

**PB-27**

## Genetic Diversity and Population Structure Analyses of *SSIV-2* Gene in Rice

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### [Abstract]

Soluble starch synthase (SS) IV-2 is one of the starch synthase gene family members and responsible for starch chain elongation interacting with other rice eating and cooking quality controlling genes (e.g., *AGPLar* and *PUL*). *SSIV-2* is mainly expressed in leaves, especially at grain-filling stage and its alleles can significantly affect rice quality. Here, we investigated the genetic diversity and population structure analyses of *SSIV-2* gene by using 374 rice accessions. This rice set was grouped into 320 cultivated bred (subsequently classified into *temperate japonica*, *indica*, *tropical japonica*, *aus*, *aromatic* and *admixture*) and 54 wild rice. Haplotyping of cultivated rice accessions provided a total of 7 haplotypes, and only three haplotypes are functional indicating four substituted SNPs in two exons of chromosome 5: T/A and G/T in exon 4, and C/G and G/A in exon 13. Including the wild, a highest diverse group (0.0041), nucleotide diversity analysis showed *temperate japonica* (0.0001) had a lowest diversity value indicating the origin information of this gene evolution. Higher and positive Tajima's *D* value of *indica* (1.9755) indicate a selective signature under balancing selection while *temperate japonica* (-0.9018) was in lowest Tajima's *D* value due to a recent selective sweep by positive selection. We found the most diverse genetic components of the wild in PCA but shared in some portion with other cultivated groups. Fixation index ( $F_{ST}$ -values) and phylogenetic analysis indicate a closer relationship of the wild with *indica* ( $F_{ST}$ =0.256) than to its association to both of *temperate japonica* ( $F_{ST}$ =0.589). Structure analysis shows a clear separation of cultivated subpopulations at every *K* value, but genetic components were admixed within the wild illustrating the same genetic background with *japonica* and *indica* in some proportion.

### [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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