Core Collection of Chickpea as a Means to Enhance Utilization of Genetic Resources in Crop Improvement

Chickpea (*Cicer arietinum* L.) is a major food legume in many countries. It is cultivated mainly in Algeria, Ethiopia, Iran, India, Mexico, Morocco, Myanmar, Pakistan, Spain, Syria, Tanzania, Tunisia, and Turkey. In 1997 it was cultivated worldwide on 11.33 million ha, with 8.80 million t production. Of the total world production 91% is produced in Asia, and in Asia, India accounts for 74.8% production. The average world productivity of 0.78 t ha^{-1} is rather low.

The importance of increased use of genetic resources to enhance the genetic potential of the crop productivity and for alleviating the biotic and abiotic stresses in chickpea is very well recognized. However, there has been a limited use of genetic resources in enhancing yield potential. One of the main reasons for this situation is the sheer large number of accessions in the ex-situ collection. The chickpea germplasm collection at ICRISAT currently comprises 16 991 accessions, which contain large variation for different traits (Table 1). This available diversity has not been properly evaluated for use in the crop improvement. Proper evaluation of such a large germplasm is feasible only for the traits to be scored easily and do not show genotype by environment (G x E) interaction. However for applied plant breeding research, genotype evaluations often require replicated field experiments, and the traits of economic importance often display significant G x E interaction. Therefore, for meaningful data, the whole collection needs to be reduced to a manageable level. Considering this, Frankel (1984)

[Frankel, O.H. 1984. Genetic perspectives of germplasm conservation. p. 161-170. *In* W.K. Arber et al. (ed.) Genetic manipulation: impact on man and society. Cambridge Univ. Press. Cambridge, England.]

suggested the need for development of core collections. A core collection is a subset of a large germplasm collection that contains chosen accessions representing the genetic diversity of the entire gene-bank collection.

Mean and range of variation for some quantitative traits in the chickpea collection at ICRISAT.

Trait	Number of accessions	Mean	Minimum	Maximum
Days to 50% flowering	16 928	62.4	31.0	107.0
Days to maturity	16 928	115.9	84.0	169.0
Flowering duration	11 208	33.6	13.0	75.0
Plant height (cm)	16 840	37.5	14.0	96.3
Plant width (cm)	16 775	40.5	13.3	124.0
Apical primary branches	16 928	1.4	0.0	12.0
Basal primary branches	16 928	2.7	0.3	15.7
Basal secondary branches	16 928	3.1	0.0	13.7
Tertiary branches	16 928	4.6	0.0	28.2
Pods per plant	16 879	40.5	3.0	251.0
Seeds per pod	16 882	1.2	1.0	3.2
100-seed weight (g)	16 928	16.8	3.8	65.4
Protein content (%)	12 973	19.5	8.0	29.6
Seed yield (kg ha^{-1})	16 356	1216.3	70.0	5130.0

For developing the chickpea core collection of ICRISAT, we used 13 quantitative traits for which data was available on > 16 000 accessions. We stratified the entire chickpea collection by the country of origin. The accessions from the small and adjacent countries with similar agro-climatic conditions were grouped together. The traits used were days to 50% flowering, plant height (cm), plant width (cm), days to maturity, number of basal and apical primary branches, number of basal and apical secondary and tertiary branches, number of pods per plant, seeds per pod, seed yield (kg ha^{-1}), and 100-seed weight (g). As these traits were measured on different scales, they were standardized using the range of trait in each group to eliminate scale differences. The standardized data was used for clustering by Ward’s method using SAS program. From each cluster about 10% accessions were randomly selected for inclusion in the core subset. At least one accession was selected even from the clusters, which had less than 10 accessions. Sixty six accessions had no evaluation data, the six randomly selected acccessions were therefore excluded from the cluster analysis. They are included in cluster number '0'.

Using the above criteria, a core collection consisting of 1956 accessions was selected. The mean, median, and standard deviation for the 13 traits used in the selection of core subset were similar for both core and entire collections. For the 11 of 13 traits, 83.7 to 100% variation range of entire collection was represented in the core collection. For basal and apical primary branches the range variation included was 62.3% and 72.5%, respectively, indicating that the core subset was representative of entire collection. The Chi-square and Wilcoxon non-parametric rank-sum tests indicated the homogeneity of distribution between entire and core collections. In the core collection, the phenotypic associations observed in the entire collection were preserved. This clearly suggested that the co-adapted gene complexes controlling these traits were properly and adequately sampled.

This chickpea core collection will be a point of entry and provides working collection to chickpea scientists to tackle diseases, pests, and other problems. It can be extensively examined for economic traits to generate information on genetic variability in the chickpea and possible relationships among traits. Overall, it will result in enhanced use of genetic resources in crop improvement and also simplify management of the gene bank. The list of chickpea entries in the core collection with the country of origin, ICC number, and cluster number are available on diskette, free of charge from H. D. Upadhyaya, Genetic Resources and Enhancement Program, ICRISAT, Patancheru 502324, A.P., India (E-mail: H.Upadhyaya@CGIAR.ORG).

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