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IDENTIFICATION OF A NOVEL LOCUS SH2-ON FOR SEED SHATTERING IN RICE (ORYZA SATIVA L.) BY COMBINING BULKED SEGREGANT ANALYSIS WITH WHOLE GENOME SEQUENCING

Seed non-shattering is an important trait related to the efficiency of seed harvesting. Takanari is a high-yielding Indica Group rice cultivar in Japan displaying an easy shattering phenotype. To reduce its yield loss caused by seed shattering a new cultivar Oonari with moderate shattering was, recently, developed as a mutant induced from Takanari by gamma-ray irradiation. The histological analysis of abscission zone (AZ) revealed no significant difference between Takanari and Oonari grown in paddy field. However, most of the spikelets of Oonari grown in greenhouse had no or reduced AZ formation, and different from that of Takanari. F3 population derived from a cross between Takanari and Oonari showed single recessive gene's segregation for moderate-shattering. To identify the candidate gene, the bulk DNA of F3 lines with the same shattering degree as Oonari and their parents, were used for whole genome sequencing. Variation-index (VI) for F3 bulk was calculated as the ratio between the number of reads with a nucleotide mutation and the total number of reads corresponding to the mutation. We identified a single base substitution (named TO20) with top VI in the terminal region on long arm of chromosome 2. This novel locus was named sh2-ON. Structure variation analysis showed that a tandem duplication containing a microRNA172 gene occurred near TO20 in Oonari. qRT-PCR analysis indicated that the microRNA172 relative expression in Oonari was about three times as high as that in Takanari. It has been reported that Apetala 2 (AP2) genes, such as SHAT1 in rice and Q gene in wheat which are both involved in controlling of grain threshing, are targets of microRNA172. Therefore, we infer that the duplication of microRNA172 might be the cause of reduced seed shattering in Oonari.

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