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## GENETIC RESOURCES — MUSEUM OR UTILITY

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### ABSTRACT

This paper presents a revision of the 'genetic resources dogma', the strategies for their conservation and utilisation which, formulated some 20 years ago had remained unchallenged and almost unchanged. As a result of these strategies, collections have become very large, too large for plant breeders to use, hence the establishment of smaller, but genetically representative 'core collections' as proposed. They could be made available anywhere, including countries like Australia and New Zealand. With adequate representation in collections of the endangered varieties of traditional agriculture — the principal genetic resources for the last 100 years — about to be achieved, future collecting can be more selective, concentrating on specific characteristics required by plant breeders, such as resistance to diseases and pests. Main emphasis should be shifted to collecting the wild relative of crops. Evaluation should become much more specific and responsive to current needs of plant breeders.

### KEYWORDS

Germplasm collections, conservation, core collections, landraces, mission oriented collecting, generalist collecting.

### AN EMBARRASSING SUCCESS?

In the last 20 years the preservation of plant genetic resources has become an issue of worldwide interest and concern which has led to extensive international and national activity. Hundreds of collecting expeditions have added over 100,000 accessions to germplasm collections, many of them newly established in the centres of genetic diversity in Asia, Africa and Latin America; and an international guardian, the International Board for Plant Genetic Resources, now presides over the growing network of genetic resources centres and their treasures.

The holdings of accessions in germplasm collections are now truly impressive, if not outright overwhelming. According to Holden (1984) there are now, in 600 collections, 1.2 million accessions in cereals, a quarter of a million of vegetables, almost 200,000 of grain legumes, and so forth. True, there is a good deal of duplication within, and much more between collections, some of it deliberate

and useful. I brought with me to New Zealand in the twenties a large part of the wheat collection then being assembled by the Cambridge Plant Breeding Institute, and large parts of this went on to other institutions. All the same, there is a massive representation in collections of all the major and many minor crops. Expert committees on crops or groups of crops agree that the massive collecting of the last 10 years could and should ease off to relatively few genuinely needed targets — and I suggest that some of these are 'stamp collecting' rather than a quest for essential and at present unrepresented alleles.

This achievement exceeds the most optimistic expectations 20 years ago. As I said initially, it is also overwhelming. For it is a fact that the use to which many, or most of these collections have been put, has been limited, in the developed countries and even more so in the developing countries from which most of the more recent accessions are derived. In some developing countries an obvious reason is the small number of plant breeders. The more abundant breeders in the United States use germplasm collections more widely, but the main targets — resistance to diseases, insect pests, or nematodes — are fairly restricted (Duvick, 1984). It may be the very size of collections which restricts their use by plant breeders to characteristics which are easily evaluated.

There is no question of the potential usefulness of germplasm collections. Clearly, the achievement of these two decades must be upheld and representative collections preserved for the foreseeable future. But I believe they should be made more accessible to breeders of today. There is a need for a new look at collections, their structure and size, and the interface they present to the plant breeder.

### THE GENETIC RESOURCES DOGMA

What has been called the genetic resources movement started some 20 years ago with the realisation that the genetic reservoirs in Vavilov's geographical centres of genetic diversity were fast disappearing as a consequence of rapid agricultural developments. There had been earlier warnings, but no sense of acute danger. Of course, germplasm collections had started a century earlier with Philippe de Vilmorin's collection of wheat that he assembled at Versailles. And all the 'classical' breeders at the turn of the century — Nilsson-Ehle in Sweden, Saunders in Canada, Farrer in Australia — had their

collections, acquired from various sources, in Farrer's case through copious correspondence with colleagues around the world. But they did not aim to capture anything like the range of genetic diversity that was to be revealed by Vavilov's discoveries.

