Morphological characterization of a minicore subset in different botanical types of Groundnut (*Arachis hypogaea* L.)

C. MADHURA, KENCHANAGOUDAR, P.V., BASAMMA AND V. SUJAY

SUMMARY

Plant genetic resources are the most valuable and essential basic raw material to meet the current and future needs of crop improvement programmes. Although there is an increase in the number of germplasm accessions in gene banks, there is no corresponding increase in their use, indicating that the collections were not being used to their full potential. Not only is the limited use of germplasm a worrisome issue, but also the large-scale deployment of a very few genotypes complicates the whole situation even more. Extensive use of fewer and closely related parents in crop improvement is contrary to the purpose of collecting a large number of germplasm accessions, and could result in vulnerability of cultivars to pests and diseases. Developing core collection (about 10% of the entire collection) has been suggested as a method of enhancing the use of the germplasm. However, even this number could be large and unmanageable if the entire accession is several thousands; A methodology to reduce the size further and select a mini-core that is about 1% of the entire collection, yet represents full diversity of the species has been developed. The minicore subset consisting of 182 accessions of which 42 of *hypogaea* bunch, 39 of *hypogaea* runner, 63 of Spanish bunch and 38 of *fastigiata* along with nine cultivars, were evaluated for 10 morphological traits to characterize and to estimate phenotypic diversity using principal component analysis (PCA). PCA showed that all the ten characters except growth habit and pod constriction contributed for multivariate. Standard clustering procedure like euclidian distance is used to separate groups of similar accessions among 195 genotypes for qualitative characters. The hierarchical cluster analysis revealed eight distinct clusters at the distance value of 10 and it revealed that to maintain the diversity due consideration could be given to botanical types as well as clusters in selecting the diverse superior germplasm accessions for use as parents in crop improvement programmes Thus their morphological characters help in differentiating accessions of the same botanical type and their use in breeding will broaden the genetic base of the cultivars.

Plant genetic resources are the most valuable, essential, and basic raw materials that allows identification of promising genes in the germplasm collection that can be incorporated in the breeding programmes to develop promising cultivars. The characterization of diversity in germplasm collection is important to plant breeders to utilize and to the gene bank curators to manage the collection efficiently and effectively for crop improvement programmes to meet the demands of increasing populations. Vavilov (1926) was the first geneticist to realize the essential need for a broader genetic base for crop improvement. He and his colleagues collected germplasm of crops and their wild relatives globally. In the wake of new agricultural development in the early 1970s, the loss of traditional cultivars and landraces seemed to be the most urgent problem, and massive germplasm collecting efforts were made to address it. As Frankel and Brown (1984) indicated, germplasm could be used, for a wider range of characters, if a smaller number of well characterized accessions were to be given priority for use in crop improvement research. To pursue the same idea, Frankel (1984) proposed manageable sampling of the collection, A core collection contains a subset of accessions from the entire collection that captures most of available diversity of species (Brown 1989a). However, even this number could be large and unmanageable if the entire accession is several thousands. A methodology to reduce the size further and select a

Correspondence to:
C. MADHURA, Department of Genetics and Plant Breeding, University of Agricultural Sciences, DHARWAD (KARNATAKA) INDIA

Authors' affiliations:
KENCHANAGOUDAR, P.V. BASAMMA AND V. SUJAY, Department of Genetics and Plant Breeding, University of Agricultural Sciences, DHARWAD (KARNATAKA) INDIA