate characterization and evaluation; and the danger that farmers abandon the cultivation of traditional landraces under economic pressures. Careful monitoring will always be needed. Conservation through use *in situ* might run the risk of losing specific alleles or genotypes as a result of continuous adaptation and a backup system through *ex situ* conservation will be required. This was emphasized by Hammer et al. (1996) who found that 96.8% of the samples collected in Albania in 1941 were still intact in the Gatersleben genebank in Germany, whereas a survey 50 years later

in the same region in Albania showed genetic erosion of about 50%. The authors concluded that this “is an amazing result as the material had to survive the Second World War and two translocations”.

The choice between conservation methods may be dictated by the biology of the species. For instance, if the cultivated species does not produce seeds (as for bananas) the choice includes on-farm conservation, maintenance in field genebanks, in vitro slow growth and cryopreservation (Sharrock and Engels, 1997). Cassava and potato represent examples of extensively studied genebanks used to develop in vitro techniques, for which a broad range of conservation options is now available.

5.3 Examples of conservation protocols

The protocols and procedures of three genebanks have been included as Appendices to this handbook. These genebanks specialize in sexually propagated, mostly outcrossing crops (grassland species), a vegetatively propagated crop (banana) and multiple crops.

5.4 Monitoring viability

Monitoring viability of stored seeds is important for conservation and much research has been carried out on germination and vigour testing. The curator has to be able to assess accurately the initial viability of accessions prior to storage and then monitor the viability of them during storage. Viability and vigour should be tested soon after regeneration, as unwarranted processing and storage of non-viable material is a waste of time and funds. Standards for viability monitoring in genebanks are included in the Genebank Standards (FAO/IPGRI, 1994). Specific procedures for viability testing are included in the IPGRI handbooks on seed technology for genebanks, on principles and methodology (Ellis et al., 1985a), as well as on specific germination information and test recommendations (Ellis et al., 1985b). Moreover, methods have been developed that require substantially less seed per test, e.g. sequential seed testing (Ellis et al., 1980).

Protocols have been developed at The International Seed Testing Association (ISTA) to test viability of numerous crop species (Ellis et al., 1985b). However, no specific management approaches for viability testing and monitoring have been developed and this has resulted in a range of practices being used. Some genebanks test all their stored seed samples at regular intervals whereas others test randomly selected accessions irregularly. It should be borne in mind

that data on the pattern of loss of seed viability over time (shape of the curve) is limited. Additional information on available protocols can sometimes be obtained from botanical gardens and associations of seed producers. When not available, such protocols have to be established and it is suggested to use an experiment-based approach, as variation has been recorded within well-known species and among populations, particularly regarding dormancy and hardiness of seed hulls. Determining seed vigour, in addition to germination percentage, could provide the genebank curator with early indications of a decrease in viability (Bewley and Black, 1994).

Substantial differences may sometimes exist in longevity among accessions of the same species and even among genotypes within the same accession. It is therefore advisable to monitor seed viability carefully. As regeneration is usually very costly and risky, from a genetic diversity point of view, it should not be undertaken unnecessarily. Therefore, it is recommended that each genebank develop its own monitoring procedures that guarantee effective and efficient conservation.

5.5 Regeneration strategies aiming at maintenance of integrity

Genebanks rarely receive sufficient material in ready condition for long-term storage. Often genebanks do not receive sufficient germplasm for all needs (conservation, distribution, health and viability testing, etc.). Moreover, germplasm distribution by genebanks requires phytosanitary certification and thus production under controlled conditions. If seed is collected from the wild, or obtained from farmers' seed stocks or markets, viability and health status are unknown. Genebanks thus have to multiply or regenerate the material to ensure sufficient quantity and quality. Regeneration under controlled conditions is crucial to ensure viability and germplasm health and to maintain genetic integrity.

Regeneration of accessions is a key process in genebank management since accessions are vulnerable to loss and change. It is also a costly process and compromises have to be frequently made without regard for the possible consequences that may become apparent much later. It was for these reasons that IBPGR published a scientific background paper for regeneration and multiplication of germplasm in seed genebanks (Breese, 1989).

More recently, a decision guide for the regeneration of seed accessions was published with the objective of facilitating the development of optimum procedures (Sackville Hamilton and

Chorlton, 1997). The guide provides curators with options to address specific regeneration requirements of different accessions, and to take account of the various circumstances under which genebanks operate. A flow chart highlighting the major decisions made during the regeneration process provides curators with a tool for optimizing regeneration management. The guide deals with the timely identification of accessions when seed quality and quantity is lacking. It also considers the regeneration of accessions to produce new seed of optimum quality and quantity (also termed rejuvenation or multiplication), with minimum loss of genetic integrity and at maximum cost-effectiveness (Sackville Hamilton and Chorlton, 1997).

Indications of genetic shift and genetic drift from studies of population genetics have led to development of procedures for multiplication and regeneration of genebank accessions that maintain genetic integrity to the highest degree possible. Molecular genetic techniques allow changes to be monitored in genetic make-up of samples in genebanks. The question of genetic instability, in particular due to somatic mutations in the case of in vitro conserved germplasm, is a real concern and needs to be given due attention for long-term conservation to be effective. True-to-type characters need to be established as part of the routine process.

As plant breeders know their crops very well, some genebanks cooperate closely with breeders in regeneration activities, or even subcontract this responsibility to a breeder. Other genebanks organize open days for breeders and other interested users, growing materials in the field to promote familiarity with genebank germplasm and create interest in further evaluation and use. In many cases regeneration is thus combined with close scrutiny of the material, including its systematic characterization. In some instances the regeneration is combined with evaluation (Engels, personal observation). However, this is generally not advisable, in particular when the curator wants to score disease resistance, since the overriding objective should be to produce healthy, high-quality seed for long-term conservation.

It has been noted that in several genebanks regeneration of stored germplasm accessions has not been regarded as an integral responsibility of the genebank. Sometimes regeneration has been financed through special projects and has created a situation that has not been sustainable. As a result, the genetic diversity maintained has been jeopardized and emergency rescue actions have been needed. To avoid such situations it is strongly

recommended that regeneration is considered to be a genebank responsibility and to make the necessary budgetary provisions for carrying it out.

5.6 Characterization and evaluation approaches

Characterizing accessions, an activity that is typically regarded as the responsibility of the genebank curator, involves determining the expression of highly heritable characters, ranging from morphological features to seed proteins and possibly including molecular markers. Such characters also enable easy and quick discrimination among phenotypes and allow simple grouping of the accessions, as well as a check on the trueness-to-type of homogeneous samples, frequently according to criteria used by breeders and other germplasm users. Genebanks should consider establishing close cooperation with plant breeders while characterizing accessions, not only during the field and laboratory activities but also earlier to decide on which descriptors to use. In addition to or instead of a molecular analysis, their scoring also allows establishment of systematic relationships among accessions and even crops, including their evolutionary relationships. This directly facilitates utilization of collections, allows detection of misidentifications and indicates possible errors made during other genebank operations (Bretting and Widrlechner, 1995). It also results in better insight in the composition of the collection and the coverage of genetic diversity. A proper characterization also makes an important contribution towards rationalizing management procedures, since it allows the curator to make well-informed decisions on where best to regenerate the material (e.g. the japonica and indica rice races findings of Rao and Jackson, 1996), to identify possible duplicates, to group germplasm accessions, etc.

Berthaud et al. (1997) proposed a modified version of the traditional three-step linear model of conservation, evaluation and use by promoting genetic enhancement and pre-breeding, relying on knowledge and activities of farmers as well as local breeders.

The environment invariably influences the expression of traits used in the (preliminary) evaluation of germplasm accessions. The most valued traits in crop improvement include yield, agronomic performance and stress resistances. It is obvious that an adequate evaluation of the collection represents an important prerequisite to effective use of the collection, as well as a major investment. The genebank manager should take every opportunity to get the

conserved material evaluated. The expression of important traits is increasingly being researched using molecular markers (Bretting and Widrlechner, 1995). Since this activity is not regarded by all genebanks as a typical genebank responsibility, but rather as a task for plant breeders and other users, close cooperation among all participants is essential to ensure useful application of results.

It is not always obvious which molecular technique to use in addressing a specific germplasm management question. IPGRI published a technical bulletin to provide curators with a guide for choosing the best and most cost-effective technique (Karp et al., 1997). CGN offers an on-line update on this issue (www.cgn.wageningen-ur.nl/pgr/).

In order to facilitate standardization of information obtained during characterization and evaluation, IPGRI coordinates the publication of Descriptor Lists in close cooperation with crop experts and genebank curators. These are consensus lists of descriptors for individual species and written in the universally understood language for PGR data, thereby contributing to a more efficient exchange of information and use of germplasm. To date 85 lists have been published (IPGRI et al., 2001).

5.7 Information management

With increased impact of globalization and political importance of PGR, the need for information on germplasm has increased. A number of examples exist of how information on germplasm can be shared. These include the Germplasm Resources Information Network (GRIN) database in the United States, which is a centralized database holding passport and evaluation data for accessions in the decentralized National Plant Germplasm System (NPGS) collections. Similarly, the CGIAR centres holding germplasm collections have computerized documentation systems and these are linked through the System-wide Information Network on Genetic Resources (SINGER). Passport data and descriptor data for a large number of European collections will shortly be available through the EURISCO database. All this information will be freely available on the Internet. An example of sharing information related to a specific crop is provided by the *Musa* Germplasm Information System (MGIS) for banana and plantain developed at the International Network for the Improvement of Banana and Plantain (INIBAP).

Most routine genebank operations generate information that is key to efficient operation of the genebank and to safe and efficient conservation. Most genebanks have computerized documentation systems that greatly facilitate the storage and maintenance of data, as well as their retrieval. These systems vary significantly from one genebank to another in their complexity. Well-developed documentation systems are operational in national genebank systems in the USA (i.e. GRIN), in the Netherlands (i.e. GENIS) and in the Nordic countries (by the Nordic Genebank).

A useful overview of the various aspects of genebank documentation can be found in the guidebook for genetic resources documentation (Painting et al., 1993). In addition, Guarino et al. (1995) presented detailed information on management approaches related to germplasm collecting.

5.8 Germplasm health and plant quarantine

Infection and contamination of accessions with pathogens may cause several problems in germplasm management. The seed longevity may be affected, characterization and evaluation may be negatively influenced, pathogens may spread in the collection and destroy susceptible accessions, and pathogens may be distributed to new sites along with the germplasm. If not properly dealt with, infection will pose quarantine problems that negatively impact on germplasm flow. Adequate management measures should be taken by the genebank to eliminate infection and contamination or at least reduce it to acceptable levels. IPGRI is currently in the process of developing a manual that addresses these issues and recently published a germplasm health guide for the management of forest seed material (Sutherland et al., 2002).

Before being incorporated into an ex situ collection, samples need to be checked for presence of pests and diseases (Frison and Jackson, 1995). In principle, all accessions intended for distribution must be healthy to limit the spread of diseases. This is particularly important in the case of vegetatively propagated crops, where there is a significant risk of spreading viruses, viroids and mycoplasmas. The genebank manager will have to devise an appropriate and detailed germplasm health monitoring strategy, taking into account national quarantine regulations. This will often entail the use of diagnostic tools or the intensive inspection of plants grown from the seed stocks to be stored for conservation and utilization. Additionally, when involved in international transfer of materials, other protocols might be applicable. FAO and IPGRI have been

working on establishing such protocols for several years and have issued a series of international guidelines for the safe movement of germplasm. Specific techniques are available, in particular for the detection of virus infections, which allow detection and eradication of diseases from a number of species. More information can be found in the FAO and IPGRI series for the safe movement of germplasm (Diekmann and Putter, 1995). Unfortunately, these guidelines were mainly developed for the major food crops. Several genebanks have included a provision in their MTAs excluding liability of the genebank in cases of unforeseen infection.

5.9 Conditions for germplasm exchange

The distribution of germplasm to users can be regarded as an ultimate goal of genebank operations, especially as it is the step that links conservation and utilization. Similarly, it is important to the genebank that new germplasm is received through collecting missions or, to avoid duplication, through exchange programmes with other genebanks.

Until the establishment of the CBD, free exchange of genetic resources was the norm. Even when improved varieties from formal plant breeding or biotechnology programmes were subject to variety rights protection, samples were available for further breeding and research. The CBD favours bilateral exchange and requires governments to regulate access to biodiversity formally. This has led to a decrease in global germplasm flows.

The concept of Farmers' Rights evolved in the mid-1980s during discussions on the IU in recognition of the contribution of indigenous peoples and farmers to the maintenance and development of genetic diversity. The disagreement on this concept resulted in increased reluctance to provide access to genetic diversity in the absence of clear guidelines, in particular regarding the sharing of benefits, another difficult and not yet well clarified and implemented objective of the CBD and the new IT.

However, although the CBD details a bilateral approach to access, it does not require it. Parties are free to agree on the system that best suits them. For genetic resources for food and agriculture, where the country of origin frequently cannot be determined, a multilateral system seems to be a more logical path to follow (Cooper et al., 1994). This recognition represented the starting point for the members of the FAO Commission on Genetic Resources for Food and Agriculture when renegotiating the IU.

In summary, the Multilateral System on Access and Benefit Sharing (MLS) under the IT sets conditions for access to collections designated to be part of this system.

The CGIAR centres, in close consultation with IPGRI and FAO, have developed and adopted MTAs that are specific contracts used to transfer genetic material. Several national and institutional collection holders have adopted similar contracts, notably the members of the European Cooperative Programme for Crop Genetic Resources Networks (ECP/GR), to regulate the exchange of germplasm and its subsequent use (see Appendix 6 for the text of the draft MTA). According to the text of the new IT, in due time a model MTA will be developed to cover exchange under the MLS. All exchange of germplasm that is not covered by the MLS, or other provisions of the IT, will be treated as a to-be-established MTA. Voluntary guidelines were adopted by the VIth Conference of the Parties of the CBD in The Hague in 2002. For more details on this subject see also Section 2.1.

It is of critical importance that germplasm accessions leaving the genebank be accompanied by relevant information, including passport, characterization, evaluation and management data as well as an import permit and phytosanitary certificate when necessary. At the same time, it is also vital for the genebank to receive feedback from users about performance of the accessions in trials, breeding activities and phenotypic traits and genotypic data.

Some strategic considerations

Increasing amounts of information are becoming available on aspects of access, benefit sharing, plant breeders' rights and patents. The issues are complex and the positions of the different stakeholders in the conservation and use of PGR sometimes conflict. Therefore, genebank managers are advised to think about formulating appropriate PGR policy, particularly regarding access. The existing or to-be-established national genetic resources committees seem to be the most logical bodies to develop or at least support such policies and regulations as they will comprise representatives of the various stakeholder groups. They will provide an excellent platform for exchange of ideas and opinions.

It will be important for genebank managers to make sure that such policies and regulations are realistic and can be implemented, that they will be conducive to the exchange of germplasm and that they

receive the full support of the user community. The following points are offered for consideration while developing policies and regulations:

(i) Legislation enacted hastily is seldom optimal. Bad legislation can hinder previously agreed and workable systems of exchange of materials.

(ii) Formulation of national policies based on voluntary guidelines and codes of conduct covering access to material and access to knowledge, including aspects of prior informed consent and mutually agreed terms, allow validation of the concepts prior to enacting legislation.

(iii) Managers of ex situ collections need to consider links to in situ conservation in biosphere reserves, national parks and protected areas, especially where management procedures involve government departments and communities. They will have to take into account benefit-sharing principles.

(iv) Similarly, linking in situ and on-farm conservation might need decisions to be made on prior informed consent, access to and protection of knowledge etc. to be made by communities. Until documentation of, for instance, a peoples' biodiversity register, the managers of ex situ collections have a responsibility not to enact regulations that might affect local methods of biodiversity management, the protection of indigenous knowledge and the local community's access to plant genetic resources.

(v) Strategies used by the genebank to evaluate materials have major implications for conservation and utilization. Recent molecular studies suggest that phenotypic evaluation on-station is likely to give only an incomplete indication of the breeding value of an accession, especially with respect to quantitative traits. In addition to the promotion of breeders' use of germplasm collections, revitalization of on-farm conservation and utilization traditions may constitute a powerful alternative tool for the genebank in its efforts towards sustainable utilization, since this is likely to reveal hidden traits. Efforts can include participatory plant breeding. In such cases the appropriate regulatory body needs to establish a framework covering access and utilization from the local to the international level. In addition, further improvement of methodology to characterize the genetic potential of germplasm by molecular means will add to better selection and utilization of germplasm.

