Allelic richness and diversity in global composite collection and reference sets in chickpea (Cicer arietinum L.)

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Abstract

Worldwide, chickpea is the fourth largest grain legume crop, predominantly grown in Asia. A composite collection of 3000 accessions profiled using 50 SSR markers, and also characterized for 24 morphological descriptors. The complete data set on 2915 accessions and 48 SSR markers was used to determine structure and diversity and for the formation of reference sets. A total of 1683 alleles were detected in the composite collection, of which 935 were rare and 748 common alleles. Gene diversity varied from 0.533 to 0.974. Group-specific unique alleles were 104 in Kabuli, 297 in desi, 69 in wild Cicer; 114 each in Mediterranean and West Asia, 117 in South Asia. Diversity analysis using DARwin-5.0 revealed Kabuli as a group genetically more diverse than other seed types. Genotypic and phenotypic distance matrices were used to identify reference sets consisting of 300 accessions. Genotyping-based reference sets captured 79% of the 1683 alleles. However, phenotyping-based reference set retained 66% alleles. Qualitative-descriptors-based reference set captured 71% alleles while quantitative-descriptors-based reference set retained 64% alleles. We imposed another condition in the DARwin program that retains 211 accessions of the chickpea mini core and then select additional 89 from the remaining accessions. When compared for allelic richness, genotyping-based reference sets again captured 78% alleles while phenotyping-based reference set could retain 69% alleles. Also, the qualitative-descriptors-based reference set retained 73% alleles compared to 69% of 1683 alleles in quantitative-descriptors-based reference set. The relative usefulness of reference sets in chickpea breeding and genomics need to be investigated.