

Composite Collection

Plant genetic resources (PGR) are the basic raw materials for future genetic progress and an insurance against unforeseen threats to agricultural production. An extensive characterization of PGR provides an opportunity to dissect structure, mine allelic variations, and identify diverse accessions for crop improvement. ICRISAT and ICARDA jointly developed a composite collection of 3000 accessions, which consists of 1956 accessions of the ICRISAT core collection, 709 accessions from ICARDA, 39 advanced lines/cultivars, 35 distinct morphological variants, 20 accessions from wild Cicer species (*C. reticulatum* and *C. echinospermum*), and 241 trait-specific (resistance to biotic and abiotic stresses, early maturity, multi-seeded pods, double podded, large-seed, high seed protein, nodulation and responsive to high input conditions) accessions. Biologically, it represents 80% land races, 11% advanced lines/cultivars, 1% wild species, and 8% accessions of unknown origin. This composite collection has been molecularly profiled using 50 SSRs in high throughput assay (ABI3700).

Genetic Structure of Composite Collection

The 48 SSR loci data on 2915 accessions were analyzed using PowerMarker V3.0 and DARwin 5.0 version. This composite collection showed rich allelic diversity (1683 alleles, 35 alleles per locus, 748 most common alleles and 935 rare alleles at 1%), group-specific unique alleles, and common alleles sharing between the species and geographical groups. Unique alleles are those detected in a group of accessions but absent in other groups. Group-specific unique alleles were 104 in Kabuli, 297 in desi, and 69 in wild Cicer; 114 each in Mediterranean and West Asia (WA), 117 in South and South East Asia (SSEA), and 10 in African region accessions. Desi and kabuli shared 436 alleles while wild Cicer with desi and kabuli, respectively, shared 17 and 16 alleles. The accessions from SSEA and WA shared 74 alleles while those from Mediterranean with WA and SSEA, respectively, 38 and 33 alleles. Desi's detected higher proportion of rare alleles (53%) than kabuli's (46%), while wild Cicer accessions were devoid of rare alleles.