

**Development of SNP-based markers of Onion (*Allium cepa* L.) using RNASEQ**

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**[Introduction]**

The onion (*Allium cepa* L.) is the most widely cultivated species of the genus *Allium*, especially it has been valued because of the pungent flavor and aroma. *Allium* species including onion has very large genome sizes ranging from approximately 10 to 20 Gbp, which have complicated genomic studies and precluded genome sequencing until recently. The objective of the current study is to develop SNP-base markers for genetic mapping and breeding program of onion.

**[Materials and Methods]**

We extracted RNA from three different tissues (root, green stem and flesh scale leaf) using two onion varieties of 'Umjinara' and 'Sinsunhwang', followed RNASEQ was conducted using HiSeq2500 platform. SNP calling among tissues was performed using transcriptome sequences.

**[Results and Discussion]**

We found 43,845, 52,180 and 52,627 SNPs from green leaf, root and flesh scale leaf, respectively and the number of common SNP among three tissues was 30,191. Through comparison with mRNA information of rice, a total of 1029 onion CAPS primers were developed and assigned to 12 rice chromosomes. Also, heat map consisting of 1808 DEGs was generated along with gene annotation for all DEG identified in the study, and sixty-nine CAPS markers were developed from DEGs. These CAPS markers might be used for genetic mapping or functional studies of onion.

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