8. Location of QTLs controlling panicle exsertion in rice (Oryza sativa L.)

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Panicle exsertion, the distance between flag and panicle, is one importantly morphological trait of rice, which seriously affected the production of seeds in hybrid rice (Yuan et al., 1988). In this study, a set of 182 BILs from a backcross of Koshihikari (*japoncia*)/Kasalath (*indica*)//Koshihikari (kindly provided by National Institute of Agrobiological Resources, Japan) was used. A restriction fragment length polymorphism (RFLP) map covering 1115.2 cM was constructed with 162 RFLP markers (Y. Takeuchi and M. Yano, unpublished data, http://www.rgrc.dna.affrc.go.jp). Their seeds were sown on 25 May, 2006. After 25d, all seedlings, with a seedling per hill were transplanted to the rice field of Shanghai Normal University, China. Before harvest, panicle exsertion for each BIL was measured. All measurements for each line were replicated six times and the average values were used for quantitative trait loci (QTL) analysis. Composite interval mapping (CIM) analysis was applied to precisely identify the QTL locations (Zeng, 1994). The CIM analysis was performed by QTL Cartographer (Wang et al., 2005). The loci with LOD value greater than 2.9 was considered as indicative of the presence of a QTL.

As a result, the both parents, Koshihikari (1.0cm) and Kasalath (1.58cm) show the differences of panicle exsertion. In addition, continuous variation and transgressive segregation (Fig. 1) were observed, which suggested that panicle exsertion was a quantitatively inherited trait in this BIL population.

Four QTLs (*q*PE-1, *q*PE-2, *q*PE-3-1 and *q*PE-3-2) were identified for the panicle exsertion with LOD value of 4.41 (chromosome 1), 2.93 (chromosome 2), 5.62 (chromosome 3) and 4.76 (chromosome 3) (Table 1 and Fig. 2) and had increased additive effects of 1.58cm from Kasalath, and 0.99cm, 1.61cm, 1.30cm from Koshihikari, respectively. This is the first report on the identification of QTLs for panicle exsertion and their chromosomal localization on the molecular map of rice. Interestingly, *q*PE-1 coincided with the qCL-1-1 for culm-length, and *q*PE-3-2 was allelic to/tightly linked to *q*CL-3, *q*PL-3-2, *q*IN1-3 for the culm length, panicle length and 1st internode length, respectively, all which were detected in the same BIL population (Yamamoto et al., 2001). The results and the tightly linked molecular markers that flank the QTLs might be useful in improving panicle exsertion of rice.



Fig. 1 Frequency distributions for panicle exsertion in BIL population derived from progeny of Koshihikari/Kasalath//Koshihikari Panicle exsertion represents the distance between flag and panicle in rice plant and its positive values indicate the degree of panicle enclosure

QTL	Chromosome	Marker interval ¹⁾	Peak LOD Value	Additive effects ²⁾ (cm)	Variation ³⁾ (%)
qPE-1	1	C86-R2625	4.41	-1.58	12.19
	2	R712-C1135	2.93	0.99	6.62
qPE-3-1	3	C944- R2856	5.62	1.61	17.16
<i>q</i> PE-3-2	3	R3228-R1925	4.76	1.30	13.07

Table 1 QTLs associated with panicle exsertion using BILs from a cross of Koshihikari/Koshihikari

1) Back bold markers indicate the nearest marker to putative QTL.

 Positive values of additive effects indicate koshihikari alleles are in the direction of increasing panicle exsertion.

3) The percentage of explained phenotypic variation



Fig. 2 Location QTLs for panicle exsertion using 182 BILs from a cross of Koshihikari/Kasalath//Koshihikari Black bar indicate marker interval of QTL detected. Black arrowheads indicate the location of peak LOD.

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