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Strategic Use of QTL Mapping to Improve the Palatability of Rice

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[Abstract]

The properties of starch play an important role in determining the palatability of rice. In addition, the gelatinization temperature (GT) of rice starch is an important factor in determining the quality of rice because it is related to the cooking time and texture of rice. For the development of high-quality rice, it is important to understand the genetic basis of palatability-related traits, and QTL analysis is an effective method to explain the genetic basis of variation in complex traits. QTL mapping related to alkali digestion value (ADV) of brown and milled rice was performed using the 120 Cheongcheong/Nagdong double haploid (CNDH) line. As a result, 12 QTLs related to ADV were detected, and 20 candidate genes were selected from the RM588-RM1163 region of chromosome 6 through screening by gene function analysis. The comparison of the relative expression level of candidate genes showed that *OsSS1q6* is highly expressed in CNDH lines with high ADV in both brown rice and milled rice. In addition, *OsSS1q6* has high homology with starch synthase 1 protein, and interact with various starch biosynthesis-related proteins, such as GBSSII, SBE, and APL. Therefore, we suggest that *OsSS1q6* identified through QTL mapping could be one of the various genes involved in the GT of rice by regulating starch biosynthesis. This study can be used as basic data for breeding high-quality rice and provides a new genetic resource that can increase the palatability of rice.

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