

Genome-wide structural and functional landscapes of SNPs revealed from the WGRS data of 179 accessions of Arachis

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Abstract

Peanut being an important food, oilseed and fodder crop worldwide, its genetic improvement currently relies on genomics-assisted breeding (GAB). Since the level of marker polymorphism is limited in peanut, availability of a large number of DNA markers is the prerequisite for GAB. Therefore, we detected 4,309,724 single nucleotide polymorphisms (SNPs) from the whole genome re-sequencing (WGRS) data of 178 peanut accessions of Arachis along with the reference genome sequence of Tifrunner. SNPs were analyzed for the structural and functional features in order to conclude on their utility and employability in genetic and genomic studies. ISATGR278-18, a synthetic amphidiploid, showed the highest number of SNPs (2,505,266), while PI_628538 recorded the lowest number (19,058) of SNPs. A03 showed the highest number of SNPs, while the B08 recorded the lowest number of SNPs. The number of accessions required to record 50% of the total SNPs varied from 11 to 13 across the chromosomes. The rate of transitions was more than that of transversions. Among the various chromosomal contexts, intergenic and intronic regions carried more SNPs than the exonic regions. SNP impact analysis indicated 2,488 SNPs with high impact due to gain of stop codons, variations in splice acceptors and splice donors, and loss of start codons. Of the 4,309,723 SNPs, as high as 46,087 had the highest polymorphic information content (PIC) of 0.375. As an illustration of application, a drought and disease resistant accessions were compared with susceptible accessions to identify the SNPs with high impact substitutions. SNPs were also identified between the two sub-genomes (A and B). This SNP resource is being used for haplotype selection and allele mining for various genes and gene families. Overall, these structural and functional landscapes of the SNPs will be of immense importance for their utility in genetic and genomic studies including reverse genetics in peanut.

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Biography

Ramesh S. Bhat has contributed significantly for the Post-Graduate teaching and Research in the area of Molecular Biology and Biotechnology. The major focus of his research has been the development of transposable element-based marker system, mapping of foliar disease resistance, taxonomic and drought tolerance traits, marker validation [using heterogenous inbred families and, various recombinant inbred line and multi-parent advanced generation inter cross (MAGIC) populations] and molecular breeding in peanut. Genomic location and properties of Arachis hypogaea miniature inverted repeat transposable element 1 (AhMITE1) were characterized. Genome-wide mutations were also studied in terms of transposon activity, SNP and CNV. Extensive analysis of DNA methylation and SNPs were carried out in peanut by his group. Two backcross lines with foliar disease resistance developed have been approved for commercial cultivation. Currently, the backcross lines developed in the

background of two elite varieties (GPBD 4 and G2-52) are under field evaluation for variety development.

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