(vi) In terms of strategic management, the genebank can learn by doing rather than wait for policy-makers' more rigid frameworks.

5.10 Development of a genebank operation manual

In the absence of agreed procedures and protocols for many routine genebank operations and in view of the increasing cooperation between regional and international genebanks, it is important that individual genebanks maintain their own accurate and detailed records of their procedures. Development of a genebank operation manual will facilitate and streamline the work at the genebank itself and enhance genebank activities and approaches. It will also allow staff, especially new staff, to assume their tasks and responsibility more easily. Furthermore, such a manual will contribute to collaboration with other genebanks, and to transparency in the execution of national and international responsibilities and help to increase trust.

In order to translate the genebank's objectives and strategies into actions, a genebank manager should at least consider the following points:

1. Identification of and compliance with scientific standards representing the best practices.
2. Interpreting these standards and the interdependency between them while translating them into a series of procedures and protocols.
3. Making decisions that are well founded on best practices in the absence standards.

As a follow-up to this, it is important to establish a detailed manual of operating procedures for all major genebank activities. The manual should be written in clear, concise language. Few genebanks have developed such manuals to date. Useful examples include those from IRRI, Philippines (IRRI, 1995), CGN, the Netherlands, currently being updated for ISO 9000 certification (van Hintum and Hazekamp, 1993) and ICRISAT, India (Rao and Bramel, 2000).

1. Introduction
2. Context of genebank management
3. Setting objectives for genebanks
4. Considerations for improved conservation and utilization concepts and strategies
5. Genebank management praxis
- 6. Rationalization of genebank management**
 - 6.1 Reasons for rationalization**
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6. RATIONALIZATION OF GENE BANK MANAGEMENT

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It has been shown that protocols for germplasm management sometimes differ considerably among genebanks, depending on their specific circumstances, objectives and other factors. Although the published genebank standards (FAO/IPGRI, 1994) cover a wide array of genebank activities, they largely focus on procedures related to storage and management of orthodox seed collections. Moreover, there has been little attempt to define procedures for optimizing management (other than for regeneration) and there is a risk that genebanks may uncritically interpret genebank standards without due consideration of their particular situation.

This chapter deals with rationalizing germplasm collection management by individual genebanks. It considers decisions to be made by the genebank curator and a parent institute for optimizing efficiency of genebank operations. It does not deal with the coordinated management of collections held by different genebanks, which requires decisions to be made by national or international bodies. Efficiency of regional or global genetic resources conservation and utilization is addressed in Chapters 4 and 8.

6.1 Reasons for rationalization

There will be occasions when a collection has been allowed to build up uncritically without due consideration for the genebank's remit and capacity. This may result in a need to rationalize the collection by eliminating unwanted accessions and either eliminating or combining duplicate accessions.

Curators are also increasingly being urged by their funding bodies to reduce costs by rationalizing (usually a euphemism for size reduction) their collections. In particular, genebanks are often criticized because many or most of their accessions are hardly ever used. Maintenance of large collections is questionable if they are used so little. An alternative is to rationalize, reducing the size of collections and the cost of their maintenance and increasing use of what remains.

Conventionally, the term rationalization has been applied only to the elimination of unwanted accessions from the entire (conservation or base) collection. However, costs can also be saved by keeping just a subset of accessions of a given collection actively available for use while continuing to conserve the entire base collection intact. This is also a form of rationalization.

When considering whether to rationalize, a genebank manager must assess the scientific and financial costs and benefits of both forms of rationalization, and must consider the consequences of a particular approach:

- If the entire conservation collection is rationalized, the eliminated accessions become permanently unavailable or very difficult to retrieve. Is this acceptable?
- What are the risks that genes or genotypes will be permanently lost?
- If only the active collection is rationalized, the eliminated accessions are only temporarily unavailable but reactivation of accessions from the base collection necessitates a delay for regeneration. Is this acceptable?
- A reactivation policy is needed to decide which accessions to reactivate. Is it possible to formulate an acceptable policy?
- What provisions are made for satisfying requests for seed of unavailable accessions? Do these form part of the reactivation policy? Options (which may vary between requests) include:
 - Offering seed of a similar accession instead (i.e. same as for rationalizing the entire collection).
 - Guaranteeing the user can have a sample within one year (following priority regeneration).
 - No provision made. An accession remains unavailable until reactivated for other reasons.
- There is a risk that the unavailable accessions will be forgotten and so become permanently unavailable. Can this risk be reduced to an acceptable level?
- If underutilization is the justification for rationalization, the curator must determine the cause of underutilization.

- Is it because the collection is larger than necessary to achieve its conservation objectives? If so, consider rationalizing the whole collection, i.e. the conservation (base) collection as well as the utilization (active) collection.
- Is it because only a small proportion of the collection is relevant to current breeding and research objectives (which are necessarily narrower than the broad long-term conservation objectives)? If so, consider rationalizing just the utilization (active) collection while retaining the conservation (base) collection intact.
- Is it because of lack of awareness of the potential value of the collection? If so, consider changing the ethos and structure of the genebank. For example, increase publicity, proactively initiate collaboration with potential users, increase interaction with users, and increase expertise of genebank staff in skills relevant to biodiversity research so that the genebank can contribute more to collaboration than just a passive seed distribution service. This may be applied instead of, or in addition to, rationalizing conservation or utilization.

It should be noted that underutilization is not per se a reason for rationalizing the entire collection. Underutilization is a reason for rationalizing utilization, not conservation. The primary prerequisite for effective rationalization (of either of the two forms above) is that it must be possible to assign a value to each accession easily, accurately and cheaply. Rationalization then involves keeping the high-value accessions, while low-value accessions are eliminated. If appropriate values cannot be assigned to accessions, rationalization cannot be effective and should not be attempted. It should also be noted that rationalization in the case of vegetatively propagated material could be a critically important undertaking to allow the genebank to continue to conserve the most important genotypes or clones (rather than losing them all). An example of such a situation has been provided by Nissilä et al. (1999).

6.2 Rationalizing conservation

Rationalization of the entire base collection may be appropriate if it is possible to identify a subset of the original collection that adequately fulfils the same conservation objectives. An economic approach implies that cost savings achieved by maintaining a smaller collection must cover costs of identifying the retained subset within a determined time. In almost all cases, rationalization of the entire conservation collection will involve some loss of

genetic integrity and, therefore, of the conservation value of the collection as a whole. Potential benefits of rationalization must be weighed against the inevitable negative consequences.

- To rationalize the entire collection, accessions must be valued on the basis of their contribution to the conservation objectives of the genebank. There are two distinct components to the process of valuing accessions: relevance to the mandate of the genebank, and the degree of similarity to other accessions in the collection. Accessions have high value if they are relevant to the conservation mandate of the genebank and have characteristics that distinguish them clearly from other accessions. The fundamental distinguishing characteristics are the occurrence of particular alleles, genotypes and genomes (combination of alleles across all loci or any combination of loci), and the frequency of alleles, genotypes and genomes. Derived characteristics are the phenotype (including phenotypic response to environment) and the origin of the accession.
- Accessions have zero value if they fall outside the conservation mandate or are genetically identical to other accessions in the collection.
- Accessions that lie within the conservation mandate but about which little is known (so that distinctiveness from other accessions cannot be assessed) should be treated as high-value accessions (at least until they are adequately characterized and evaluated, when their value may be reassessed).

Elimination of unwanted accessions because they fall outside the mandate of the genebank can be a cheap and cost-effective approach to rationalization. However, the genebank should consider conservation obligations on a broader scale and determine whether the unwanted accessions should be transferred to another genebank with a different mandate, instead of simply being destroyed. Consultation with FAO or IPGRI or regional plant genetic resources networks is recommended before destroying accessions.

Another potentially cheap and cost-effective approach can be the elimination of unwanted accessions on the basis that they were donated by another genebank and that the MOS is held by the donating genebank or elsewhere. Before eliminating such accessions the curator should confirm with the original source that the MOS remains safe and viable. However, the efficacy of this approach depends on the ability to trace the history of such accessions back to their original source. This requires good documentation in all genebanks involved in its history. In addition,

in many cases, especially with outbreeding species, the accession will have undergone genetic changes through sampling drift and through genetic contamination, shift and drift during regeneration at one or more stages beginning with the moment of subsampling the MOS. Before deciding to eliminate a donated accession that is known to have its MOS safe and intact, the genebank curator will need to consider whether the likely extent and value of these genetic changes merit conserving the accession in addition to the distant MOS. If, for example, a donated sample is different from the MOS and has been intensively characterized and evaluated, discarding the donated accession effectively discards the valuable data as well, which may represent an unacceptable loss.

Increasing attention is being given to rationalizing collections by identifying and combining or eliminating duplicate accessions. Duplicates may be identified on the basis of having a common origin—two accessions derived from the same original sample by subsampling, seed exchange and regeneration are historical duplicates. Alternatively, biological duplicates may be defined on the basis of their genetic similarity. The concept of biological duplication embodies degrees of similarity, from sharing similar identified alleles to having all alleles present at identical frequencies.

Historical duplicates are often difficult to identify because of (a) frequent failure to adhere to the standard of maintaining a copy of all passport data with every accession and (b) errors in typing, transcribing, translating or transliterating passport data. These problems prevent the routine application of software to identify the duplicates and necessitate intensive manual comparison of accessions by staff with excellent knowledge of the collections. Labour costs are therefore high. Even then, reliability is low. Moreover, for genetically heterogeneous and variable accessions, historical duplicates are usually not biological duplicates, so that combining or eliminating historical duplicates would cause a loss in genetic integrity or diversity respectively even if they could be accurately identified.

If rationalization is to be based on combining or eliminating duplicates it would clearly be preferable, from the perspective of minimizing the resulting loss of genetic integrity of the collection, to determine which accessions are true (i.e. biological, not just historical) duplicates. However, this is an even more formidable task than identifying historical duplicates. Conventional trials for characterization and evaluation of germplasm are inadequate for the detection of biological duplicates for three reasons:

1. The objective of conventional breeders' trials is detection of extreme phenotypes by assessing large numbers of accessions. Accurate identification of the most extreme phenotype is less efficient than provisional identification of a group of accessions that probably includes the extreme phenotype. As such, conventional trials have low statistical power, often using only two or three replicates and using rapid, but not necessarily accurate, scoring protocols. Such trials do not have sufficient statistical power to identify biological duplicates. For this purpose, it would be necessary to repeat trials, increase replication and accurately measure phenotype and genotype—at correspondingly much higher cost.
2. Most conventional programmes for characterization and evaluation focus on the phenotype. Yet for the purposes of identifying duplicates the genotype is important. Molecular tools are now available for identifying genotypes, although they remain much more expensive than conventional characterization programmes and are not in routine use. The problem further increases if the accession consists of a population or a mixture of genotypes.
3. Most importantly, even with the most detailed methodology, accessions that differ in potentially important genes may be incorrectly identified as duplicates if not characterized for those genes. This will always occur unless the entire genome of every plant of every accession is sequenced—and this is currently not feasible. Conventional trials and molecular analyses based on random DNA markers focus on only a very small number of characters and indeed ignore many agronomically important traits that can be expensive to measure, such as quality and tolerances to cold, drought, disease and other stresses.

For the last of these three reasons, it is inevitable that a major loss of genetic integrity will occur if duplicates are defined purely on the basis of their measured genetic similarity. Arguably, the risk of unacceptable loss of genetic integrity caused by combining two accessions may be small if they are known to be historical as well as biological duplicates. If they have the same origin, then failing to detect a difference between them for the measured traits may indicate that they have not undergone genetic changes since separation. This, it could be argued, would leave reasonable grounds for supposing they are biological duplicates at other loci. On the other hand, if they are biological duplicates at the measured loci but are not of the same origin, the likelihood of their also being biological duplicates at other loci is extremely low.

Inevitably, rationalization of the conservation collection will involve decisions based on incorrect information. Biologically unique accessions can be incorrectly identified as duplicates of other accessions and be eliminated or combined. To guard against such errors, consideration should be given to continuing storage of the eliminated accessions in the archive collection instead of disposing of them. The feasibility of this option depends on storage costs being low. If the archive collection is used in this way, when rationalization errors are discovered, eliminated accessions can simply be reincorporated into the conservation collection. Any damage done to the collection caused by rationalization is thus repaired.

In conclusion:

- Rationalization of the entire collection will always result in some degree of genetic depletion.
- To identify duplicate accessions it is essential to use both historical and biological criteria.
- Identification of historical and biological duplicates is costly.
- Rationalizing collections by identifying and combining or eliminating duplicates is unlikely to reduce the running costs of a genebank unless storage and maintenance costs are also exceptionally expensive.
- If discarded accessions are disposed of, the resulting genetic damage to the collection is permanent and care must therefore be taken to ensure accurate identification of duplicates.
- If, instead of being disposed of, the accessions are stored at low cost in the archive collection, the genetic damage is theoretically reduced, enabling less stringent, and therefore less costly, criteria to be used to identify duplicates.

6.3 Rationalizing utilization

Rationalization of an active collection involves keeping only a subset of the full collection available for immediate distribution, leaving the full base collection intact and thereby not compromising conservation objectives. In practice, rationalized active collections will usually be a composite of several subsets identified using different criteria.

Underlying this concept is a fundamental question that has not been adequately addressed in the past: "How much of the collection of a genebank should be immediately available for use?" It is often considered obvious that the whole collection must be kept immediately available. There is, after all, no reason to conserve germplasm *ex situ* unless it is utilized. In keeping with this

philosophy, many genebanks are mandated to maintain immediate access to all accessions of their collections, thus ruling out any consideration of rationalizing the active collection. One might question the underlying logic: it is acceptable to make some accessions permanently unavailable by rationalizing the entire collection, yet unacceptable to make some accessions temporarily unavailable by rationalizing the active collection and retaining them in the base collection. Yet in most genebanks most accessions remain unused.

Firstly, this is because so few accessions are highly valued. It is widely recognized that only a tiny percentage of germplasm has high current agronomic value. In exactly the same way, at any one time and for any one objective, only a small proportion of the available gene pool will be of high value. In this respect, it is immaterial whether the objective is breeding or research, or how value for the objective is defined. For example, the value of an accession for immediate breeding or research can be defined in terms of:

- Its yield potential (and components and determinants of yield such as photosynthetic efficiency, canopy architecture, tillering properties, rooting characteristics, etc.), quality (protein, minerals, fats, carbohydrates, tannins, vitamins, flavour compounds, medicinal compounds, strength for building, etc.), stress tolerance (heat, cold, drought, flooding, disease, trampling, lodging, shade, competition, nutrient supply, soil compaction, etc.) and its breeding system.
- GxE (genotype by environment) interactions for any of the above (including GxE for the biotic environment—farmers, pests, pathogens, competitors, symbionts, herbivores, pollinators, rhizosphere organisms—as well for the abiotic environment).
- Genotype: genes that determine the above phenotypes or their response to environment, or linked genes, or genotypes and genetic backgrounds contributing to gene by gene interactions.
- The underlying molecular, biochemical, physiological and developmental processes and mechanisms involved in the pathway from genotype to phenotype for any of the above.
- Passport data (environment, farming systems and sociology) and therefore contributions to knowledge of the distribution of diversity.
- What is not known about an accession may be as important as what is known about it in determining its use value. For example, accessions with no characterization or evaluation data should be given high priority for internal use by the genebank in its own screening programme. Newly collected accessions

often generate exceptionally high interest among the user community, precisely because so little is known about their phenotype or genotype.

- The difference between the accession and other accessions in any of the above. For example, studying accessions with extreme contrasting passport data is an efficient approach to understanding the distribution of genetic diversity in relation to the origin of accessions.

Germplasm collections can be used for a range of purposes and for each only a few accessions are likely to be useful. Only a few objectives can be tackled at any one time, even by large organizations, so only a few accessions will be used.

Even if there is insufficient information available to define the value of accessions for a given objective, it is still often inefficient to screen the entire collection. The core collection concept can represent the first stage of a more efficient screening programme. Results from the preliminary screening are then used to define a new subset of the collection that may be of greater value.

It cannot be expected that any more than a small number of accessions from a germplasm collection can be used at any one time. Those used will be relevant to prevailing plant breeding objectives and scientific research programmes. It should not be regarded as a failing of a genebank that the vast majority of accessions are not used. It is far more important that potentially useful accessions can be identified and are available.

