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Disentangling Evolutionary Pattern and Haplotype Distribution of Starch Synthase III-1 (*SSIIIb*) in Korean Rice Collection

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[Abstract]

Soluble starch synthases (SSs) elongate α -glucans from ADP-Glc to the glucan nonreducing ends and play a critical role in synthesizing resistant starch in the rice. A total of 10 SSs isoforms were reported in rice, including granules-bound starch synthase I (*GBSSI*), *GBSSII*, starch synthase I (*SSI*), *SSIIa* (*SSII-3*), *SSIIb* (*SSII-2*), *SSIIc* (*SSII-1*), *SSIIIa* (*SSIII-2*), *SSIIIb* (*SSIII-1*), *SSIVa* (*SSIV-1*), and *SSIVb* (*SSIV-2*). SSIII proteins are involved in forming the B chain and elongating cluster filling chains in amylopectin metabolism. The functions of *SSIIIb* (*SSIII-1*) are less clear as compared to SSs. Here, we sought to shed light on the genetic diversity profiling of the *SSIII-1* gene in 374 rice accessions composed of 54 wild-type accessions and 320 bred cultivars (temperate japonica, indica, tropical japonica, aus, aromatic, and admixture). In total, 17 haplotypes were identified in the *SSIII-1* coding region of 320 bred cultivars, while 44 haplotypes were detected from 54 wild-type accessions. The genetic diversity indices revealed the most negative Tajima's D value in the temperate-japonica, followed by the wild type, while Tajima's D values in other ecotypes were positive, indicating balancing selection. Nucleotide diversity in the *SSIII-1* region was highest in the wild group (0.0047) while lowest in temperate-japonica. Lower nucleotide diversity in the temperate-japonica is evidenced by the negative Tajima's D and suggested purifying selection. The fixation index (F_{ST}) revealed a very high level of gene flow (low F_{ST}) between the tropical-japonica and admixture groups ($F_{ST} = -0.21$) followed by admixture and wild groups (-0.04), indica and admixture groups (0.02), while low gene flow with higher F_{ST} estimates between the temperate-japonica and aus groups (0.72), tropical-japonica and aromatic groups (0.71), and temperate-japonica and admixture groups (0.52). Taken together, our study offers insights into haplotype diversity and evolutionary fingerprints of *SSIII-1*. It provides genomic information to increase the resistant starch content of cooked rice.

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