Indeed it was Vavilov who started systematic, representative collecting. He set the pattern for what I have called 'generalist' collecting. His and his colleagues' main concern was to assemble and study genetic diversity and its evolution. Useful traits such as disease resistances were appreciated, but they were not the main objective. The latter, however, was the case in many of the extensive collections made by the US Plant Introduction Service in the first half of this century. Such 'mission-oriented' collecting has a specific target. It may be resistance to a biotype of a pathogen, or pasture strains suitable for particular environments. The target is of immediate concern. In contrast, 'generalist' collecting attempts to assemble a representation of the existing allelic distribution for current and future use in research, or in breeding for objectives which at present may not even be recognised.

The latter, in a nutshell, was the philosophy which motivated the genetic resources movement. Systematic generalist collecting would assemble representative samples of the genetic diversity of economic plants, to be preserved for current and future work. This philosophy emerged at an international conference convened by FAO and IBP (The International Biological Programme) at FAO in Rome in 1967 (Frankel and Bennett, 1970). It was widely accepted and became the basis of international activities, since 1975 stimulated and co-ordinated by the International Board for Plant Genetic Resources (IBPGR). Its ramifications formed what one might call the 'genetic resources dogma'. Five principles were conceived in 1967:

- Highest priority to preservation of the threatened landraces.
- Generalist instead of mission-oriented collecting.
- Representativeness through large collection size.
- Evaluation essential for use.
- Preservation in storage, instead of frequent regeneration or preservation in cultivation or in mass-reservoirs.

#### **Landraces as the highest priority**

There was general agreement on foremost attention being given to the collecting and preservation of landraces of major crops. They had been the traditional sources of the modern cultivars and were still widely drawn upon by breeders; and throughout the Vavilovian centres they were now extensively threatened by the rapid spread of greatly improved modern cultivars. The FAO Panel of Experts on Plant Exploration and Introduction, which from 1967 to 1974 played a major part in formulating strategies, listed priority targets for collecting which later were refined and extended by IBPGR after its establishment in 1975.

In the main, landraces were and are of interest because they have been found to contain a great diversity of genetic elements of agronomic value which plant breeders attempt

to incorporate in the genotypes of locally adapted cultivars. These elements can be as small as a single gene, or they can comprise a sizeable part of the genotype. Indeed, in the country of origin a local landrace may be the receptor and an introduction the donor.

The importance of wild relatives of crop species as potential genetic resources has repeatedly been emphasised (e.g., Harlan, 1976, 1984). Various authors have suggested that representative collections of wild relatives are needed for research and for assessment of their potential contributions to breeding, encouragement coming from outstanding successes such as the use of wild relatives in tomato breeding. It had, however, been part of the dogma that wild species receive priority only in case of acute danger of extinction, hence collecting activities have been on a restricted scale.

Now that representative collections of landraces are more or less accomplished and that interest in and concern for wild relatives has grown among biologists and plant breeders, the time has come for a redistribution of priorities. This is recognised by the IBPGR (IBPGR Secretariat, 1984, p.9) in its strategy for the coming years. Moreover, there is increasing evidence that wild relatives can be rich reservoirs of genetic diversity, richer indeed than the derived domesticates. Landraces of barley collected in several districts of Iran, and a representative collection of wild barley, *Hordeum spontaneum*, from Israel, were compared for variation at 19 common allozymic loci. Mean number of alleles per locus and degree of polymorphism were substantially higher in the wild barley than in the landraces, and lowest in the synthetic barley crosses 21 and 34, illustrating the progressive loss of variation with advancing selection under domestication (Brown and Munday, 1982). On a broader scale, Harlan (1984) emphasizes the 'ecological amplitude' of wild relatives, often exceeding that of the domesticated species by a wide margin. He also provides a long list of hybrids between wild species and their cultivated relatives, showing heterosis or transgressive segregation for yield, with hybrid sugar canes and octoploid strawberries as outstanding examples. Finally, Ladizinsky (1985) points to the founder effect in the domestication of many species due to isolation by mutation or allopolyploidy, resulting in a narrow genetic base compared with the wild ancestral source.