Moreover, rationalizing the entire collection with a view to increasing utilization, as has often been recommended, threatens the future value of the collection. Breeding and research objectives frequently change, requiring a change in the pattern of utilization of a collection. This need for continual change is a current and constant reality. For example, within the past decade, grass breeding objectives at IGER (Institute of Grassland and Environmental Research, Aberystwyth) have had to change from breeding for yield in intensively managed high-input grasslands, to breeding for quality, then to breeding for extensive low-input systems, then for stress tolerance, and then for amenity use (sports turf, park grassland etc.). There have been major changes in the need for grass genetic resources and it would have been impossible to satisfy those needs if the grass germplasm collection had been inappropriately rationalized any time in the past.

On these grounds, the assumption that the whole collection should be maintained immediately accessible is questionable. It seems logical that rationalization of the collection to increase the efficiency of utilization should be based on rationalizing utilization itself, not on rationalizing conservation efforts. Recognition of this simple logic has the added advantage that rationalizing the entire (conservation) collection can be undertaken purely on the basis of improving the efficiency of conservation, without compromising requirements for efficient utilization.

It is therefore recommended that any genebank with a mandate to keep all accessions available for immediate distribution should consider the extent to which that mandate reduces the efficiency of utilization and should consider revising the mandate.

The previous paragraphs identify two reasons for utilizing only a subset of the full collection: (1) only some accessions are useful for current objectives and (2) even if it is not known which accessions, using a core collection is usually more cost-effective than screening the entire collection. There are two corresponding components to the process of assessing the value of accessions for current utilization: relevance to current utilization objectives, and dissimilarity from other accessions.

- Accessions have high use value if they are known to be highly distinctive from other accessions.
- Accessions have high use value if they are currently valued for breeding and research objectives (discussed above).
- Accessions have low use value if their distinctiveness from other accessions is low or unknown and their value for current breeding and research objectives is low.

Note the close correspondence with determining the value of accessions for conservation. Instead of relevance to the conservation mandate of the genebank, relevance to current utilization mandate(s) is more important. Instead of genetic duplication of other accessions, distinctness (of genotype or of origin) from other accessions is emphasized. Note also that identifying the most distinct accessions is a much easier task than identifying duplicate accessions, whereas assigning value to current breeding and research objectives will usually be more demanding than identifying relevance to the conservation mandate.

Rationalization of the active collection may lead to significant cost savings if:

- The conservation (base) and utilization (active) collections are maintained as physically distinct entities (see Chapter 4).
- It is relatively expensive to maintain an accession in the active collection accessible for immediate use, and relatively cheap simply to conserve an accession in the base collection. Maintaining an accession in only the base collection reduces costs but renders it unavailable for immediate distribution.

The genebank may actually be able to increase the efficiency of utilization if the following also holds true:

(i) Genebank staff can efficiently, economically and accurately identify the accessions that will contribute most to achieving current breeding and research objectives. To do this, they must be able to:

- Understand and monitor changes in breeding and research objectives, through interacting and collaborating with the primary users.
- Have a good understanding of the ecological, evolutionary, geographical and sociological processes controlling the distribution of biodiversity in the mandate species in general and within the collection in particular.
- Have a good understanding of the structure of the genebank database.
- Have reliable, relevant data in the database.
- Have expertise in data management, GIS and statistical analysis.
- Have access to the information technology tools necessary to apply the expertise.

These attributes and skills must be sufficient to enable the genebank staff to translate users' statements of their current breeding and research objectives into search criteria and a formal statistical/GIS analysis to identify the best accessions for use.

(ii) A conventional core collection (a subset of the entire collection designed to include most of the genetic diversity present in the full collection) is formed to satisfy requests that were not predicted during the previous process. In most cases potential users ask for accessions that are not immediately available but can be offered a genetically similar accession from the core collection.

(iii) The majority of requests for seed come from users and collaborators with whom genebank staff may interact closely. This reduces the number of requests that are satisfied by offering similar accessions from the core collection, and ensures that such

requests are only from casual users who contribute little to the objectives of the genebank.

(iv) A two-tier body of users is implicit in development of the above: priority collaborators whose needs are considered and analyzed carefully and for whom the active collections is rationalized, and casual users whose needs may be less well fulfilled. This may be contrary to the mandate of some genebanks. In some cases, such as the CGIAR centres, their global mandate cannot be amended. In other cases, curators may wish to consider the possibility of achieving the genebank's utilization objectives more efficiently and completely by setting up a network of priority collaborators.

(v) A routine protocol should be established by which genebank staff continually revise objectives and reassess the currently most valuable accessions. Accessions should not be allowed to remain permanently unused and forgotten.

6.4 Subdividing accessions

Conservation

Subdividing genetically variable accessions may in some cases help conservation by reducing genetic variation within accessions. This, in turn, reduces genetic changes through subsequent subsampling and regeneration.

In general, the approach is only effective for accessions of inbreeding species that comprise a physical mixture of two or more distinct pure lines. However, splitting can disturb the genetic integrity of a landrace, though it might be possible to reconstitute the original landrace simply by combining the component lines. Farmers maintain some landraces (e.g. of common bean and sorghum) as mixtures. The farmer reconstitutes the mixtures annually by selecting the appropriate mixture of seeds from the previous harvest. In this case, subdividing the accession into its components could improve maintenance of genetic integrity.

For outbreeding species, subdividing accessions will seldom help conservation of genetic integrity.

Utilization

Subdividing genetically variable accessions may promote utilization by separating alleles or genotypes of particular importance to plant breeders and researchers.

Subdivision of an accession to facilitate utilization relies on there being alleles or genotypes of value in themselves that are better utilized separately from the rest of the accession. However, subdividing multiplies the number of entities to be maintained and is therefore likely to increase maintenance costs. Therefore, the decision to subdivide must consider the trade-off between increasing value and increasing cost.

Who should decide whether to subdivide? Who should subsequently maintain the subdivided material? Should the original sample also be maintained? There are no simple answers to these questions. The user may decide, or, if the genebank is sufficiently familiar with current breeding and research objectives, the genebank may proactively subdivide, in order to encourage potential users to use the alleles or genotypes that the genebank thinks are of potential value. The latter approach requires the genebank to maintain a high level of interaction with users, and may be particularly effective if genebank characterization and evaluation procedures enable effective identification of variants.

If the user is a breeder, it may be appropriate for the subdivided line(s) of interest to be incorporated into the breeder's collection, with only the original accession being retained by the genebank. This has no cost implications for genebank maintenance. If the user is a scientist without a working collection, subdivided lines will be lost unless included in the genebank.

Details on the question of lumping or splitting accessions can be found in a recent IPGRI publication (Sackville Hamilton et al., 2002) and in van Hintum et al. (2001).

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7. ECONOMIC COSTS OF GENE BANK OPERATION

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With increasing expectations on genebanks to make operations more cost efficient and with the importance of having more detailed cost data for the curator to make informed decisions, this chapter deals with aspects that provide the reader with a better insight on both the theory and the methodology to calculate costs and to interpret these correctly.

7.1 Introduction

Though the size of ex situ collections has expanded substantially over the past few decades, scant information exists on fundamental issues such as the economic benefits from or the costs of conserving germplasm. Conceptual advances in estimating benefits have been hindered by the fact that crop genetic resources generate values with multiple dimensions. Progress in empirical analysis has also been hampered by measurement difficulties—since only some dimensions of the value of crop genetic resources are revealed in market prices. (An economist's taxonomy of values associated with crop genetic resources is presented in Box 2, with relevant references.)

In contrast to the economic benefits of conserving germplasm ex situ, costs of conservation can be estimated directly by compiling the data from records kept by genebank managers (Burstin et al., 1997; Epperson et al., 1997; Pardey et al., 2001). One reason for focusing on costs rather than benefits is that if the costs of conserving an accession are shown to be lower than any sensible lower-bound estimate of benefits, for many decisions, it may not be necessary to undertake a challenging exercise in benefit estimation. In any case, cost

information is crucial when a genebank manager pursues the objective of minimizing operational costs subject to the technology and funding that is available.

This chapter provides an economic framework for estimating the costs of operating genebanks. The framework enables genebank managers to address questions of interest to them. Following a brief background on the economics of genebank operation, the methodology for calculating costs is summarized. To illustrate the methodology, the final section presents excerpts from a comprehensive study of the CIMMYT genebank, conducted by Pardey et al. (2001). However, one caveat is of particular importance. It must be emphasized that the example we present is most directly applicable to plant species that can be conserved as seed samples. Therefore, though the framework may be adapted to species with other modes of reproduction, cost estimates derived in

Box 2. A taxonomy of value and some key references

The value derived from crop genetic resources is broadly categorized as use value and non-use value. Sometimes referred to as existence values, non-use values reflect the satisfaction individuals or societies may derive simply from knowing that something exists, independently of whether it is used (Krutilla, 1967). It is difficult to imagine, however, that many people (other than a few specialists) derive pleasure only from being assured that crop genetic resources are housed somewhere in a genebank. Instead, crop species are conserved precisely because they are thought to possess alleles of potential use to human society. Most value associated with the accessions in a genebank collection is derived from their use rather than their mere existence. Use value includes current use value and expected future use value, as well as the value of retaining the flexibility to respond to some unknown, future event—termed option value. Overviews and surveys discussing the sources of economic value in crop genetic resources are numerous, including Pearce and Moran (1994) and Swanson (1996).

Both current and future use values can be estimated through market prices when a product or good, such as grain or seed, is traded. We can use forms of 'hedonic analysis' to ascertain the current value for productivity enhancement of crop genetic resources embodied in crop varieties (Evenson and Lamarié, 1998). A genebank collection, in contrast to a breeder's working collection, exists to a large extent in order to respond to future, unforeseen challenges, and therefore the expected future use value of a genebank collection is an important component of its total value. We can, with some methodological difficulty and a number of caveats, calculate a present value of expected future benefits from direct use of germplasm in crop improvement. We do so by combining the probability of finding useful material with its predicted productivity benefit once it is found and incorporated into new varieties. The time required to search for and incorporate useful genes into well-adapted germplasm affects the magnitude of expected benefits in a major way because of the time value of money.

this fashion are likely to differ substantially among crops (potato vs. wheat vs. maize) and according to the improvement status of the material (wild vs. cultivated barleys).

7.2 The basic economics of genebank operation

The framework of production economics provides an instructive approach for analyzing a genebank facility and its operations. The essential notion of production economics is that outputs are produced with some combination of inputs. The institutions and technological environment that prevail at a point in time predetermine the combination of inputs, though these factors change over time. Applied to the case of a genebank, the inputs of labour, equipment and acquired seeds or planting materials are processed to produce outputs in the form of stored, viable seeds

Option value is similar to expected future use value conceptually, but distinct from it in practice. For example, we might use the past incidence of changes in rust disease pathogens or other major pest outbreaks to predict the expected future value of certain types of accessions as sources for new sources of resistance for a known pest. However, there are some pests and other environmental events for which we have no prior knowledge at all. Accessions, and collections of accessions, can have option value related to this uncertainty—but determining its magnitude is difficult.

Crop genetic resources are public goods and market prices generally fail to capture the full value of public goods. While recent changes in intellectual property rights may alter the public good nature of crop genetic resources, the problem of relying on market prices to assign value to streams of direct use benefits from utilization of accessions in crop improvement is likely to persist. Finally, there are many current and future uses of genebank accessions other than their direct use in breeding new crop varieties—and many of these are contributions to other types of public goods, such as knowledge.

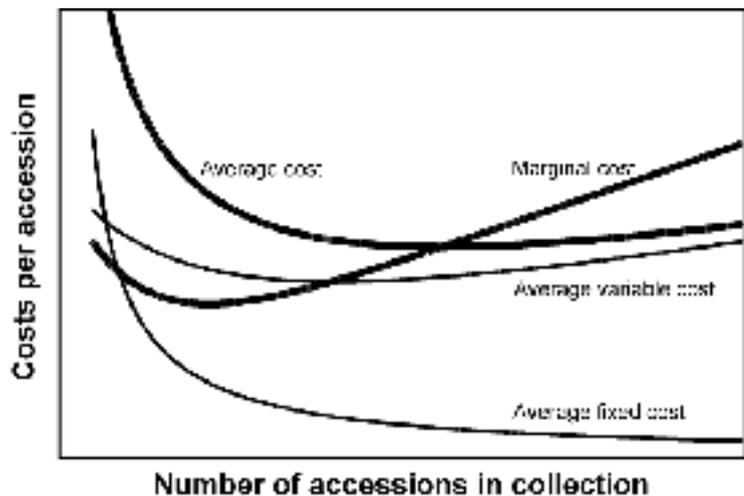
Alongside conceptual overviews of the sources of value, several theoretical economic models have analysed the value of genetic resources (for example, Brown and Goldstein, 1984; Weitzman, 1993; Polasky and Solow, 1995; Simpson et al., 1996; Evenson and Lamarié, 1998). By contrast, there are few published examples that use empirical data to estimate the value of genebank collections. Evenson and Gollin (1997) traced the flow of rice germplasm from the International Rice Research Institute into improved varieties grown in the developing world, and estimated that adding 1000 accessions to the collection was associated with annual income of \$325 million in present value terms. Gollin et al. (2000) studied several cases of the search for resistance among germplasm stored in a wheat collection at CIMMYT genebank, drawing inferences about the optimal size of collections and the conditions under which marginal accessions may or may not have high value. Zohrabian (2000) estimated the lower-bound value of an additional accession in the US soybean collection, concluding that while the value may not be great in absolute terms, it more than justified its cost.

and accompanying information. Properly stored seeds and other materials with relevant information can be disseminated immediately for current use, or placed in the storage facility as options that can be exercised (repeatedly if necessary) in future years.

Total costs of genebank operations are broadly classified as variable (labour and non-labour), capital and quasi-fixed. Quasi-fixed inputs are often termed 'human capital,' referring to skilled labour with scientific expertise such as genebank managers and laboratory scientists. Technicians and temporary workers, or those paid on an hourly basis, are treated as variable labour inputs. As a practical matter, we have identified variable inputs as those that are sensitive to the size of the operation, capital inputs as those that are not and quasi-fixed inputs as a group of inputs that are neither fixed nor variable, but 'lumpy.' A quasi-fixed input is 'lumpy' in the sense that it is a discrete, indivisible unit that cannot be adjusted easily with fluctuation in the extent of genebank operations; it is variable in that it is more easily adjusted than a capital item such as the building itself.

Costs in each class can be then summarized in terms of average and marginal costs. For example, average annual storage costs can be calculated as the total costs of storage in any year divided by the number of accessions in a stored collection. Depending on the type of inputs used in production, average cost can be represented in terms of average variable costs, average fixed costs or the sum of both. In the case of storage, average fixed cost decreases monotonically as the number of accessions increases, unless a new

Figure 2. Hypothetical average and marginal costs per accession.



building must be constructed. By contrast, average variable cost is in general U-shaped (Figure 2). As the number of accessions increases from a small size, the operation becomes more efficient and average variable cost decreases. After a certain minimum level of cost, it increases with the number of accessions due to excessive use of variable resources given fixed factors. The marginal costs of storage would be the increase in total costs of storage that are incurred when another accession is added to the collection.

In practice marginal costs are difficult to estimate even with a long time series of historical data, since they depend on the size of the collection. Theory principles are often used to 'guess' marginal cost. We can assume that (i) over the relevant size range, marginal costs are constant, (ii) curators operate at the most efficient point possible, where average costs have reached a minimum level and are equal to marginal costs or (iii) either capital or quasi-fixed inputs are utilized at a less-than-full capacity, so that marginal costs are always less than average cost. For practical purposes, the third case is generally assumed and the average costs are interpreted as upper bounds of the corresponding marginal costs.

7.3 Analyzing the cost of genebank operations

Data

Table 1 provides some examples of cost elements for each genebank operation by type of input. All staff with post-graduate degrees has been classified as quasi-fixed labour, though the role of staff rather than their degree or title is a more relevant criterion. Commercial rental rates often serve as estimates of the annualized cost of capital. However, if these data are unavailable, data on purchase prices and the expected service life of the item, combined with a real interest rate (nominal interest rate minus inflation rate), are all that is necessary to estimate them directly (see equation below).

The annual user cost of a capital item that is purchased at time zero for X dollars with service life n years is given by

$$PV_0^n = X + \frac{X}{(1+r)^n} + \frac{X}{(1+r)^{2n}} + \frac{X}{(1+r)^{3n}} + \dots = \frac{X}{1-a^n}, \text{ where } a \equiv \frac{1}{1+r} < 1$$

and r is the interest rate.

Table 1. Examples of cost elements in genebank operation.

