

The use of *ex situ* conserved plant genetic resources

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Received 24 March 2003; Accepted 27 March 2003

Abstract

Plant genetic resources are conserved so that they can be used to improve crop plant production and in other ways. However, it is often asserted that use of *ex situ* conserved germplasm is inadequate and that genetic diversity maintained in genebanks is underutilized. In part, this reflects an incomplete recognition of what constitutes use of plant genetic resources, and of the many different ways in which material from genebanks contributes to improved agricultural production. Based on recent information from surveys of distribution of germplasm from genebanks, and from surveys of users, we suggest that the evidence indicates that there is substantial use of *ex situ* conserved materials for a wide range of different uses. We suggest that barriers to use of *ex situ* conserved germplasm may often result from a lack in numbers of users, and from limitations in capacity to effectively utilize the genetic diversity present in genebanks to reduce genetic vulnerability and increase sustainability in modern production systems.

Keywords: distribution; genebank accessions; genebanks; genetic diversity; germplasm conservation

Introduction

Plant genetic resources are conserved in order that they may be used now and in the future. (FAO, 1998)

In this statement, the Food and Agriculture Organization (FAO) restated an almost universally held belief about crop plant germplasm conservation which is viewed as utilitarian in nature, aimed primarily at supporting improved agricultural production. However, this strong commitment to use by those involved in the conservation of plant genetic resources has been accompanied, almost from the beginning, by a concern with the inadequacy of

that use. In the early 1960s, Simmonds (1962) argued that germplasm collections were poorly used and inaccessible to their primary users and these concerns have been regularly repeated and discussed over the last 40 years (e.g. Frankel and Brown, 1984; Holden, 1984; Marshall, 1989; McPerson *et al.*, 1996; Smale and Day-Rubenstein, 2002). At the same time, the amount of *ex situ* conserved germplasm has continued to grow so that, by 1998, FAO estimated that there were probably over 6 million accessions conserved in over 1300 genebanks throughout the world (FAO, 1998).

Paralleling the concern with the use of conserved germplasm has been an increasing concern with the amount of genetic and crop diversity within production systems (e.g. National Research Council, 1972). Has modern agriculture led to a dependence on too few

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cultivars of too few crops? This is a much wider debate than one which is mainly concerned with how much conserved germplasm is used. But clearly there are close links. Increasing the diversity in production systems is likely to lead to greater use of conserved germplasm and greater use of collections is likely to lead to increased diversity in production systems.

Sustainable production, with its emphasis on decreased inputs of non-renewable resources, is also commonly expected to require the use of additional genetic diversity in production systems (Whitten and Settle, 1998). Certainly, many traditional production systems, which are often cited as examples of sustainability, continue to be characterized by relatively high levels of both between-crop and within-crop diversity (Jarvis *et al.*, 2000; Watson and Eyzaguirre, 2002). There is also an increasing recognition that these production systems contribute to the conservation of crop genetic diversity and an acceptance that, in many cases, conservation *through use* (in production) is as important as conservation *for use* (in *ex situ* collections) (FAO, 1998).

Despite the importance accorded to use of conserved germplasm, and the recognition that developing more sustainable production requires improved use of genetic diversity, there is little information on the extent and nature of use of material conserved *ex situ* (FAO, 1998). In fact, there is considerable confusion about what constitutes use of the germplasm stored in *ex situ* collections. In this paper we propose to explore what should be regarded as 'use' of *ex situ* conserved germplasm and to review available information on the extent and nature of that use. Finally, we will try to identify barriers to improved use and the ways in which they may be overcome. In doing this we will try to explore some of the wider issues linking improved use of genetic resources in *ex situ* collections with increasing the amounts of diversity in production systems.

What constitutes use of *ex situ* conserved germplasm?

It is often assumed that use of *ex situ* collections equates to 'use by plant breeders in crossing programmes'. Thus, Peeters and Williams (1984) refer exclusively to use by plant breeders in their paper 'Towards better use of genebanks with special reference to information'. This narrow perception needs to be corrected. Use of genetic resources can involve a wide range of different, but often interrelated, actions. These can include characterization and evaluation of material, use of accessions for biological and agricultural research and direct use (e.g. for restoration or production), as well as use in plant breeding programmes.

Characterization and evaluation

Describing the characteristics of accessions in a genebank is recognized as an essential activity by genebank managers and by organizations supporting them such as International Plant Genetic Resources Institute (IPGRI) and FAO (Hawkes *et al.*, 2000). IPGRI differentiates between characterization and evaluation. The former involves determining characteristics of accessions that 'enable an easy and quick discrimination between phenotypes ... are generally highly heritable, can easily be seen by the naked eye and are equally expressed in all environments'. Evaluation involves characteristics that are susceptible to environmental differences but are generally useful in crop improvement (e.g. agromorphological traits, biotic and abiotic resistances, or nutritional properties) (see e.g. IPGRI *et al.*, 1995). The traditional view has been that characterization will normally be the responsibility of genebank managers while evaluation will typically be carried out elsewhere (e.g. IPGRI *et al.*, 1995).

