Plant Genetic Resources Management and Conservation Strategies: Problems and Progress

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Abstract

The conservation of plant genetic resources has developed into an important technical, socio-economic and political concern over the past forty years or so. With the successes of the Green Revolution in the sixties and the concomitant losses of landraces of the major food crops, especially in developing countries, it became apparent that coordinated efforts to collect and conserve these threatened resources were needed. Genebanks were established in almost every country based on a two-tiered conservation concept that was developed for the storage of orthodox seed-producing cereal crops. However, vegetatively propagated and recalcitrant seed producing species, as well as other materials for which the genebank concept did not work, became increasingly threatened and also needed to be conserved. New techniques and strategies were called for. With the ratification of the Convention on Biological Diversity (CBD) in 1992, considerable awareness was raised about the importance of conserving biodiversity, its sustainable use and the need for equitable benefit-sharing arrangements. The discussions that, among others, led to the CBD gave a real boost to in situ and on-farm conservation brought to light the realization that adequate management practices for genetic resources conserved in farmers' fields and home gardens were badly needed. This paper deals with important PGR management and conservation approaches taken by both public and non-governmental institutions, assesses their constraints and describes the progress made towards their further development.

INTRODUCTION

The conservation and use of plant genetic resources is an evolving scientific discipline. It has undergone dramatic changes over the last 50 years or so, partly as a reaction to changes in the overall concern about the environment, including the role agriculture plays in this context, partly caused by developments in relevant technologies as well as by significant political and legal changes. It is also an area that attracts considerable attention from civil society and in recent years in particular it has enjoyed significant political interest, especially with regard to questions concerning access and benefit-sharing.

It is against this background that this paper on conservation and management strategies has been written, with a special emphasis on the historical developments of conservation and use concepts and strategies in relation to changes in, for example, ownership and access questions, approaches to socio-economic development, in particular in developing countries, technological developments and collaborative arrangements. This first section concludes with a review of some of the major problems that genebanks currently face. The paper then presents a proposal for a modified ex situ conservation (long-term) concept, including suggestions on how to optimize linkages between conservation and utilization strategies. It then looks at suggestions and options for rationalized conservation and use approaches. In the final section some conclusions are drawn for horticultural crops based on their specificity with regard to some key characteristics for their effective and efficient utilization.
A HISTORICAL REVIEW OF PGR MANAGEMENT AND CONSERVATION STRATEGIES

The Early Days

With the discovery of the Mendelian laws at the end of the 19th century scientific plant breeding was initiated and with it the awareness that genetic diversity is the foundation for genetic advancement. Consequently, plant breeders began to create their own breeding collections for the crops they were working with. Possibly the most famous germplasm collections established during the 1920s and 1930s are those based on the work of Vavilov at St. Petersburg. The majority of the collections were assembled through both collecting missions in the centres of diversity of the target species, and through exchange with other genebanks, plant breeders and collectors. The collecting efforts were clearly biased towards the diversity the breeder needed for his/her programme, i.e. very targeted and selective. The successes of plant breeding, in particular as part of the Green Revolution during the 1960s, resulted in significant replacements and losses of the landraces and this, eventually, saw the genetic foundation of these successes start to erode. This process led eventually to a global systematic collecting effort, coordinated by the International Board for Plant Genetic Resources (IBPGR, the precursor institute of the current International Plant Genetic Resources Institute, IPGRI), one of the Centres of the Consultative Group on International Agricultural Research (CGIAR). As a result of this coordinated effort almost 220,000 germplasm accessions, predominantly threatened landraces of the major food crops and their wild relatives, were collected worldwide and stored in genebanks of the CGIAR and of national plant genetic resources programmes across the world.

