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Genomic Variations of Korean Sesame Varieties

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Sesame (*Sesamum indicum*), the oldest oilseed crop, is grown mainly in tropical and subtropical areas as an important source of vegetable oil and protein to human. 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 wildly. The purpose of this study is to identify genomic variations in Korean sesame varieties and diverse genotypes, which could be useful for improvement of sesame cultivars.

[Material and Methods]

A total of twelve sesame genotypes were used for detection of genetic variation, including 7 Korean varieties, 3 from China and India, and 2 accessions from National Agrobiodiversity Center. Resequencing of all materials was performed using Illumina HiSeq platforms. The softwares used for SNP development were BWA, Samtools, Picard, GATK and SnpEff.

[Results and Discussion]

The amount of raw genome sequence data from different varieties ranged from 3.5 Gbp (YuzhiDS899) to 33.0 Gbp (Swetha). After quality trimming, the total of remaining sequence data is 121.7 Gbp with the range of sequencing depth of 6.5-64x. After read mapping on the Zhongzhi13 reference genome, the properly mapped read numbers ranged from 26.0 million to 252.8 million with 20x mapping depth on average. In the comparisons between each cultivar and Zhongzhi13, YuzhiDS899 showed the lowest total SNP number of 97,505, with an SNP density of 0.36 per kbp, whereas Swetha showed the highest total SNP number of 1,157,417 and an SNP density of 4.2 per kbp. We identified 5,396,381 SNPs among the 12 sesame genotypes. As a result of annotation of all SNPs detected, 52,147 SNPs, only one percentage of SNPs, were located in the genic region. Of the genic region SNPs, 12,885 SNPs were detected from coding sequences, which were classified into 6,253 synonymous SNPs and 6,632 non-synonymous SNPs. SNP matrix will be analyzed to integrate individual SNPs of each genotype and the SNPs specific to Korean varieties will be detected to develop genetic markers for Korean cultivar identification and genetic diversity analysis.

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