Genetic Diversity and Discovery of Unique SNPs in Five Country Cultivars of Sesamum indicum by Next-Generation Sequencing

Authors : Nam-Kuk Kim, Jin Kim, Soomin Park, Changhee Lee, Mijin Chu, Seong-Hun Lee

Abstract : In this study, we conducted whole genome re-sequencing of 10 cultivars originated from five countries including Korea, China, India, Pakistan and Ethiopia with Sesamum indicum (Zhongzho No. 13) genome as a reference. Almost 80% of the whole genome sequences of the reference genome could be covered by sequenced reads. Numerous SNP and InDel were detected by bioinformatic analysis. Among these variants, 266,051 SNPs were identified as unique to countries. Pakistan and Ethiopia had high densities of SNPs compared to other countries. Three main clusters (cluster 1: Korea, cluster 2: Pakistan and India, cluster 3: Ethiopia and China) were recovered by neighbor-joining analysis using all variants. Interestingly, some variants were detected in DGAT1 (diacylglycerol O-acyltransferase 1) and FADS (fatty acid desaturase) genes, which are known to be related with fatty acid synthesis and metabolism. These results can provide useful information to understand the regional characteristics and develop DNA markers for origin discrimination of sesame.

Keywords : Sesamum indicum, NGS, SNP, DNA marker

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