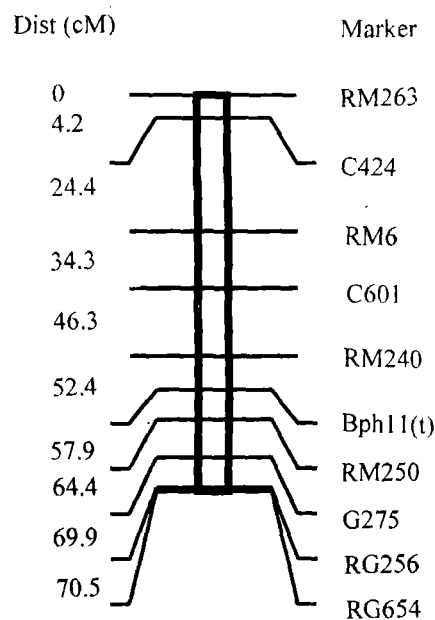


### RFLP and SSR mapping of a new gene for brown planthopper resistance introgressed from *O. eichingeri* into cultivated rice (*O. sativa* L.)

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Nine brown planthopper (BPH) resistance genes have been registered so far, but of them only *Bph1*, *bph2*, *Bph3*, *bph4*, *Bph9*, and other three unregistered genes *Bph10(t)*, *Bph(t)*, *bph(t)* were located on chromosome 3, 4, 10, and 12, respectively, by using traditional and molecular mapping methods. To use the genes for BPH resistance in rice breeding and production, interspecific hybrids between cultivated rice and accessions of *O. eichingeri* ( $2n = 24$ , CC), a wild rice species from Africa, with strong resistance to BPH and whitebacked planthopper were produced. The  $F_1$  plants from the interspecific cross between 02428 and one accession of *O. eichingeri* were resistant to BPH biotype 1 and 2, indicating that BPH resistance is under dominant control. A segregation population from a resistant introgression line which derived from backcrossing to 02428 containing 82 plants were analyzed for BPH resistance. The numbers of resistance and susceptible plants were 61 and 21, respectively, fitting the 3 : 1 ratio, while the segregation ratios of RFLP and microsatellite markers in the segregation population fitted to the ratio of 1 : 2 : 1. A linkage group on chromosome 2 was constructed by using software MAPMAKER. The alignment of five RFLP and four microsatellite markers on chromosome 2 was identical to that of the known molecular maps constructed by Harushima et al (1998), Temnykh et al (1999), and Shen et al (1998). The newly discovered BPH resistance gene called *Bph11(t)* was located between RM240 and RM 250 with a distance of 6.1 and 5.5 cM to the two markers, respectively (see figure). This is an useful

information for further fine mapping and marker-aided selection of this new BPH resistance gene for rice improvement. □



#### RFLP and SSR mapping of *Bph11(t)* on rice chromosome 2.

Map distances were presented in centimorgans (Kosambi function) in the left of the chromosome.

### Type correlation analysis between six morphological trait index and eight isozyme loci

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Indica-japonica differentiation is the majority for differentiation of Asian cultivated rice (*O. sativa* L.). Sun et al proposed to distinguish indica and japonica by using the parameter  $P_j$  value which was quantified from six isozyme loci associated with indica and japonica differentiation, and the classification was consistent with the method of Cheng's "six combined morphological trait index" (CMT index). In this study, we analyzed the correlation between the six morphological traits and eight isozyme markers for indica-japonica classification by using 100 rice lines.

One hundred lines were classified by CMT index, and analyzed using eight isozyme loci following the methods described by Sun and Glaszmann. Among them, 32 DH lines were derived from Gui 630 (typical indica)/02428 (wide

compatible japonica), 60 DH lines derived from JX 17 (typical japonica) / ZYQ (typical indica), 4 parents, and 4 control varieties (IR36, Nanjing 11, Ballila, and Akihikari). The analysis of type correlation between CMT index and eight isozyme loci were operated.

The six type correlation coefficients between the CMT index and the eight isozyme markers were all significant. The correlation coefficient of the first pair of type variable of morphology and isozyme was 0.6718. In the first synthetic factor U1 of morphology, the coefficient of X4 was the largest while in the first