


Genebank
Chickpea
Taxonomy
Germplasm Collections
Core Collections
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Reference Set
Random Core Selection
Genebank
Chickpea Mini Core

A core collection is a chosen subset of large germplasm collection that generally contains about 10% of the total accessions and represents the genetic variability of entire germplasm collection. The purpose of a core collection is to improve the use of genetic resources in crop improvement programs. In many crops the number of accessions contained in the genebank are several thousands, and a core subset consisting of 10% of total accessions would be an unwieldy proposition. In this article we have suggested a two-stage strategy to select a chickpea mini core subset consisting of only about 1% of the entire collection held in trust at ICRISAT's genebank (16,991 accessions). This mini core subset still represents the diversity of the entire core collection. The first stage involves developing a representative core subset (about 10%) from the entire collection using all the available information on origin, geographical distribution, and characterization and evaluation data of accessions. The second stage involves evaluation of the core subset for various morphological, agronomic, and quality traits, and selecting a further subset of about 10% accessions from the core subset. At both stages standard clustering procedure was used to separate groups of similar accessions. A mini core subset consisting 211 accessions [Click here for List of accessions](#) from 1,956 core subset accessions, using data on 22 morphological and agronomic traits, was selected. Newman-Keuls' test for means, Levene's test for variances, the chi-square test and Wilcoxon's rank-sum non-parametric test for frequency distribution analysis for different traits indicated that the variation available in the core collection has been preserved in the mini core subset. The most important phenotypic correlations which may be under the control of coadapted gene complexes, were also preserved in the mini core. This mini core subset, due to its drastically reduced size, will prove to be a point of entry to proper exploitation of chickpea genetic resources.