Both characterization and evaluation should be regarded as forms of use of genetic resources because the information obtained by undertaking the activities involved (growing the plants, describing specific properties, collecting, analysing and summarizing the data and making it available to other users) all involve carrying out activities on the accessions and adding to their value. The information contributes to the body of knowledge on a crop, enabling us to determine the range of diversity that exists and the forms that it takes, and to identify the specific accessions that may be required for different specific purposes. Characterization and evaluation make genebank collections more useful for other objectives and increase their value to other users.

Characterization and evaluation of large collections can be particularly valuable and important. A large number of accessions may have to be tested (used) in order to find the few that have the desired traits, and one of the great values of large genebank collections is that they allow us to do this. Chang (1989) reports that the International Rice Research Institute (IRRI) found 401 accessions of *Oryza sativa* resistant to whitebacked planthopper out of 48,554 tested and that 26 accessions were found to be resistant to yellow stem borer out of 22,920 tested. Similarly, Holbrook and Anderson (1995) reported that they found 112 peanut accessions resistant to late leafspot in their collection of 7432 accessions.

Although some evaluation may be trait-specific, involving large numbers of accessions being screened for only one characteristic, much characterization and evaluation is carried out for many traits at the same time. The activities (and the costs involved in these activities) provide information on many different aspects of accession

performance. Information can therefore be obtained not only on range of trait expression and specific characteristics but also on associations and correlations between traits. Preliminary information on heritability will also become available. Clearly these data are useful (and are used) even when no further activities will be undertaken with many of the accessions for many years.

Evaluation of accessions can become complex and detailed and be carried out by specialist groups of users. Examples of this type of evaluation might include determination of specific nutritional properties such as vitamin content or oil content (e.g. Velasco and Mollers, 1998) or response to stresses that are governed by complex interactions of characteristics such as drought or salinity tolerance (Belkhodja *et al.*, 1994). Genebanks repeatedly ask that this information is sent to them so that it can be incorporated in their databases on accessions. Unfortunately, it is clear that this is often not done and the amount of this type of evaluation and the way the information obtained is used, is largely unquantified and unquantifiable unless it results in published research papers (see below).

Use in research

Use of *ex situ* conserved accessions in research is extensive and important. Jackson *et al.* (1999) commented that thousands of rice accessions were sent to and used by rice researchers throughout the world. In their view, this use of germplasm accessions 'contributes to rice science, and facilitates the deployment of germplasm accessions that are actually used in breeding'. Research using germplasm accessions provides knowledge of the range of expression of traits and of the correlations between them, heritability and genetic control of specific characteristics, the biochemical pathways involved in expression of traits and their molecular genetic control.

The extent to which agricultural research makes use of *ex situ* conserved genetic resources is difficult to determine. Three international journals are devoted to reporting research on or with plant genetic resources (*Genetic Resources and Crop Evolution*, *Plant Genetic Resources Newsletter* and *Plant Genetic Resources: Characterization and Utilization*). These currently publish over 100 papers per year which deal largely with the collection and conservation of genetic resources, and the extent and distribution of genetic diversity.

Dudnik *et al.* (2001) found that 22% of the papers published in four international journals (*Crop Science*, *Euphytica*, *Plant Breeding* and *Theoretical and Applied Genetics*) in 1996 made use of material that came from *ex situ* collections. Most common topics of research included quantifying genetic diversity, investigating

biotic and abiotic stress resistance, breeding research, studies on molecular markers, performance of agromorphological and quality traits, and taxonomy and phylogeny. The survey suggested that 80% of authors came from developed countries or from institutes of the Consultative Group on International Agricultural Research (CGIAR) and that 90% of the material used came from developed country or CGIAR genebanks. This may reflect publishing habits as well as the more limited opportunities researchers in developing countries have to publish material in international English language journals.

It would be useful to have further surveys of this type. Much of the research using genebank materials is likely to be reported in national or regionally based journals or in crop newsletters rather than in international journals. Thus, reports from China suggest substantial use of Chinese material in research (e.g. Gao Weidong *et al.*, 2000) largely published in Chinese language journals.

In practice, the boundary between research and evaluation is often rather blurred. Good and detailed evaluation will be published in research journals or will lead to the identification of specific accessions for particular pieces of research, such as the inheritance of individual traits or the physiological, biochemical and molecular bases of differences in expression observed in different accessions. In this respect, the dramatic advances in molecular genetics are beginning to have an impact on evaluation and characterization (<http://www.cgn.wageningen-ur.nl/pgr/>). It is likely that molecular genetic evaluation will become increasingly routine for the better-endowed genebanks and that research increases which uses genetic resources to determine how differences in gene expression are effected.

