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ABSTRACT BOOK

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Using genetic and genomic resources to broaden the genetic base of cultivated groundnut

Upadhyaya HD^{*}, Dwivedi SL, Varshney RK, Hoisington DA, Gowda CLL

International Crops Research Institute for the Semi-Arid Tropics (ICRISAT),
Patancheru PO 502 324, India

^{*}Address for correspondence: h.upadhyaya@cgiar.org

Groundnut is highly self-pollinated tetraploid crop with $2n = 40$ chromosomes and ~2800 Mb genome. ICRISAT genebank at Patancheru, India has the largest collection: 14,968 cultivated accessions from 92 countries and 451 wild relative accessions representing nine sections and 44 species. For enhancing the use of germplasm, core and mini core collections were developed that when evaluated identified several new sources of variation for agronomic traits and resistance to biotic and abiotic stresses. Further, a composite collection of 1000 accessions, which also included 184 mini core accessions, has been molecularly profiled using 21 SSRs and formed a reference set of 300 most diverse accessions (<http://www.generationcp.org>). Genetic populations are being developed for mapping of genes associated with beneficial traits. These are useful resources to analyze genetic relationships and identify marker trait associations using linkage disequilibrium and association mapping. Unlike past, several genomic resources are now available to research community: high throughput platforms including DArT technology, SSRs, BAC libraries, ESTs, and genetic linkage maps.

Narrow genetic base further constraint the researchers to cope with evolving pests and diseases pressures and variation in environmental stresses. Re-synthesis pathway that also generates additional diversity has proven useful to transfer genes from wild to cultivated species in some polyploids. Amphidiploids have been developed in groundnut using wild progenitor and other species. Our studies indicate that synthetic amphidiploids in addition to diseases and pest resistance can also be used to enhance agronomic traits such as earliness, 100-seed weight and pod yield.