

Fine mapping of a grain weight QTL on rice chromosome 8 using near isogenic lines derived from a cross between *Oryza sativa* and *O. rufipogon*

Xiaobo Xie, Mi-Hee Song, Fengxue Jin, Dong-Beom Yoon, Sang-Nag Ahn*

Department of Agronomy, College of Agriculture and Life Sciences, Chungnam National University, Daejeon 305-764, Korea (*ahnsn@cnu.ac.kr)

A QTL for 1,000-grain weight (TGW) was detected near the SSR marker RM210 on chromosome 8 consecutively at $P=0.0001$ from BC_2F_2 to BC_3F_4 derived from a cross between the Korean japonica cultivar Hwaseongbyeo and *Oryza rufipogon*. The *O. rufipogon* allele increased grain weight in the Hwaseongbyeo background in an additive manner. Using sister BC_3F_3 near-isogenic lines (NILs), gw8.1 was validated and mapped to a 6.1 cM region in the interval between RM42 and RM210 ($P=0.0001$). Substitution mapping with eight BC_3F_4 sub-NILs further narrowed the interval containing gw8.1 to about 306.4 kb between the markers RM23201.CNR151-RM30000.CNR99. A yield trial using homozygous BC_3F_4 sister sub-NILs and the Hwaseongbyeo recurrent parent indicated that the NIL carrying *O. rufipogon* DNA across the entire gw8.1 target region between RM42 and RM210 outyielded its sister NIL (containing a Hwaseongbyeo substitution in the RM42-RM210 interval) by 9% ($P=0.0292$). The higher yielding NIL (containing the larger *O. rufipogon* introgression) produced 19.3% more grain than the Hwaseongbyeo recurrent parent ($P=0.0180$). This result suggests that gw8.1 contributed to grain yield. Analysis of one NIL at BC_3F_4 indicated that the phenotypic variation for TGW is associated with variation in grain shape, specifically grain length ($P=0.0001$). The locus, gw8.1 is of particular interest because of its independence from undesirable height, maturity and grain quality trait. SSR markers tightly linked to the grain weight QTL will facilitate cloning of the gene underlying this QTL as well as marker-assisted selection for increased grain weight in an applied breeding program.

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