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Granule-Bound Starch Synthase I (*GBSSI*): An Evolutionary Perspective and Haplotype Diversification in Rice Cultivars

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[Abstract]

Granule-bound starch synthase I (*GBSSI*), encoded by the *waxy* gene, is responsible for the accumulation of amylose during the development of starch granules in rice endosperm. Despite many findings on waxy alleles, the genetic diversity and evolutionary studies are still not fully explored regarding their functional effects. Comprehensive evolutionary analyses were performed to investigate the genetic variations and relatedness of the *GBSSI* gene in 374 rice accessions composed of 54 wild accessions and 320 bred cultivars (temperate japonica, tropical japonica, indica, aus, aromatic, and admixture). GBSS1 coding regions were analyzed from a VCF file retrieved from whole-genome resequencing data, and eight haplotypes were identified in the *GBSSI* coding region of 320 bred cultivars. The genetic diversity indices revealed the most negative Tajima's D value in the tropical-japonica, followed by the aus and temperate-japonica, while Tajima's D values in indica were positive, indicating balancing selection. Diversity reduction was noticed in temperate japonica (0.0003) compared to the highest one (wild, 0.0044), illustrating their higher genetic differentiation by F_{ST}-value (0.604). The most positive Tajima's D value was observed in indica (0.5224), indicating the *GBSSI* gene domestication signature under balancing selection. In contrast, the lowest and negative Tajima's D value was found in tropical japonica (-0.5291), which might have experienced a positive selection and purified due to the excess of rare alleles. Overall, our study offers insights into haplotype diversity and evolutionary fingerprints of *GBSSI*. It also provides genomic information to increase the starch content of cooked rice.

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