During the course of the abovementioned developments a practical ex situ conservation strategy was developed for the storage of predominantly orthodox seed producing food crops, and coordinated by the IBPGR to maintain in perpetuity the allelic integrity and identity of a sample (Frankel and Soulé, 1981). This two-tiered model, which consisted of a base collection for long-term conservation and an active collection, for short- to medium-term storage of germplasm material for distribution to users, was widely accepted and applied, including the global network of base collections. The central role in this conservation concept was played by so-called genebanks. The drying of the harvested seed to a relatively low seed moisture content (somewhere in the range between 3 and 7%, depending on the species) and their subsequent storage at a relatively low temperature (-18°C for the base and +5°C for the active collection) formed the technological basis of the concept. Seed processing, viability testing and monitoring, regeneration and data management were seen as the principle responsibilities of the genebank, alongside the characterization and preliminary evaluation of the collections. Plant breeders were expected to carry out the so-called further evaluation. However, this simplified ex situ conservation strategy was clearly biased towards agricultural (cereal) crops that produce orthodox seeds and was based on the assumption that there would be a frequent and high demand for the use of the material stored in the active collections, and that cooperation between base and active collections would be intense. Although more than 1,300 genebanks and germplasm collections were reported to exist in 1996, maintaining more than 6 million samples of approximately 16,500 species, including 8% accessions of vegetable species, 4% fruits and 4% root and tubers (FAO, 1998), it would be wrong to conclude that this conservation strategy is perfect. A critical analysis will be made on this in the next section.

It should be noted that until the first half of the 1980s germplasm was regarded as an item of “common heritage of humankind”, an item that could be made freely available to users for their use in breeding programmes or other research. This notion was the foundation of the International Undertaking on Plant Genetic Resources, a legally non-binding agreement between more than 100 countries on the conservation and use of agricultural plant genetic resources, established by the FAO in 1983. Simultaneously, the contributions of farmers to the generation and maintenance of genetic resources were
recognized in the concept of “Farmers’ Rights”, a right that was declared compatible with Plant Breeders’ Rights (PBRs). During the discussions that eventually led to the conclusion of the Convention on Biological Diversity in 1992, the sovereign rights of States over the biodiversity (including plant genetic resources for food and agriculture - PGRFA - as a sub-section) within their borders, together with the increasing importance of intellectual property rights (IPRs), had a significant impact on the availability of the genetic resources which will be described later.

The 1980’s and Early Nineties

The initial strong focus on the collecting of threatened landraces gradually made place for a much broader interest and a more comprehensive approach towards the safeguarding of PGRFA for current and future use. This led to a significant increase in the number of species that was included in ex situ conservation programmes, usually coordinated by genebanks, ranging from major food crops to medicinal plants, traditional leafy vegetables and other minor, usually by research neglected, crop species. The already mentioned weak linkages between base and active collections, were expected to be overcome with the formation of crop specific regional or global germplasm networks (Perret, 1991). The central role of databases was seen as critically important.

The noted broadening in scope of conservation also resulted in a more determined effort to include crops that were vegetatively propagated and/or perennial species. This led to the need for and development of techniques for the storage of germplasm in the form of tissue cultures, i.e. the so-called in vitro conservation (Ashmore, 1997), and concepts and strategies for the management of in vitro collections were developed (IBPGR, 1986). The lack of long-term and safe storage methods of tissue-cultured germplasm led to the further development of cryopreservation, i.e. the storage in or above liquid nitrogen. This approach has gained considerable attention and protocols for the storage of an increasing number of species have been developed. During the 1980s procedures for the maintenance of germplasm collections in so-called field genebanks were developed. Due to the complementarity of these two methods special attention was paid to the interface between in vitro and field genebank collections, and recommendations were made on how to optimize this complementarity (Engelmann, 1999).

During the same period a special effort was made to search for low-input ex situ conservation approaches. One of the main constraints encountered, especially in many developing countries, is the strong dependency on a reliable electricity supply for cold chamber and drying rooms operating in genebanks. Therefore, the search for alternatives for this dependency, as well as for other low-energy input conservation activities, was given high priority. One of the approaches is based on the assumption that very dry seeds, stored at higher temperatures than the “standard recommendation”, could still achieve an acceptable storage life. Another low-input conservation research area dealt with sun- and shade-drying procedures, with the aim of obtaining seed lots of an acceptable seed moisture content and initial viability, followed by subsequent storage in hermetically sealed containers that would allow at least medium-term storage. Results are encouraging with significant differences observed between species. The formation of well-structured collections that adequately represented genetic diversity, either of an entire species or for a given trait, became a matter of concern when germplasm collections became large. The establishment of so-called core collections has become an important instrument for genebanks to contribute to improved use of ex situ stored germplasm collections, especially for crops where large collections exist (van Hintum et al., 2000). The significant developments in the molecular genetics area, in particular achievements related to marker technology and geographic information systems (GIS), were factors that began to influence conservation and use strategies, although possibly not to the extend possible.