Operations	Non-capital			Capital
	Quasi-fixed	Labour	Non-labour	
Information management (including data analysis)	<ul style="list-style-type: none"> Information manager Data analyst 	<ul style="list-style-type: none"> For data entry For equipment maintenance 	<ul style="list-style-type: none"> Computer supplies Publication related expenses Software licences 	<ul style="list-style-type: none"> Servers Computer equipment
General management	<ul style="list-style-type: none"> Genebank head or genebank manager 	<ul style="list-style-type: none"> Secretaries Unallocatable labour 	<ul style="list-style-type: none"> Office expenses Electricity Unallocatable expenses 	<ul style="list-style-type: none"> Buildings Unallocatable equipment
Storage (medium-term and long-term)	<ul style="list-style-type: none"> Genebank curator 	<ul style="list-style-type: none"> For maintaining and operating refrigeration equipment and facility 	<ul style="list-style-type: none"> Electricity for storage rooms 	<ul style="list-style-type: none"> Cold storage room Refrigeration equipment Storage shelves and seed containers
Viability testing	<ul style="list-style-type: none"> Genebank curator 	<ul style="list-style-type: none"> Lab technician Worker 	<ul style="list-style-type: none"> Chemicals and supplies 	<ul style="list-style-type: none"> Lab equipment and supplies
Acquisition	<ul style="list-style-type: none"> Genebank curator Scientist for seed health testing 	<ul style="list-style-type: none"> Lab technician Temporary worker 	<ul style="list-style-type: none"> Chemicals and supplies Seed envelopes 	<ul style="list-style-type: none"> Lab equipment and facility
Safety duplication	<ul style="list-style-type: none"> Genebank curator 	<ul style="list-style-type: none"> Temporary worker 	<ul style="list-style-type: none"> Packing supplies Shipping cost 	
Dissemination	<ul style="list-style-type: none"> Genebank curator 	<ul style="list-style-type: none"> Lab technician Temporary worker 	<ul style="list-style-type: none"> Chemicals and supplies Packing supplies Shipping cost 	<ul style="list-style-type: none"> Equipment and facility
Regeneration	<ul style="list-style-type: none"> Genebank curator Field manager 	<ul style="list-style-type: none"> Field worker Equipment technician Temporary worker 	<ul style="list-style-type: none"> Chemicals and supplies for fields Fuel for vehicle Electricity for drying machine 	<ul style="list-style-type: none"> Farming land Screenhouse Seed dryer Seed cleaning equipment
Characterization	<ul style="list-style-type: none"> Field manager Lab scientist 	<ul style="list-style-type: none"> Field worker for agronomic characterization Lab technician for molecular characterization 	<ul style="list-style-type: none"> Lab chemicals and supplies 	<ul style="list-style-type: none"> Lab equipment and facility
Evaluation	<ul style="list-style-type: none"> Field manager Lab scientist 	<ul style="list-style-type: none"> Lab technician Field worker 	<ul style="list-style-type: none"> Lab chemicals and supplies 	<ul style="list-style-type: none"> Lab equipment and facility
Pre-breeding	<ul style="list-style-type: none"> Field manager Lab scientist 	<ul style="list-style-type: none"> Lab technician Field worker 	<ul style="list-style-type: none"> Lab chemicals and supplies 	<ul style="list-style-type: none"> Lab equipment and facility
Other research	<ul style="list-style-type: none"> Genebank curator Lab scientist 	<ul style="list-style-type: none"> Lab technician 	<ul style="list-style-type: none"> Lab chemicals and supplies 	<ul style="list-style-type: none"> Lab equipment and facility

The category of information management includes all activities related to database management and publications. Software licensing fees and skilled labour for database operations constitute a large portion of information management costs. General management includes all administrative operations and other activities that are not directly attributable to specific cost categories. Electricity services, physical facilities and computers, which may be used in other operations but whose total costs cannot be disaggregated, are also classified here. Capital items that are charged on a lease-basis within the organization, such as computers or vehicles, can be treated as non-labour rather than as capital costs. Management encompasses all genebank operations, and its cost should be allocated to each individual operation according to its managerial complexity and relative importance.

The major cost items in seed storage are the electricity for the refrigeration system and the capital equipment. The cost of viability testing consists of supplies and the labour of laboratory technicians. The category of acquisition includes the costs of seed health testing and seed handling. The cost of collection from remote regions might also be included.

Both safety duplication and dissemination involve packing and shipping seed samples, though dissemination is much more frequent and costly than duplication. Part of the costs for seed health testing (including capital items) should be allocated to the category of dissemination costs when phytosanitary certificates are required.

Regeneration is one of the most expensive activities in genebank operations. This category includes both the fieldwork (e.g., land preparation, planting, weeding, harvesting, etc.) for seed production and the seed processing (such as drying and cleaning) for storage.

Economic analysis of the data

Once each cost element has been assessed and management costs have been allocated to operations, the overall composition of costs and relative magnitude of each element can be examined. The sum of all elements then represents the total annual economic cost of operating the genebank.

One point that may require emphasis is that the annual economic cost estimated here may differ from the annual genebank budget in several respects⁴. First, overhead costs may be omitted from a genebank budget but included in its economic cost. If a genebank is operated as part of a larger institution, it shares some

⁴ Though institutions have endeavoured to achieve full financial transparency through 'full economic costs' accounting, the annual budget is still different from the economic cost defined here.

administrative services (library, financial and security services) with other programmes⁵. Second, the cost of programme-wide operations such as seed health testing should be allocated according to the proportion accomplished by the genebank, but an annual genebank budget may include all or none of these costs. Third, annualized capital costs (including the costs of physical facilities, land and other donated equipment) are fully represented in the economic cost, while only parts of them may be considered in an annual budget.

The average cost of each operation is calculated by dividing the total cost by the number of accessions processed. We can then compare average costs among operations or in a single operation over time to indicate efficiency. Questions related to the lumping and splitting of accessions might also be addressed within this framework. Based on these figures, we can estimate the average cost of storing an accession for one year or in perpetuity. For practical purposes, as explained above, average cost can in turn be taken as an estimate of marginal cost.

The average cost of storing an accession depends critically on the status of each accession and the genebank protocol. If the accession is viable and is stored in sufficient quantity, then the cost of conserving it for one year is very low. If the accession must be regenerated due to either low viability or low stock, then the cost includes regeneration and viability testing. The same logic applies to the cost of distributing accessions to clients.

The magnitude of the cost of conserving an accession in perpetuity depends not only on the status of the accession but also on the time frame of each operation and the real rate of interest. Most genebanks have their protocols regarding the intervals of some operations such as viability testing, regeneration and dissemination. For example, depending on the crop, the interval of viability testing can be set at 5 or 10 years, and the regeneration interval can range from 20 to 30 years for seeds in medium-term storage and up to 100 years for those in long-term storage. The regeneration interval is further affected by the magnitude of demand for the accession. For accessions demanded with high frequency, regeneration is required more often to replenish the stock. The pattern of requests for seed samples is difficult to predict, but it is possible to estimate the dissemination interval using historical dissemination data. The interest rate can be assumed to range from 2% to 6%.

⁵ One way to assess such costs is to multiply relevant genebank costs by the overhead rate of the institution.

7.4 An example: Wheat conservation at the CIMMYT genebank

As an illustration, we present some of the results of a study by Pardey et al. (2001) to estimate the costs of operating the wheat and maize genebanks at the headquarters of the International Center for the Improvement of Maize and Wheat (CIMMYT), Mexico. The goal of the study was to determine whether continued conservation of genebank accessions was justified and to assess the level of long-term financial commitments that would be required to do so. Below, the major steps in the analysis are reviewed with reference to the CIMMYT wheat collection. Interested readers should consult the published article for details regarding assumptions, further interpretation and analyses of the maize collection.

Tables 2 and 3 contain information on the costs of inputs used to conserve and distribute a total of 123000 wheat accessions in the CIMMYT genebank (in US dollars unless otherwise indicated). Capital input costs are shown in Table 2. Based on the CGIAR guidelines for capital depreciation, the service life is assumed to be 7 years for vehicles, 10 years for equipment and up to 40 years for physical facility. The authors used current replacement costs instead of historical purchase prices in order to ensure a consistent cost series for all capital items regardless of purchase year. The annualized costs of capital in the right-hand column of Table 2 are derived using an interest rate of 4%.

Table 3 incorporates all annual operating costs related to conservation and distribution of wheat germplasm. Numbers in parenthesis under each heading refer to the number of accessions processed for that operation. For example, 5800 new accessions were acquired and 14250 samples were disseminated in 1996. The overhead rate applied is the official CIMMYT rate 22.14%⁶. The costs under the column labelled 'capital' in Table 3 are the annualized costs from Table 2. In Table 3, the capital costs associated with seed testing in Table 2 have been allocated between acquisition and dissemination.

Total costs from Tables 2 and 3 are summarized in Table 4, and average costs are estimated for each type of operation. Information and general management costs are assigned to each operation in Table 3⁷. Total variable cost is the sum of the total labour and non-labour costs. Average quasi-fixed and variable costs are the basis for the economic analysis of conservation costs presented next.

⁶ Methods for calculating overhead rates vary by institution. Here, the overhead rate represents the ratio of indirect costs (central administration, library, security, bioinformatic service, etc.) to direct cost (research costs).

⁷ The shares of the management costs allocated to each operation are 15% for medium-term storage, 5% for long-term storage, 5% for acquisition, 10% for germination testing, 35% for regeneration, 5% for duplication and 25% for dissemination (these shares were estimated through interviews with genebank managers).

Economic analysis

Pardey et al. (2001) estimated the annual expenditure for conserving wheat germplasm in CIMMYT genebank at \$326785, though this figure was later adjusted downwards to \$270138 given some exceptional regeneration costs during the study year (Table 4). About 64% of the annual cost involved labour (both labour and quasi-fixed), while about a quarter of the total cost related to capital inputs. Although the investment required to build a genebank is substantial, when viewed on a representative annualized basis, the overall genebank operation is not particularly capital-intensive. A substantial portion of the labour cost is quasi-fixed in nature.

Table 2. Annual capital input costs (US\$) for conserving wheat germplasm at CIMMYT.

Source: Pardey et al. (2001)

Items	Service life (year)	Replacement cost (US \$)	Annualized cost (US \$)
Medium-term storage		277 765	19 979
Storage facility	40	174 051	8455
Storage equipment	10	81 979	9718
Backup power system	10	8205	973
Seed container	25	13 530	833
Long-term storage		274 485	19 753
Storage facility	40	174 051	8455
Storage equipment	10	81 979	9718
Backup power system	10	8205	973
Vacuum sealer	10	2000	237
Seed container	50	8250	369
Germination testing		12 650	1 052
Germination testing facility	40	6400	311
Germination chamber	10	6000	711
Other lab equipment	10	250	30
Regeneration		206 500	23 464
Screenhouse	10	112 000	13 277
Vernalizer	10	12 000	1423
Seed drying equipment	10	25 000	2964
Seed processing facility	40	30 000	1457
Seed processing equipment	10	1500	178
Vehicle	7	26 000	4165
Seed health testing (incl. for acquisition and dissemination)		14 428	1 659
Seed health facility	40	1296	63
Greenhouse	10	1080	128
Lab/office equipment	10	10 445	1238
Jacuzzi equipment	10	672	80
Vehicle	7	936	150
General capital		34 800	2 390
General facility	40	24 800	1205
Office equipment	10	10 000	1185
Total capital cost		820 628	68 298

Hence, within a certain range of activity, the overall costs of conservation do not increase dramatically as the number of accessions increases.

Activity	Non-capital Quasi fixed	Labour	Non- labour	Capital
Acquisition (5800)	5186	5397	2907	995
Seed health testing	4246	1902	1949	-
Introductory planting	-	1996	431	-
Seed handling	-	520	-	-
Overhead	940	978	527	-
Medium-term storage (123 000)	7609	2858	1962	19979
Storage management	6230	-	-	-
Climate control	-	2340	1606	-
Overhead	1379	518	356	-
Long-term storage (75 000)	4566	2858	3312	19 753
Storage management	3738	-	-	-
Climate control	-	2340	2712	-
Overhead	828	518	600	-
Germination testing (12 000)	3044	3493	244	1052
Germination testing	2492	2860	200	-
Overhead	552	633	44	-
Dissemination (14 250)	29 717	2051	5172	664
Dissemin. management	22 428	-	-	-
Seed health testing	1902	851	984	-
Packing and shipping	-	828	3250	-
Overhead	5387	372	937	-
Duplication (35 000)	3044	2779	5186	-
Packing and shipping	2492	2275	4246	-
Overhead	552	504	940	-
Regeneration (22 000)	38 047	36 451	18 011	23 464
Field operation	24 920	21 134	9688	18 865
Seed processing	6230	8710	5058	4599
Overhead	6896	6607	3625	-
Information management	-	22 900	611	-
Maintaining database	-	18 749	-	-
Other expenses	-	-	500	-
Overhead	-	4151	111	-
General management	30 437	9771	13 832	2390
Managerial staff	24 920	8000	-	-
Computers	-	-	4900	-
Electricity	-	-	1425	-
Other expenses	-	-	5000	-
Overhead	5517	1771	2507	-
Total	121 649	88 559	51 236	68 297

Table 3. Annual operating costs (US\$) for conserving and disseminating wheat germplasm at CIMMYT. Numbers in parenthesis are the number of accessions included in the activity each year.

Source: Pardey et al. (2001)

Table 4. Total and average costs (US\$) for wheat genebank operations at CIMMYT.

Source: Pardey et al. (2001)

Activity	No. of accessions	Total capital cost	Total quasi-fixed cost	Total variable cost	Average capital cost	Average quasi-fixed cost	Average variable cost
Medium-term storage	123 000	20 338	12 175	11 887	0.17	0.10	0.10
Long-term storage	75 000	19 873	6 087	8 526	0.26	0.08	0.11
Acquisition	5 800	1 115	6 707	10 659	0.19	1.16	1.84
Germination testing	12 000	1 291	6 087	8 449	0.11	0.51	0.70
Regeneration	22 000	24 301	48 700	67 996	1.10	2.21	3.09
Safety duplication	35 000	120	4 566	10 320	0.00	0.13	0.29
Dissemination	14 200	1 261	37 326	19 002	0.09	2.63	1.34
Total		68 298	121 648	136 839	1.93	6.82	7.48

Table 5. Average cost (US\$) of conserving a wheat accession for one year at CIMMYT.

Source: Pardey et al. (2001)

	Accession already stored no regeneration	Accession newly acquired no regeneration	Accession already stored regeneration	Accession newly acquired regeneration
Conservation cost	0.19	3.61	3.45	8.08
Long-term storage	0.19	0.19	0.19	0.19
New introduction				
Acquisition	-	2.99	-	2.99
Initial germination testing	-	-	-	1.21
Initial duplication	-	0.43	-	0.43
Germination testing	-	-	0.61	0.61
Regeneration	-	-	2.65	2.65

The cost of storing an additional accession for one more year is equal to the sum of average quasi-fixed and average variable costs per accession, excluding collection from remote regions. Table 5 illustrates the sensitivity of the annual cost to the status of the sample, including its time in storage, time to last regeneration or germination test. If the sample is known to be viable, the average cost of holding an accession of wheat is only 19 cents. If the sample needs to be regenerated because it failed the germination test, the cost of keeping it for another year jumps to \$3.45 for an accession. If a newly introduced accession is viable and of sufficient size that seed multiplication is not required, the average cost of incorporating and storing it for one year is \$3.61. The cost rises to \$8.08 if the sample must be regenerated at the time of introduction.

Here it should be realized that actual costs will vary greatly between genebanks across the world, due to huge differences in salaries and in purchasing and maintenance prices for equipment and facilities.

7.5 Consequences of adding or eliminating accessions

To assess the economic costs of either adding or eliminating accessions, we need to begin by constructing cost tables of the type presented above. Next, we need to consider the impact of adding or eliminating accessions on each of the activities presented in Tables 3 to 5 (or equivalent breakdowns for genebanks other than CIMMYT). The relevant considerations are described in Chapter 3.

The nature of the economic assessment depends on the magnitude and conditions of restructuring that is being considered:

- If the adding and/or eliminating are to be undertaken with no change in capital infrastructure, then we can simply ignore the capital costs in Tables 3 to 5.
- If it is to be undertaken with no change in the complement of senior scientists, then the 'Total' for quasi-fixed costs must be held constant. Holding these constant implies that any increase in quasi-fixed inputs for one activity must be accompanied by an equivalent reduction in quasi-fixed inputs for other activities.
- If the genebank is assigned a non-negotiable fixed total budget, then the same applies to the total for variable (labour plus non-labour) costs.

Then, for each cost component of each activity, two key estimates must be generated.

