Conservation and Utilization of Plant Genetic Resources – Future Directions

M. Mackay[1], R. von Bothmer[2] and B. Skovmand[3]

[1]Australian Winter Cereals Collection, Tamworth Agricultural Institute, Calala NSW 2340, Australia; [2]Swedish University of Agricultural Sciences, SE-230 53 Alnarp, Sweden; [3]Nordic Gene Bank, SE-230 53 Alnarp, Sweden, e-mail: michael.mackay@dpi.nsw.gov.au

Abstract: The conservation of plant genetic resources became a recognised venture in the early 20th century due largely to the work of people like N.I. Vavilov and H.V. Harlan. International impetus was subsequently realized following the activities of scientists like O. Frankel, J. Harlan and J. Hawkes in the 1970s and 1980s. The principle focus over the past century was largely on collection and storage of plant genetic resources, with utilization receiving less resources and attention. One reason for this is that utilization has been largely considered the responsibility of breeders. Evaluation has most often been addressed using plant breeding philosophies, which focus more on discarding, or culling, material. Evaluation of plant genetic resources should focus on identifying useful germplasm for specific purposes. Traditional methods of discovering new genetic variation remain effective, but have been supplemented by some newer approaches. These include the systematic evaluation of large numbers of accessions, the core collection concept and employing molecular biology and statistical techniques to study diversity. There is currently an unprecedented demand for plant genetic resources to support plant improvement. We still, however, face difficulty in the effective and efficient identification of those accessions most likely to possess the novel genetic variation being sought by breeders. The future holds numerous opportunities for further developing how we conserve and use plant genetic resources, and how well we do this. It is suggested that we could use new technologies to greater advantage in both the conservation and utilization of plant genetic resources.

Keywords: plant genetic resources; conservation; utilization; gene bank efficiency; gene bank management; core collections; germplasm identification

Man only began to domesticate plants and animals during the last 10 000 years (Baker 1970). Most of the food on which mankind now relies comes from relatively few crop species, the number of which has decreased steadily (Harlan 1992) over the last hundred years. Until late in the 19th Century, following the rediscovery of Mendel's work, man and the domesticated crop species essentially co-evolved within the boundaries provided by nature. Early plant breeders (e.g. R. Biffen, United Kingdom; A. Blount, United States of America; W. Farrer, Australia; K.A. Flyaksberger, Russia; H. Nilsson-Ehle, Sweden and N. Strampelli, Italy) changed all this. They began to understand the laws of inheritance and observe some of the genetic diversity made available by millennia of interaction between man, plant and the environment, and pioneered the science of plant breeding. They analysed crop needs and then selected parents with different desirable attributes to hybridize, or cross, and selected combinations of the chosen attributes within the segregating progeny.

Soon after hybridization became a standard plant improvement practice the full extent of the available genetic variation began to be appreciated. In the 1920s N.I. Vavilov initiated a drive to collect, classify and use the genetic variation of all crops of potential value to the Soviet Union. His objective was primarily plant improvement, but in the process he recognised the richness of the diversity

Table 1. The principle recommendations of the FAO/IBP Conference of 1967 (Frankel & Bennett 1970)

1.	Determine the location and nature of PGR in the field
2.	Survey the material in existing collections
3.	The efficient utilization of PGR requires that they are adequately classified and evaluated
4.	Conservation requires strong emphasis because its importance was not yet fully appreciated
5.	Importance of documentation, at all stages, was recognised and highlighted
6.	The geographic dispersion, complexity, magnitude and importance of this programme demand international co-ordination, guidance and administrative backing at the highest level

available, which eventually led to his postulation about centres of origin and/or diversity. H.V. Harlan recognised in the 1930s that modern barley cultivars were displacing the traditional farmers varieties and foresaw that our collections would become invaluable resources (Harlan 1936).

