

Fine mapping of a grain weight quantitative trait locus, qGW6, using near isogenic lines derived from *Oryza rufipogon* IRGC105491 and *Oryza sativa* cultivar MR219

ABSTRACT

Grain weight is a major component of rice grain yield and is controlled by quantitative trait loci. Previously, a rice grain weight quantitative trait locus (qGW6) was detected near marker RM587 on chromosome 6 in a backcross population (BC2F2) derived from a cross between *Oryza rufipogon* IRGC105491 and *O. sativa* cv. MR219. Using a BC2F5 population, qGW6 was validated and mapped to a region of 4.8 cM (1.2 Mb) in the interval between RM508 and RM588. Fine mapping using a series of BC4F3 near isogenic lines further narrowed the interval containing qGW6 to 88 kb between markers RM19268 and RM19271.1. According to the Duncan multiple range test, 8 BC4F4 near isogenic lines had significantly higher 100-grain weight (4.8 to 7.5% over MR219) than their recurrent parent, MR219 ($P < 0.05$). According to the rice genome automated annotation database, there are 20 predicted genes in the 88-kb target region, and 9 of them have known functions. Among the genes with known functions in the target region, in silico gene expression analysis showed that 9 were differentially expressed during the seed development stage(s) from gene expression series GSE6893; however, only 3 of them have known functions. These candidates provide targets for further characterization of qGW6, which will assist in understanding the genetic control of grain weight in rice.

Keyword: Fine mapping; Grain weight; *Oryza rufipogon*; Quantitative trait locus; Near isogenic lines