First, we must determine the impact on the number of accessions to be processed each year. For storage this is simple, as each added accession and/or eliminated accession can be directly reflected in the total number of accessions. For germination testing there will be, at least in the long-term, a pro rata increase/decrease associated with adding or eliminating accessions. For regeneration there might be complex dependencies on usage. For dissemination and characterization the genebank manager may have greater flexibility in choosing which and how many accessions are disseminated and characterized each year, independently of the number stored.

Second, we must determine the impact on the efforts required to maintain the quality of the accessions processed each year and hence estimate the effect on average costs per accession. This is probably one of the most difficult parts of the process. As outlined above, existing analyses of genebank costs are retrospective, first calculating total economic cost and then estimating average cost by dividing the total cost by the number of accessions. For planning to add or eliminate accessions, managers need to estimate future average costs per accession that will result from a change in management procedures. For example, after careful consideration of the elements of the handling procedure, we might estimate that the average costs per accession will rise by 10%.

Then, the manager's best estimate of the change in total costs would be given by multiplying the expected change in costs per accession multiplied by the change in total numbers of accessions processed annually. By doing this we shall have completed the achievable half of the economic analysis—impacts on economic costs. The remainder—impacts on value—is beyond the scope of this document and beyond the achievements of any genebank analysis undertaken to date.

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8. SHARING RESPONSIBILITIES

*Emile Frison,
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Suzanne Sharrock
and Bert Visser*

This chapter deals with aspects of sharing responsibilities with other genebanks and institutions with the aim of making the operations more cost-efficient, more effective and, in particular, more sustainable.

8.1 Introduction

The 1970s saw an increasing number of initiatives focus on international collaboration in the area of plant genetic resources conservation, chief among which was the establishment of IBPGR in 1974. IBPGR recognized the need to divide the task of global collecting and conservation activities and also adopted a regional approach based on the Vavilovian centres of diversity. In the 1970s, following a conference in Beltsville in 1972, several further regional centres were set up (Ethiopia, Costa Rica), but were under political pressure from the beginning. It soon became clear that the idea of a regional centre in one country, serving several other countries in the same region, was generally not acceptable. Countries were not prepared to be dependent on institutions outside their borders (Pistorius, 1997). As a result of this failure of the regional approach, IBPGR and later IPGRI recognized the necessity to work at the national level and began to focus on strengthening national programmes for conservation and use of plant genetic resources. However, the need for sharing responsibilities remained clear, and today this is being addressed through the development of collaboration largely through networking, taking both regional and crop-based approaches.

The IT and the GPA on PGRFA each stress the importance of global collaboration. The former IU agreed on the development of an international

network of genebank collections (Art. 9). The GPA recognizes the promotion of networks for plant genetic resources as a priority activity (no. 16) and in particular focuses on the need for regional and international networks and an appropriate complement of crop-based, thematic and in situ oriented networks. The text of the new IT on PGRFA mentions again (Art. 17) the relevance of international networks. In conclusion, the policy framework supports and encourages the formation of networks. Various networks at different levels exist and some of these are addressed below.

8.2 Why is collaboration in germplasm management important?

In the 1970s and 1980s, in recognition of the threat of genetic erosion, a massive collecting effort took place and the accessions in today's genebanks are largely the result of this. This means that huge collections of plant genetic resources now exist in genebanks (approximately six million samples; FAO, 1998). However, it is also clear that many countries lack the resources to maintain the material for which they, or the international community, committed resources to collect. At the same time, some other countries have excess storage capacity. Furthermore, while targeted safety duplication of existing collections is far from complete, it is also believed that there may be a significant amount of unwanted over-duplication of samples (FAO, 1998). The need for rationalization of collections and the sharing of facilities/resources, wherever possible, through regional and international collaboration is therefore a priority.

Apart from the need for collaboration for the sake of efficiency, the interdependence of countries for plant genetic resources is another important reason for collaboration. Crops such as cassava, maize, groundnut and beans, although originating in Latin America, are now staple food crops in many African countries. Similarly, it is estimated that in Brazil, almost half the population's plant-derived energy comes from three major cereal crops—rice, wheat and maize—all of which originated in other parts of the world (FAO, 1998). Thus countries are highly interdependent with regard to the supply of new genes for crop improvement. Closely related to this is the fact that many countries have made extensive collections of genetic diversity from the centres of origin of the crops they are interested in. Thus important diversity of many species is being held in genebanks far removed from their countries of origin. With the coming into force of the CBD in 1993, under which the sovereign rights of countries over their genetic resources was recognized and used as one of the basic principles of the Convention, the issue of restoration of genetic

diversity (or repatriation of materials) must also be addressed. Collaboration between countries is essential to ensure the continued access to, and exchange of, plant genetic resources.

As well as the interdependence of countries and regions with regard to the exchange of plant genetic resources, it is also clear that there is interdependence in the area of technology. Conservation and germplasm management technologies are generally more advanced in developed countries, while many of the latter may be considered relatively diversity-poor. On the other hand many diversity-rich countries are less developed and still lack the technologies that allow secure, cost-effective conservation of their genetic resources. The benefits of collaboration between technology-rich and diversity-rich countries are clear.

Finally, international collaboration helps to give prominence to germplasm management activities and to maximize germplasm diffusion and utilization. A genebank or a network actively involved in collaboration is more likely to attract support at the national level. Moreover, partnerships developed in the framework of the genebank may spill over into other areas of crop research. The reverse of this being that a genebank working in isolation may be easily seen as unimportant and therefore is likely to lose support.

What are the benefits of shared responsibilities?

It is clear that one of the major aims of sharing responsibilities for germplasm management is to increase the efficiency of overall conservation efforts. The most expensive tasks of a genebank are those of characterization, evaluation and regeneration of accessions. Sharing responsibilities in these areas could go a long way towards addressing existing backlogs, as well as contributing to cost-savings for individual genebanks. For example, genebanks located in different environments can provide the different growing conditions required for the regeneration of individual accessions.

Another important area of collaboration is that of sharing information about accessions. Shared information is an essential element in promoting the evaluation and utilization of conserved material and in raising the awareness of the importance of conservation activities. Collaboration between genebanks or networks is also necessary in ensuring the security of conserved material through adequate duplication and in promoting increased exchange of genetic resources.

Improved international collaboration would also result in an increase in sharing and transfer of knowledge and technologies, contributing to capacity building at the national level and promoting collaborative research in other areas. Collaboration could also facilitate the rationalization of conservation activities with, for example, the identification of unnecessary duplicates contributing to a reduction in the numbers of accessions being maintained in individual collections. This would be reflected either in reduced conservation costs or in the release of resources to allow a better coverage of other species presently under-represented in genebanks. Finally, it is believed that ensuring collaboration between strong national programmes is the best way of building an effective global system for the conservation and utilization of plant genetic resources.

8.3 Constraints to sharing responsibilities

A number of constraints to the development of collaboration and the sharing of responsibilities for germplasm management have been identified. One major obstacle is the focus on national structures and the confirmation of sovereign rights of nations over their plant genetic resources resulting from the CBD. For many years slow progress made in the negotiation of access to germplasm and in benefit sharing in the framework of both the CBD and the IT on PGRFA served as a further disincentive to collaboration among countries. Moreover, in order to participate effectively in collaborative projects, strong national structures bringing together the involved ministries, especially those in charge of agriculture and environment, and trained staff are required—and these are often lacking. In many countries the lack of recognition of the importance of plant genetic resources activities means that few incentives have been put in place to encourage further development and little funding for collaborative initiatives is available. Furthermore, research systems in general lack mechanisms to reward initiatives in collaboration. Thus researchers are not encouraged to develop a partnership mentality.

8.4 What can be shared?

Documentation/information

Information is an essential element for collaboration in germplasm management. Information adds value to accessions in genebanks and sharing such information thus enhances the value and usefulness of conserved material. Furthermore, as a first step in sharing conservation responsibilities, it is necessary to know exactly what is being maintained where. Sharing information is also crucial

in relation to germplasm exchange, restoration activities and knowledge of in situ genetic diversity. Several examples of genebank information management systems have been presented in Section 5.7. A recent example is set by the EU-funded EPGRIS project, which aims to offer the potential user a single entry point to the collections maintained by European collection holders. The EURISCO database will offer passport data available on those collections. For more information about EURISCO and EPGRIS, the web site is: <http://eurisco.ecpgr.org> (available from September 2003).

Conservation and duplication

As mentioned earlier, many countries are unable to cover the costs of conserving their local plant genetic resources as well as providing for the genetic resources needed for their breeding activities. Sharing responsibilities for conservation and duplication can help to overcome this problem. Thus, within a region one country may take responsibility for conserving the diversity of one crop while another focuses on a different crop. This approach is particularly useful for countries having to deal with a range of species, each with different conservation requirements. Sharing responsibilities in this way allows individual genebanks or networks to take on a crop-specific focus and to develop a high level of expertise for specific crops. Alternatively, countries might seek to share tasks by agreements based on geographical coverage, in particular taking into account responsibilities for genetic resources developed in the country.

Distribution of germplasm

Germplasm distribution can be a labour intensive, expensive and time-consuming task for a genebank and sharing the responsibility for this can therefore bring substantial benefits. In the case of vegetatively propagated crops in particular, distribution is closely associated with germplasm health and there may be benefits in encouraging distribution to be handled in a more centralized fashion. Thus certain genebanks could take on responsibility for ensuring the health status of germplasm before distribution and undertake this activity on behalf of other genebanks. This is currently the case for the banana and plantain collections maintained by INIBAP.

Germplasm characterization and evaluation

Much greater efforts are required to complete the characterization and evaluation of germplasm in collections. The lack of adequate and useful information about conserved germplasm is considered to be the main reason for the lack of utilization of such materials. This is an area where shared responsibilities are important and in

the case of evaluation more or less essential. As most traits are environment-dependent, evaluation must take place in the appropriate environment, and preferably in several different locations (multi-site evaluation). Crop networks can play an important role in this regard.

Another aspect of evaluation where sharing tasks is important is in the identification of useful traits—for example, through testing under specific conditions of stress or in the presence of certain pests and diseases, especially those not present in the country where the material is being conserved. Furthermore, the use of specialized technologies, such as for the molecular analysis of germplasm, is likely to be restricted to those countries where the expertise and technologies are available. This is therefore another area where collaboration between countries is important.

Core collections

A core collection is a subset of an entire collection that represents, with a minimum of repetition, the genetic diversity of a crop species and its wild relatives (Johnson and Hodgkin, 1999). Core collections are not intended to replace existing collections but to present potential users with as much diversity as possible in a smaller subset of samples. The creation of a core collection can help to greatly increase the utilization of accessions conserved in a genebank and is thus considered an important aspect of genebank management. The identification of a core collection obviously requires input from a wide range of specialists and is therefore considered an area where international collaboration is important.

Pre-breeding

Pre-breeding and 'germplasm enhancement' involve the transfer of genes and gene-combinations from various sources into more useable breeding material. Breeders can make rapid progress using pre-bred materials in crop improvement and are therefore reluctant to introduce new genetic material from wild or landrace sources into their normal breeding lines. However, it has been noted that the genetic base of many major economic crops is very narrow and it has been recommended that efforts be made to address this issue. Pre-breeding and germplasm enhancement are ways to facilitate the introduction of new genetic material into existing breeding programmes. However, as pre-breeding and germplasm enhancement are activities at the interface between germplasm conservation and utilization, it is often unclear if it should be the responsibility of the curator or the breeder. It is generally considered that pre-breeding is a pre-competitive activity which commercial breeders cannot afford in the short-term. Many public research

institutions and universities have done pre-breeding in the past, but current scarcity of long-term research funds means that this activity is now being neglected. Lack of pre-breeding has negative implications for the use of germplasm stored in genebanks as well as on the long-term sustainability of crop production. Greater international collaboration could help to address this problem, by facilitating the increased use of global crop genepools and enhancing the efficiency of pre-breeding.

Responsibilities for training

Many countries still have insufficient numbers of adequately trained staff to run national plant genetic resources programmes. However, significant training capacity does exist in many parts of the world. Sharing responsibilities for training would allow available resources to be focused on building up the capacity of a limited number of institutes, in order for these institutes to take on a regional training function. Bringing together PGR scientists from different countries for training would also help to build a foundation for future collaborative activities between these countries. International collaboration could also help in the development of modules on plant genetic resources suitable for inclusion in national university courses on agriculture and related subjects.

Research

There are a number of research activities pertinent to germplasm management that can be addressed through collaborative research projects. These include areas such as the development of molecular markers, research on optimal storage conditions, cryopreservation etc. Collaboration in such research allows progress to be accelerated as well as spreading the costs of the research.

8.5 Requirements for sharing responsibilities

In order to build collaborative programmes where responsibilities are genuinely shared, a number of essential elements are required. These include:

- Information/documentation system: Any collaboration requires the exchange of information. In the area of germplasm management, all participants in the collaboration must be able to exchange information in a common format about the germplasm being managed. A common data management system is essential.

- Means of communication: A communication system, equally accessible to all partners, is another essential element for developing collaboration.
- Structure for collaboration: While collaboration *per se* may be a commendable goal, it is unlikely to be successful unless it is formalized within some type of structure. Useful models for collaboration include networks and charters.
- Agreed standards and guidelines: Sharing responsibilities requires that tasks be divided amongst collaborating partners. An important prerequisite to ensure that tasks are performed in an acceptable way is to adopt commonly agreed standards and guidelines.
- Trust: Collaboration and sharing responsibilities are not possible if there is no trust among partners. Such trust can be developed in various ways, such as staff exchange visits, training programmes, development of agreed standards etc.

8.6 Structures for collaboration

National networks or programmes

The successful conservation and utilization of plant genetic resources involves action by a wide range of people in every country—policy-makers, planners, scientists, germplasm curators, breeders, teaching institutions, rural communities, NGOs and farmers. Effective coordination mechanisms are required at the national level to enable these actors to participate efficiently. Mechanisms to coordinate plant genetic resources activities exist to some degree in many countries. Such mechanisms can take the form of a centralized national programme, such as the one in Ethiopia, where the Institute of Biodiversity Conservation and Research administers all plant genetic resource activities. Other countries have formalized sectoral PGR programmes, where different institutes undertake different aspects of conservation and utilization, while a coordinating committee governs policy and planning decisions.

In many countries, genebanks are the focal point for national PGR programmes, although they typically lack satisfactory linkages with other sectors and actors. In particular, there is a need to link *ex situ* and *in situ* conservation through evaluation, genetic enhancement, breeding and seed distribution programmes. One example of a successful networking initiative at the national level can be found in France, where 25 networks (for cereals, forest trees, fodder and lawn crops, vine etc.) involving a wide range of players, including both the public and private sector and NGOs, have been established. Within the framework of these networks, the public and

the private sectors share responsibility for the conservation, evaluation and regeneration of the genetic resources (BRG, 1999) (see www.brg.prd.fr).

Bilateral agreements between countries

Bilateral agreements between countries are more likely to be of a broader nature than those between individual genebanks or networks. While the central focus may be conservation of specific genepools, the collaboration is more likely to include a wider range of activities, including training and research. An example of this type of collaboration is that between the Netherlands and Germany for the conservation of sugar beet, potatoes and chicory.

Bilateral agreements between genebanks

One of the simplest forms of collaboration is a bilateral agreement between two genebanks or networks. Here the two institutions agree to share the tasks for conservation of specific genepools. An example of this is the collaboration between CGN (Netherlands) and Wellesbourne (UK) for the conservation of vegetable species. In this particular example, each genebank takes responsibility for conserving the genepool of a particular species on behalf of both institutes.

Although institutional agreements are attractive and relatively easy to establish, they are very dependent on the views of genebank management and less embedded in national policies.

Another well-known example of bilateral collaboration is formed by numerous collecting missions, in which parties may share crop expertise, regeneration and characterization capacity, access to storage facilities and funds in order to conserve germplasm from a particular country and make it available for use.

Bilateral collaboration offers the attraction of relative simplicity over regional networks. Decisions can be more far-reaching because they involve fewer parties but the impact may be limited because of the small number of players.

Bilateral agreements may result in major cost savings for regeneration and characterization as well as the expertise to carry out efficient and reliable regeneration. A necessary condition for such agreements to be successful is that national users do not feel hindered by the location of a collection in a foreign collaborating genebank as this would negatively influence utilization of the germplasm. Thus, implementation of such agreements requires

intensive and formal communication with the national user community and is most likely to be successful between neighbouring countries.