Almost another half century passed before the full value of the genetic diversity of our crop and pasture plant species began to be more widely acknowledged in a world that was rapidly becoming smaller with advances in transport and communication. The Food and Agricultural Organization of the United Nations (FAO) began to take an interest in facilitating seed exchange and published a study on "Plant exploration and introduction" in 1958 (1992). FAO continued to facilitate a range of activities associated with seed exchange and cataloguing genetic stocks (FAO 1959) and was a major player in generating wider interest through, for example, meetings such as the 1961 Technical Meeting on Plant Exploration and Introduction (Whyte & Julén 1963). Sir Otto Frankel was instrumental in bringing FAO and the International Biological Programme (Frankel 1987) together to convene the FAO/IBP Technical Conference on the Exploration, Utilization and Conservation of Plant Genetic Resources, Rome, 1967. This conference brought together a group of experts (later called the Panel of Experts on Plant Genetic Resources) for the purpose of developing an international plan for the conservation of plant genetic resources, or PGR (Pistorius 1997). The principle recommendations that arose from the 1967 conference, in effect, largely charted the course of PGR at the national and international levels, almost to the present time. These recommendations touched all aspects of PGR from exploration to utilization (Table 1) and provide a useful yardstick for measuring the development of PGR to the current time.

Many PGR activities of the 1960s, 1970s and beyond responded, wholly or in part, to the 1967 conference. *Ex situ* gene banks became a growth industry, collection missions were conducted in many parts of the world, storage conditions were studied, the distribution of primitive varieties and related species were determined. On reflection, these activities resembled a 'gold rush' to collect and store the wealth of diversity from Vavilov's centres of genetic diversity that were being proclaimed by the burgeoning PGR community.

The subsequent efforts to realise the 1967 conference recommendations met with varied success. The purpose of the conference was to set up a global network (Pistorius 1997) that would involve base, active and working collections. The high-level international cooperation and funding necessary to achieve this objective did not eventuate at the time. As reflected later by Harlan (1992), "The trend today is toward national collections and collections maintained by individual or corporate plant breeders. Networking does not seem politically feasible at this time."

Some members of the Panel of Experts (through FAO) presented the case to the Consultative Group on International Agricultural Research (CGIAR) in 1971 (Pistorius 1997). Through the establishment of the International Board for Plant Genetic Resources (IBPGR, later the International Plant Genetic Resources Institute, IPGRI) and its IARC (International Agricultural Research Centres) gene banks, the CGIAR provided a version of an international network that promoted, stored and distributed PGR. Despite the early achievements of IBPGR, concern about the on-going ownership of, and access to, PGR under such an arrangement eventually resulted in considerable focus moving towards legal issues relating to the regulation and exchange of PGR (Pistorius 1997, provides a detailed account). This concern ultimately led, by way of the Convention on Biological Diversity (CBD) in 1992, to PGR being removed from a "common heritage of mankind" category into

a "sovereign rights of states" classification. The International Treaty on Plant Genetic Resources for Food and Agriculture, the precise operational details of which are still being negotiated, could significantly influence some aspects of PGR activities in the future.

In the meantime a recent report asserts that over 97% of the 1470 gene banks in the world do not "meet international standards for managing long term conservation" (Qualset & Shands 2005). The report further claims that one in six, of the 6 million samples held in these gene banks, are degenerating – presumably at an unacceptably high rate. With these statistics in mind, and the benefit of being able to use hindsight in reflecting on the success, or otherwise, of PGR activities over the previous few decades, it is an opportune time to look towards some practical directions for the conservation and utilization of PGR into the future.

CONSERVATION

The term conservation embraces many PGR activities. A number of disciplines have active interests in the conservation of PGR (Figure 1). Here we want to concentrate on several of the more fundamental gene bank aspects of PGR conservation. To do this, however, we would like to begin with recognising the diversity among gene banks around the globe. We then want to concentrate on discussing a few elementary gene bank conservation activities. Our idea is to focus on some practical steps that will help make gene bank conservation activities not only more efficient, but also effective. In other words, addressing the essential gene bank PGR activities using the most appropriate methodology.

