

Composite Collection

As part of Generation Challenge Program, to create a public platform that will use molecular methods to unlock genetic diversity and put it to use in better crops for the world's poorest farmers, a global composite collection comprising 1000 accessions representing the 13,632 germplasm accessions that are conserved at ICRISAT genebank was developed (Table 3). The composite collection include elite germplasm, released cultivars, genetic stocks, accessions both resistant and susceptible to abiotic and biotic stresses, mini core developed at ICRISAT genebank and its comparator, representative accessions from each cluster of core collection, contributions from crop specialists working in different disciplines, wild species that are easily crossable with cultivated pigeonpea. Considering the heterogeneity of the accessions, 12 plants per accession were selected for DNA extraction following a high-throughput procedure, and the DNA was pooled to capture within accession variation (Upadhyaya et al. 2005).

Twenty SSR markers with highly significant correlations ($r^2 > 0.9$) were identified. Preliminary analysis detected 144 alleles, ranging from 5 (PGM109) to 24 (CCB8) with a mean of 12.0 alleles per locus Mean Polymorphic Information Content (PIC) value was 0.345 (ranging from 0.094 to 0.525). Phylogenetic tree constructed based on biological status revealed that both cultivated and wild accessions formed distinct clusters (Fig. 1). All the accessions belonging to seven wild *Cajanus* species grouped together in a separate cluster except few, which grouped with the cultivated accessions.

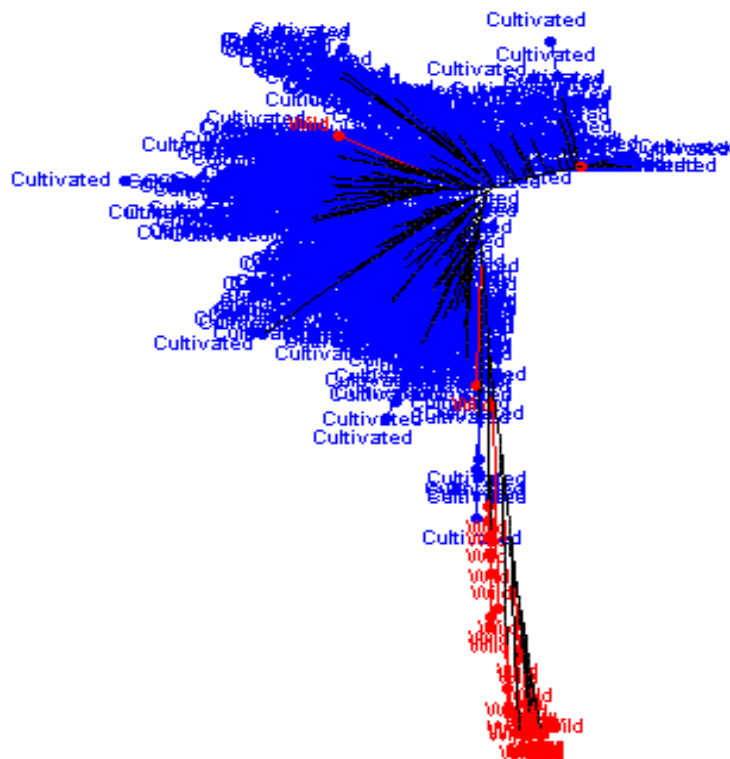


Figure. Tree diagram of 955 accessions with 12 SSR markers.

Blue: Cultivated, Red: Wild

Genetic Structure of Composite Collection

Analysis of 20 SSR markers data on 952 accessions detected 197 alleles, of which 115 were rare and 82 common alleles. Gene diversity varied from 0.002 to 0.726. Biologically, group-specific unique alleles were 60 in wild types and 64 in cultivated types. Among the cultivated accessions, 37 were in indeterminate (NDT) type, geographically, 32 in Asia 4 (Southern Indian provinces, Maldives, and Sri Lanka), 7 in Asia 6 (Indonesia, Philippines, Thailand), 5 in Asia 3 (Central Indian provinces), and four in Asia 1 (North western Indian provinces, Iran, and Pakistan). Only two alleles in Africa differentiated it from other regions. Wild and cultivated types shared 73, DT (Determinate) and NDT shared 10, DT and wild shared 4, and the NDT and wild shared 20 alleles. Asia 1 shared 4 alleles with Asia 3 and 3 alleles with Asia 4. Asia 4 shared 6 alleles with Asia 3 and 5 with Asia 6. Wild types as a group were genetically more diverse than cultivated types. NDT types were more diverse than the other two groups based on flowering pattern (DT and SDT: Semi-determinate).