

Core Collections of Plant Genetic Resources

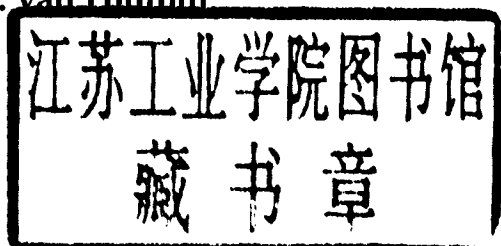
Editors: T. Hodgkin, A.H.D. Brown,
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Edited by

**T. Hodgkin, A.H.D. Brown, Th.J.L. van Hintum
and E.A.V. Morales**



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Preface

Work on conserving crop plant genetic resources has always been concerned as much with the effective use of the resources as with conserving variation *per se*. Core collections can make an important contribution to both objectives and, over the past decade, have become an increasingly important part of discussions on conserving and using crop germplasm more effectively. The IBPGR/CGN/CENARGEN workshop on 'Core Collections: Improving the Management and Use of Plant Germplasm Collections', held in Brasília in August 1992, was convened in response to this upsurge of interest in core collections among plant germplasm experts in order to bring together in a single volume a wide range of relevant information on the subject. CGN had been at the centre of the action, described in this volume, to develop a barley core collection and IBPGR (renamed IPGRI in 1994) had received many requests for advice on the use of a core collection and for information on how to construct one. CENARGEN, one of the world's largest and most active national genetic resources institutions, was among the organisations giving serious consideration to doing so.

In the late 1980s, IBPGR had worked on the development of a position paper on core collections, based on literature then available. That effort became bogged down in contentious academic views on sampling theory and was not pursued. By 1992 there was a much greater sense of urgency about the matter because many genetic resources institutions were looking to the core collection as a means of addressing some urgent management problems. The aim of the workshop and of this publication, therefore, was not merely to refine the concept but to examine how it has been applied in order to develop some practical solutions to the problems facing gene bank managers and genetic resources users in the 1990s.

The problems for which core collections might offer solutions are felt to be essentially of two kinds, both having their origin in the way in which genetic resources work has developed over the past 20 years. In the early 1970s the loss of traditional cultivars and landraces in the wake of new agricultural developments seemed to be the most urgent problem and a massive collecting effort was made to address it. In the first place, more genebanks were established — many more than could have been foreseen at that time. The volume of the collections that have been assembled worldwide has far outgrown the management resources and regimes of these facilities, collectively. Second, the use that has been made of these collections to bring about economically significant improvements in yield and profit has been patchy and often not up to the expectations of governments. Generally, this has been because gene bank managers have been unable to cope with the major task of evaluating their material to enable crop breeders to select from it the samples most likely to meet their needs.

As originally described by O.H. Frankel in his article on 'Genetic perspectives of germplasm conservation' (in Arber, W. et al. *Genetic Manipulation: Impact on Man and Society*, published in 1984

by Cambridge University Press, UK), a core collection is a limited set of accessions of a crop species and its wild relatives which would represent, with a minimum of repetitiveness, the genetic diversity of a crop species and its wild relatives. This subset of the whole collection would provide potential users with a large amount of the available genetic variation of the crop gene pool in a workable number of accessions. It would therefore be useful to plant breeders seeking new characters which require screening techniques not possible with a large collection. Because each of the accessions in a core collection is, to some extent, representative of a number of accessions (from a particular area of the world or with some shared characters), the core can also be used as a point of entry to the active or base collections of a crop. Detailed research can be carried out on a core to obtain an effective picture of the characteristics of the gene pool as a whole.

The core collection concept has aroused considerable worldwide interest and debate within the plant genetic resources community. It has been welcomed as a way of making an existing collection more accessible through designating a small group of accessions that would be the focus of evaluation and use and would provide an entry point to the larger collection which it aims to represent. However, concerns remain that the available knowledge of genetic diversity is still not sufficient, in any crop, to enable a meaningful core to be selected and that many of the useful characters occur at such a low frequency that they would almost always be omitted from a small core collection, no matter how it was selected. A more general concern that has been expressed is that the development of a core collection will lead to a neglect of the rest of the collection and a reduction in the resources available to work on non-core accessions.

In 1989 IBPGR carried out a worldwide survey of institutions and researchers known to be involved in developing core collections. Over 20 projects were identified involving grain legume, vegetable and fruit crops, and descriptions of established core collections of okra, wild *Glycine* species and winter wheat already existed. Since that time there has been increasing interest in core collections and further projects have been initiated. The analysis of genetic diversity in collections, to assist in their management and use, has also increased.