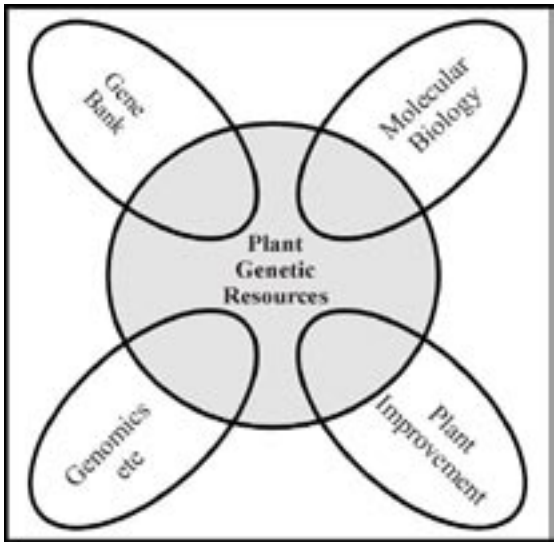

Figure 1. Plant genetic resources functions are undertaken by a variety of disciplines

Types of gene banks and their mandates

Different gene banks have different mandates, often formulated by national, regional or other interests. The gene banks managed by the IARCs usually have a global role (e.g. the CIMMYT wheat collection), some gene banks fulfil a regional role (e.g. Nordic Gene Bank), while many gene banks address national or crop specific objectives (e.g. Australian Winter Cereals Collection).

As well as global/regional or crop/species orientated mandates, there is also considerable variation among gene banks in their functions and activities. In addition to basic conservation activities, some gene banks have a requirement to undertake research into a variety of PGR areas, such as the study of genetic variation and its distribution, or the evaluation of accessions for pre-determined attributes. Other gene banks might have been established to formalize the conservation activities of associated plant improvement programs. There will obviously be a number of additional models for gene banks, but the point is to recognize and respect that these differences occur.

We believe it would be useful to categorise these functions and identify those that are essential to the conservation of PGR. In the context of this paper, we are referring to the *ex situ* conservation of PGR, which we see as a gene bank responsibility. The essential conservation functions undertaken by gene banks include acquisition, multiplication and regeneration, storage, distribution, and associated documentation – passport and characterization data, as well as practical seed management information.

With increasing competition for funds available for PGR activities, it is reasonable to partition these activities into those that are absolutely essential to gene bank function, those more aligned with basic research, and those of a more applied research nature. In this way it might be possible to direct those funds required to undertake essential gene bank activities where they are most urgently required. Hammer (2003) suggested that primary PGR research has difficulty competing with some

PGR associated activities that can produce results more rapidly.

Types of plant genetic resources

General types of PGR (Table 2) have been identified on at least three separate occasions (Frankel 1970, 1984; Alercia *et al.* 2001). These different types generally represent distinctive genetic structures, potential as sources of novel genetic variation, and type and quality of the information associated with them.

Modern cultivars are the result of over one hundred years of pro-active plant breeding that was based upon millennia of co-evolution between man and crop, and represents highly specialised gene blocks that display wide adaptation. The modern breeder usually adds one, or a few, new traits at a time to an existing successful agronomic background. In contrast, pre-breeders are often concerned with the identification and transfer of specific traits into acceptable genetic backgrounds and generally broadening the diversity base. While most types of PGR can be of interest in fundamental research activities, it is more often the landraces and non-cultivated types that are targeted as sources of novel genetic variation for breeding activities, especially for overcoming biotic and abiotic stresses (for example, Harlan 1977). More recent examples of landraces providing solutions in cereals include tolerance and resistance to boron toxicity in soils, resistance to Russian wheat aphid (*Diuraphis noxia*) (Mackay 1995) and through use of physiological traits (Skovmand *et al*. 2001).

Based on general patterns of PGR usage we can begin to ask questions about how we should manage the different types of PGR. For example, depending on the nature of the trait being sought, we could choose to include or exclude obsolete and current cultivars in an evaluation project seeking genetic variation for an entirely new trait.