Direct use

While direct use of accessions in production or in some other way is not common for crop plants, it is much more common for forage or agroforestry materials. Direct use may not always be aimed at specific production objectives, there may be wider environmental concerns such as rehabilitation of specific environments that have become over-grazed or polluted by industrial waste. To date, surveys have not really allowed us to determine how extensive this kind of use is because they too have been targeted mainly at users of crop plants.

Over the last decade there has been an increasing interest in the direct use of crop genetic resources as part of the response that might be made to war disasters and other events that result in severe loss of planting material by communities or countries. The view has been expressed that, in many cases, aid agencies respond to these events with planting material that is not optimal

for farmers in the affected areas, who might benefit more from receiving locally adapted materials obtained from a suitable genebank (Richards and Ruivenkamp, 1997). At the same time there appears to be a growing demand by some farmers to receive back materials that have been placed in genebanks and which changing circumstances (e.g. increased prices of fertilizers and other inputs) are making more attractive.

Plant breeding

The inclusion of accessions in plant breeding crossing programmes and their subsequent development of released cultivars are the most generally recognized use of genetic resources. Most crop cultivars contain some accessions from genebanks in their pedigree and various calculations have been made of the very extensive benefits that have come from use of these materials (Evenson *et al.*, 1998).

In the next section we will present information on the scale of use of genebank material in breeding programmes but two problems in arriving at an adequate quantification of the extent of use in plant breeding should be recognized. Firstly, there is often a linked process from characterization and evaluation through identification of possible parent material and selection of progenies to final release of new cultivars. At all stages material is discarded having been fully used and the contribution of the discarded material is seldom recorded and is difficult to quantify. Secondly, once useful traits from a genebank accession have been transferred to improved cultivars, these will commonly become the source of the traits in future. The accession will have been recorded as used only once despite the fact that the traits it provided continue to be included in all future varieties.

How much use is there?

Two approaches have been used to determine the extent of use of *ex situ* conserved germplasm. The first involves determining numbers of samples of different crops distributed by genebanks, and who they were sent to, so as to try to ascertain what they were used for (usually based on information given by the requestor of material). The second involves surveying known recipients of material to find out how they used the material they received. Both have obvious problems in relation to their ability to determine accurately the amount and type of use and some of these are noted below. Furthermore, in only one case (China; Gao Weidong *et al.*, 2000), do published data exist which allow direct comparison of genebank distributions with users' actions for the same material in the same country.

Distribution of germplasm from genebanks

FAO (1998) reported on the percentage of the number of accessions distributed each year for a number of national and international genebanks. Their analysis was based on reports from the participating countries (www.fao.org/WAICENT/FAOINFO/AGRICULT/AGP/AGPS/pggrfa/wrlmap_e.htm). FAO noted that only a handful of the 66 countries that report having national genebanks distribute more than 10% of accessions annually. Examples of countries which distributed more than 10% included Germany which claimed to distribute 17% (of which 20% were supplied to breeding programmes), Pakistan (10%), Thailand and Ecuador (42%). Most international centres were reported to have distributed more than 10% annually with IRRI, for example, being cited as distributing 16%.

FAO admitted that the indicator used was 'admittedly crude' and, interestingly, discussed the levels of use in almost apologetic terms, as though seeking to excuse what it perceives as a low level of use. It is not clear why distribution of less than 10% of the accessions per year should be regarded as low usage and what might be regarded as average or even high usage. However, the report noted that there were substantial differences between crops with Cuba reporting that 50% of the citrus and potato collections are distributed each year as compared with only 5% for rice. A further difficulty in interpreting the data is that it is not always clear whether countries are reporting numbers of samples distributed or numbers of accessions distributed (with the possibility that many samples were distributed of some accessions). The report from Canada, for example, uses samples and accessions interchangeably.

The data in the different Country Reports confirm that there were large differences between crops in the amount of distribution. The USA reported ranges in percentage of collection distributed from 14% (for maize and *Phaseolus vulgaris*) to 75% for *Pisum sativum* for the 10 most requested crops over a 3-year period (1992–1994). There were also large year-to-year fluctuations suggesting that any analysis of use should include data from a number of years. Some countries provided data on the type of recipients but this was very variable. Canada separated federal government, university, private company, non-governmental organizations (NGOs) and provincial government recipients. The Institute for Plant Genetics and Crop Research, Germany provided information on the different types of use and reported that 25% were used for screening purposes, 40% for 'other evaluation', 18% for breeding, 9% for research and the rest for other uses. In contrast, the Bundesforschungsanstalt für Landwirtschaft, Germany distinguished between recipients and reported that 62% of recipients were research institutes, 16% were breeders,

16% were private users and 6% were members of the German association of private breeders (GFP).

