

Construction of a DNA database and development of novel SNP markers for Cabbage(*Brassica oleracea* L) identification using GBS technology

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[Introduction]

The construction of a DNA database for identify the Cabbage(*Brassica rapa* L) has been made possible by the development of novel single nucleotide polymorphism(SNP) markers using next generation sequencing(NGS) technology. For the development of novel SNP marker associated with agronomic trait; (A) side face of blade, (B) color of outside leaf, (C) incision of outside leaf, (D) conservancy of leaf, GBS(genotype by sequencing) was performed with core 48 variety of cabbage. We did not select molecular markers for associated with agronomic trait through Manhattan plot analysis. But the 56,210 SNPs loci were discovered among 48 core cabbage variety by GBS(Genotype by sequencing) and then 39 SNP loci that indicated most high read depth were initially applied to select SNP markers for identification of persimmon varieties. Finally 25 SNP markers were developed for identification of 106 cabbage varieties and constructed of a DNA database. Average polymorphism information content (shannon's information index) was 0.547, ranging from 0.335 to 0.693. Genetic distance of clusters ranged from 0.0625 to 0.8400 by unweighted pair-group method with arithmetical average based on Jaccard's distance coefficients. These novel SNP markers will useful for variety identification related to seed dispute and distinctness, uniformity and stability (DUS) test for cabbage.

Keywords: SNP, GBS, cabbage, DUS

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