The IBPGR survey clearly showed how important the core collection approach was becoming to the management and use of plant genetic resources. However, it also revealed a number of problems in effectively developing this approach. After considering the nature and variety of the work in progress, the potential importance of core collections in developing countries, and the problems of taking the concept further, the co-sponsors identified the pressing need for a publication to provide a theoretical and practical basis for the further development of cores to improve genebank management and promote the use of germplasm collections.

The workshop in Brasília provided a timely opportunity to engage in healthy scientific debate focused on the issues involved in developing core collections and the contributions such collections might make to current germplasm management problems. A long period of preparation went into the event. CENARGEN kindly offered to make available its excellent facilities in Brasília and a programme committee representing the three sponsoring organisations selected speakers and topics to approach the subject from various perspectives so as to throw light on such questions as: Can a core collection be a useful tool for streamlining the management of a large genetic resources collection? If so, how should such a collection be constructed and how can it be made most effective as a management tool? Can a core collection help to facilitate effective access to a large collection by users and thus help to

channel germplasm more efficiently from conservation into breeding programmes, biotechnology programmes, etc? If the potential is there for a core collection to be used in this way, how can it be realised in practice?

It was no surprise that final, definitive answers to these questions did not emerge from the week of deliberations in Brasília. However, the presence of experts working on different facets of these questions, and in a variety of crops, had the very positive outcome of bringing together the numerous strands of relevant knowledge, stimulating debate and establishing collaboration. The publication of the contributions, revised in the light of workshop discussions, should help to refine the theory and practice of core collections in particular, and to develop more effective ways of conserving and using plant genetic resources in general.

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Part 1

INTRODUCTION

1.1

The core collection at the crossroads

A.H.D. BROWN

Abstract

National gene banks are now entering an era of increased activity and responsibility, particularly for their own indigenous crop germplasm. Their programmes need to cover all phases of germplasm activities, and yet have to operate with limited resources. The core collection offers a way to meet these challenges. A core collection consists of a limited set of accessions derived from an existing collection, chosen to represent the genetic spectrum in that collection. The concept has met criticism in four areas: that the rest of the collection is vulnerable to decay or disposal; that the bias towards representing diversity ignores usefulness; that the system is too inflexible; and that variation within accessions is ignored. Most of these concerns appear to arise from misuse or misunderstanding of the core approach.

Gene banks handling clonal crops, or species with recalcitrant seeds, can gain much from using core collections. Field gene banks are expensive to run and prone to loss. The core approach can guide the choice of accessions for growing in the field and those for developing and using *in vitro* methods. The principles of stratified, representative sampling in the core concept also apply to the choice of populations for conservation *in situ*. The need for choice arises from the cost of such strategies in crop species and the limit on areas for the preservation of wild species. A better use of limited resources will enable specific scientific goals (such as the discovery of new resistances) to be achieved. Large numbers of new deposits could swamp national gene banks. Some selection is unavoidable to prevent the loss of significant components of their collections, and core collections could assist in dealing with excess numbers. Further, a core will render a collection more workable for the user, and thus ensure support for its conservation in the longer term.

Those of us charged with the responsibility of conserving plant genetic resources have challenging work ahead. Recent events that have shaped our current situation include the almost universal adoption of the Food and Agriculture Organisation (FAO) Undertaking on Plant Genetic Resources and the launching of the International Plant Genetic Resources Institute (IPGRI). These developments have brought new enthusiasm for, and emphasis upon, national programmes of plant genetic resources conservation. We are challenged to do a better job assembling, managing, conserving and using collections, particularly of our indigenous genetic resources.

Yet at the same time these tasks must be achieved with limited resources. In addition, it is important to address all phases of gene bank activities — from collection through to actual use of the genetic variation in plant improvement programmes. A hindrance to fulfilling all these functions is the unrestrained growth in the number of accessions in collections and the amorphous nature that collections can take on.

Recognising that the sheer size of a germplasm collection could deter its use, Frankel (1984) proposed that it could be pruned to a 'core collection'. The core collection would represent 'with minimum repetitiveness, the genetic diversity of a crop species and its relatives'. The remaining accessions would not necessarily be discarded but would be managed as a 'reserve collection'.

Since this proposal, we have examined the rationale, purposes and general principles of core collections (Frankel and Brown, 1984; Brown, 1989a, b). As to the size of a core collection, sampling theory of selective neutral alleles in finite populations indicated that about 10% drawn randomly from the whole collection was relatively efficient in retaining its allelic variation (about 70% retained). However, this could be improved by stratifying the collection into groups of related accessions and selecting 10% from each group. A number of core collections have now been formed and others are described in this volume. In addition, there has been much debate as to the reasons for core collections and ways to form them. In this chapter, I will begin by reviewing many of the issues, and then outline the steps and questions involved in selecting cores, with a special focus on clonal crops.

WHAT IS A CORE COLLECTION?