As already mentioned, the access conditions to genetic resources gradually changed from a “common heritage” notion to a “national sovereignty” principle, a change that was strongly facilitated, if not initiated, by the negotiations that took place in preparation for the conclusion of the CBD and Agenda 21. In addition, a drastic change
took place in the area of intellectual property rights (IPRs), in the sense that patents became a widely applied form of protecting inventions and discoveries, including in plant sciences. Through the advances in molecular genetics, numerous genes and gene constructs were patented and, more recently, plant varieties are also protected by patents, particularly in the USA. These developments resulted in a much more restricted attitude to sharing germplasm with others, in particular researchers in other (developed) countries, and bilateral arrangements rather than multilateral exchange procedures were preferred, in particular for plant species that had a potential use for commercialization. The use of material transfer agreements (MTAs) for the exchange of germplasm samples was initiated.

Another important change with regard to the conservation and use of genetic resources took place during this period. A much more “people oriented” conservation approach began to be implemented and this led, among other things, to much more participatory research and decision-making as well as “governance” approaches. The important role in particular of development oriented non-governmental organizations (NGOs) should be mentioned in this context, as well as an increased involvement of civil society at large in environment protection and conservation actions. As a consequence, stronger links between conservation and development were sought and established.

As a result of the aforementioned changes, in particular spurred by the CBD negotiation process, the importance of and attention paid to in situ and on-farm management of genetic resources drastically increased. This will be discussed in further detail in the next section.

**From the Early 1990’s until Present Day**

The changes with regard to ownership over and access to genetic resources, equitable sharing of benefits that derive from their use, the protection of intellectual property as well as the revolutionary developments in the information and molecular genetics areas, continued to have a continued strong impact on the conservation and use approaches in the nineties. How these changes influenced the various (political) positions of nations can be appreciated in the re-negotiation process of the International Undertaking that began in 1993/94 and resulted finally in a legally binding agreement on the conservation, use and facilitated access to PGRFA. This International Treaty on Plant Genetic Resources for Food and Agriculture (IT) was concluded in November 2001 and endorsed by 116 countries (Cooper, 2002). The peculiarities of PGRFA compared to biodiversity in general, e.g., difficulty to apply the country of origin concept, the strong interdependency of nations on genetic diversity for crop improvement, the critical role of these resources in traditional agriculture and in food security, formed the basis for the establishment of a multilateral rather than a bilateral system for their exchange (Cooper et al., 1994). This thinking eventually led to the establishment of a multilateral system for 34 food crop species as well as temperate forage species as part of the IT, an agreement that keeps the genetic resources of these listed species formally in the public domain and facilitates easy access to and utilization of these resources.