Storing and managing PGR

The science of successfully storing PGR is not being addressed here. We are more concerned with questions about how different types of PGR might be treated and will use orthodox type seeds as an example.

Broadly speaking there are three main regimes for orthodox seed storage:

Long term storage at 6–8% moisture content at around –18°C.

Medium term storage at about +4°C.

Short term under ambient conditions.

Gene banks contain advanced, or improved, cultivars as well as other types of PGR. Within gene bank operations there is a tendency to treat all accessions in the same manner. For example, if it has been decided that 1000 seeds should be stored for each accession, then this standard is usually applied to all accessions. We should question why 1000 seeds of an accession that is an obsolete cultivar of a self pollinating species are being stored. Similarly, should such an accession be placed in long term or medium term storage?

Table 2. Types of plant genetic resources

Alercia *et al.* (2001)	Frankel (1984)	Frankel (1970)
Wild Weedy	Wild relatives of crop species	Wild and weed species related to cultivated species
Traditional cultivar/landrace	Landraces	Primitive varieties or landraces
Breeding/research material, including mutant/genetic stock		Special genetic stocks such as resistance stocks, genetic and cytogenetic material, induced mutations etc.
Advanced/improved cultivar Other	Modern varieties, current and obsolete	Pbsolete cultivars Cultivars in current use

After accepting that there are different types of germplasm and that there are different storage options available, there is an opportunity to make use of this knowledge in achieving more rational conservation strategies. The practice of applying broadly based standards across an entire collection should be re-examined with a view to developing discerning methods that address the logical differences between types of PGR and storage options. This is just one example of how we can re-evaluate the PGR conservation standards that we currently accept (for gene bank functions) in order to achieve astute management practices.

Eliminating unnecessary duplication and minimising redundancy have often been raised as important gene bank management issues. The full contribution that new and developing technologies, such as molecular biology and informatics, can make to these PGR activities is still to be fully realised. Already there are a number of examples of these technologies supporting traditional gene bank methods in identifying duplication (Zhang *et al*. 2001) and redundancy (Phippen *et al.* 1997).

Documenting PGR

Documentation is an essential component of PGR conservation. Passport data is essential for correct identification and characterization data is helpful to the management and classification of PGR. This was duly recognised and promoted by the 1967 FAO/IBP conference. Over time it almost seems that the systematic documentation of PGR has become a discipline in its own right. During the compilation of the global wheat inventory only a subset of the FAO/IPGRI multi crop passport descriptors were actually used (Mackay & Skovmand 2003). The pertinent question we wish to raise is which information is essential, which information is helpful, and which information is redundant?

Marshall and Brown (1981) questioned the value of elaborate characterization to breeders. Frankel (1984) suggested that systematic documentation might have led to the 'development of centralized information systems with large numbers of descriptors and descriptor states', and went on to question if there was redundancy in documentation. These words, from more than twenty years ago, can serve to remind us that we could reconsider the type and quantity of information required for the rational conservation of PGR in gene banks, perhaps employing some method to estimate the quality of the information under consideration.

We believe there is considerable scope to develop and achieve more judicious documentation systems for PGR in gene banks. Of course there will be other needs for documentation of PGR outside essential gene bank functions, such as evaluation data, but we advocate that these requirements should be supported separately, i.e. not from core gene bank funds.

Characterization

Characterization (sometimes called classification) data can have multiple applications in gene banks. This type of data usually relates to highly heritable morphological traits and is sometimes extended to include some basic agronomic attributes, such as plant height and a measure of maturity, which can be less heritable but more useful.

Within the gene bank, characterization data is helpful in categorising accessions into groups for breeders to select from for evaluation purposes. For example, a bread wheat breeder might request soft, red grained accessions with a specific height and maturity range. Another valuable application of characterization data is in maintaining quality control. In the Australian Winter Cereals Collection (AWCC) the same characterization data is collected each time an accession is regenerated. Cross-referencing the data with that collected on previous multiplication or regeneration occasions ensures the integrity of a number of gene bank operations.