The most complete survey of germplasm distribution in the literature is probably that undertaken on the use of Chinese *ex situ* collections (Gao Weidong *et al.*, 2000). Distribution data on 10 crops (rice, wheat, maize, soybean, cotton, *Citrus*, Peking cabbage, cucumber, mulberry and tea) for 1984–1998 were collected and analysed. At the same time, surveys were carried out of recipients of the material to find out how it had been used.

There were large differences between crops with respect to numbers of samples distributed and the number of samples per 100 accessions per year. For the major cereals for which large collections exist (rice and wheat) the numbers of samples distributed annually were substantial although the percentage of the collection distributed was low (Table 1). For cabbage, cotton and cucumber, where smaller collections were maintained, the percentage distributed was higher (cucumber, 13.5 samples/100 accessions/year; cabbage, 14.0; cotton, 14.9). An exceptionally high use was reported for citrus with 127.5 samples/100 accessions/year, over the 15-year period of the survey.

Much larger numbers of cultivars and advanced lines were distributed than land races, genetic stocks or wild relatives. Overall, 61% of the samples distributed were advanced lines or cultivars while 22% were land races, 4% were wild relatives and 2% genetic stocks. However, there were marked differences between crops. Nearly 60% of the *Citrus* material distributed was germplasm of wild relatives or land races and the same was true for soybean.

Data also exist on distribution of germplasm from the international genebanks of the CGIAR. Iwanaga (1993) reported that the 'active germplasm distribution index' (AGDI—equivalent to the number of samples/100 accessions/year) for *Phaseolus* varied from 43.3 to 254.8 between 1977 and 1991 with an average of 111.4 over 15 years. By comparison with Chinese data, these figures

from Centro Internacional de Agricultura Tropical (CIAT) were very high and recent data suggest that current levels of distribution are somewhat lower.

The SINGER website (www.singer.cgiar.org) provides information on the transfers of materials from the international collections of the CGIAR institutes to users outside the system. Of course, the institutes themselves make very significant use of the materials in their own investigation, research and breeding work so the data substantially underestimate use of these collections. Iwanaga (1993) noted that 75% of the *Phaseolus* samples distributed by CIAT over 15 years were used in other CIAT programmes. However, some preliminary analysis of the SINGER data has led to important findings relevant to understanding patterns of use.

Analysing flows of material transfer from CGIAR genebanks over 25 years showed that most of the material (81%) went to developing country users and that, for some crops, flows of material between regions were particularly important. In groundnut, some 60% of transfers involved movement of material to a different region from that in which it was collected (Fowler *et al.*, 2001). The importance of international movement of germplasm and the role that it has played in supporting the global development effort was a key element in the development of the recently agreed Treaty on Genetic Resources for Food and Agriculture.

The material transfer data available on the SINGER database confirm the existence of substantial fluctuations in numbers of accessions transferred over years. Differences between crops are also marked (Table 2). Sample/accessions transfer levels are lower for cereal crops than for grain legumes. The high transfer figure for banana and plantain germplasm (57.7) should also be noted although, rather surprisingly, transfers for potatoes and cassava were rather low (7.2 and 6.0 samples/100 accessions/year, data not shown).

An important aspect emerging from the SINGER data is that one can distinguish between samples distributed and

Table 1. Distribution of samples from Chinese germplasm collections, 1984–1998 (data from Gao Weidong *et al.*, 2000)

Crop	Number of accessions	Samples distributed	Samples distributed/100 accessions/year
Rice	73,323	57,750	5.25
Wheat	42,811	53,010	8.25
Maize	15,967	4910	2.05
Soybean	31,206	18,100	3.87
Cotton	6724	15,000	44.61
Citrus	1041	19,911	127.51
Peking cabbage	1665	3505	14.03
Cucumber	1474	2980	13.48
Tea	2527	7885	20.80
Mulberry	1757	1692	6.42

Table 2. Average transfers per year from CGIAR genebanks to non-CGIAR recipients for the 5 years 1996–2000 for barley, sorghum, rice, lentil, bean, groundnut, chickpea and *Musa*

	Accessions	Accessions transferred	Samples transferred	Accessions/100 accessions	Samples/100 accessions
Barley (ICARDA)	24,230	1671	2109	6.90	8.70
Sorghum (ICRISAT)	36,586	2152	2516	5.88	6.88
Rice (IRRI)	84,961	1784	2078	2.10	2.45
Lentil (ICARDA)	10,004	1482	1686	14.81	16.85
Bean (CIAT)	32,513	1457	2321	4.48	7.14
Groundnut (ICRISAT)	15,342	1810	2062	11.80	13.44
Chickpea (ICRISAT)	17,250	2200	2497	12.75	14.48
<i>Musa</i> (INIBAP)	947	n.a.	546	n.a.	57.7

