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Identification of Genomic Variations among 12 Korean Sesame Varieties

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[Introduction]

Sesame, *Sesamum indicum* L, is called the queen of oil seeds because of the highest oil content among oilseed crops. It is grown widely in tropical and subtropical areas. In Korea, over seventy cultivars have been developed through pure-line selection and cross-breeding etc. However, application of molecular markers or genomic information in sesame breeding is not explored widely. The purpose of this study is to identify genomic variations in Korean sesame varieties which would be used for diversity study and sesame breeding.

[Material and Methods]

A total of twelve Korean sesame varieties developed in Rural Development Administration were used for identification of genetic variations. Resequencing of all materials was performed using Illumina HiSeq platforms. The softwares used for data analysis were Trimmomatic, BWA, Samtools, Picard, GATK and SnpEff.

[Results and Discussion]

The amount of raw genome sequence data from twelve sesame varieties ranged from 11.9 Gbp (Pyoungan) to 28.6 Gbp (Gangheug). After quality trimming, the total of remaining sequence data is 206.8 Gbp with the range of sequencing depth of 30.1~72.2x. After read mapping on the Zhongzhi13 reference genome, the properly mapped read numbers ranged from 61.0 million to 161.9 million with 34.1x mapping depth on average. To compare the variants among 12 varieties, SNPs and InDels of the locus having all the mapped reads derived from twelve varieties were finally chosen and its number was 1,059,977 in total. Among 1,046,828 homozygous diallele removing multiallele and heterozygous diallele, the variants with PIC values > 0.4 were totally 267,286 including 226,590 SNPs and 40,696 InDels. Some of high PIC InDels > 20 bp will be used in genotyping of 46 Korean sesame varieties. Furthermore, KASP markers as the high-throughput genotyping system would be developed using high PIC variants across 13 sesame chromosomes. InDel and KASP markers will play a strong role in accelerating marker-assisted breeding in sesame, as well as the studies about genetic diversity and cultivar discrimination.

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