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Haplotyping and Evolutionary Studies on *GBSSII* Gene in Korean Rice Collection

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[Abstract]

Granules-bound starch synthase II (GBSSII), one of the isoforms of granule-bound starch synthase (GBSS), is responsible for amylose synthesis by expressing in non-storage tissues such as leaf, stem, root, and pericarp. Up to date, little is known about this gene functions and basic knowledge of heritable characteristics of this gene, *GBSSII*. We identified functional haplotypes and performed evolutionary analyses on the *GBSSII* using 374 rice accessions (320 Korean bred and 54 wild) based on the classified groups. A total of 14 haplotypes were found, and almost all haplotypes (13) were functional, carrying 19 non-synonymous SNPs in two exons (exons 1 and 2). The lowest nucleotide diversity was detected in *Tropical japonica* (0.00145), while the highest *pi*-value was in *Aus* (0.01081), illustrating the signal of this gene evolution. The highest Tajima's *D* value in *Aus* (1.6380) indicates *GBSSII* gene domestication signature under balancing selection, while the lowest Tajima's *D* value in *Temperate japonica* (-0.8243) highlights that they were under positive selection, which may be purified due to the excess of rare alleles. The highest genetic differentiation was observed between *Tropical japonica* and *aroma* ($F_{ST} = 0.921928$). In contrast, the highest interbreed level was detected in *Aus-admixture* ($F_{ST} = -0.20157$). The genetic relatedness between and or among the wild and cultivated subpopulations was revealed through PCA, population structure, and phylogenetic analyses.

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