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Genetic Diversity and Characterization of *DPE1* Gene in Rice Germplasm

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[Abstract]

Disproportionating Enzyme 1 (DPE1) is an α -1,4-D-glucanotransferase that cleavages the α -1,4-glycosidic bonds and transfers glucosyl groups. In rice endosperm, it participates in starch synthesis by transferring maltooligosyl groups from amylose and amylopectin to amylopectin. Here, we investigated the haplotype variations and evolutionary indices (e.g., genetic diversity and population structure) for the *DPE1* gene in 374 rice accessions representing seven subgroups (*wild*, *indica*, *temperate japonica*, *tropical japonica*, *aus*, *aromatic*, and *admixture*). Variant calling analysis of *DPE1* coding regions leads to the identification of six functional haplotypes representing/occupying 8 nonsynonymous SNPs. Nucleotide diversity analysis revealed the highest π -value in *wild* group (0.0556) compared to other cultivated groups, of which *temperate japonica* showed the most reduction of genetic diversity value (0.003). A significant positive Tajima's D value (1.6330) of *admixture* highlights sudden population contraction under balancing selection, while *temperate japonica* with the lowest Tajima's D value (-1.3523) showed a selection signature of *DPE1* domestication which might be the cause of excess of rare alleles. Moreover, these two subpopulations exhibits a greater differentiation ($F_{ST}=0.0148$), indicating a higher genetic diversity. Our findings on functional *DPE1* haplotypes will be useful in future breeding programs, and the evolutionary indices can also be applicable in functional studies of the *DPE1* gene.

[Acknowledgement]

This work was supported by National Research Foundation of Korea (NRF) grants by the Korean government (MSIT) (No. NRF-2022R1A4A1030348), "Cooperative Research Program for Agriculture Science and Technology Development" (Project No. PJ015935) of the Rural Development Administration, and Korea Institute of Planning and Evaluation for Technology in Food, Agriculture and Forestry (IPET), Ministry of Agriculture, Food and Rural Affairs (MAFRA)(322060031HD020).

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