Prior to this development, but closely related to the same philosophy of placing genetic resources of food crops in the public domain, the conclusion of agreements between the Centres of the CGIAR and the FAO in 1994 should be mentioned. In these agreements the Centres formally accepted responsibility to conserve the germplasm collections for the long-term, to manage them according to international standards, to not claim ownership and IPRs over the designated accessions, and to distribute them with an MTA (spell out) to third parties under the same conditions (Hawtin et al., 1996). Through this arrangement, and under the auspices of the United Nations (i.e., FAO), more than 500,000 accessions of the most important food crops were formally placed in the public domain and kept freely available to any bona fide user. The CGIAR System-wide Information Network for Genetic Resources (SINGER) allows free public access to accession-level passport information and other relevant information on the material held in trust by the Future Harvest Centres and, thus, facilitates their use in improvement
activities (SGRP, 2000). For more information on SINGER: http://singer.cgiar.org. With the increased interest and research efforts with regard to the in situ and on-farm conservation and use of PGRFA a strong impetus was given to the central role of people in this approach. Renewed interest was developed towards questions regarding how traditional farmers manage their crops, usually as landraces or primitive varieties, how they select preferred genotypes, how the genetic diversity levels at the farm and community levels are being maintained, etc. (Brush, 1995). After almost ten years of work on on-farm management with partners in nine countries around the world IPGRI has drawn the conclusion that the continued use of traditional cultivars by farmers in many production systems makes a significant contribution to the maintenance of the so important genetic diversity in agro-ecosystems. The on-farm management of genetic resources can also provide a natural link between conservation and development and, in a more indirect manner, provide opportunities for broadening the genetic basis of crops in a particular production area (Jarvis et al., in press).

Closely related to the above development is the increased interest in participatory research and management approaches in the area of PGR management. Participatory plant breeding became an important method for breeders in the CGIAR and elsewhere to ensure that farmers’ needs are being addressed in the breeding process, that their traditional knowledge would be included in decision making and that the necessary decentralized approaches would lead to better locally adapted varieties (Eyzaguirre and Iwanaga, 1996; Friis-Hansen and Sthapit, 2000).

Critical Review of Current Genebank Strategy

As has been already noted before, the current and widely used genebank strategy has been largely based on the requirements of and conservation experiences with seeds of the major cereal species, i.e., with an orthodox storage behaviour. We know that many of the species that are being conserved ex situ do not produce orthodox seeds, if any at all, or the curator wants to conserve germplasm material as a clone, i.e., through vegetative propagation. In addition, the strategy was based on the assumption that the use of the germplasm accessions stored in the active collections would be such that the stocks would deplete before the seeds would lose their viability. This assumption certainly does not apply to many genebank situations as the use of germplasm accessions is much less and many accessions have to be regenerated due to decreasing viability.

When the ex situ conservation strategy was designed it was certainly not envisaged that genebanks would maintain many species, sometimes hundreds and, as a consequence, the attention to individual accessions and species is sometimes rather superficial. It might well happen that the basic information required to make decisions for the effective maintenance of the germplasm is lacking. These circumstances do lead to increased costs for the conservation efforts while the budgets of many genebanks have decreased over the years. Consequently, the demand for more cost-efficient approaches has increased and many genebanks are looking for opportunities to lower their expenses, either through a reduction of their responsibilities, by applying less expensive (and sometimes technically questionable) procedures.

Besides the foregoing, increased concerns that conserved germplasm material is not being optimally used have also led to a rethink of the traditional conservation strategy. Conserved material should be readily available along with the information that users need in order to facilitate their use. With the new molecular genetic tools, as well as with much more powerful information management technologies, a revision of the strategy was possible and some suggestions for more effective and cost-efficient ex situ germplasm management are proposed in the following section.

A REVISED EX SITU CONSERVATION STRATEGY

The ideas and suggestions presented in this and the next section have been adapted from a chapter authored by Sackville Hamilton, Engels and van Hintum (Sackville
Hamilton et al., 200X) in an IPGRI publication “A Guide for Effective Germplasm Collection Management” which is currently being finalized.

Four different collection types are proposed for the efficient and cost-effective conservation and use of germplasm accessions. The base and the security back-up collections provide jointly the conditions for long-term conservation. The active collection is meant for the storage of samples for research and distribution purposes. The archive collection provides an additional security for accessions that would otherwise have been eliminated from the genebank. The definitions of these four collection types are:

1. 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) not available for distribution.

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

3. The **security back-up collection** comprises accessions of the base or active collection deposited at a location different from that of the base or active collection for safety purposes only.

4. The **archive collection** consists of germplasm accessions that are stored but not actively maintained. The genebank does not have responsibilities for conserving or distributing these accessions.

The actual application of these different types will be described below, starting with long-term conservation and then looking at the linkages between conservation and utilization. The possibilities for cost-saving approaches and/or the introduction of technical improvements will be emphasized.