So far we have considered genetic resources — domesticated as well as wild — as sources of genetic elements for recombination with adapted cultivars. One may call this 'gene introduction', as distinct from 'plant introduction' which transfers and adopts individuals or populations, cultivars or ecotypes. In the New Zealand or Australian context, the introduction of pasture species and ecotypes in the first half of the century is a familiar example. Introductions of this kind are for direct use, subject to natural or deliberate selection or recombination. Pasture species are, of course, wild species, as are forest or medicinal species where introduction and improvement in the main is also on a population basis. However, similar circumstances occur in domesticates where plant breeding is

absent or is not likely to go beyond selection of populations or genotypes. This is the case in many minor crops, and, for most crops, in some developing countries — at least for the time being. In such circumstances collections should be restricted to representative and relevant cultivars or ecotypes, rather than cater for a plethora of diversity which is unlikely to be used.

#### **Mission-oriented v. generalist collecting**

As mentioned previously, a good deal of the collecting done about the middle of the century was directed to capture specific targets of interest to breeders at the time. The dogma was critical of such collecting which it sought to replace by an all-embracing policy of generalist collecting. It advocated the abandonment of mission-orientated collecting, at least until the immediate emergency in the most threatened areas had been met. With the advent of IBPGR a comprehensive and well-funded strategy of generalist collecting became a reality, and a substantial proportion of the allelic diversity within crop species can now be expected to be preserved in germplasm collections.

This does not mean that every allele that may be required is located in some germplasm collection. Clearly it is not possible to collect in every site which may harbour a crop species, let alone its wild relatives. Representation expresses a probability but by no means a certainty. Hence gaps are bound to occur for any but common alleles, and if a source is known the need could be satisfied by mission-oriented collecting. Indeed, it would now be justified for mission-oriented collecting to become the prominent strategy, with generalist collecting restricted to filling-in gaps.

#### **Is large beautiful?**

As remarked above, collections are now very large. They also are generally available, through agreement between national or international authorities and IBPGR. Yet they are very little used. This applies widely in both developing and developed countries. For example, the 5-year plan of the IBPGR Regional Committee for S.E. Asia for 1985-89 (IBPGR, 1984), referring to the substantial collections now available in the region, states that 'very little of these collected materials has been utilised in the breeding programmes.' No doubt the small number of plant breeders in the regions is part of the reason. But even in the United States the majority of breeders of the principal crops resort to their own small working collections for breeding materials (Duvick, 1984). The exceptions are some of the large International Agricultural Research Institutes.

Clearly the reasons for the limited use of germplasm collections apply widely and appear to be intrinsic in the genetic resources system as it has developed in the last decade. In the first instance, the limitations appear as management problems: excessive size, inadequacies of evaluation, lack of breeder participation. Basically limitations arise from an inadequate perception of the genetic contributions to be derived from germplasm

collections. In the absence of such perspectives, safety was sought in numbers. To paraphrase a famous maxim by the late Dr Schumacher, 'large is beautiful' became the dogma of germplasm conservation. No doubt this was justified by the sense of urgency in the face of the imminent world-wide threat to the traditional sources of genetic diversity, the landraces. I have come to recognise, however, that Schumacher's actual phrase, 'small is beautiful', may be the key to the wider use of collections. For the plant breeder, the accessibility and usefulness of a collection is likely to be in inverse proportion to its size, provided the loss of genetic information is within tolerable limits (cf. Frankel and Soule, 1981, pages 243-244, 249-251).

