**6. Identification and mapping of two new loci for hybrid breakdown in cultivated rice**

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Hybrid breakdown, which is one of the reproductive barriers in cultivated rice, is found in the progeny of cross between Indica and Japonica rice varieties. The genetic basis of this phenomenon can be elucidated by assuming a set of two complementary loci as postulated by Oka (1957). Under this postulate, the parental genotypes would be $A_1 A_1 a_2 a_2$ and $a_1 a_1 A_2 A_2$, respectively, and segregants with one or zero dominant gene, such as $A_1 A_1 a_2 a_2$, $a_1 a_1 A_2 A_2$, and $a_1 a_1 a_2 a_2$, would express the hybrid weakness. Here we report the chromosome location of novel genes controlling hybrid breakdown in Asian cultivated rice using DNA markers.

Japonica rice variety, Sasanisiki was used as a tester to screen hybrid breakdown among Asian cultivated rice varieties. Weak plants with shorter plant height and fewer tillers occurred in the $F_2$ of crosses with several varieties from Assam, India. One of the Assam accessions, ARC10303 was used for further genetic analysis. The $F_1$ plants between Sasanishiki and ARC10303 were normal and the segregation ratio in the $F_2$ fit the expected ratio, 11 normal and 5 weak by the chi-square test. The $B_1F_1$ plants segregated into 3 normal and 1 weak when Sasanisihiki was backcrossed to the $F_1$, whereas the segregation ratio in the $B_1F_1$ did not fit to 3 normal and 1 weak when ARC10303 was backcrossed to the $F_1$ (Table 1). Analysis of 84 $F_2$ plants using 98 DNA markers identified the two chromosomal regions where the segregation of the marker allele associated with normal and weak plant-type are located. One is on chromosome 6 and the other is on chromosome 11, difference based on the expected model without contradiction. The alleles from ARC10303 at the locus on chromosome 6 and those from Sasanishiki at the locus on chromosome 11 produced weak plants. These regions differ from the loci for hybrid weakness in the $F_1$ or $F_2$ and later generations previously reported (Fukuoka and Okuno 1997, Fukuta et al. 1998, Ichitani et al. 2000, Kubo and Yoshimura 2002). The chromosomal locations of the two loci designated as *hwg1(t)* and *hwg2(t)* were determined by linkage analysis of 104 and 99 $B_1F_3$ plants, respectively. *hwg1(t)* is located between marker loci *RM7193* and *C214* at a distance of 3.4 and 2.4 cM on chromosome 6, while the other *hwg2(t)* is located between marker loci *RM206* and *RM254* at a distance of 5.1 and 1.1 cM, on chromosome 11 (Fig. 1). DNA marker analysis confirmed that the deviation of the segregation ratio in one of the $B_1F_1$ populations was due to distorted segregation that was not observed in the $F_2$ population.

Table 1. Segregation ratio for plant-type observed

| Generation | Cross combination | Number of plants | | Ratio expected | $\chi^2$ |
|---|---|---|---|---|---|
| | | Normal | Weak | | |
| $F_1$ | S/A | 10 | | 1:0 | |
| $F_2$ | S/A | 60 | 38 | 11:5 | 2.58 |
| $BC_1F_1$ | S/A//S | 37 | 15 | 3:1 | 0.41 |
| | S/A//A | 48 | 6 | 3:1 | 5.56 |

S: Sasanishiki, A: ARC10303

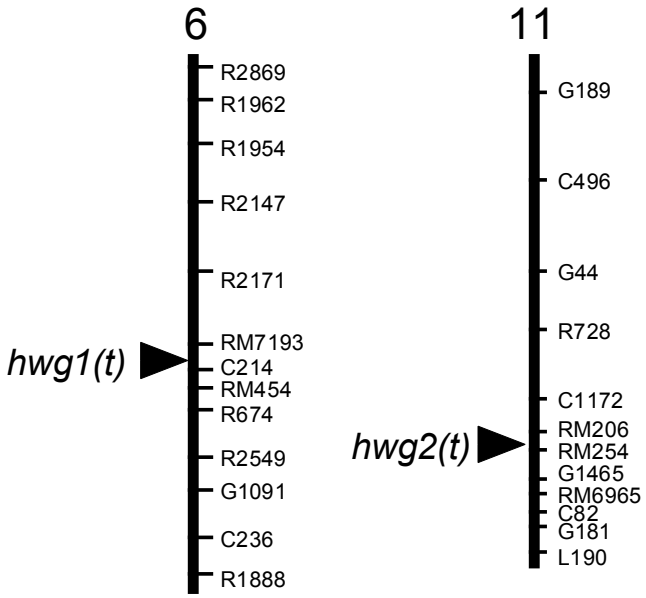


Fig.1. Chromosomal locations of *hwg1(t*) and *hwg2(t)*.

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