**Long-term Conservation**

Ad 1. The most important feature of the base collection is the so-called “**Most Original Sample**” (MOS). The MOS should be identified to be genetically as close as possible to the original population that it is intended to represent. The MOS should be prepared and stored in the best possible conditions for safe long-term survival and seed from the MOS should never be distributed for use. One sub-sample, (the so-called “**primary MOS**”), should be stored in the genebank responsible for its conservation and the number of seeds that it should contain will depend on the number of seeds required for regeneration and for viability monitoring. For additional security, a second smaller sub-sample (the “**secondary MOS**”) should be sent to a distant genebank, as a security backup to be maintained under black-box arrangements in conditions at least as good as those used for the primary MOS. The distant genebank will be contracted to store the secondary MOS in defined “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 and should contain just enough seeds to regenerate the MOS. A viability monitoring routine should be established to ensure detection of the need for regeneration before the MOS dies. When the MOS begins to lose viability, it should be regenerated under the best possible protocol for maintaining genetic integrity and producing high quality seed.

Ad 2. This collection type has no long-term conservation function.

Ad 3. Just as a duplicate of the conservation (=base) collection of one genebank should be sent for safe storage to a distant genebank, the genebank should provide black-box **security back-up collection** facilities for base collections stored elsewhere. Storage conditions should be the same as, or better than, those for the distant base collection(s), i.e., optimal for long-term storage, and will be normally the same as for the local base collection. A security back-up collection is used only for disaster recovery, e.g., accidental loss of accessions by fire or loss of entire collection as a result of civil unrest. Beyond provision of the best possible storage conditions, the local genebank holding the security back-up takes no further responsibility for ensuring that accessions remain viable and should never use, regenerate or distribute germplasm from the security back-up.
Ad 4. In certain cases a genebank may also choose to store other germplasm accessions at low cost which do not represent a base collection (possibly only applicable to seed storage), while denying responsibility for conservation or distribution, i.e., to “archive” germplasm accessions for (opportunistic) reasons of eventuality only. Like the security back-up, [the difference is that there is no original] accessions in the archive collection should be maintained in optimal conditions for long-term survival, but with no further investment in monitoring or maintaining viability and genetic integrity.

Combining Conservation and Utilization Strategies

This section deals with the handling of accessions stored for research and distribution in the so-called “active collection”, and with how that is linked with the long-term conservation of the germplasm in the base collection. There are numerous storage options, and the only general rule is the genebank uses the “best economically viable” conditions. Some typical scenarios are presented as examples:

• For species with orthodox seed storage characteristics, it is common to keep the active collection of seed at approximately 5% seed moisture content and between 0 and 4°C, which often gives more than adequate longevity to avoid regeneration for viability reasons.
• Storage at room temperature may be an acceptable option if utilization is heavy and additional regeneration is relatively cheap and effective compared with cold storage.
• As these storage conditions are not optimal they might result in more frequent regeneration of the material in the active collection. This must however not be allowed to interfere with effective conservation of the MOS.
• At the other extreme, it can be economically more effective to keep the active collection in long-term storage with the base collection, since this will require the operation of only one rather than two storage systems.

RATIONALIZING CONSERVATION AND UTILIZATION COLLECTIONS

This section deals with germplasm collection management procedures by individual genebanks that lead to more cost-efficient or technically more effective approaches. It considers decisions to be made by the genebank curator and/or its parent institute, for the purpose of optimizing efficiency of the genebank operation by eliminating unwanted accessions from the entire conservation (or base) collection (i.e., rationalization type 1) and/or to only keep a subset of the accessions actively available for utilization while continuing to conserve the entire base collection intact (type 2). Considerations to decide whether or not to “rationalize” a collection must be based on an assessment of the scientific and financial costs and benefits of both types of rationalization, which include:

• If the entire conservation collection is rationalized, the eliminated accessions are made permanently, or at least semi-permanently, unavailable. 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 re-activation of accessions from the base collection necessitates a delay for regeneration. Is this acceptable?
• What provisions are made for satisfying requests for seed of unavailable accessions? Do these form part of the re-activation policy?
• 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 what is the cause of underutilization.
Rationalizing Conservation Collection