In earlier sections we have come to the conclusion that germplasm collections have become museums, too large to use. They need to be reduced in size to make them operational. The problem is how to achieve representativeness within greatly reduced numbers. In the context of genetic resources, genetic representativeness is assumed to follow from ecogeographic representativeness, though every other source of information should be used to safeguard genetic distinctiveness and to reduce redundancy. We have proposed a 'core collection' which would be as representative as can be contrived on the basis of available information (Frankel and Brown, 1984). First, there are the passport data used in the IBPGR system of characterisation which, hopefully, contain biogeographical information (place of origin or breeding site) and parentage of breeders' cultivars. Such information provides the basis for defining groups of ecologically and genetically related accessions. Then there are biosystematic data, developmental data, records of distinctive 'observable characters' (see below), and genetic markers such as isozymes. All these can be used to form groups of phenotypically similar accessions using multivariate clustering techniques. These groups can be sampled to form a core collection. Accessions not included in the core collection are retained as a 'reserve collection' which can be resorted to for rare alleles, or to follow up leads from the core collection. The transformation is essentially a computer operation which does not involve physical change.

So far the core collection is merely a concept, although at least two attempts to establish one are now under way. The main advantage is to make a representation of a crop's germplasm available to all. I well remember the informative and educative value of the wheat collection here at Lincoln, quite apart from its practical uses. New testing and breeding methods have opened new channels of use which make accessibility of germplasm even more desirable. Indeed, core collections would make world collections accessible to breeders anywhere, and certainly in Australia and New Zealand.

#### **Evaluation — for what, and by whom? The breeder's responsibility.**

It is one of the tenets of the genetic resources dogma that without evaluation there can be no utilisation. This is undoubtedly true, but there were few clear ideas about what

should be evaluated, apart from overly comprehensive, and hence unrealistic, lists of descriptors, or whose responsibility evaluation should be.

Let us first consider 'evaluation for what'. In a paper called, 'The theory of plant breeding for yield' written here at Lincoln 40 years ago (Frankel, 1947) I divided the characters of concern to plant breeders into two categories:

- 'Observable' or strongly expressed characters — can be readily identified in single plants or their progenies, although this may require special conditions such as the presence of a pathogen, or a specific — usually extreme — environment, but not a multiplicity of diverse environments. They are simply, or if polygenic, strongly inherited and can be readily selected for in hybrid generations.
- Non-observable, variable or complex characters — are subject to environmental variation. They are largely responsible for differences in yield or adaptation. Inheritance is polygenic. Evaluation of accessions may require replicated tests in multiple sites. However, with the exception of plant introductions, such tests are irrelevant since accessions are used as donors in crosses with other genotypes.

In my view this distinction is both real and important and, if understood, should help to end the prevailing confusion about evaluation.

Evaluation carried out on germplasm collections — as distinct from breeders' working collections — is generally confined to observable characters. An appropriate example is the collection of the International Rice Research Institute (IRRI) because of the excellence of the collection and the comprehensive nature of its evaluation (Chang, 1980; table reproduced in Frankel and Brown, 1984). From the list of characters evaluated it is evident that they fall within the definition of observable characters, though many of them require specific environments or specific tests for identification — tests in specific, not multiple environments. Evaluation for observable characters may be done by the curator, with the participation of specialists — entomologists, pathologists, physiologists — which is the case at IRRI and other International Institutes. However, in many instances it needs to be checked by the breeder, e.g., for interaction with local biotypes.

Evaluation of germplasm collections must be breeder oriented. Targets should either be known to be of interest to breeders, or directly nominated by them. To assert that evaluation is essential for utilisation makes sense only if utilisation is assured after evaluation.

Finally to the evaluation of non-observable (or variable) characters, with yield as the paradigm. Multi-environment tests have been proposed to assess the potential of accessions. However, in the evaluation of alien germplasm accessions it is not their own yield performance but their genetic interaction with locally adapted cultivars that is the objective of the test, and this can only be ascertained in tests for combining ability with them.

Clearly such tests could not be contemplated on collections numbering tens of thousands, but the formation

of core collections should bring them into the realm of feasibility: many large breeding establishments make hundreds, or thousands of crosses each year. The new hybridising agents make it possible to test large numbers of accessions for combining ability with a locally adapted genotype. Being breeding material, in distinction from germplasm accessions, the  $F_1$ 's should be tested in multi-environments.

