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Development of dCAPS Markers for Identifying the Relationships in Korean Oat (*Avena sativa* L.) Varieties using Transcriptome Analysis

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[Introduction]

Cultivated oat (*Avena sativa* L.), having high protein contents, is an important cereal crop for human being. Oat have been getting the limelight as a health food owing to well-being trend recently. Oat has a large genome size and is a self-pollinated allohexaploid with a basic chromosome number of 2n=6x=42, consists of A, C and D sub-genome. The development and application of molecular markers has been relatively slow in oat compared with other crops. Meanwhile, there is a growing need for identifying the relationships at the DNA level in oat germplasm as in other crops, and to use this information for genomic analysis and implements for molecular breeding. Molecular markers were developed for gene discovering, linkage map construction and identifying the relationships among germplasm in oat, based on RFLP, AFLP, RAPD, SSR and SNP technologies. RFLP is not a PCR based DNA marker, difficult to use because of using hybridization probe and time consuming method for checking the polymorphism. The other type of DNA markers is insufficient to utilize and doesn't have universal characteristic for using in other germplasm with different background. Recenty, research results were published identifying the genetic relationships between Korean oat varieties using previous reported SSR markers and developed EST-SSR markers. In here, we developed dCAPS (derived cleaved amplified polymorphic sequence) markers for identifying the relationships in Korean oat varieties using SNPs in intragenic regions by RNA-Seq technique. The RNA-Seq technique has benefit for identify the sequence variation in intragenic regions at low cost and use this information for development DNA marker in crop with large genome size without reference genome sequence data.

[Materials and Methods]

Korean oat varieties, Choyang, Daeyang, Darkhorse, Gehl, Gwanghan, Hispeed, Ilhan, Okhan, Samhan and Swan were used for extraction of total RNA. Total RNA of each variety was extracted using RNeasy Mini Kit (Qiagen) following the manufacturer's instruction and subsequently used for CDNA synthesis. The CDNA, which has length range from 200 to 400 bp, was selected for sequencing analysis. Each of RNA-seq reads was assembled by trinity based on the de novo assembly technique. The longest assembled read was used unigene as reference sequence of gene. The assembled read was aligned along with unigene and variety specific SNP was discovered. The dCAPS marker was developed using variety specific SNPs by dCAPS Finder 2.0.

[Results and Discussion]

Total of 638 high-quality SNPs were selected as variety specific. Total of 571 dCAPS marker were designed using this SNPs. In the future, it will be verified that each of marker works well, and shows the distinctive cutting band after applying the restriction enzyme. The relationships will also be identified among Korean oat varieties and DNA marker set could be established for individualizing among Korean oat varieties.

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