Subregional programmes

Within regions, and particularly within subregions, countries usually have many crops and much plant genetic diversity in common. It is therefore likely that plant genetic resource programmes will have similar objectives and the benefits of collaboration are clear. An example of subregional collaboration is that of the NGB. This genebank holds the base collection of accessions from Denmark, Finland, Iceland, Norway and Sweden. The individual collaborating countries hold active collections. A similar arrangement has existed for many years in Southern Africa where the SADC Plant Genetic Resources Centre (SPGRC) in Zambia acts as regional centre for SADC member states. The former is a joint Nordic institute reporting directly to the Nordic Council of Ministers. The latter programme consists of a regional plant genetic resources centre, the Southern African Development Community (SADC) Plant Genetic Resources Centre (SPGRC) and is also a network of national plant genetic resources programmes and centres to coordinate activities at the national level and to preserve the indigenous PGR material, which forms the natural crop heritage of the region.

Yet another example of subregional collaboration is formed by the Nordic-Baltic black-box agreement on safety duplication, providing for the storage of backup collection materials from the Baltic States on the premises of the NGB.

Regional networks

One of the most successful examples of collaboration at the regional level is that of the European Co-operative Programme for Crop Genetic Resources Networks (ECP/GR) (see www.ecpgr.cgiar.org). This network is aimed at ensuring the long-term conservation and increased use of plant genetic resources in Europe. It is governed by a steering committee of national representatives and overall co-ordination is provided by IPGRI. The programme operates through 10 broadly focused networks dealing with groups of crops or general themes related to plant genetic resources. ECP/GR is financially maintained by modest contributions of the member states and mostly depends on contributions in kind by the genebanks in the region. The network has invested substantially in joint evaluation projects and in the establishment of joint crop databases and core collections. Currently 35 countries participate in ECP/GR. One of the initiatives

developed is the European Information Platform on Crop Genetic Resources that was developed to facilitate access to information about genetic resources conserved in genebanks throughout the region. The information platform provides access to regional/global crop-specific databases and contact information for institutions in the region active in crop genetic resources conservation and utilization. A European Plant Genetic Resources Search Catalogue with passport data on ex situ collections maintained in Europe, accessible via the Internet and termed EURISCO, is currently being developed (<http://www.ecpgr.cgiar.org/>).

A number of other regional networks exist in Africa, Asia and the Americas (e.g. EAPGREN in eastern Africa and SPGRC in southern Africa; RECSEA in Southeast Asia; TROPIGEN and REDAFIT in South America; REMERFI in Central America and Mexico; CMPGR in the Caribbean).

Another crop-specific network includes the Latin American Maize Programme (LAMP), a network for germplasm evaluation and regeneration supported by USDA/ARS, Pioneer-HiBred and a number of national programmes. Subsequent development of core subsets as well as seed regeneration and conservation activities of Latin American maize landraces were coordinated by CIMMYT maize genebank activities upon termination of LAMP as a Latin American maize germplasm conservation network (Tabla, 1999).

A network should not be an objective in itself, but should rather be a mechanism to facilitate collaboration and address needs. Networks may be commodity or regionally based. Regional networks have a comparative advantage in dealing with the practical conservation of collections, policy, regional task sharing and species or themes of regional importance. Crop networks have a comparative advantage in addressing species and themes of global importance.

Regional and subregional collaboration offer the advantages of simpler logistics and common interests and cultural heritage when compared with global programmes, which are therefore often crop-specific. They may also have a greater impact than bilateral forms of collaboration. National PGR programmes and national genebanks should endeavour to strengthen these regional networks by active contributions to their activities and active participation in their planning.

International crop networks

Crop networks are an excellent means of bringing together specialists from different fields on a global or regional basis to set priorities for the management of a particular crop gene pool. This usually involves the formation of a shared database of all accessions in ex situ collections, the strengthening of collaboration in collecting and evaluation of germplasm and the promotion of a more effective utilization of the available genetic resources.

One of the earlier crop networks to be established was the World *Beta* Network in 1989. The crop database and the network, which includes the USA, Japan, Iran, Egypt and India, is coordinated by Germany (BAZ). The network meets biannually and is one of the few such networks to receive some support from the private sector.

Within the framework of the global barley network, the mutual benefits to be gained from sharing the workload of genetic resources conservation are well recognized. Tasks such as establishing a common European Barley Information System, identification of duplicates and organization of a safety duplication network cannot be carried out in one country alone. Activities relevant to the EU Programme are being performed within ECP/GR, often as 'input in kind', involving most EU and many non-EU countries. The European Barley Database (EBDB) (http://www.ipk-gatersleben.de/barley/EU_barley.htm) contains data on 92 000 accessions from 36 institutions in 29 countries, among them 36 000 from EU and 31 000 from project partners. EBDB will form the basis for identifying duplicates and gaps. The International Barley Core Collection (BCC) is also being established, comprising accessions from worldwide collections, including a European subsection.

In addition, several crop-specific networks have been established for CGIAR mandate crops by the relevant CGIAR centres, such as the Global Wheat Genetic Resources Network coordinated by CIMMYT and CIAT's Global Cassava Genetic Resources Network, and by FAO for non-CGIAR crops. In the case of bananas and plantains, INIBAP assumed global responsibility for germplasm conservation and distribution following a meeting held in 1984.

The major network relevant for genebanks is the System-wide Genetic Resources Programme that coordinates the conservation activities of the CGIAR centres. Together, the genebanks that participate in this programme contain more than 500 000 accessions of all major staple crops and distribute approximately 100 000 samples of germplasm, excluding breeding lines and improved materials, each year to users in many countries in the world.

Initiatives for global collaboration are born from the recognition that collaboration at the global level brings added value compared with collaboration at lower integration levels.

8.7 Other examples of collaboration

A host of examples of other institutional collaboration exists, both based on task sharing as well as aimed at technology transfer and training. Such collaboration is vital for genebanks with few resources and a major contribution to global objectives of conservation and utilization as formulated in the GPA.

Germplasm standards and decision guides

A number of publications have appeared as a result of international collaboration in the area of genetic resources management. These publications help to provide common standards for use in genebanks, thus making it easier for genebanks to work together. They can also be used as teaching tools. The development of such standards and technical guides requires bringing together experts from a wide area and thus constitutes an important type of collaboration. Moreover, bringing people together in this way, for the purposes of developing a common understanding, helps to promote future possibilities for collaboration. For example, collaboration in coconut research has increased significantly following meetings of coconut scientists to revise the Descriptor List for Coconut and to develop Technical Guidelines for the Safe Movement of Coconut Germplasm. This collaboration is carried out in the framework of COGENT (International Coconut Genetic Resources Network) and has resulted in the development of the International Coconut Genetic Resources Database (CGRD) that contains data from 25 sites in 18 countries and is shared with coconut breeders worldwide.

Training programmes

Development of training programmes at the international and regional level plays an important role in bringing people together. A large number of plant genetic resources scientists in developing countries have been trained through the MSc course at the University of Birmingham. Training programmes of this type not only bring people together, thus laying the foundations for future collaboration, but also provide the opportunity to emphasize the need for and benefits of collaboration in the minds of future planners and policy-makers. Future initiatives may increasingly take advantage of the Internet as a tool for long-distance learning.

8.8 How can we make collaboration work?

The importance of crop databases as an essential element in collaboration has already been noted. Without the basic information on what is being conserved where, collaboration is difficult, if not impossible, to initiate. Another important element is trust. Partners in any collaborative project must have confidence in their fellow participants and believe that activities are being conducted in an optimal way. As mentioned earlier, scientific exchange visits, training programmes and the use of common standards and guidelines can go a long way towards helping to build mutual trust.

In all collaborative ventures, there must be a willingness to participate, even if this means losing individual control of some activities. The ability to be able to accept shared responsibilities and thus shared credit for achievements is important. Incentives, in terms of appropriate funding mechanisms, opportunities to learn new skills, possibilities to visit other institutes and participate in meetings, can also help to encourage the development of collaboration. Specific projects, such as the identification of core collections, can be used as a springboard for the development of bigger initiatives. One suggested way of increasing collaboration is the twinning of genebanks.

The success of a network is strongly linked to the willingness of participants and the sense of ownership they have in the network. In commodity-focused networks, scientific leadership, which can be provided by a scientific committee, needs to be complemented by an institution that assumes a coordinating function, with sufficient time and financial resources to ensure that the network remains active. The role of the coordinator must be active but not dominate. An institution able to play an 'honest broker' role in the coordination of a network can be determining factor for a durable and successful collaboration.

8.9 Promoting public awareness

Public awareness of the importance of plant genetic resources is the key to mobilizing appropriate support at the national and international level for conservation. A targeted public awareness programme, using well-documented examples of the vulnerability of important crops and highlighting positive examples of the benefits of collaboration, is an important mechanism for generating support. Within countries, public awareness can help to involve communities, non-governmental organizations and the private sector in national plant genetic resources activities, thus ensuring a

broader base for conservation. Similarly, at the international level efforts should be made to enlist the help of well-known and influential people to attract attention to the issues.

8.10 Conclusions

The need to ensure the safe, long-term conservation of plant genetic resources is indisputable but the burden for ensuring such conservation falls unevenly across countries. Some of the countries with the greatest diversity of plant germplasm are those least able to devote resources to conserving it. Given that countries are highly interdependent with regard to plant genetic resources, it is logical that conservation responsibilities should be shared among countries. However, the development of collaborative initiatives and true partnerships is not easy. Networking is one means by which the different players can be brought together and this chapter provides some examples of successful networking approaches. Other mechanisms for bringing partners together also exist and some of these are proving successful. At the global level, however, much greater efforts are still required to enhance collaboration in germplasm management. Without greater sharing of responsibilities, efficient conservation of important genetic resources will never be achieved. It is hoped that through raising the awareness of the importance of germplasm conservation, as well as of the benefits of collaboration, progress will be made towards the development of a truly participatory global conservation system.

9. References

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2. Context of genebank management
3. Setting objectives for genebanks
4. Considerations for improved conservation and utilization concepts and strategies
5. Genebank management praxis
6. Rationalization of genebank management
 - 6.1 Reasons for rationalization
 - 6.2 Rationalizing conservation
 - 6.3 Rationalizing utilization
 - 6.4 Subdividing accessions
7. Economic costs of genebank operations
8. Sharing responsibilities
- 9. References**

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APPENDIX 1

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APPENDIX 2

Genebank standards and quality assurance

*Ehsan Dulloo
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The conservation of germplasm in genebanks in the form of seeds requires that the genetic integrity of the material conserved be maintained to the highest standard over prolonged periods of time. For this to happen, it is necessary to set standards based on current scientific knowledge and available technologies for the proper handling and storage of seeds in genebanks that will ensure their conservation over the longest time possible, without the need for frequent costly regeneration. The importance of maintaining the highest standards in genebank management cannot be over-emphasized given the sheer number of accessions held globally in the ex situ collections of plant genetic resources. These total over six million accessions (FAO, 1998). As a result of these large collections of the most important and threatened crop germplasm, most genebanks around the world are facing difficulties in managing their collections to the highest standards (FAO, 1998). Over 45% of the global collections need regenerating and countries are experiencing many difficulties in this (Rao and Engels, 1998). One of the conclusions reached in the FAO State of World Report on Plant Genetic Resources for Food and Agriculture (FAO, 1998) is that "While each continent contains a small number of genebanks operating in conformity with the highest international standards, much of the material in the remaining facilities is stored under conditions that threaten its genetic integrity."

In 1975, the Panel of Experts on Plant Exploration and Introduction, established by FAO, made the first recommendations on preferred and acceptable standards to be adopted in storing seeds for long-term conservation (FAO, 1975). This was followed by standards recommended by the IBPGR working group on engineering, design and cost aspects of long-term seed storage facilities in 1976 (IBPGR, 1976) and later by the IBPGR advisory committee on seed storage in 1985 (IBPGR, 1985). At the request of the FAO Commission on Plant Genetic Resources in 1991, a panel of experts was convened to work with FAO and IBPGR to assess and refine genebank standards in the light of advances made in seed storage technology. The recommendations of this expert consultation, which were endorsed by the FAO Commission in 1994

and subsequently published by FAO and IPGRI (FAO/IPGRI, 1994), constitute the international standards used to date in national, regional and international genebanks.

Those standards for genebanks include specific definitions of base and active collections as well as acceptable and preferred targets for routine genebank operations. It has been recognized that there are inherent problems in setting standards and that many genebanks, particularly in developing countries, are stretching their meagre resources in trying to adhere to the preferred standards, thereby undermining their ability to sustain these collections in the long term. It is debatable whether these standards are still realistic, particularly in the developing countries, and whether they should be modified. The need for establishing a quality assurance system for genebanks and a plan for implementation should be part of this discussion. This is particularly important when genebanks cooperate in networks and responsibilities need to be shared among partners. It is hoped that this publication will assist in promoting more informed decision-making. General recommendations for routine genebank operations are included below.

Standards for routine genebank operations

1. Seed processing for storage

Seeds must be cleaned, dried, tested and packaged before being stored. The time spent between harvesting and storage can be critical for the long-term viability of seeds. It is therefore important that seeds are processed as quickly as possible. Often seeds cannot be processed immediately and it is recommended that they are maintained under temporary conditions (usually suboptimal storage conditions) for the minimum amount of time. It is further recommended that pre-drying in cloth bags immediately after harvest, and sometimes even before threshing, is a good idea. Seeds should be kept under as favourable conditions as possible so that temporary storage initiates the drying process. It was also suggested that a seed moisture content level suited to the storage temperature be established to avoid rapid deterioration of the seeds.

Controlled humidity and temperature of processing area

In the humid tropics, where ambient temperature and relative humidity are high, consideration must be given to the environmental conditions in the processing area. It is recommended that seed

packaging is done in an ancillary room to the drying room, with controlled humidity and temperature, in order to avoid any condensation forming on the seeds.

Chemical treatment of seeds after harvest

It has been recognized that chemical treatment of seeds may be detrimental to seed quality but may be necessary if temporary storage is prolonged and pests and diseases are likely to be a problem. Consequently it is recommended that all apparatus used should be routinely fumigated to reduce the risk of infection and spread of diseases.

2. Seed drying procedures

In general, seeds should be dried as quickly as possible to maintain viability. Many genebanks in developing countries cannot adequately operate dehumidified drying chambers due to unreliable supplies of electricity and high capital costs. They often use low-cost technologies such as silica gel in specially constructed cabinets and/or sun drying to achieve the desired low moisture content for storage. Such technologies are quite effective and can be recommended in cases where costly drying rooms cannot be operated. It is emphasized that while some flexibility should be maintained the standard for drying should focus on the conservation objective rather than on the kind of technology used. Samples should be properly dried so that seed quality and viability are maintained. This means that the desirable seed moisture content (for long-term storage somewhere between 3 and 7%, depending on the species) should be reached as soon as possible without risking unnecessary seed quality loss. The temperature of the drying room or area should be chosen accordingly and might be about 15–25°C. As the optimum seed moisture content varies among species it might be best to use salt solutions that lead to an equilibrium of the seeds with the relative humidity specific for that salt solution.

3. Purity and health testing

The objective of the standard is to attempt to store seeds as cleanly as possible, free from weed seeds, pests and diseases. It is recommended that there is no chemical treatment of the material in the base collection to control pests and diseases. However, it is recognized that disease indexing, especially for viruses, is important and should be done wherever possible. This is particularly important for germplasm maintained and distributed in vegetative form, either as cuttings, tubers or as tissue.

4. Storage conditions

The currently recognized standards for base and active collections are as follows:

Base collection—acceptable standard is sub-zero temperature and preferred standard is -18°C , with 3–7% seed moisture content (depending on species).

Active collection—conditions that retain viability above 65% for 10–20 years. The standards also recognize that, in general, a reduction of the seed moisture content is more cost-effective than controlling the storage temperature.

5. Accession size in storage

The minimum amount of seed required in storage depends on the expected number of seeds that will be used and on the degree of genetic uniformity. For the base collection seeds are required for viability monitoring tests and for at least two regenerations (see also Sections 4.2 and 6.2). The Genebank Standards recommend:

Base collection—acceptable standard is 1000 viable seeds (absolute minimum) and preferred standard is 1500–2000 seeds, calculated as the minimum sample size for at least one regeneration plus one regeneration for an active collection and several viability monitoring tests. More seeds will be required in the case of genetically heterogeneous accessions.

The genebank standards for accession size apply in principle only to the base collection, i.e. for conservation purposes, and not to the active collection. IPGRI published a decision guide on regeneration of accessions in a seed collection (Sackville Hamilton and Chorlton, 1997) that provides guidance on how to optimize seed quantity in relation to usage for base collection and target quantities for the active collection.