Like many timely and appropriately named ideas, that of the core collection has already begun to diverge. Let us start with the original concept put forward by Frankel and Brown (1984) and Brown (1989a, b):

A core collection consists of a limited set of accessions¹ derived from an existing germplasm collection, chosen to represent the genetic spectrum in the whole collection. The core should include as much as possible of its genetic diversity. The remaining accessions in the collection are called the reserve collection².

The entries in the core are chosen primarily to be representative. They are ecologically or genetically distinct from one another. Within the primary constraint of covering the genetic spectrum and ecological range, the aim should then be to maximise the genetic diversity. This implies that the core should not contain duplicates and should minimise similarity between its entries. For example, the sampling would include single-spaced points along an ecological gradient (a spectrum) rather than be restricted to a few repeats from both extremes (maximum diversity).

-
- 1 The term 'accession' is used in this chapter to refer to a sample maintained in the whole collection. The term 'entry' is used to refer to any accession or subline from it that is selected for inclusion in the core.
 - 2 The workshop on which this volume is based resolved that the term 'reserve collection' should not be formally recognised by the International Board for Plant Genetic Resources (IBPGR). However, the concept itself must be discussed in this chapter, and the term is used solely in that context.

While it might be convenient to speak in the singular of a core for a whole group of related species, such as the core for perennial *Glycine* species (Brown et al., 1987), in practice core selection for each species is made separately. Indeed, the sampling procedure and intensity are likely to differ between the crop species, its progenitor or close wild relatives and its distant relatives.

At least two modifications to the core concept have been proposed. One is to alter the term itself to 'core subsets' in order to 'underscore the fact that these are not separate collections, but a set of designated accessions within an existing collection' (National Research Council, 1991). The term 'core set' would be simpler, as the prefix 'sub-' is redundant. This approach may be appropriate for collections that are under no pressure to be reduced in size and for which no physical separation of the core from the rest of the collection is planned. However, separation of the core and some reduction of the total size may be needed in collections with burgeoning numbers, and for these collections the original term is appropriate. More importantly, it has precedence.

A second modification proposes the use of the term 'core' for sets of accessions that a curator has chosen as examples in the collection for a specific purpose, such as a core set for tolerance of acid soils, and another for rust resistance (Mackay, *Chapter 4.4, this volume*). However, this use of the term 'core' is confusing and lacks legitimacy because it has been used previously to denote a genetically representative set (Frankel and Brown, 1984; Brown, 1989a). Why not just incorporate the specific purpose for which a set has been chosen into its name (for example, an 'acid-soil tolerant set' or a 'rust-resistant set')?

A new development of the core concept has arisen from cutting the linkage of a core to a specific, existing germplasm collection and applying the concept to a crop species as a whole. Thus the core collection for that crop would consist of a limited number of entries chosen to represent the genetic diversity of the species and its wild relatives for breeding and research. It would be a synthetic core, assembled from the various cooperating germplasm collections or from fresh sampling of wild or crop populations. The most ambitious project of this type so far is the Barley Core Collection project initiated by the European Cooperative Programme for the Conservation and Exchange of Crop Genetic Resources (Knüpffer, *Chapter 4.1*).

I wish to stress the differences between the synthetic core collection and a core collection attached to a specific gene bank. The first and most important difference is that the synthetic core is of more assistance to germplasm use than to gene bank management. It forms a set of entries in addition to those held in a national collection that will be managed as a new and distinct unit. In contrast, a core collection is taken from an existing collection — it does not have to be gathered from several sources. Second, the synthetic core relies on an international committee of experts on that crop to agree on its composition. In contrast, a curator can implement the original concept directly by nominating its entries from the current holdings.

These and other uses of the term 'core collection' are likely to continue. However, the rest of this chapter focuses on the original conception. From the definition of 'core collection' we now turn to the 'why' and the 'how' in assembling and using core collections.

THE FUNCTIONS OF A CORE COLLECTION

Core collections have many roles to play in the management and use of genetic resources. This is because most activities in gene bank management require the curator to make choices or to set priorities among accessions because of limited resources. It is usually not logical or efficient to start at accession

number 1 and work sequentially through all accessions in the collection. The germplasm operations for which a core collection offers distinct advantages are:

