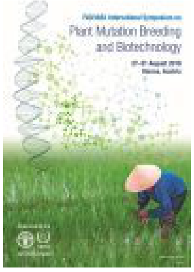

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FINE MAPPING AND CANDIDATE GENE ANALYSIS OF THE QUANTITATIVE TRAIT LOCUS GW8. 1 ASSOCIATED WITH GRAIN WEIGHT IN RICE

A quantitative trait locus (QTL) gw8.1 was identified in the population derived from a cross between the elite japonica cultivars; 'Hwaseong'and Oryza rufipogon (IRGC 105491). Near isogenic lines (NILs) harboring the O. rufipogon segment on chromosome 8 showed increased grain length and weight compared to those of the recurrent parent, Hwaseong. This QTL was mapped to a 175.3-kb region containing 28 genes, of which four were considered as candidates based on the presence of mutations in their coding regions and as per the RNA expression pattern during the inflorescence stage. Leaves and panicles obtained from plants harvested 5 days after heading showed differences in gene expression between Hwaseong and gw8.1-NILs. Most genes were upregulated in O. rufipogon and gw8.1-NIL than in Hwaseong. Scanning electron microscopy analysis of the lemma inner epidermal cells indicated that cell length was higher in gw8.1NIL than in Hwaseong, indicating that gw8.1might regulate cell elongation. Among the candidate genes, LOC_Os08g34380 encoding a putative receptor-like kinase and LOC_Os08g34550 encoding putative RING-H2 finger protein were considered as possible candidates based on their functional similarity.

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