Systematic testing of largely untested germplasm combinations might open up unforeseen possibilities of genetic innovation. Such an attempt might be seen as a responsibility of large international or national breeding institutions. But it seems appropriate that large private concerns which increasingly are emerging in the industrialised countries play an active part in evaluating and introducing new sources of germplasm rather than regarding the whole of R and D as the responsibility of public institutions.

Whatever the objective or scope of the operation, evaluation for non-observable characters is meaningful only in the breeder's own environment, and under his supervision. The sometimes suggested multi-environment tests are an expensive, yet ineffective evasion of the breeder's responsibility for evaluation.

### Conservation

The only precept of the dogma which has stood the test of time — and of critical thinking — is conservation. Indeed, it is as necessary as ever. Conservation is being extended by bringing formerly recalcitrant seeds into the fold of conventional ones, and by developing cryopreservation as a major conservation technology. Seed conservation along the lines first specified by the FAO Panel of Experts has been generally accepted and is now practised — with help from IBPGR — in developing countries as well as in developed ones and in the International Institutes of Agricultural Research. The seeds of the earth are now reasonably safe and a public resource.

### SUMMARY AND CONCLUSIONS

After 20 years of genetic resources movement and 10 years of international activity guided by IBPGR, the objectives formulated at the beginning of the era are within reach. A fair representation of the landraces of most of the major and of many minor crops is reasonably secure, for the use of all, now and in the foreseeable future. Collecting targets can now be more specific in response to plant breeders' needs which cannot be satisfied from existing collections; and we now know better where to collect.

We no longer need to concentrate on threatened landraces as we did in the past decades, at the exclusion of wild relatives from first priorities. There now is a widespread and growing interest in using them as gene resources, and some of them are now threatened in some habitats. There is good reason for developing collecting strategies for wild relatives, designed to build up representative collections with a minimum of genetic

redundancy (Brown and Marshall, 1986).

Similar principles could now be applied to existing collections for the purpose of making them more manageable, not only in maintenance, but, more importantly, in evaluation and utilisation. A representative core collection could achieve this end, while the larger reserve collection would remain as a standby. Only experience can show whether this can increase and widen the use being made by plant breeders.

Evaluation strategy must advance from generalities to breeder-oriented specific objectives. So far — and understandably — such objectives have been, and are observable characters. These will no doubt continue in first place. But non-observable characters, with yield as the paradigm, must not be excluded. The core collection would make this possible. But evaluation would need to be interactive — i.e., in genetic interaction with adapted genotypes. This can only be done by the breeder in his own environment. Innovative breeding makes demands on resources which may be beyond the traditional small private breeder, but should not be beyond those of the large companies which are coming to the fore. Indeed they have a responsibility to share R and D with public institutions. But the latter must remain in the field to maintain the public interest in continuing scientific and technological advance.

## REFERENCES

Brown, A.H.D., Marshall, D.R. 1986. Wild species as resources for plant breeding. Proceedings of the DSIR Plant Breeding Symposium 1986. *Agronomy Society of N.Z. Special Publication 6*: 9-15.

Brown, A.H.D., Munday, J. 1982. Population-genetic structure and optimal sampling of landraces of barley from Iran. *Genetica 58*: 85-96.

Chang, T.T. 1980. The rice genetic resources program of IRRRI and its impact on rice improvement. *In: Rice improvement in China and other Asian countries*. pp. 85-105. IRRRI, Los Banos.

Duvick, D.N. 1984. Genetic diversity in major farm crops on the farm and in reserve. *Economic Botany 38*: 161-178.

Frankel, O.H. 1947. The theory of plant breeding for yield. *Heredity 1*: 109-120.

Frankel, O.H., Bennett, E. 1970. Genetic resources in plants — their exploration and conservation. IBP Handbook No. 11. Blackwell Scientific Publications, Oxford & Edinburgh.