Rationalization of the entire (conservation = base) collection may be appropriate if it is possible to economically identify a subset of the original collection that adequately fulfils the same conservation objectives. “Economically” in this context means that the cost savings achieved by maintaining a smaller collection must pay for the cost of identifying the retained subset within a specified number of years, i.e., conducting a cost-benefit analysis. 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 this inevitable negative impact. 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. Elimination of unwanted accessions on the basis that they fall outside the mandate of the genebank can be a cheap and cost-effective approach to rationalization.

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.

Rationalizing collections by identifying and combining or eliminating duplicate accessions is receiving increasing attention. Duplicates may be identified on the basis of having a common origin – two accessions derived from the same original collected sample by sub-sampling, seed exchange and regeneration are “historical duplicates”. Alternatively, “biological duplicates” may be defined on the basis of their genetic similarity. 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 truly (i.e., biologically, not just historically) duplicates. However, this is an even more formidable task than identifying historical duplicates.

The rationalization of the conservation collection will, inevitably involve erroneous decisions, in which biologically unique accessions are incorrectly identified as duplicates of other accessions and so inappropriately eliminated or combined. To guard against such errors, consideration should be given to continue the storage of the eliminated accessions in the archive collection instead of disposing of them. The feasibility of this option depends on the cost of storage being low. If the archive collection is used in this way, then, when rationalization errors are discovered, the “eliminated” accessions can be simply retrieved into the conservation collection, and the genetic damage to the collection caused by rationalization is repaired. Conversely, if the eliminated accessions are disposed of completely, the genetic damage caused by rationalization is permanent and irreparable, and consequently greater care must be taken to minimize the damage. In conclusion:

- Rationalization of the entire collection will always genetically damage the collection to some extent.
- To identify duplicate accessions it is essential to use both historical and biological criteria.
- Identification of historical duplicates and biological duplicates are both exceptionally costly exercises.
- Therefore, rationalizing collections by identifying and combining, or eliminating duplicates, is unlikely to reduce the cost of running a genebank unless storage and maintenance costs are also exceptionally expensive.
- If the “victims of rationalization” are simply disposed of, the resulting genetic damage to the collection is permanent and hence great care must 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 reversible, enabling less stringent, and therefore less costly, criteria to be used to identify duplicates.
Rationalizing Utilization Collection

Rationalization of the utilization (= active) collection could involve only keeping a subset of the full collection available for immediate distribution while leaving the full base collection intact and thereby not compromising conservation objectives. 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 utilization?” 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.

Collections can be utilized for a vast range of objectives. For each one of these objectives, only a limited number of accessions will be useful, but for each objective a different range of useful accessions might be found. At any one time, only a few objectives can be tackled even by large organizations, so only a few accessions will be utilized. It is therefore correct that only a small proportion of a collection will be utilized in any given timeframe.

Even if we do not have sufficient information 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 provide the first stage of a more efficient screening programme, in which initially only the core collection is screened, and results from the preliminary screen are used to define a new subset of the collection that may have greater value.

Therefore, attempting to force frequent utilization of all accessions in the collection would be scientifically inappropriate and financially wasteful. It is more appropriate and efficient to utilize only the small proportion of each collection that is relevant to current objectives for utilization. Underutilization of most accessions should not per se be regarded as a failing of a genebank. On the contrary, it should be recognized that the almost non-use of the majority of accessions is actually a desirable component of efficient utilization of the genetic diversity available in the collection. It is understood that such efficient use can only be achieved if and when the accessions in the collection are being correctly characterized and evaluated for those traits desired by the user. Far more important than the amount of use of each accession is the appropriateness of use.

Moreover, rationalizing the entire collection with a view to increasing current utilization, as frequently recommended in recent years, threatens the future utilization value of the collection (Sackville Hamilton, 2000). Breeding and research objectives frequently change, which in turn require a change in the pattern of utilization of a collection. This need for continual change is a current and constant reality, not simply a vague risk for some undefined time.