Musa data refer only to the years 1993–1995.
n.a., not available.

accessions distributed. As noted above, one accession may be distributed many times so that distribution of large numbers of samples may not reflect use of large numbers of accessions. Generally, while some accessions are distributed many times, most accessions are distributed only once or twice but there are marked differences between crops. For sorghum from the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) it was found that 55% of the accessions were distributed only once or twice and less than 10% were distributed more than 10 times over the period of 25 years analysed. Wild *Cicer* spp. provided a marked contrast with over 60% of the accessions distributed five to eight times. The relation between numbers of samples and numbers of accessions distributed can also be examined in respect of the proportion of accessions distributed at least once over any given period. In the case of the CGIAR genebanks there again appear to be marked differences between crops. Some 35% of IRRI rice accessions were distributed at least once even though the number of samples distributed over the same period is substantial. In contrast, most of the accessions of the ICRISAT groundnut, chickpea and sorghum collections had been distributed at least once to non-CGIAR users (94%, 87% and 84%, respectively).

Some studies have been done on the recipients of samples from CGIAR genebanks. They have been classified by type into National Agricultural Research Services (NARS), universities, private and 'other'. The most important recipients have been NARS and universities but the percentage varies depending on crops. The amount of material distributed to the private sector has been very small, with the greatest amount being for maize (*ca* 5%). Very low levels of distribution to private users were also characteristic of the national genebanks included in the FAO (1998) analysis.

The levels of use reported here appear similar with those of other developed country genebanks. Th. van Hintum (personal communication) reported that use

levels of material stored by Centrum Voor Genetische Bronnen Nederland (CGN), Netherlands ranged from 5.7% and 6.3% per annum for barley and oats over the period 1993–2002 to 60.0% and 70.1% for *Allium* and lettuce. Again one sees a much higher use level for vegetable collections than for cereal ones. In this case use of *Brassica* spp. and potatoes was intermediate (35.4% and 38.4%, respectively).

Use of germplasm from genebanks

The other approach to documenting use of *ex situ* conserved materials has been by conducting and analysing surveys of users. These surveys range in approach from analytical and quantitative, focusing on the different uses made of different amounts of material, to more subjective, concerned with users' opinions of different aspects of supply and use of material.

The most detailed and quantitative survey was carried out by Gao Weidong *et al.* (2000) as a component of their study of distribution and use, as noted above. Surveys were distributed to over 650 users in China and overseas and case studies were carried out at 13 institutions with plant breeding responsibilities for the crops studied. Overall, Gao Weidong *et al.* (2000) reported that 21% of the distributed material was used in screening and evaluation, 9% was used in research, 8.1% in breeding and 2% in some other form of use (including direct use). They reported that some 60% of the material was 'not used' but this figure includes material received by the different institutions for conservation purposes rather than simply unused (Gao Weidong, personal communication). Unfortunately, the authors do not provide any breakdown of different use patterns for different crops although they do distinguish between different types of germplasm. Thus, cultivars and advanced lines are more likely to be used in breeding than land races and wild relatives, while genetic stocks are most likely to be used in research. A problem

with these data (as with other data on use) is that users do not necessarily make a clear distinction between numbers of samples received and numbers of accessions received. If they request repeat samples of the same accession they may still regard this as a single acquisition.

Through their survey of 13 breeding centres, Gao Weidong *et al.* (2000) provided important data on the ways in which material might be expected to flow through use programmes and contribute to cultivar production. For rice they found that 9% of the germplasm received by the centre was used in breeding and that over the 15-year period of the survey 376 cultivars were produced which contained about 300 genebank accessions in their pedigree. Breeding is a long-term business and genebank accessions distributed in the last 5 years of the survey period would be unlikely to find their way into released cultivars within the survey period. There were substantial differences between crops both in respect of the proportion of distributed material that ended up in the breeding centres and in the subsequent fate of the material. Very large percentages of soybean accessions were reported as used for breeding (34% of material received or 4633 accessions) whilst very few accessions found their way into finished cultivars (36 accessions in 292 cultivars or 0.27% of accessions received). In contrast 163 (or 10%) of the 1662 cotton accessions received by the breeding centre were used in the production of 192 cultivars.

The earliest surveys of users were carried out by Peeters and Williams (1984) and Peeters and Galwey (1988). These were limited in scope, concerned primarily with ascertaining use by plant breeders of genebank collections, and with attempting to determine the needs of plant breeders. Other users were more or less completely ignored and there was little information about the amount of material used by plant breeders and how it was used. Peeters and Galwey (1988) reported that genebanks were principally used to obtain new sources of disease resistance, but that even for this purpose, most of the barley breeders and nearly half of the *Allium* breeders used breeder's lines or advanced cultivars. They noted that 75% of barley workers and 25% of *Allium* workers surveyed used genebanks regularly.

