PB-32

Characterization of *PUL* Haplotypes and Its Evolutionary Analyses in Korean Rice Accessions

Thant Zin Maung[1], Yong-Jin Park[1,2]*

[1]Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 32439, Republic of Korea
[2]Center for Crop Breeding on Omics and Artificial Intelligence, Kongju National University, Yesan 32439, Republic of Korea

[Abstract]

Pullulanase (PUL), a debranching enzyme, has been utilized in hydrolyzing the α-1,6 glucosidic linkages in starch, amylopectin, pullulan, as well as related oligosaccharides. It has also been indicated that PUL is a novel indicator of inherent RS (Resistant Starch) formation in rice. In this study, we performed haplotype analysis on 320 bred rice accessions, and additional 54 wild accessions were added to study genetic diversity along with other population-based analyses of the *PUL* gene. Through these investigations, we summarized a total of 10 functional (non-synonymous) SNPs from 7 different exons on chromosome 4. There were 10 haplotypes, of which only six haplotypes were functional, implicating different subpopulations. Diversity reduction was noticed in *temperate japonica* (0.0005) compared to the highest one (*aus,* 0.0154), illustrating their higher genetic differentiation by F_{ST}-value (0.926). The highest Tajima's *D* value was observed in *indica* (3.6613), indicating *PUL* gene domestication signature under balancing selection, while the lowest Tajima's *D* value was found in *temperate japonica* (-2.2191) which might have undergone under positive selection and purified due to the excess of rare alleles. PCA, population structure, and phylogenetic analyses provide information on the genetic relatedness between and or among the cultivated subpopulations and the wild based on *PUL* genomic region.

*Corresponding author: Tel. +82 41-330-1201 E-mail. yjpark@kongju.ac.kr