

8. Fine mapping of *PGWC-7* for rice appearance quality in rice (*Oryza sativa* L.)

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Percentage of grains with chalkiness (PGWC), one of rice appearance quality, varies in different rice varieties. A high PGWC results in lowering the density of starch granules and the grains are more prone to breakage during milling (Del Rosario et al. 1968). Also, since both longitudinal and transverse cracks occur easily in chalky kernels when the grain is steamed or boiled, chalkiness reduces the palatability of cooked rice (Nagato and Ebata 1959, Hiromoto et al. 2007). Because the Japanese and North Chinese market prefer sticky rice, the rice grains with a chalky appearance are easily recognized and result in low sale prices. On the other hand, rice cultivars with chalkiness are useful for the production of special food, an example of which is sake, a Japanese liquor.

So far, the differences in grain chalkiness in different rice varieties are poorly understood at the molecular level. Thus, it is imperative to determine the underlying biochemical mechanism for grain chalkiness, by fine mapping and identification of the major QTLs of PGWC.

Previously, a set of chromosome segment substitution lines carrying overlapping chromosome segments of Pai64S in a genetic background of elite cultivar 9311 had been constructed by our laboratory (Xiao et al. 2005). In this study, an isogenic line (IL) in the set of chromosome segment substitution lines, encoded as IL51, showed significantly higher PGWC than that of 9311 in the phenotype observation of two consecutive years, 2006 and 2007 (Fig.1, $P < 0.001$). By genotype analysis, we found IL51 harbored only a segment of the long arm of chromosome 7, which indicated that the high PGWC of IL51 may result from the introgression of Pai64S.

To fine map the locus, one secondary population of 3237 F_2 lines derived from the cross IL51/9311 was further constructed. First, 400 F_2 lines was useful for QTL detection in the segment from the introgression of Pai64S. The *PGWC-7* locus was primarily mapped in the interval between RM21925 and RM21974, on the long arm of chromosome 7. Next, twenty-five SSR markers located around this genomic region were selected to screen for polymorphism between IL51 and 9311. All of the extreme F_2 lines with low PGWC were useful for fine mapping, and the phenotypes of the recombinant lines were repeatedly tested in F_3 lines. Finally, the *PGWC-7* locus was mapped to the interval between ZH3 and ZH5, with 0.7cM from ZH3 on one side and 0.1cM from ZH5 on the other side (Fig. 2).

In this study, we found that *PGWC-7* locus was tightly linked with the marker ZH5, which can be useful for marker assisted selection breeding of rice quality.

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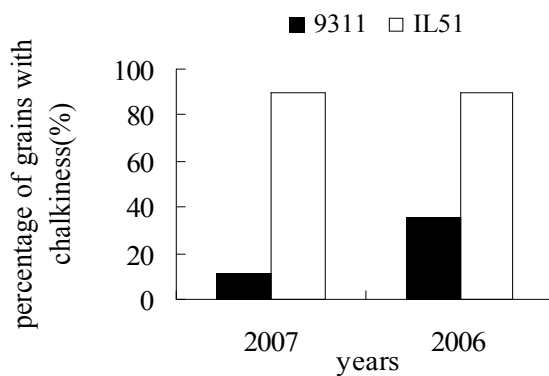


Fig. 1. PGWC of 9311 and IL51 in 2006 and 2007

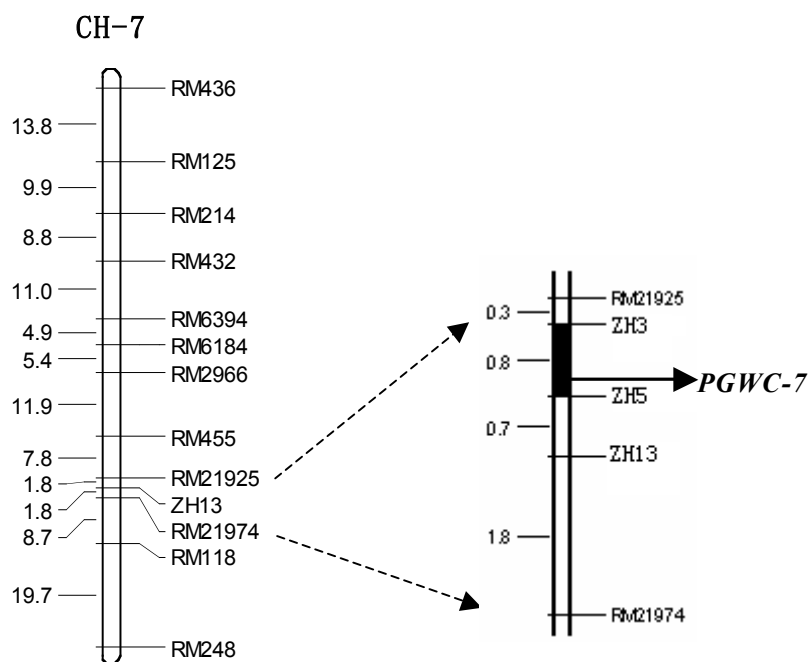


Fig. 2. Location of the *PGWC-7* locus on the molecular linkage map of chromosome 7

References

Del Rosario A. R., V. P. Briones, A. J. Vidal, B. O. Juliano, 1968. Composition and endosperm structure of developing and mature rice kernel. *Cereal Chem.* 45: 225–235.

Nagato K. and M. Ebata, 1959. Studies on white – core rice kernel II. On the physical properties of the kernel. *Proc. Crop. Sci. Soc. Jpn* 28:46–50.

Xiao Y. H., L. L. Liu, L. Jiang, C. G. Lu, C. Y. Yu, W. W. Zhang, J. S. Zuo, H. Q. Zhai, J. M. Wan, 2005. Development of the chromosome segment substitution lines (CSSLs) derived from a hybrid rice cross, Pai64S/9311 with super high yield potential. *Rice Genet. Newsl.* 22:17-19.

Yamakawa H., T. Hirose, M. Kuroda, T. Yamaguchi, 2007. Comprehensive expression profiling of rice grain filling-related genes under high temperature using DNA microarray. *Plant Physiology* 144: 258–277.