Frankel, O.H., Brown, A.H.D. 1984. Plant genetic resources today: a critical appraisal. *In: Genetics: new frontiers. Proceedings XV International Congress Genetics 4*: 3-13.

Frankel, O.H., Soullé, M.E. 1981. Conservation and evolution. Cambridge University Press, Cambridge.

Harlan, J.R. 1976. Genetic resources in wild relatives of crops. *Crop Science 16*: 329-333.

Harlan, J.R. 1984. Evaluation of wild relatives of crop plants. *In: Crop genetic resources: conservation and*

evaluation. J.W. Holden and J.T. Williams (eds). Allen & Unwin, London. pp. 212-222.

Holden, J.H.W. 1984. The second ten years. *In: Crop genetic resources: conservation and evaluation*. J.W. Holden and J.T. Williams (eds). Allen & Unwin, London. pp. 277-285.

IBPGR. 1984. IBPGR Regional Committee for Southeast Asia, Five-year plan for action 1985-89. IBPGR, Rome.

IBPGR Secretariat. 1984. The IBPGR in its second decade. An updated strategy and planning report. IBPGR, Rome.

Ladizinsky, G. 1985. Founder effect in crop-plant evolution. *Economic Botany 39*: 191-199.

## SYMPOSIUM DISCUSSION

Dr M.B. Forde, Grasslands Division, DSIR

Most of your address has been based on crop genetic resources. Pasture plant genetic resource collections are very far behind — should we be taking note of the lessons learnt in crops?

Frankel

No, certainly not on the same scale. I think we over did it on crops, and also breeding of the kind that you get in crops is unlikely to be widespread in pasture plant breeding.

Dr Forde

In sorting collections into core and reserves, I presume you still intend to maintain all the lines in the reserve collection?

Frankel

Yes, although some core collections may be so successful that the reserve collection will not be called upon perhaps for a decade and it may be felt that it is not needed, I hope the reserve collections will be maintained. The maintenance of most seeds is very inexpensive because they have a very long shelf life.

Dr R.I. Brawn, Seed Consultant

What do you see as the future of collecting in third world countries that are concerned about the stealing of their resources.

Frankel

The stealing of resources is not a real threat — a few heads taken from a crop of barley are not depriving anybody — the owner of the crop, the country it is growing in or the science in that country — of anything whatsoever. If it is brought into an international collection it will in fact be safe — for the country of origin, as for anywhere in the world. In this way we have saved an enormous amount of material, and indeed material comes back to the developing country itself. For example, the dwarfing genes of wheat and rice which were discovered by the Japanese, not quite a developing country even at that time, would never have been discovered wherever they came from, in these cases I suppose from China. Many of the genes that have been used in different countries have been

discovered in the developed countries and not for many many years, perhaps never, would have been discovered in the countries of origin.

Incorrect claims are made of stealing of genetic resources. For example in Pat Mooney's first book *Seeds of the Earth*, he describes an Australian plant collector taking *Medicago* seeds from Libya without paying for them because he collected them himself from the soil. Then he took them home, changed them a little and sold them back to Libya. What in fact happened was an Australian collecting mission collected in Libya as in other parts of the Mediterranean, and brought back hundreds of annual *Medicagos*, a few of them made commercial use and seed was sold to Libya as it was sold in Australia or anywhere else.

I think it is time that scientists stood up to such claims.

Dr W. Bushuk, University of Manitoba

In view of the likely probability that we will soon be able to construct or synthesise genes for specific characters, do you feel that the needs for collections still remain the same or will they be modified in the future?

Frankel

There are two answers to this. Firstly, we are still a long way from manufacturing genes for any purpose and for many characters there are numerous genes that are required. Secondly, there are gene assemblies in our collections, not only individual genes, and the plant breeder looks for gene assemblies. We shall never be able to manufacture anything of the kind that nature has manufactured by way of gene assemblies. So, I believe collections, at least for the foreseeable century, are unlikely to be wholly out of date.