The descriptors included in the characterization data should be chosen to fulfil these two functions, categorising and quality control, as well as to be compatible with the mandate of each individual gene bank.

UTILIZATION

As mentioned previously, it became widely accepted that systematic characterization and evaluation were prerequisites for utilization. An early advocate of this assertion later withdrew support (Frankel 1984), due largely to the recognition that significant quantities of the information being collected or assembled were either not very useful or redundant. We are not implying that information

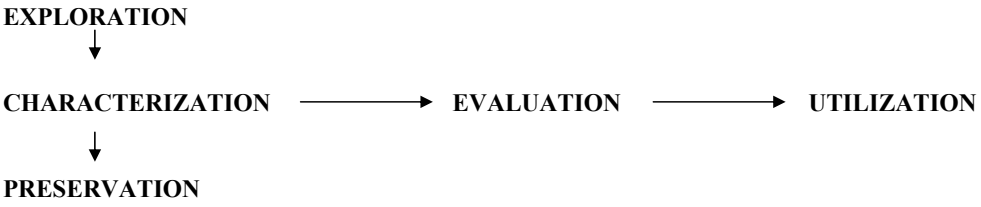

Figure 2. Stages in the conservation and utilization of plant genetic resources (after Marshall & Brown 1981)

is not necessary, or that evaluation is not part of the overall process. We do, however, suggest that utilization is a process that involves a number of logical steps to be successful.

Distinguishing between characterization, evaluation and utilization

Marshall and Brown (1981) identified a number of stages in programs that conserve and utilize PGR (Figure 2). They note that the restricted resources available for each stage limit the numbers of accessions that can be effectively processed in such programs.

Here we want to distinguish between the conservation and utilization processes. We will only address the steps involved with utilization – the horizontal process in Figure 2. Characterization data can be put to use in a number of ways in gene banks. The application of characterization data for utilization purposes requires clarity in terms of a) what is the utilization objective and b) the value of different types of information in achieving the utilization objective. In other words, we need a valid reason to evaluate accessions – there has to be a problem to be resolved. In addition, there also needs to be compelling reasons to use characterization data in identifying those accessions that might contain the variation which is anticipated will solve the problem.

According to our understanding of the utilization process, once a production obstacle has been recognised the next task is not to evaluate, but to gather information and/or knowledge about all aspects of the problem. For example, answers to the following questions could provide sufficient information and knowledge about a problem to allow the breeder to initiate thinking about which particular groups of germplasm might contain the genetic variation being sought: Where does the problem exist? How can we identify genetic variation relating to the expression of the problem? Where else in the world does the problem occur? What other scientists might have some knowledge or experience with this problem? Are there any environmental parameters correlated with the problem?

It is only after sufficient information and knowledge has been obtained that attempting to identify sources of new genetic variation can begin. It is also possible that, during the course of information and knowledge gathering, a ready-made solution is identified and negates the need to find novel genetic variation. On the other hand, if a new solution has to be discovered, we can then explore ways in which we might identify those PGR that are most likely to contain the genetic variation we are seeking. Thus, we can combine the information we gather to resolve a specific problem with any other available information, including characterization data, to achieve our objective. To summarize, utilization requires the assembly and creative use of different types of information before candidate accessions for evaluation can be identified. It is only after the candidate accessions have been identified, and appropriate screening methodology is available, that the evaluation phase can begin. This model of the utilization process can be illustrated in Figure 3.

We believe that this general process has been the most common way by which breeders, and others, have intuitively utilized PGR for the last century. There will always be exceptions to any attempt to define a process like the utilization of PGR, however, our experience and knowledge supports the general process described above as being very successful over time.