6. Initial testing and viability monitoring

The Genebank Standards provided for initial testing and viability monitoring are adequate and are summarized below:

An initial test should be carried out on a minimum of 200 randomly drawn seeds at, or soon after, receipt of the seed lot. For the base collection it is advised to do a first monitoring test after 5–10 years storage (depending on storage conditions and storage behaviour of the species in question) on 50–100 randomly drawn seeds (also see Section 7.2.1.1 Regeneration Decision Guide). Subsequent test intervals depend on the accession performance, but might well be

more than 10 years. Before deciding on regeneration, especially when sufficient seeds are still available, it is advised to perform another viability test to avoid unnecessary regeneration.

The active collection may undergo a periodic test every 5 years (depending on storage conditions and expected life span of accessions).

When storage conditions are the same for base and active collections, the base collection standards can also be applied to the active collection.

7. Regeneration

The timely regeneration of accessions is an essential genebank activity to maintain the viability and genetic integrity of the germplasm. Because of the requirement for specific knowledge, particular conditions and high costs, regeneration represents a major problem for many genebanks. The decision guide on regeneration of accessions in seed collections (Sackville Hamilton and Chorlton, 1997) provides detailed information on regeneration standards.

Initial viability should exceed 85% but may be lower for some species for which this standard is inherently difficult to attain.

When viability of the base collection drops below 85% of the initial value, 100 seeds or more, depending on requirements, are used for regeneration to ensure maintenance of genetic integrity. It is advised to regenerate sufficient seeds for the active collection in order to retain genetic integrity and to meet demands, and regenerate from the base collection every 2 to 3 cycles of multiplication of the active collection to avoid large differences between the base and active collections. In general, it is suggested to use procedures that retain genetic integrity, in particular isolation techniques that allow strict control of unwanted outcrossing.

8. Documentation

Information in a genebank documentation system should preferably include passport, management, characterization and evaluation data. As a minimum, the system should include available passport data and data on viability status and seed stocks.

9. Standards for distribution

Upon request all users should receive a sample with a sufficient number of seeds to cover the genetic diversity represented in the accession adequately and to allow for proper experimenting. The

sample should be accompanied by detailed identification data as well as adequate information on the accession, in particular passport data and, if available, characterization and evaluation data. Also, where appropriate, information should be included on the viability status of the accessions and on the proper germination conditions for the distributed seeds. Alternatively, reference to this information as available on the genebank's website may be offered in those cases for users with access to the Internet. If the genebank adopts an MTA, it is suggested that users sign it before any germplasm is distributed. Quarantine conditions should be met. Ideally, depending on national policies and regulations, there should be no difference made in the treatment of domestic and foreign users.

10. Security of the collections

It is recommended that the genebank search actively for collaborating genebanks that are willing to store safety duplicate collections, in order to safeguard the collections in cases of emergency. Hosting institutes should be in the position to offer at least the same quality of storage conditions as those of the original genebank. Different collections may be duplicated in different collaborating genebanks, and arrangements for safety backup might be reciprocal.

Temperature of the cold room facilities and RH of the drying rooms should be continuously monitored if possible. A proper monitoring system should be installed to warn of power cuts and potentially deleterious changes in storage conditions. Similarly, proper fire fighting equipment should be installed. In most cases a backup power supply is advisable unless guarantees can be obtained for restoring electricity supply within few hours.

The safety of personnel working in the coldrooms should be optimized through the development of proper procedures that eliminate the risk of persons becoming trapped in the coldrooms.

While it was recognized that the current IPGRI/FAO genebank standards are adequate and represent the best practice for genebanks, participants observed rigid non-creative compliance to these standards in some countries with limited facilities. In other countries standards were regarded as an ideal only to be aimed at. Genebank managers should make sound decisions in interpreting standards and the interdependency between them. Quality control of genebank operations was considered to be an important prerequisite for effective collaboration, germplasm exchange and reliable data management. An international certification system for

genebanks may be considered. Genebanks should always establish a detailed manual of operational procedures. These procedures should be described in detail and include the standards that are used.

APPENDIX 3

Case study on collection management at the Institute of Grassland and Environmental Research, Genetic Resources Unit⁸

Ruaraidh Sackville Hamilton

Mission

The mission of the Genetic Resources Unit (GRU) at the Institute of Grassland and Environmental Research (IGER) is to undertake high-quality research on the ex situ conservation, understanding and utilization of biodiversity of temperate forage grasses and legumes, as part of the overall strategic research programme of the institute. The GRU is not required to act simply as a passive seed-supply service. The mission requires conservation of grassland genetic resources to the highest possible standard, active promotion of utilization through collaboration, and acquisition of the knowledge required for efficient conservation, utilization and collaboration.

Biological constraints

The remit of the genebank covers many species of temperate forage grasses and legumes. Most produce orthodox and long-lived seed under good storage conditions. Most are obligate outbreeders, possibly resulting in substantial genetic changes occurring through seed exchange and multiplication, and necessitating careful regeneration. Many have also commonly become established as feral populations, posing high risk of contamination in field plots. Most have small seeds, enabling use of small sealed aluminium foil containers for storage rather than large jars. Evaluation of grasses is undertaken in 1-m² plots sown at 1000 seed m⁻², requiring a relatively large number of seeds to be included in each seed exchange packet. In many species, seed dormancy is an important feature, but generally mechanisms for breaking dormancy are well established.

Genebank management infrastructure

Breeding and genetic resources are financially and administratively independent. Interaction is managed as a collaborative association between equal partners. All seed is dried to approximately 5% seed moisture content with self-indicating silica gel and is then heat-sealed in aluminium foil laminate pouches. The base collection is kept in deep freezers at -20°C or -25°C. Active collections reside in breeders' seed stores at 2°C. Quarantine is maintained and regeneration is carried out in high-quality purpose-built glasshouses

⁸ <http://www.igergru.bbsrc.ac.uk/>

with isolation chambers constructed to meet international quarantine standards, eliminating cross-contamination. Taking balanced bulks further reduces genetic changes during regeneration. Full documentation of passport data and seed transactions is established in a database, making use of MS Access.

Storage costs are low—around 0.2 per accession per annum. Utilization costs (characterization, evaluation, seed exchange and associated additional regeneration) are several orders of magnitude higher. Costs of rationalizing by identifying duplicates are higher.

Genebank management strategy

Conservation strategy

The IGER collection is small and storage capacity is not a limiting factor. The cost of storage is low, but the costs of identifying duplicates are high. Historical duplicate accessions are likely not to be biological duplicates and the probable frequency of duplicates is low. Any attempt to rationalize by combining or eliminating duplicates would either be exceptionally expensive and eliminate few accessions (if stringent criteria are applied to identify duplicates) or would seriously damage the genetic integrity of the collection (if less stringent criteria were applied so that more accessions were eliminated). Therefore, the base collection at IGER will not be rationalized in the foreseeable future, on the grounds that it would increase rather than reduce costs and would undermine the GRU conservation objectives.

Utilization strategy

At the end of section 6.3 there is a set of criteria outlining the conditions under which rationalizing utilization might reduce costs and increase the efficiency of utilization. All these criteria are satisfied at IGER. Utilization of the collection is therefore heavily and proactively targeted at a dynamically defined subset of accessions. Prospective users are encouraged to use accessions from the subset if appropriate. No resources are invested in keeping accessions available that are not regarded as being of high current value or that exist in the conventional core collection. This significantly reduces maintenance costs and releases resources that enable genebank staff to undertake more detailed research and improve knowledge and utilization.

Since storage costs are low, seeds of an accession are not removed from the active collection even following a decision that the accession is not of sufficient value to current breeding and research objectives. Only the expensive maintenance operations (viability testing, regeneration, characterization and evaluation) are stopped.

Seeds remain available for distribution until stocks run out; they then remain unavailable until they are regenerated following a positive decision that the accession is being reintroduced into the active collection.

Thus the active collection of seed available for immediate distribution includes:

- Accessions identified as being of high value to current objectives.
- The core collection, maintained to ensure a high probability of satisfying potential requests for seed for various reasons (by providing, if not seed of the requested accession, then at least seed of a genetically similar accession).
- Remnant seeds of accessions that are no longer actively maintained.

A significant amount of staff time is invested in ensuring the targeted subset of accessions remains optimal, changing quickly in response to any change in objectives. When an inactive accession (i.e. one that is currently not available for distribution) is identified as being needed for current breeding or research, it is immediately regenerated from the base collection and added to the active collection. The process of identifying such accessions takes one of two forms, active or passive, as follows.

Active: genebank staff interact closely with the major users to identify changes in breeding and research objectives. This is a continuous iterative process in which breeders and other scientists identify current objectives and genebank staff identify ways in which the genebank can respond to any changes. Experience has shown that several iterations may be required to combine the breeders' and scientists' perceptions of their objectives with the genebank's knowledge of the collection and thence to identify the appropriate response by the genebank. Responses range from changing the status of individual accessions to a full reanalysis of the database and redefinition of which accessions should be kept available. The process of discussion and reassessment is forward-looking, to minimize delays while reactivated accessions are regenerated.

Passive: a specific request for an accession of which there is not currently enough seed for distribution leads to the following process:

- The appropriate European Central Crop database is searched to determine whether the accession is held elsewhere.

- The genebank database is searched to find the most similar accession for which seed is available.
- A discussion is held with the prospective user on whether either of these alternatives is acceptable.

If neither is acceptable, further discussions are held to determine whether the accession should be activated by regenerating seed from the base collection (necessitating a delay of up to a year before seeds are available). A judgement has to be made whether the prospective user intends to initiate breeding or research for an important new objective that merits a change in status of the accession, or indeed a more comprehensive reassessment of the status of other accessions as well. A casual one-off request will not lead to a change in status if it is considered unlikely to contribute significantly to the objectives of the institute or to be followed up by further requests for the same accession. Conversely, multiple requests for the same accession, or a request that might lead to relevant collaborative research, will effect reactivation (possibly with regeneration funded through a joint grant proposal). As a last resort, if the user believes no alternative is acceptable and wishes to proceed without collaboration, irrespective of the strategic implications for IGER, and is prepared to pay for the costs of regeneration, the GRU will undertake to regenerate the accession as a top priority. The affiliation of the prospective user is not an explicit criterion in the decision (although in practice internal users will tend to be favoured because internal users and the genebank both have to contribute significantly to the same strategic objectives of the institute).

Passport data and associated ecogeographical analysis are critically important in targeting accessions for utilization. For many traits, the environment of origin can be a good predictor of genotype, provided evolutionary responses to different environments are well understood. Obtaining that understanding is a GRU research objective.

Focusing all the research efforts on the few accessions in the active collection may risk condemning accessions that are only stored in the base collection to stay there because of the relatively limited amount of information on them. This could lead to a reduced overall use of the collection in the long-term. Avoiding this is an important part of the GRU research and decision-making process and involves reactivating poorly studied accessions for inclusion in GRU's research.

APPENDIX 4

Case study on the collection management strategies of the Centre for Genetic Resources, the Netherlands

*Theo van Hintum
and Bert Visser*

Mission

The Centre for Genetic Resources, the Netherlands (CGN) is part of the DLO Foundation, forming the umbrella for the research institutes of Wageningen University and Research Centre. CGN maintains the Dutch genebank for plant and animal genetic resources for food and agriculture under a mandate of the government of the Netherlands. In addition, CGN is involved in on-farm conservation programmes.

CGN's mission is to contribute to global conservation efforts. CGN considers as a leading principle the notion that the value of germplasm depends on the knowledge about it and availability of that germplasm. In this context, CGN recognizes the need to integrate ex situ and in situ conservation approaches and the will to collaborate with all stakeholders.

CGN has traditionally adhered to a policy of unrestricted availability of germplasm held in its genebank. In the interest of keeping this material available for future research and utilization, CGN has undertaken not to claim legal ownership over the germplasm held in its genebank or to seek any intellectual property rights over that germplasm or related information.

Background

The collections of CGN include 20 crops and total accessions currently amount to 21000. All accessions are maintained as base collections and active collections. CGN has particularly focused on vegetable crops. The priority crops include both self-fertilisers and outbreeding species, e.g. cabbage, peppers, potato, tomato, eggplant, onion and grassland species. Seed longevity varies but may be rather limited for some species, e.g. those of onion and lettuce. The total number of accessions distributed and used for research purposes amounts to 5000–6000 each year. Costs of labour and facilities in the Netherlands are very high when compared with those in most other countries.

Because of these parameters (share of outbreeders, limited longevity, high use level, high labour costs) the budget allocated to regeneration of the germplasm represents a substantial part of the total genebank budget and rationalizing collection management is therefore of paramount importance.

Bulking and splitting of collections, well-founded strategies for germination rate testing and revisiting the concept of guaranteed availability of all accessions in the active collection are investigated to curb total spending on regeneration.

Basic procedures

All accessions in the CGN collections are maintained under long-term storage conditions. The quality of the seeds is regularly monitored and regeneration is carried out with the greatest care to avoid loss of genetic variation. CGN adheres to the following simple procedures:

When an accession is to be added to the CGN collection, it is documented and the seed quality and quantity are checked. If needed, the germplasm is regenerated before it is added to the collection.

All CGN accessions are stored at both -20°C (base collection) and +4°C (active collection). Before storage, the seeds are cleaned, dried and packed in vacuum-sealed aluminium foil bags. The viability of the seeds in the base collection is monitored systematically. If necessary an accession is rejuvenated. Upon rejuvenation the seeds of both the active and the base collections are replaced. If the stock of an accession in the active collection is exhausted, it is replenished with seeds from the base collection. If the remaining seed quantity in the base collection is insufficient to replenish the active collection, the accession is regenerated. After regeneration the seeds of both the active and the base collection are replaced. Upon request users receive, free of charge, a small amount of seed per accession. Requests are handled promptly, generally within a month.

Detailed procedures

1. Requirements for uptake

A number of requirements have to be met if inclusion in the CGN collection is to be considered. They are listed below:

The original sample should contain at least 3000 seeds in the case of self-pollinating crops and 4500 in the case of cross-pollinating crops. For some large-seeded crops, such as broad beans, the threshold is 1500 seeds.

The sample should be pure and clean; the purity of the sample is checked visually and if necessary the sample is cleaned of impurities.

In general the germination rate should be at least 80%. In case of material that is difficult to regenerate, e.g. because of climatic constraints, lower levels of germination may be accepted. If the germination rate does not meet the criteria, the sample is rejuvenated before uptake.

In parallel to the physical check-up, the accompanying information on the accession is studied. Based on these data it is decided whether the accession also qualifies for uptake with regard to uniqueness and importance of the accession, reliability of passport data and the threat of genetic erosion.

An accession is only split if the sample consists of different crop species or, in the case of wild populations, if different genera can be distinguished.

2. Seed handling and storage

For uptake, or following each regeneration, the seeds are air-dried, threshed, cleaned, dried under controlled conditions and packed. The basic procedures are described below. During all these procedures, the identity of the samples is checked by comparing the labels inside and outside the bag. Procedures may differ in non-essential details for some crop collections (data available).

After harvesting, the bagged and labelled samples are partially dried at 20°C and 30% RH, resulting in seed moisture content of about 12%. Before threshing, the material is temporarily stored under controlled conditions, the seed moisture content remaining at approximately 12%.

Dried samples are threshed using a small winnowing machine (Clipper). Seeds and debris are separated using differences in seed size, specific gravity and floating speed, by passing the sample through a combination of different sieves (round or slit sieves) and air flow devices. Peas and beans are threshed by hand, since mechanical threshing damages the seeds.

After threshing, the seeds are checked for uniformity of shape and size using indented cylinders. To maintain sample variation, these procedures are not too discriminative. For crops such as tomato, pepper and eggplant, the seed cleaning procedures differ considerably (details are available). During and after cleaning, the samples are again checked visually for purity and damage.

After cleaning, the samples are dried in a room at 15°C and 15% RH until they reach equilibrium humidity, which will differ from crop to crop (mainly depending on oil content).

The seed samples are packed in laminated aluminium foil bags. The bags consist of 3 layers: the inner layer of 80 µm polyethylene, an intermediate layer of 12 µm aluminium foil and an outer layer of 12 µm polyester. Four different sizes of bags are used, depending on the size of the seed samples.

For storage, five different types of samples are distinguished:

1. User sample, a small quantity of seeds that is distributed to users.
2. Germination sample, containing seeds that are used to monitor the viability of the accession.
3. Regeneration sample, which is maintained to enable regeneration of the accession.
4. Duplication sample, which is shipped to another genebank as a backup.
5. Residual sample, containing the remaining seed of the sample, used to produce additional batches of user and germination samples when necessary.

