

PB-31

Functional Haplotypes and Evolutionary Analyses of *SBE1* in Collected Rice Germplasm

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[Abstract]

The starch-branching enzymes (*BEs*) are responsible for synthesizing the amylopectin, which plays an important role in determining the structural and physical properties of starch granules. *BE* has two differently functioning isoforms (*BEI* and *BEIIa/b*) based on their difference in the chain-length pattern by the degree of polymerization (DP), which mainly contributes to the amylopectin chain length distribution in starch biosynthesis. In this study, we investigated functional haplotypes and evolutionary analyses of *SBE1* in 374 rice accessions (320 Korean bred and 54 wild). The analyses were performed based on the classified subpopulations. Haplotype analysis generates a total of 8 haplotypes, of which only four haplotypes were functional carrying four functional SNPs in four different exons of *SBE1* on chromosome 6. Nucleotide diversity analysis showed a highest *pi*-value in *aromatic* group (0.0029), while the lowest diversity value was in *temperate japonica* (0.0002), indicating the signal of this gene evolution origin. Different directional selections could be estimated by negative Tajima's *D* value of *temperate japonica* (-1.1285) and positive Tajima's *D* value of *tropical japonica* (0.9456), where the selective sweeps were undergone by both positive purifying and balancing selections. Phylogenetic analysis indicates a closer relationship of the wild with most of the cultivated subgroups indicating a common ancestor for *SBE1* gene. *F_{ST}*-values indicate distant genetic relationships of *temperate japonica* from all other classified groups. PCA and population structure analysis show an admixed structure of wild and cultivated subpopulations in some proportions.

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