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Erratum

Mapping QTLs influencing rice floral morphology using recombinant inbred lines derived from a cross between *Oryza sativa* L. and *Oryza rufipogon* Griff.

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In Fig. 3, chromosome 3, "L" should read "3L".

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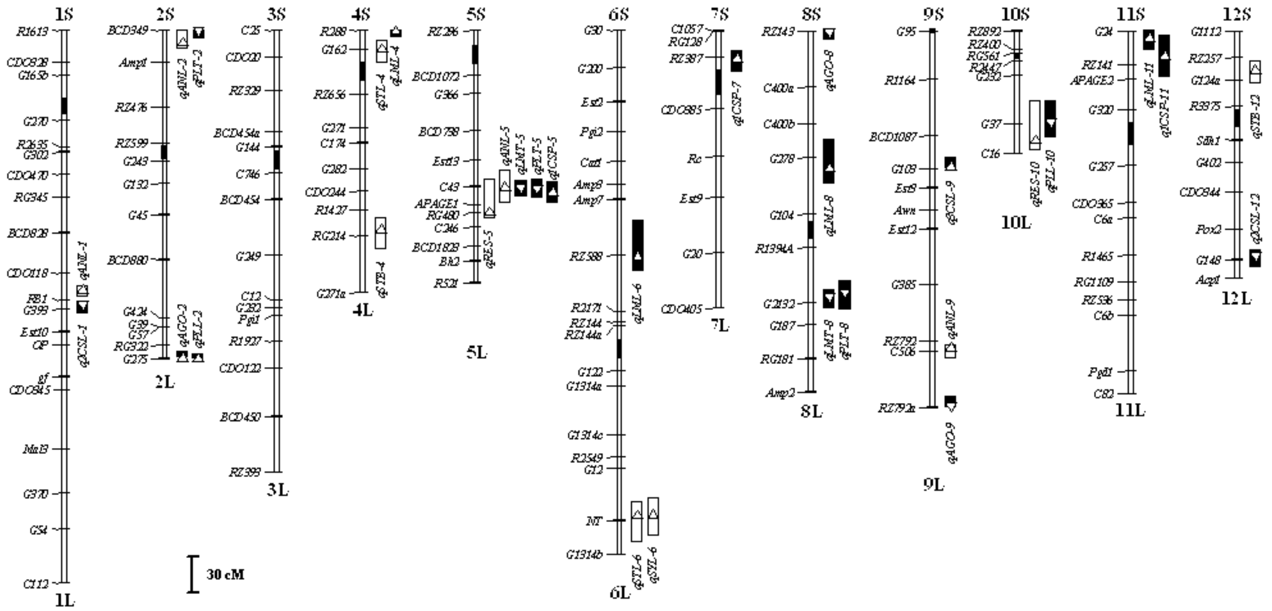

Fig. 3 Mapping of QTLs for floral traits on the rice linkage map. The linkage maps consisted of 147 markers including 121 RFLPs, 17 isozymes, two protein markers (*APAGE1, 2*), one RAPD marker (*RB1*) and six morphological markers (*OP, NT, Awn, gf, Bh2* and *Rc*) (Cai and Morishima 2002). The orientation of each chromosome was obtained from known maps (Causse et al. 1994; Harushima et al. 1998). The *black regions* on chromosomes represent the estimated centromere regions (Singh et al. 1996). The numbers, *S* and *L*, indicate each short and long chromosome arm, respectively. Markers are indicated on the left of each chromosome. *Triangles and boxes* on the right of each chromosome represent LOD peaks of putative QTLs and their one-LOD support intervals (Lynch and Walsh 1998), respectively. *White, gray and black boxes* indicate pistil, stamen and glume QTLs, respectively. *Upward and downward triangles* indicate that the presence of the W1944 and Pei-kuh alleles increase each trait, respectively