The Development of 'Core Collections' for *Beta* Germplasm

B. V. Ford-Lloyd and M. J. Lawrence

School of Biological Sciences,
University of Birmingham,
Edgbaston, Birmingham, UK

ABSTRACT

Proposals are made for the development of core collections of *Beta* germplasm. These could be represented by no more than 200 accessions for each major section of the genus. The basis for their development is discussed, and the advantages accruing from their development in terms of improved prospects for germplasm maintenance and complete evaluation within the World Beta Network are highlighted.

Additional Key Words: Beet, genetic resources, diversity, evaluation

A major issue in genetic resources conservation has been the size of collections in relation to their effective management and use. The large collections in genebanks may severely hinder appropriate genebank practices. The maintenance of such collections and the handling of requests for germplasm samples is time-consuming and expensive. While the entire world collection of *Beta* germplasm cannot be described as being large in comparison to, say, that of rice at the International Rice Research Institute where 80,000 accessions are held, nevertheless the 5000 or so accessions of *Beta* do present the World Beta Network with problems.

Seed rejuvenation is a major problem in many of the collections, seed stocks are often low (particularly for annual forms), and viability is often unmonitored (particularly for section Corollinae). It has so far proved impossible to attract major funding for large-scale coordinated evaluation programs to take place, so that, outside the United States, evaluation now proceeds through individual cooperation of breeders within the IIRB on an ad hoc basis.

THE DEVELOPMENT OF CORE COLLECTIONS

One answer to these problems is to develop core collections, as has already been done for barley, cassava and *Phaseolus* (Hodgkin, T., pers. comm.). In broad terms, the core collection was envisaged by Frankel (1984) as being a subgroup of accessions of any germplasm collection which would incorporate, with minimum redundancy, the genetic diversity of a crop species and its relatives and which, to all intents and purposes would form the 'active collection' for germplasm evaluation and distribution, with the remainder of the germplasm being kept as a 'reserve' collection.

How is the choice of core material to be made? Brown (1989a) has identified stratified sampling as being more efficient than purely random sampling. This involves dividing the collection into nonoverlapping groups, and then taking samples from each group. The ways in which the groups are established may vary depending upon the crop species, but could depend upon taxonomy, passport data, or ecogeographical information.

In terms of the size of the core collection, Brown (1989a) has argued that the core should consist of about 10% of the whole collection, up to a maximum of about 3000 accessions, for each species. He estimates that, at this level of sampling, the core will generally contain over 70% of the alleles present in the whole collection (Brown, 1989b).

SAMPLE SIZE FOR GENETIC RESOURCE COLLECTIONS

An alternative approach to this problem is provided by the recent work of Lawrence et al. (1994), who considered the size of sample required to capture at least one copy of each allele at each of a number of independently inherited loci at a given probability. Their calculations indicate that, provided the sample size chosen gives a very high probability of conserving the alleles of a single locus, this size is also sufficient to give a high probability of conserving at least one copy of each allele at k loci. Thus, if it is assumed that the genome of a species, whose individuals set 90% of their seed by self-pollination, contains 40,000 structural loci (Nei, 1987), and that 40% of these loci are polymorphic (Hamrick, 1989), a sample size of 172 gives a probability of 0.999999828 of conserving all of the alleles at the 16,000 polymorphic loci, even if the frequency of one allele at each locus is only 0.05. If the individuals of the species set more than 10% of their seed by cross-pollination or the frequency of the least frequent allele at some of the 16,000 polymorphic loci is greater than 0.05, the probability of conserving at least one copy of each allele at each locus is even higher than this. In practice, therefore, it should be relatively easy to conserve all or very nearly all of the alleles of a population in a random sample of 172 plants.

Lawrence et al. (1994) further argue that since the aim of genetic conservation is to conserve all of the genes of a target species, it follows that it is the species, rather than its constituent Mendelian populations, that should be regarded as the population from which samples are to be drawn; that is, a sample size of 172 taken from the species as a whole should be sufficient to give a very high probability of conservation. This suggests that a sample of size 200, rather than of the size 3000 suggested by Brown (1989b), should be sufficient to conserve all or very nearly all genetic diversity within a core collection, even if the individuals of the species of interest set most of their seed by cross-pollination.

CORE COLLECTIONS OF *BETA*

Are core collections of *Beta* warranted? Given the likelihood of discontinuity of variation between the sections of *Beta,* it would be necessary to develop cores for each of the major sections. A core of 200 accessions of section Beta would allow for adequate representation of both wild and cultivated forms. Accessions of sections Corollinae and Patellares are fewer than of section Beta and probably require fewer accessions in their core collections, say 100 each. It would probably be wise to select the core material on both geographical and taxonomic criteria.

What would be the benefits? Firstly it would provide a means by which a broadly representative sample of *Beta* germplasm could be adequately maintained and duplicated for safety purposes. Secondly it would provide material on which intensified evaluation could take place within a framework of international collaboration. This evaluation could include the use of the newer molecular techniques of RFLP and RAPD for the identification of diversity. Comparisons using more conventional measures could also be made. There are 137 evaluation descriptors in the 'Descriptors for Beta' (IBDGR/CGN,1991). Effective evaluation for these descriptors together with the development of molecular markers for diversity such as RFLP and RAPD cannot be carried out by one institute or laboratory alone. Neither can such a comprehensive study be spread across all the *Beta* germplasm currently in storage. Core collections would therefore provide the necessary focus for such work to commence.

LITERATURE CITED

Brown, A. H. D. 1989a. Core collections: a practical approach to genetic resources management. Genome 31: 818-824.

Brown, A. H. D. 1989b. The case for core collections. Pages 136-156. *In* A. H. D. Brown, O. H. Frankel, D. R. Marshall and J. T. Williams (eds). The Use of Plant Genetic Resources. Cambridge University Press, Cambridge.

Frankel, O. H. 1984. Genetic perspectives of germplasm conservation. Pages 161-170. *In* W. K. Arber, K. Llimensee, W. J. Peacock and P. Starlinger (eds). Genetic Manipulation: Impact on Man and Society. Cambridge University Press, Cambridge.

Hamrick, J. L. 1989. Isozymes and the analysis of genetic structure in plant populations. Pages 87-105. *In* D. E. Soltis and P. S. Soltis (eds). Isozymes in Plant Biology. Chapman and Hall, London.

IBPGR/CGN. 1991. Descriptors for Beta. International Board for Plant Genetic Resources, Rome/Centre for Genetic Resources, the Netherlands.

Lawrence, M. J., Marshall, D. F. and Davies, P. Sample size for genetic conservation. Euphytica (submitted).

Nei, M. 1987. Molecular Evolutionary Genetics. Columbia University Press, New York.