The surveys by Peeters and Williams (1984) and Peeters and Galwey (1988) were conducted over 15 years ago and more recent surveys suggest a more positive approach to the use of genetic resources by breeders and by other users. McFerson *et al.* (1996) contacted a range of crucifer germplasm users and reported that those surveyed expected use of genebank material to increase steadily but were generally somewhat dissatisfied with accessibility and quality of documentation. The users surveyed by van Soest (2001) were generally positive in their appreciation of the CGN (Dutch

genebank) and expected to continue needing material from it. They considered the genebank was especially important for providing wild relatives and land races which they did not expect to maintain in their own collection. Disease resistance was by the far the most important trait of interest and they strongly emphasized the need for information, preferably online through the internet.

ten Kate and Laird (1999) reviewed use of plant genetic resources from the perspective of access to the resources and benefits from their use. Use is seen very largely from a private plant breeder's perspective and the information presented is essentially anecdotal. The view presented is that breeders avoided using primitive material (land races or wild relatives) if at all possible and preferred adapted improved materials. While this is certainly true, it does not really help determine the amount of use made of genebanks, the way in which that use occurs and how it might be improved.

Widrechner *et al.* (in preparation) surveyed use of *Amaranthus*, *Brassica*, *Cucumis* and *Helianthus* materials distributed by the North Central Regional Plant Introduction Station, Ames, Iowa, USA. The response rate to the questionnaire was low (12%) but suggested quite substantial use was being made of the distributed materials. Some 89% of respondents characterized and evaluated the germplasm received and 138 research projects were described resulting in over 100 publications of which over 80% were in peer-reviewed journals. One-third of the respondents reported that the germplasm had been or was being used in breeding programmes and 21 reported direct use of germplasm received.

Substantial use of US germplasm collections was also reported by Smale and Day-Rubenstein (2002) in their survey of non-USA recipients of germplasm of 10 crops maintained in US genebanks (barley, beans, cotton, maize, potato, rice, sorghum, squash, soybean and wheat). Almost half the recipients came from developing countries, with most belonging to non-commercial organizations (76.6%). The numbers of recipients from commercial companies was very small (4.5%). As with other surveys, disease resistance was identified as the most important trait sought. Most significantly, within the brief 5-year period covered by the respondents 11% of the germplasm accessions distributed had already been incorporated into a breeding programme, 43% were still being evaluated and 28% of the samples were reported by recipients to be useful in other ways. Smale and Day-Rubenstein (2002) reported that applying these percentages to the total numbers of samples distributed during the surveyed period would suggest that as many as 18,000 accessions distributed by US genebanks may have been used in breeding programmes and in other ways and some 27,000 may still be under evaluation.

All these surveys have sought information from users on their perceptions of problems of obtaining material from genebanks and bottlenecks to use. Of course there are always reports of poor-quality material with low germination and of misidentification. However, overall, the findings from the surveys have been remarkably consistent with regard to the most commonly reported concerns. The availability of information about accessions is a first priority identified by almost all surveys. This is especially the case for information on biotic and abiotic stress response, i.e. resistance to pests and diseases and to environmental stress such as salinity, cold or drought. This is interesting because it used to be argued that evaluation was the concern of the user since the traits concerned were subject to environmental factors and should not be undertaken by genebanks. However, it appears that today's users would like to have evaluation data on accessions preferably in a form that can be queried interactively. This is possible for SINGER-linked collections, the US collections through GRIN and a number of other country genebank collections such as Australia's.

Related to information is a concern with resource availability. Most surveys show that both users and genebank managers are aware that funding is insufficient to enable the information needs of users to be fully met. Recent developments with respect to the establishment of a Global Conservation Trust give some hope that improvements may be possible in this area, although funds will first be needed to secure the resources and ensure their proper maintenance and reproduction.

The existence of policy instruments that support germplasm exchange is also a commonly mentioned concern of users. This has a number of different aspects which range from a concern with phytosanitary regulations that may limit exchange of material to much wider concerns regarding access and benefit sharing that have been central to the development of the recently agreed International Treaty on Genetic Resources for Food and Agriculture (<http://www.fao.org/ag/cgrfa/itpgr.htm>).

Towards an improved understanding of use of plant genetic resources

Although the data are limited, it is possible to reach some conclusions about use of plant genetic resources and the information needed to provide an adequate understanding of use. The most recent surveys suggest that there is substantial use of genetic resources and this can take many different forms. It is clear that information on patterns and extent of use is valuable and allows genebank managers to meet users' needs better and to improve their own management procedures

(regeneration, multiplication, characterization, provision of information, etc.). It can also increase the awareness of the user community of the availability and value of conserved germplasm. Finally, it provides the detailed evidence needed to convince funding agencies of the desirability of investing in conservation.

