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SNP Marker Discovery Base on Trait-association in Cabbage (*Brassica oleracea* L.) Using GBS Technology

Eun-Jo Shim[1], Dong-Min Kim[1], Hyun-Jung Kim[1], Su-jin Lee[1], Hye-Won Kim[1], Mi-Su An[1], Sun-Young Ko[1], Seung-In Yi[1], Jin-Kee Jung[1]*

[1]Seed Testing & Research Center, Korea Seed & Variety Service, Gimcheon, 39660, Korea

[Introduction]

The cabbage (*Brassca oleracea* L.) is a widely cultivated vegetable species integral to human diets, with a classification of cultivar groups based on the specialized morphology of their edible structures(kales, chinese cabbages, Brussels sprouts, broccoli, kohl rabi and cauliflower). The cabbage's genome was known as self-fertilizing diploids(2n=2x=18) chromosomes. The cabbage varieties were commonly classified as 3 types; red, white, savoy cabbages and so on. The purpose of this study is developing SNP markers which is significantly linked to agronomic trait with 96 cabbage cultivars using GBS (genotype-by-sequencing) technology.

[Material and Methods]

For this study, we performed a GBS-sequencing with 96 cabbage varieties, for Plant variety protection and register of import and production, stored in KSVS (Korea seed variety service) archive. GBS libraries are constructed using *ApeK*I digestion and adapter ligation. The ds DNA were digested using *ApeK*I 10 unit(75°C, 16 hr) and ligated using T4 DNA ligase(75°C, 16 hr). The ds DNA and adaptor mixture were cleaned up using QIAquick PCR purification kit. Thermal Cycler using the following condition: denaturation of 30s at 98°C, 18 cycles of 10s at 98°C, 30s at 60°C and 30s at 72°C elongation was completed by a final extention of 5min at 72°C. The genomic sequence within this version of Ensembl includes 33,459 scaffolds (>200 bp) with an N50 of 850 kb that was assembled at NRC-Saskatoon using a hybrid approach from Illumina, Roche 454 and Sanger sequence data. The assembly has been orientated and assigned to the nine pseudochromosomes using dense genotype-by-sequencing genetic maps. Gene prediction of the assembled genomic scaffolds was conducted by JCVI and NRC-Saskatoon using MAKER and PASA. Functional annotation for the gene models is provided through similarity to Arabidopsis thaliana genes. Associations were calculated using TASSEL software.

[Results and Discussions]

The results of GBS analyses were identified 17,148 SNP loci among total 270,718 SNP loci for novel SNP marker for cabbage variety identification. All of SNPs are evenly distributed in each 9 chromosomes. The phylogenetic tree, PCA and population structure was constructed with reliable 17,148 SNP loci and most of varieties were clearly classified with each population. These GBS analysis results will be useful in these SNPs for develop novel marker which is correlated with agronomic traits and available Fluidigm analysis.

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*Corresponding author: Tel. +82-54-912-0231, E-mail. jinkeejung@korea.kr