In view of the foregoing 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 the conflicting requirements of 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.

There are two reasons for utilizing only a subset of the full collection: (1) only some accessions are useful for current objectives, and (2) even if we do not know which those accessions are, utilizing 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 a high utilization value if they are known to be highly distinctive from other accessions.
• Accessions have a high utilization value if they have significant importance for
  current breeding and research objectives.
• Accessions have a low utilization value if their distinctiveness from other accessions
  is low or unknown and their value for current breeding and research objectives is low.

  Rationalization of the utilization collection may lead to significant cost savings if:
• The conservation (base) and utilization (active) collections are maintained as
  physically distinct entities, and
• It is relatively expensive to maintain an accession in the active collection accessible
  for immediate utilization, and relatively cheap simply to conserve an accession in the
  base collection. Maintaining an accession in the base collection only, unavailable for
  immediate distribution, then reduces costs.

  The genebank may actually be able to increase the efficiency of utilization if the
  following also holds true:
1. Genebank staff can efficiently, economically and accurately identify the accessions
   that will contribute most to achieving current breeding and research objectives.
2. A conventional core collection is formed to satisfy requests that were not foreseen in
   the previous process. Therefore, in most cases potential users requesting accessions
   that are not immediately available can be offered a genetically similar accession from
   the core collection.
3. The majority of seed requests are from users and collaborators (external and
   international, as well as internal) with whom genebank staff may interact closely. This
   minimizes the proportion 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.
4. Implicit in the above is the development of a two-tier class of users: priority
   collaborators, whose needs are considered and analyzed carefully and to which
   rationalizing the (active) collections is tailored, and casual users whose needs may be
   less well met. This may be contrary to the mandate of some genebanks. In some cases,
   such as the CGIAR Centres with a global mandate, the mandate is unalterable. 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.
5. A routine protocol should be established by which genebank staff continually revise
   perceived objectives and re-assess which are the “currently most valuable accessions”.
   Accessions should not be allowed to remain permanently unused and forgotten –
   otherwise there is indeed no reason to conserve them.

HOW DO THESE DEVELOPMENTS IMPACT ON HORTICULTURAL SPECIES?

So far this paper has been very general in its reference to germplasm, in so far as no
distinction has been made between any type of crop or species, e.g., horticultural versus
agricultural crops. However, this does not mean that no principle differences between
species or groups of crops exist from a conservation and/or utilization perspective. Rele-
vant generic biological aspects of a crop/species considered for inclusion in a genebank
that should be addressed by the curator in order to choose the most suitable method or
procedure for the conservation and the facilitation of the utilization, include the following.

**Germplasm Management**

Does the target species produce seed and what are its storage characteristics (i.e.
orthodox, intermediate or recalcitrant)? What decisions have to be made on methods of
conservation and are complementary methods needed? A very useful reference database
on seed storage behaviour is provided by IPGRI (Hong et al., 1996).

What is the genetic variation between and within samples or accessions, i.e.
populations, mixtures, pure lines or clones? How can regeneration be carried out so that it
will reduce chances of genetic drift and drift? (see also Sackville Hamilton and Chorlton,
1997).
1. If sexually reproduced, what is the degree of outcrossing, and if not zero how does the level affect genebank operations? Under which conditions and to what extent is the level of contamination with pollen from other accessions or from commercially grown neighbouring crops or wild relatives during regeneration acceptable or unavoidable? (Sackville Hamilton and Chorlton, 1997).

2. What is known about fecundity, i.e. what is the number of seed produced compared to the number of seed sown? Can seed production be optimized to match expected demand for seed? (Sackville Hamilton and Chorlton, 1997).

3. What is known about seed longevity of the target species and possibly of individual accessions of the target species, under the chosen storage conditions? What is the optimum seed moisture content that would allow the highest longevity under the given storage conditions? (see also Walters and Engels, 1998).

4. How much is known about genetic variation within and between accessions in terms of seed longevity? How can viability monitoring over time be tailored to fit individual accessions? Is it known if certain pathogen infections lead to differential effects on the longevity of the seed or tissue?