However, there is a real need for information from a larger number of different genebanks, from a wider range of situations with respect to size, geographical location and objectives than has been surveyed so far. Work done to date provides valuable guidance on how these studies should be conducted and the type of information that should be collected.

A major conclusion from the work surveyed in this paper is that the extent and patterns of plant genetic resource use are much more complex than can be adequately represented by any single simple measure. Information is needed on numbers of samples distributed compared with the total numbers of accessions, the relationship of sample numbers distributed to numbers of accessions distributed, and the proportion of accessions in a collection distributed over any period. Marshall (1989) also emphasized the importance of using the number of independent requests as a measure of use and Th. van Hintum (personal communication) has also noted the importance of this information. These different indicators all need to be estimated over a number of years to take account of the considerable year-to-year fluctuations that may occur. Distribution activities that reflect management concerns (e.g. for safety duplication) need to be separated from distribution for different uses.

The estimates of use reported above should be regarded as preliminary and indicative, requiring further checking and analysis. As far as we can ascertain, characterization and evaluation work carried out by genebanks was not included in any of the use data analysed although evaluation carried out by separate organizations would have been included. Thus all the data underestimate use for evaluation and, probably, research carried out by genebanks. Further, as noted above, the SINGER data presented here do not include transfers of materials within the CGIAR system although these are quite likely to constitute well over half of the transfers occurring (Jane Toll, personal communication; Iwanaga, 1993).

Very substantial differences were reported between crops with respect both to the numbers of samples distributed and to the ratio of these to the size of their respective collections. For cereal crops, while sample numbers were large, the numbers of samples distributed per 100 accessions per year was often below 10 and nearly always below 20. The data suggested that sample/100 accession numbers were higher for grain legumes and vegetables and highest for fruit. Since the collections are often very much smaller the numbers of

samples distributed were also smaller. This might suggest more intensive use of vegetable and fruit collections than of cereal crops but, more importantly, it shows the dangers of comparing genebank distribution data without taking account of the crop content of the collections.

It is clearly important to distinguish between sample use and accession use and to relate information on these to the different factors that will influence patterns of sample and accession distribution. Most accessions will probably be used on a fairly regular basis in small collections that can be handled by those involved in evaluation or research. In contrast, most accessions will be very rarely distributed from large collections with well-developed core collections. The importance of accepting that long time frames are needed in any analysis of use must be emphasized. After preliminary characterization and evaluation, some accessions in large collections may only be used once or twice every 50 years without being regarded as under-used.

There are now very large numbers of genebank users or requestors of material. Widrlechner *et al.* (in preparation) reported 713 different recipients of NRCPIIS germplasm over 10 years for *Amaranthus*, *Brassica*, *Cucumis* and *Helianthus* and Smale and Day-Rubenstein (2002) reported 1063 different non-US recipients for the 10 crops they surveyed over a 5-year period and noted that US *ex situ* conserved germplasm was sent to over 237 countries, territories or departments over the 10 years 1990–1999. Unfortunately the number of requests was not reported. One suspects, although data on this are not available, that lack of knowledge of the existence of collections is no longer the important factor it was in the survey on *Allium* germplasm use reported by Peeters and Galwey (1988).

The survey data suggest that evaluation, research and plant breeding are often linked and that material may often flow through a use system. At the same time it can also enter or leave the system at any point, depending on the objectives of the different workers, and the results obtained with the material. Where there are close links between genebank, researchers and breeding programmes, the flows can be fairly easily followed but, where this is not the case, it is much more difficult to determine the process of use. Again, although the evidence is very limited, there seem to be significant differences between crops. In some crops relatively larger numbers of accessions enter crossing programmes than in others, as seen in China (see above). Similarly, while it has been reported that 11% of material in CIMMYT (International Maize and Wheat Improvement Center) wheat crossing blocks is land race or unimproved (CIMMYT, 1997), the use of such materials in maize is universally acknowledged to be exceptional (Tallury and Goodman, 2001). Gaining an adequate

understanding of flows of germplasm (and genes) through evaluation, research and breeding programmes and developing adequate ways of assessing these from the point of view of improving use of genetic resources will require specific case studies on selected crops.

The continuing low use of genebank collections by commercial companies has been noted in all surveys where this has been recorded. Interestingly, Smale and Rubenstein (2002) found that commercial companies receiving samples from the USA were twice as likely to come from developing countries as from developed countries. While there are very real reasons why private plant breeders make little use of genebank collections (ten Kate and Laird, 1999), there is a need for better information on the situations in which they do want genetic resources and the capacity of genebanks to meet their needs. For example, are there marked differences between crops and between types of material with respect to private breeders' needs and is there particular information that can usefully be provided to support their improved use of genebanks?

