Identifying Useful Germplasm for Crop Improvement Using Core, Mini Core and Molecular Marker Approaches

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Abstract

Plant genetic resources (PGR) are critical components of plant breeding efforts aimed towards increasing food security. The establishment of ex situ colletions has been the result of several decades of global efforts to conserve plant biodiversity. The need of large variability by plant breeders, concern about potential loss of the variability, and non-availability of low cost tools to identify similarities and dissimilarities among accessions have led genebanks to hold large germplasm collections. As a result about 6 million accessions are held in 1308 genebanks in the world. ICRISAT genebank contains more than 114 000 accessions of chickpea, peanut, pigeonpea, sorghum, pearl millet and six small millets. However, only a very small fraction of the vast diversity available has been used in the breeding programs due to the lack of information on traits of economic importance. Development of a representative core collection (10% of entire collection), has been suggested as a means to enhance utilization of PGR. We have developed core collections of our five mandate crops and finger millet. In crops where number of accessions is in several thousands, even a core collection would be unwieldy to handle. Therefore, we have proposed a strategy to select a mini core collection (1% of entire collection), representing the species diversity to enhance proper exploitation of PGR. Mini core collections consisting 211 accessions of chickpea (total 17 000) and 184 accessions of peanut (14 310) have been selected and are being used in assessing molecular diversity of collections at ICRISAT. We have identified diverse sources of early-maturity, high yield, tolerance to drought and low temperature at germination, oil and protein contents in peanut, and for early-maturity and large seed size in kabuli chickpea through evaluation of core/mini core collections. The molecular characterization of core and mini core collections and trait specific germplasm will result in identifying genetically diverse parents and efficient gene mining. Their use in breeding programs will result in enhancement of the trait and broaden the genetic base of cultivars.