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Developing Genomic Resources For Facilitating Molecular Breeding In Cultivated Groundnut (*Arachis hypogaea* L.)

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With an objective to develop large scale genomic resources in cultivated groundnut, efforts are being made at ICRISAT, in collaboration with its partners, to generate molecular markers like simple sequence repeats (SSRs) and Diversity Array Technology (DArT). For instance, ~250 novel SSR markers were developed either from genomic DNA libraries or mining gene sequences from *aeschynomenoid*/ *dalbergoid* and *genistoid* clades of the Leguminosae. Similarly a DArT array comprising of 5600 features has been developed. These markers together with others available in public domain or accessible through collaborators are being/have been used to detect polymorphism between parental genotypes of four mapping populations namely TAG 24 × ICGV 86031, TAG 24 × GPBD 4, ICGS 44 × ICGS 76 and ICGS 76 × CSMG 84-1. In general, 6-10% polymorphism has been observed with the SSR markers tested. Genotyping of polymorphic markers has facilitated development of genetic maps with moderate marker density (56-165 per cross) for respective mapping populations. Detailed QTL analysis for drought component traits and disease resistance, by using single marker analysis (SMA), composite interval mapping (CIM) and epistatic interaction analysis is underway. Nevertheless, one major QTL, contributing upto 54.4% phenotypic variation for rust resistance has been identified in TAG 24 × GPBD 4 population which has been validated using diverse germplasm and mapping populations. In summary, such efforts on development of genomic resources like SSRs, DArTs, genetic maps and identification of QTLs will be of great help for facilitating molecular breeding and improve crop productivity of cultivated groundnut.

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