Surveys of users' opinions on use have provided a consistent picture of their concerns and needs. Most importantly, there is a continuing demand for improved access to information and to increased amounts of information with respect to passport, characterization and evaluation data. Marshall (1989) expressed reservations about whether lack of evaluation data was a major constraint to germplasm use but the surveys suggest that the more data genebanks can provide the better and that evaluation data on biotic and abiotic stress response are particularly welcome. The fact that increasing numbers of genebanks provide this information online tends to confirm this view. Monitoring the use of online information may become an important aspect of monitoring use of *ex situ* collections.

Surveys have also shown that users perceive the policy framework as an important determinant of their access to plant genetic resources. However, there is little data on the way in which policy factors affect use. None the less the issues of ownership and of realization of benefits have frequently been cited as inhibitors of germplasm distribution both within countries (Gao Weidong *et al.*, 2000) and in exchange of materials between countries. Further studies are clearly needed on policy aspects to identify the constraints and determine their significance.

We have suggested that a first essential step in improving use of plant genetic resources conserved *ex situ* is an adequate basis of knowledge of current patterns of use and of associated problems and bottlenecks. There is clearly substantial use of *ex situ* germplasm and it is producing significant benefits. However, the detailed information required to identify key problems and develop improved practices does not yet exist. As noted above, there is a need for a

number of studies, in different parts of the world, to provide information on different crops in different situations. These would be particularly useful if they followed broadly the same procedures and adopted common approaches. One of the major problems with analysing the data to date has been that the different procedures used in different studies make comparisons between results extremely difficult. Comparative information will be particularly important if we want to help genebanks by identifying procedures that can help to improve distribution and use of *ex situ* conserved resources.

Improving the use of plant genetic resources

While genebanks can do much to support improved use of genetic resources, and to ensure that information and materials are available to users, the actual amounts used depend, to a significant extent, on the numbers of users (e.g. see Engels, 2002) and the ways in which they approach and make use of the diversity present in crop gene pools. The amount of research, pre-breeding (or germplasm enhancement) and breeding work on specific crops, and the ways in which diversity is used in this work, will have a very substantial effect on use of *ex situ* resources, i.e. the level of demand is an important determinant of the amount of use.

The numbers of plant breeders and of research scientists in relevant disciplines in many developing countries remains very low. Funds committed to plant breeding in particular, and agricultural research in general, have remained almost static since the 1980s in many parts of the world. In some areas, such as Africa, available funds have actually decreased (e.g. see Tripp and Byrlee, 2000). An area of particular concern to a number of commentators (e.g. Knight, 2003) has been the decline in germplasm enhancement work or pre-breeding. As shown above, there often seems to be a more or less continuous process from evaluation to use of material in plant breeding programmes and a break in this process (e.g. lack of adequate research to determine heritability of a character or pre-breeding to transfer a trait to a more appropriate background), will have a marked negative effect on use of *ex situ* conserved germplasm.

In contrast to the largely unchanged (or even reduced) size of the traditional user community, especially in developing countries, there are signs that a new group of users is beginning to make significant use of *ex situ* collections. Molecular genetic methods have now advanced to the stage where they can cope adequately with significant numbers of accessions from genebanks. The potential of using molecular methods to detect new useful variation in genebank collections has been widely recognized (Karp, 2002; Kresovich *et al.*, 2002).

Dudnik *et al.* (2001) noted that a significant number of research articles using genetic resources involved using molecular methods.

The size of the user community is not the only important factor that determines demand for genetic resources in *ex situ* collections. Current plant breeding and agricultural production practices tend to limit the possibility of increasing the amount of diversity used. Very few plant breeding programmes have procedures that make full use of available diversity. This need to broaden the base of plant breeding programmes has been recognized in a number of crops and some approaches that increase the use of diverse germplasm have been developed and adopted (see, e.g., Simmonds, 1993; Kannenberg and Falk, 1995; Pollack and Salhuana, 2001). At the same time the narrow genetic base that exists for a number of crops, especially in the USA, has been recognized (Bowman *et al.*, 1996; Gizlice *et al.*, 1996) as has the importance of reducing the potential vulnerability that results in such situations (National Research Council, 1972).

While it is important to ensure that the diversity present in *ex situ* collections is well used, this will not always lead to an increase in numbers of accessions distributed or involved in some specific area of use. Firstly, as genebank managers improve the information they provide to users these users will be better able to identify the most appropriate accessions for their purpose. This might lead to an increased number of requests, but a decreased number of samples distributed. Secondly, the quality and value of the specific aspect of use is as important as the numbers of accessions used. It would be a mistake to rely wholly on quantitative data to determine whether genebanks are being well used, what matters is a full identification of all the benefits.

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