The intention is that each accession is maintained by having at least one sample for safety duplication, one sample for regeneration and five samples for germination tests. There is usually a single residual sample. In cases where the seeds are very large, two residual samples are packed. Depending on the expected demand by users, the number of pre-packed user samples varies per crop between four and eight bags.

The number of seeds stored per sample type depends on the crop. In general the user sample contains 100 seeds, the germination sample 200 seeds, and the regeneration and duplication bags between 100 and 400 seeds. The number of seeds in the residual sample is recorded by weight. After the samples of different sizes are prepared, they are bagged, put under slight vacuum and sealed. After the samples are sealed, the bags are labelled. The label contains the following data: accession number, crop name, scientific species name, variety or other name, the date the sample was made, the type of sample (user, germination, multiplication, duplication or residual sample).

CGN uses both long- and medium-term storage facilities (detailed description of facilities is available). The user samples are kept in a numbered box at +4°C for medium-term storage. The other sample types (regeneration samples, germination samples and residual samples) are kept in a numbered box at -20°C for long-term storage. The numbered boxes are placed on numbered shelves in the storage rooms grouped by crop. The storage location (box and shelf) is recorded in the CGN information system.

3. Monitoring germination

The interval between two viability checks depends on the expected seed longevity of the crop. Crops with a short storage life are checked more frequently than crops with a long storage life. The lettuce collection is subject to viability checking after 8 years, whereas the cereal collections are checked every 15 years. An official seed-testing agency using 200 seeds, according to the ISTA rules, carries out most germination tests. If the germination percentage has dropped by 15% compared with the previous measurement, rejuvenation of the accession is planned for the following season.

4. Monitoring and replenishing user samples

An inventory of the number of available user samples is made annually using data from the CGN information system. Accessions with only one remaining user sample (lettuce, spinach) or no user samples at all (for crops with a lower turnover) are marked. New user samples are prepared using the residual sample as a source. For this purpose the residual sample is transferred from the long-term storage facility at -20°C to the medium-term storage facility at +4°C and left at +4°C for one day to prevent condensation forming on the seeds during handling. New user samples are stored in medium-term storage (+4°C) and the residual sample is returned to the long-term facility at -20°C.

5. Regeneration

The procedures for regeneration differ per crop or crop group. They have been documented in detail elsewhere.

6. Distribution

To ensure continued free availability of its germplasm, CGN requests from all recipients of its germplasm prior written agreement with its policy of unrestricted access to germplasm provided. Therefore, to obtain germplasm from CGN, the bona fide user should sign an MTA. Upon receipt of the completed and signed MTA, CGN will send the requested germplasm to the user. For frequent users the option is offered of signing a general MTA,

covering all subsequent requests until further notice. CGN considers all institutional users as bona fide users, including public and private sector users, i.e. breeding companies, research organizations and organizations of farmers or growers, whether from the Netherlands or other countries. For budgetary reasons it does not accept requests for germplasm from individuals.

APPENDIX 5

Case study on collection management of the International Network for the Improvement of Banana and Plantain (INIBAP)⁹

*Suzanne Sharrock
and Emile Frison*

Mission

INIBAP's mission is to increase the sustainable productivity of banana and plantain (*Musa* spp.) grown on smallholdings for domestic consumption and for local and export markets.

In order to achieve this, INIBAP has four major objectives. One of these relates specifically to the conservation and use of *Musa* genetic resources: "To organize and coordinate a global research effort on banana and plantain, aimed at the development, evaluation and dissemination of improved cultivars and at the conservation and use of *Musa* diversity."

The International *Musa* germplasm collection

Since 1985, INIBAP has been maintaining the International *Musa* Germplasm Collection. This is the world's largest collection of *Musa* germplasm and it is maintained in vitro at the INIBAP Transit Centre (ITC), located at the Katholieke Universiteit Leuven (KUL), Belgium. The collection forms part of the international network of ex situ collections maintained under the auspices of FAO. As such, INIBAP maintains the collection in trust for the world community.

Number and types of accessions

The germplasm collection currently consists of 1144 accessions, of which 933 make up the in trust collection. The remainder of the collection consists largely of improved materials provided by breeding programmes. Overall, the collection consists of 10% advanced (improved) hybrids, 75% cultivars and 15% wild species.

Conservation strategy

INIBAP's aim is to ensure that diversity representing the genus *Musa* is safely conserved, that this germplasm is maintained in the public domain, and that it is made freely available to all bona fide users. The collection is currently maintained under medium-term storage, using in vitro slow-growth conditions. A start has been made to ensure the long-term conservation of the collection using cryopreservation. To date, 44 accessions have been cryopreserved.

⁹ INIBAP is a programme of the International Plant Genetics Resources Institute (IPGRI), a Future Harvest centre.

The ultimate aim is to place the whole collection in cryopreservation for long-term storage while also maintaining a duplicate in vitro active collection for distribution. All germplasm is tested for the presence of viruses and only accessions free from virus particles are made available for distribution. INIBAP supports strategic research in the areas of cryopreservation, virus detection and virus therapy in order to improve the efficiency and effectiveness of its germplasm conservation and distribution activities.

Detailed procedures

Introducing new accessions

The accessions in the genebank are representative of a large part of the entire diversity in *Musa*. However, some gaps are known to exist, especially in relation to wild species. INIBAP therefore continues to provide support to targeted collecting missions. All new accessions acquired by INIBAP are the subject of a germplasm acquisition agreement. Such agreements ensure that the germplasm remains in the public domain. INIBAP has also developed a separate agreement for the acquisition of improved varieties from breeding programmes.

Each new accession is established in vitro from a single shoot tip and at the first multiplication a bacteriological test to detect endophytes is carried out. If endophytic bacteria are detected, an antibiotic treatment (Rifampicin 100 mg/l) is used or the accession is re-established from a single meristem. All new accessions are tested for viruses at one of three Virus Indexing Centres supported by INIBAP. Only virus-free accessions are made available for distribution. Currently 64% of the accessions in the collection are available for distribution. Research on virus therapy is ongoing with the aim of eliminating viruses from infected accessions in the collection.

Medium-term conservation

Accessions are maintained in vitro in the form of proliferating shoot tips. Each accession is maintained in 20 different tubes. The growth medium used is Murashige and Skoog (MS medium), supplemented with 2.25 mg/l benzylaminopurine (BAP), 0.175 mg/l indoleacetic acid (IAA), 30 g sucrose and 2 g/l gelrite. In order to reduce growth rates, the cultures are maintained at a low temperature (16°C) and light intensity of 25 $\mu\text{m}^2/\text{sec}$. Under these conditions, sub-cultures are required approximately every 12 months. All cultures are monitored monthly for vigour, presence of contamination, blackening, necrosis and hyperhydricity. Poorly growing and contaminated cultures are removed from the collection. Sub-culturing is carried out when the number of tubes for any accession falls to eight.

Rejuvenation

Many of the accessions in the collection have been subcultured more than 10 times and there is the possibility that somaclonal variation occurs. A system of field verification and rejuvenation has therefore been instituted. This system allows accessions to be verified in the field in their country of origin. Once they are confirmed as true to type, the accessions are re-established in culture from duplicate plants maintained in the KUL greenhouse.

Duplication

For reasons of safety, approximately half the collection is maintained in vitro as a duplicate black box collection at CATIE, Costa Rica and TBRI, Taiwan. A large number of accessions are also maintained as duplicates in field genebanks, maintained by NARS and other regional/international agricultural research organizations. The identification of duplicates is facilitated by the participation of many Musa germplasm curators in the INIBAP-coordinated Musa Germplasm Information System (MGIS).

Long-term conservation

The aim of INIBAP is to ensure the long-term safety of the collection by cryopreserving all accessions. Research has been conducted over the last few years and three alternative methods have been developed that are suitable for the different genotypes in the collection. To date, 44 accessions of 8 genome groups are cryopreserved.

Characterization and documentation

Information on the accessions in the collection is essential. Such information adds value to the accessions and helps to encourage greater use of the collection. Passport and characterization data for all accessions maintained by INIBAP are available in the Musa Germplasm Information System (MGIS) managed by INIBAP, and are also on the Internet through SINGER. MGIS is a decentralized germplasm information management system that allows curators of Musa collections to manage and exchange germplasm information. Each curator manages data and provides regular updates to INIBAP for inclusion in the central database. MGIS is based on the IPGRI/INIBAP/CIRAD 'Descriptors for Musa' and contains passport, characterization and evaluation data for accessions, as well as information related to germplasm distribution. For the accessions maintained by INIBAP, characterization data are collected using molecular, cytological and morphological methods. This work is carried out in collaboration with various partner organizations.

Distribution

One of the most important functions of the genebank is the distribution of germplasm. Accessions are distributed *in vitro*, either in the form of proliferating tissues or as rooted plantlets. Cultures are packed in Cultusak® aseptic polyethylene bags and five plants/tissue masses are provided per accession. All germplasm is distributed under an MTA and different agreements are in place for in-trust accessions and improved varieties. In order to facilitate germplasm distribution, INIBAP supports the establishment of national and regional multiplication centres that have the capacity to distribute large numbers of plants. Around 1000 accessions¹⁰ are distributed annually and 88 countries have received germplasm from INIBAP.

¹⁰This does not mean 1000 different accessions. The same accession may be distributed many times in one year.

The MTA in Box 3 is an example for improved varieties.

Box 3. Sample of the Material Transfer Agreement that is being used by INIBAP for the transfer of improved varieties of *Musa*

1. The International Network for the Improvement of Banana and Plantain as part of International Plant Genetic Resources Institute (hereinafter referred to as INIBAP) grants the germplasm listed hereunder and related information to the recipient under the terms and conditions of this agreement.
2. This germplasm has been acquired by INIBAP from breeding programme(s) (hereinafter designated as ‘the Supplier’) under terms and conditions set out in the “Agreement(s) for the acquisition of improved varieties of *Musa*”.
3. The recipient agrees not to claim ownership over this germplasm, nor to seek intellectual property protection over the received germplasm. The recipient further agrees to ensure that any subsequent person or institution to which it may make the samples of this germplasm available is bound by the same provision.
4. The recipient may use this germplasm for research, evaluation and production in accordance with the terms of this agreement.
5. The recipient, when distributing this germplasm, will clearly state that it was originally provided by the Supplier(s), as specified in the germplasm list. The recipient is required to obtain the same commitment from any subsequent recipient to whom it may further distribute this germplasm.
6. The recipient is required to:
 - a) enter into an agreement with the Supplier(s) prior to:
 - *in vitro* propagation of planting material for sale,
 - production of fruit for export,

APPENDIX 6

Interim Material Transfer Agreement for Plant Genetic Resources for Food and Agriculture of the European Cooperative Programme for Crop Genetic Resources Networks

The (name of the institution) maintains a collection of plant genetic resources accessions under a mandate of / in agreement with (national mandating authority). The (name of the institution) seeks to conserve the genetic resources that it maintains and to promote the sustainable utilization and the fair and equitable sharing of the benefits arising out of the utilization of these genetic resources. This agreement aims to contribute to these objectives.

PREFERRED TEXT

In the interest of encouraging research and utilization of and yet not hamper further access to and use of the accessions held in its collection, the (name of the institution) holds the accessions in trust under the terms of an agreement between the (name of the institution) and (national mandating authority).

ALTERNATIVE TEXT

In the interest of keeping the accessions available for future research and utilization, the (name of the institution) declares legal ownership over the accessions held in its collection.

The (name of the institution) provides access to the germplasm held in its collection in accordance with the provisions / under the conditions / of the Convention on Biological Diversity and the International Treaty on Plant Genetic Resources for Food and Agriculture. Access to the germplasm held in its collection will be granted according to the following two categories:

Category 1:

In case the accession(s) transferred concern(s) plant genetic resources for food and agriculture listed in Annex 1 of the International Treaty on Plant Genetic Resources for Food and Agriculture, facilitated access to such accessions will be in accordance with the provisions of that Treaty, in particular its articles 10, 11 and 12.

Category 2:

In case

- the accession(s) transferred concern(s) plant genetic resources for food and agriculture that are not listed in Annex 1 of the International Treaty on Plant Genetic Resources for Food and Agriculture and
- the accession(s) transferred was/were either developed by (name of the institution) and/or was/were acquired prior to the entry into force of the Convention on Biological Diversity or,
- if acquired after the entering into force of the Convention on Biological Diversity, the accession(s) transferred was/were obtained under an agreement that it/they could be made available unrestricted for any agricultural research or breeding purposes,

PREFERRED TEXT

facilitated access to such accessions will be in accordance with the provisions of the International Treaty on Plant Genetic Resources for Food and Agriculture, in particular its articles 11 and 12.

ALTERNATIVE TEXT

access to such accessions will be in accordance with the Convention on Biodiversity and in particular with the provisions on access in articles 11, 12, 13 and other relevant articles of the Bonn Guidelines on Access to Genetic Resources and Fair and Equitable Sharing of the Benefits Arising out of their Utilization of the Convention on Biological Diversity, where applicable, and in addition to the conditions stated below.

This Material Transfer Agreement does not cover transfer of accessions acquired after the entry into force of the Convention on Biological Diversity and under mutually agreed terms.

Recognizing the obligations and responsibilities referred to above, the (name of the institution) grants access to accessions from its collection under the conditions specified below:

The recipient hereby agrees

- to solely access the transferred accessions(s) for the purpose of utilization and conservation for research, breeding and training for food and agriculture, excluding chemical, pharmaceutical and/or other non-food/feed industrial uses;
- not to claim any intellectual property or other rights that limit the facilitated access to the plant genetic resources for food and

agriculture, or their genetic parts or components, in the form received, over the transferred accession;

- to ensure that any subsequent person or institution to whom he/she may make available samples of the transferred accession or material that was essentially derived¹¹ from the accession received is bound by the same provisions of this agreement and undertakes to pass on the same obligations to future recipients;
- in case he/she commercializes a product that is a plant genetic resource for food and agriculture and that incorporates germplasm under this Material Transfer Agreement, he/she shall pay to the mechanism referred to in Article 19.3f of the International Treaty on Plant Genetic Resources for Food and Agriculture an equitable share of the benefits arising from the commercialization of that product, except whenever such a product is available without restrictions to others for further research and breeding, in which case the recipient who commercializes is encouraged to make such payment;
- to indemnify the (name of the institution) against any claims arising out of the use of the transferred accession;
- to furnish the (name of the institution) with the relevant performance data produced by the recipient arising from the characterization and evaluation of the accession, or its parts and components. Upon request of the recipient these data will only be made publicly available after an embargo period of ALTERNATIVE TEXTS three years/five years;
- if publications result from the use of the transferred accession or its parts and components, to acknowledge the (name of the institution) as the supplier of the accession and send copies of such publications to the (name of the institution);
- to send copies of intellectual property, in particular patent, protection application reference numbers citing use of the transferred accession to the (name of the institution);
- to assume full responsibility for complying with the recipient nation's quarantine and biosafety regulations and rules governing the import or release of genetic material.

¹¹ Germplasm shall be deemed to be essentially derived from other germplasm (the initial accession) when (i) it is predominantly derived from the initial accession, or from germplasm that is itself predominantly derived from the initial accession, while retaining the expression of the essential characteristics that result from the genotype or combination of genotypes of the initial accession, (ii) it is clearly distinguishable from the initial accession and (iii) except for the differences which result from the act of derivation, it conforms to the initial accession in the expression of the essential characteristics that result from the genotype or combination of genotypes of the initial accession.

The phytosanitary condition of the accession is warranted only if and as described in the attached phytosanitary certificate. The (name of the institution) makes no warranties as to the safety or title of the accession, nor as to the accuracy or correctness of any passport or other data provided with the accession. Neither does it make any warranties as to the quality, availability or purity (genetic or mechanical) of the transferred accession.

[The recipient shall defray the expenses for a phytosanitary declaration, if requested.]

In case of contractual disputes arising under this MTA, arbitration can be sought by any of the Parties to this Agreement according to international arbitration treaties. Each party to the dispute shall appoint an arbitrator, and the two arbitrators shall designate by common agreement the third arbitrator who shall be the Chairman of the arbitration tribunal.

Samples of the following accession(s) are supplied expressly conditional on acceptance of the above terms of this agreement. The recipient's acceptance of the accession(s) constitutes such agreement to the conditions above.

The (name of the institute) requests the applicant to complete this agreement by authorised signature of ordering institute, corporation or person:

Name of recipient _____

Institution _____

Full address _____

Authorised signature _____ Date _____

Name and title _____

For the (name of the institution), _____

(position title) _____ Date _____

