

## 5.6 Characterization and evaluation approaches

Characterizing accessions, an activity that is typically regarded as the responsibility of the genebank curator, involves determining the expression of highly heritable characters, ranging from morphological features to seed proteins and possibly including molecular markers. Such characters also enable easy and quick discrimination among phenotypes and allow simple grouping of the accessions, as well as a check on the trueness-to-type of homogeneous samples, frequently according to criteria used by breeders and other germplasm users. Genebanks should consider establishing close cooperation with plant breeders while characterizing accessions, not only during the field and laboratory activities but also earlier to decide on which descriptors to use. In addition to or instead of a molecular analysis, their scoring also allows establishment of systematic relationships among accessions and even crops, including their evolutionary relationships. This directly facilitates utilization of collections, allows detection of misidentifications and indicates possible errors made during other genebank operations (Bretting and Widrlechner, 1995). It also results in better insight in the composition of the collection and the coverage of genetic diversity. A proper characterization also makes an important contribution towards rationalizing management procedures, since it allows the curator to make well-informed decisions on where best to regenerate the material (e.g. the japonica and indica rice races findings of Rao and Jackson, 1996), to identify possible duplicates, to group germplasm accessions, etc.

Berthaud et al. (1997) proposed a modified version of the traditional three-step linear model of conservation, evaluation and use by promoting genetic enhancement and pre-breeding, relying on knowledge and activities of farmers as well as local breeders.

The environment invariably influences the expression of traits used in the (preliminary) evaluation of germplasm accessions. The most valued traits in crop improvement include yield, agronomic performance and stress resistances. It is obvious that an adequate evaluation of the collection represents an important prerequisite to effective use of the collection, as well as a major investment. The genebank manager should take every opportunity to get the

conserved material evaluated. The expression of important traits is increasingly being researched using molecular markers (Bretting and Widrlechner, 1995). Since this activity is not regarded by all genebanks as a typical genebank responsibility, but rather as a task for plant breeders and other users, close cooperation among all participants is essential to ensure useful application of results.

It is not always obvious which molecular technique to use in addressing a specific germplasm management question. IPGRI published a technical bulletin to provide curators with a guide for choosing the best and most cost-effective technique (Karp et al., 1997). CGN offers an on-line update on this issue ([www.cgn.wageningen-ur.nl/pgr/](http://www.cgn.wageningen-ur.nl/pgr/)).

In order to facilitate standardization of information obtained during characterization and evaluation, IPGRI coordinates the publication of Descriptor Lists in close cooperation with crop experts and genebank curators. These are consensus lists of descriptors for individual species and written in the universally understood language for PGR data, thereby contributing to a more efficient exchange of information and use of germplasm. To date 85 lists have been published (IPGRI et al., 2001).