5. How large are the seeds and how many are needed per lot for regeneration or for distribution? What volume of seed is needed per accession in order to represent the genetic variation within that accession adequately? What are the most appropriate storage containers and should sub-samples of accessions be stored to facilitate their management? (Sackville Hamilton and Chorlton, 1997).

6. Can accessions effectively and efficiently be regenerated under the prevailing conditions at the genebank or should collaboration with (an)other genebank(s) under better environmental conditions be sought?

7. If material is to be stored as vegetative material, what is its precise conservation purpose? Is it to be handled as a narrow sample of variation for clonal selection/use and kept in a field genebank, or in an in vitro collection (Ashmore, 1997), or is it managed as a much wider genetic provenance aimed at use, as for instance is being done for some multipurpose trees? How many accessions or provenances can be maintained, and where, in terms of land area and/or laboratory facilities?

8. If material is clonal and in vitro culture is selected as a means of conservation or disease eradication, is the technology to be used linked to rapid multiplication facilities (Morales, 2002)? 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?

Miscellaneous Genetic Resources Issues Regarding Horticultural Crops

With the aforementioned generic biological questions answered it will be helpful for the curator to take additional, and in many cases species-specific characteristics and aspects into consideration that might require special procedures or approaches for the management of horticultural genetic resources for their conservation and utilization. The following list is certainly not complete and should be treated as indicative for the kind of aspects the curator should consider.

- The species diversity of horticultural crops is much higher for horticultural than for agricultural crops. Many of these species are of minor economic importance and have only a local or regional distribution. The amount of information known about them is frequently limited. Filling these gaps might be an important task for genebanks.

- This high species diversity might easily lead to operational constraints at the genebank, partly caused by lack of expertise and/or adequately established specific procedures, and partly due to lack of the necessary infrastructure.

- Many of the horticultural species are outbreeders and, consequently, need due attention when being regenerated. Adequate isolation procedures need to be followed.

- Because of the sometimes rather small “niches” that horticultural crops occupy breeding efforts have to pay attention to the importance of adaptation and, consequently, will require access to adapted germplasm (in particular local varieties, landraces and wild relatives) from the area for which the variety is bred. This means
that genebanks should aim at ensuring that the genetic diversity for any horticultural crop is adequately sampled and represented in the collections. Furthermore, it seems that decentralized breeding efforts would better “fit” in this situation and that possibly participatory breeding approaches should be considered as part of the breeding strategy.

- Seed supply systems of the majority of the “minor” horticultural crops are informal and limited in their geographical extension. Such systems are, in general, sensitive to outside “interference” and can easily breakdown. As they are essential for the local improvement of these crops and, thus, for the sustainable management of the genetic diversity for these species, it will be important to also “conserve” these systems as part of the overall conservation and use strategy. National plant genetic resources programmes should include such considerations in their conservation strategies.

- For many horticultural (as well as for agricultural) species pre-breeding efforts are critically important as part of the overall breeding efforts. However, with the shift of research activities from the public to the private sector in many countries, and with an over-emphasis on molecular breeding the traditional pre-breeding efforts by universities, governmental research institutes and others are very much at stake, certainly to the detriment of future breeding. Solutions for this problem will have to be found at both national and international levels, possibly by adjusting the existing policies that currently exist with regard to pre-breeding.

- For many horticultural crops are included in the multilateral system of the International Treaty, e.g., the following genera are included: Asparagus, Beta, Brassica, Citrus, Daucus, Fragaria, Malus, Phaseolus, Pisum, Solanum and Vicia. As only the listed species will enjoy the benefits of “facilitated access” it can be expected that this will have consequences for the ease of access to the germplasm of the non-listed species, most likely requiring more bureaucracy and more limitations in the use of these resources. It is anticipated that (horticultural) species that are predominantly commercially exploited (e.g. ornamentals, medicinal species, spices and others) will receive most attention and restrictions with regard to their use as genetic resources and, consequently, how their benefits will be shared.

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