The early Australian wheat breeder, William Farrer (1845–1906), provides a timeless example of the process. Beginning in about 1886, Farrer recognised a number of production and quality problems in Australia's fledgling wheat industry. He developed long range communication with scientists in Europe, Africa and North America, with whom he discussed the problems and their possible

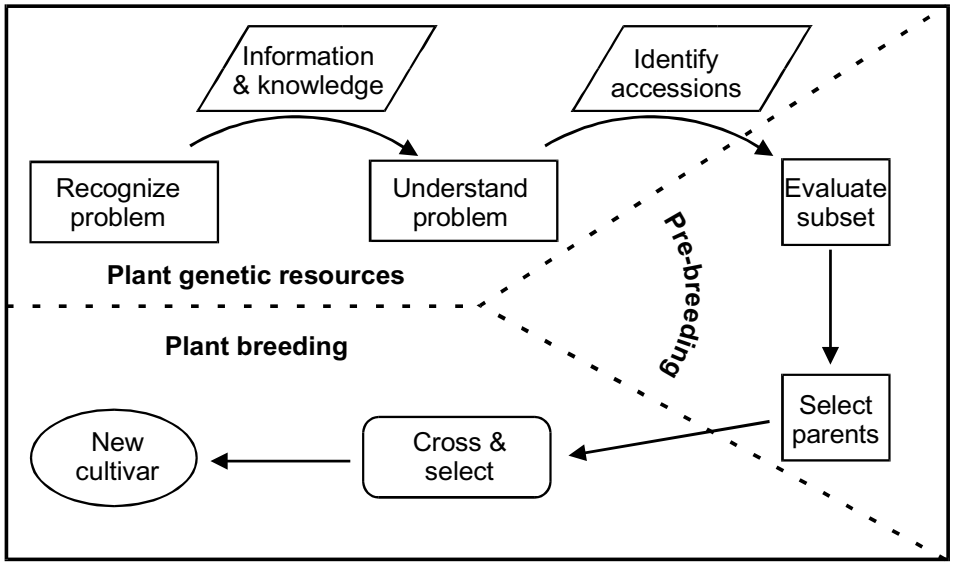

Figure 3. Illustration of germplasm utilization processes showing nominal allotment of components into primary disciplines

solutions. Based on the knowledge he gained, Farrer gathered a significant collection of wheats (about 1000 by 1896) which he evaluated and ultimately selected some as parents for hybridization. From among the progeny Farrer selected a number of genotypes which became some of the first purpose bred wheat cultivars in the world.

With the benefit of hindsight it now seems rather naive to place systematic evaluation as a prerequisite to utilization. Of course accessions must be evaluated, or screened, in order to identify the presence of desirable traits. However, it is not possible to predict those attributes for which breeders will be seeking genetic variation at some time in the future.

The identification of those accessions most likely to contain the genetic variation being sought by breeders is seen as a crucial step in the overall utilization process. For some reason it seems to have been generally overlooked in the past – probably because it was done intuitively and perhaps it was never considered important enough to record in the literature.

Core collections and utilization

Frankel (1984) proposed the core collection concept to place the emphasis for wide usage of a collection on the genuine diversity it contained, rather than its quantitative size. When applied, the "pruning procedure would result in assembling accessions representing, with a minimum of repetitiveness, the genetic diversity of a crop species and its relatives". The very definition of the core collection implies its value in making large collections more accessible, and many examples of core collections are available in the literature (Chabane & Valkoun 2004; Okpul *et al*. 2004; Zewdie *et al*. 2004; Schmidt 2005). Studies of core collections have also provided excellent insights into PGR conservation issues, such as the management and extent of diversity within collections (Hu *et al*. 2000; Fajardo *et al*. 2002).

Breeders most often have a specific objective in mind when they are seeking new sources of genetic variation, such as overcoming a productivity constraint or improving a quality attribute. While a core collection will provide the breeder with a smaller set of accessions to evaluate, it will not necessarily guarantee a positive result, especially if the allele being sought is rare, as it is intended to represent general rather than specific diversity. A subset of accessions identified on the basis of their probable diversity for the specific trait being sought would provide a more rational means of utilization. So, while the core collection has merit for gene bank management, its direct application to utilization will not be as effective. So, while there can only be one core collection of a larger collection, the general concept of reducing the effective size to identify specific diversity can still be used to develop trait specific subsets of accessions (Mackay 1995).

