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Comparative analysis of whole genome re-sequence data of two soybean genotypes with contrasting rust disease resistant trait and identification of putative SNP markers in NBS-LRR disease resistance genes

*Milind Ratnaparkhe*, ICAR-Indian Institute of Soybean Research, Madhya Pradesh, India

Asian soybean rust, caused by *Phakopsora pachyrhizi*, is one of the most serious diseases of soybean. Use of rust resistant soybean varieties is the most economical and safe strategy for management of rust. In this study we performed whole genome re-sequencing of soybean accession EC241780 which shows resistance to soybean rust.

A total of 374 million raw reads were obtained out of which high quality reads were mapped to reference genome of Williams 82. Overall 287.3 million reads (76.64%) of total reads were mapped to the genome and out of total aligned reads 203.5 million reads (70.84%) mapped uniquely to the reference genome. Based on the stringent parameters, we filtered 1,799,343 SNPs and 225,572 InDels between the reference Williams 82 genome and EC241780. Comparative sequence analysis identified 414,924 SNPs and 48,962 InDels between of two soybean accessions JS335 and EC241780 (Rust resistant). Genomic annotation in EC 241780 and JS 335 revealed that majority of the SNPs and InDels falls in the intergenic region based on current gene model and only 2.9% of SNPs and 1.03% of the Indels falls within the coding region of the genome. Functional annotation of SNVs in both the genotypes revealed that mostly the variants resulted in mis-sense (53% of total variants) and silent (40% of variants) changes in the coding regions. SSR predictions were performed on soybean accession EC241780 and cultivar JS335. A total of 323,986 and 353,820 SSRs were predicted for EC241780 and JS335 respectively. We also conducted genome wide search for NBS-LRR genes for phylogenetic and evolutionary studies and identified unique SNP markers in rust resistant line EC241780. Our study offers high-density coverage of SNP, Indel and SSR markers across the entire soybean genome, which could be utilized for high-resolution genotyping and marker assisted breeding for rust resistance in soybean.