- *Addition of new accessions:* The core collection provides a reference set for deciding whether new samples arriving at a gene bank are worth adding to the collection, or even to the core itself. Does the new sample resemble any current core entry? If so, are there enough of this type in the whole collection already? If not, should the sample be a new core entry? The core may help in identifying gaps in the collection.
- *Conservation:* The core contains material of highest priority for conservation. It should have first call on the monitoring of viability by routine seed testing. Curators faced with the task of regenerating and multiplying a large and neglected collection could attend to the core first. Duplicates held at other gene banks for safety should include the core entries. The representative nature of the core makes it suitable for developing new methods of conservation (such as ultra-dry seeds, *in vitro* or cryogenic storage).
- *Characterisation:* The core is the suitable material for developing an adequate list of descriptors. A sufficient number of characters and states should be used to distinguish between its entries.
- *Evaluation:* It is for this task that the core collection has most to offer (Frankel and Brown, 1984). The core enables a logical and efficient two-step procedure to be carried out in sampling the whole collection. Its entries can be the first to be evaluated for expensive or complex traits. It provides a set of materials covering the range of variation in the whole collection for developing new methods of evaluation that would be sound for the whole collection. Further, by focusing evaluation on a restricted set of accessions, the core assists the development of a multivariate database to study the interrelationships between characters and between kinds of data (passport, characterisation and evaluation characters).
- *Germplasm enhancement:* The breeding of desirable characters from alien genetic backgrounds into locally adapted stocks is a lengthy and expensive process. The core forms a reduced set of representative accessions for testing general combining ability with local germplasm in the search for yield enhancement (Frankel and Brown, 1984; Abel and Pollak, 1991; Spagnoletti Zeuli and Qualset, Chapter 5.1).
- *Germplasm distribution:* Designation of a core can help to accelerate the response to requests because core samples can be multiplied and packaged in advance, ready for dispatch. More importantly, it provides an opportunity to distribute representative germplasm on a reduced scale.

The general feature of most of these benefits is that the judicious reduction of the number of accessions to be handled in one operation saves resources. These resources are available for a more complete range of activities to be conducted in greater depth and thoroughness because the entries are representative of the collection (Morales, Chapter 5.3).

CRITICISMS OF THE CORE COLLECTION CONCEPT

If the core can serve curators in so many ways, why has it not been implemented more widely? Numerous objections to the core concept and stratification of germplasm collections have already

appeared or can be foreseen. These objections can be grouped under four headings: vulnerability of the reserve collection; bias towards diversity rather than usefulness; inflexibility of core entries; and lack of validity in sampling variation.

Vulnerability of the reserve collection

Several criticisms revolve around concern for the reserve collection (Marshall, 1989; National Research Council, 1991). This concern is that a core collection might threaten the size of the total collection as administrators seek economies and dispose of the reserve as excess to needs. The approach may lead to combining materials or simply neglecting germplasm that is not part of the core. In general, the division of a collection into core and reserve may threaten the 'integrity' of a carefully assembled collection.

These criticisms assume that the core collection is an entity on its own. We have always stressed that a fundamental role of the core is that it is a guide to the whole collection. Another role is that it fosters better conservation of germplasm (Brown, 1989a). No reduction of collection size is involved. Indeed, the appraisal of all the accessions in hand needed for setting up a core collection can produce evidence for increasing the total collection size through targeted collecting in particular areas. Most collections in gene banks do not have unassailable 'integrity' because their contents reflect uneven or historic sampling effects (Frankel and Soulé, 1981).

The need to reduce the size of some collections because of a shortage of resources will arise whether or not a core has been set up. Indeed, as national programmes become increasingly responsible for local genetic resources, they are in danger of being swamped by large numbers of new deposits. The practical bottlenecks that limit international acquisition (such as costly periodic exploration, shipment and quarantine) are not in place to check such growth. To use Holden's (1984) phrase, national programmes will have to 'deal with the deluge' of local material. Some selection seems inescapable, particularly for clonal crops (*see below*).

Bias towards representing diversity rather than usefulness

The fact that entries in the core are chosen to represent the genetic spectrum of the collection has led some authors to claim that the core forms a suboptimal sample. They feel it ignores the relative ease of making the crosses needed to use a character in breeding and that it is directed more at the needs of the molecular biologist and geneticist than at those of the breeder.

These claims can be disputed. Suppose a new resistance is sought from a gene bank and, from a search of the core, this resistance is found in a wild relative. This does not necessarily mean the breeder would stop screening and start crossing. The decision may well be to examine more material from the rest of the collection of the cultivated species to seek other resistances. The breeder may prefer a weaker resistance than that first found, if it is in a better genetic background. The benefit that the first search of the core has provided in this case is a resistance phenotype as a yardstick, and possibly a useful resource if no other options appear. Consider the case of the resistances to soybean leaf rust found in wild perennial *Glycine* species which have so far been extremely difficult to transfer to soybean. Such resistances have proved very useful because they uncovered cryptic pathotype variation in the pathogen to which the generally susceptible crop species is blind (Burdon and Speer, 1984).

It is true that in many instances the core is unlikely to contain the single most 'useful' source of a character for the breeder. However, as the first sampling of a two-step process, it provides a logical