Molecular biology

There are several ways in which molecular biology techniques can contribute to the conservation of PGR. Detection of duplication and redundancy in gene banks are two of the most attractive and obvious applications. Emerging applications include the study of genetic variation within species to estimate the diversity of particular collections, and how well they represent available diversity. Whilst these techniques can provide useful information about such variation, the cost involved in the evaluation of large collections suggests efficiencies are needed (Dreisigacker *et al*. 2005) to allow widespread usage for this purpose.

In terms of utilization, while these techniques offer promise for the future they do not appear to be sufficient on their own to identify adaptive potential (Weising *et al*. 2005).

Germplasm identification

To successfully utilize PGR collections we need to be aware of the types of germplasm they contain, the information that is available and, most importantly, what objective is being sought. While it might be impossible to predict the future value of an accession held in a gene bank, it is possible to identify sets of accessions that are more likely to contain the genetic variation being sought, for a particular purpose, using a logical process like the one described above.

A prototype system that combines the biological information managed by a gene bank with environmental information, using geographic information system (GIS) technologies, is being developed to identify candidate accessions for resolving specific breeding objectives. Called the focused identification of germplasm strategy (FIGS), the system has been used to develop a virtual collection by combining the 17 000 bread wheat landraces from ICARDA (International Centre for Agricultural Research in the Dry Areas), the N.I. Vavilov Research Institute of Plant Industry (VIR) and the Australian Winter Cereals Collection (AWCC). The collecting site geo-coordinates for these landraces contribute one layer of data in the total system. Other layers already developed and included are long-term temperature and rainfall data, agro-ecological zoning schemes and estimates of potential salinity incidence. FIGS has been used to develop candidate subsets of landrace accessions for evaluation against drought conditions, salinity and powdery mildew (*Blumeria graminis f*.sp. *tritici*) (K. Street, person. commun.). It is intended that the FIGS system will be available for general use via the internet.

CONCLUSIONS

A number of issues relating to PGR conservation and utilization have been raised and some opportunities for future progress identified. The list is not intended to be exhaustive, but rather to highlight the type of opportunities that exist for progressing into the future.

In terms of the conservation of PGR and gene banks, there is clearly some scope to distinguish exactly which activities are the primary responsibility of the gene bank, and those for which others should assume responsibility. Through delineation of these the gene bank can focus on fulfilling those absolutely essential conservation activities that can provide the basis of additional, more applied, conservation functions to be undertaken by others at a later time. For example, systematic classification of PGR is the task of systematics specialists, not curators or breeders. If this type of work is to be undertaken within the gene bank the necessary expertise and resources should also be provided. Likewise, evaluation is the task of breeders and pre-breeders and not the responsibility of gene banks and curators, unless it is agreed that the resources and skills to undertake such activities will be made available to a particular gene bank to perform these tasks. It is, however, important that gene banks are active participants in evaluation because they can contribute significant expertise to, for example, the identification and selection of candidate accessions.

How PGR are actually utilized has been the subject of considerable discussion for many years. Prerequisites were described and methods proposed. We believe that a critical component of the PGR utilization process, identifying candidate accessions, has been largely overlooked in the past. The reason for this probably relates to the largely undocumented and intuitive way in which breeders have actually accomplished utilization. Novel ways of applying new technologies, such as GIS, offer a way of formalising the identification of subsets of accessions that have a greater chance of containing the genetic variation being sought by breeders.

In the case of both the conservation and the utilization of PGR, the term rational is proposed to encourage sound reasons for performing these activities in gene banks. Rational conservation implies basing our conservation activities on logical scientific principles rather than on a whim or unsubstantiated claims. Likewise, rational utilization has similar implications and excludes the possibility of undertaking utilization activities without having a specific goal. In contrast, efficient utilization implies doing something with a minimum of waste, expense or unnecessary effort, but does not ensure that there is some rational purpose behind the utilization activity.

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