

Identification of the low-tillering gene in rice (*Oryza sativa* L.)

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Objectives

The genetic mechanism and allelic relationship between the low-tillering in two Japonica-type rice varieties Aikawa 1 and Shuho were clarified, and the chromosomal location was also identified with molecular (DNA) markers, to apply for the breeding program targeting to develop the new plant type as one of gene sources.

Results

The genetic mechanisms of low-tillering in two Japonica-type rice, Aikawa 1 and Shuho, were clarified and the controlling gene was identified on rice chromosomes using molecular markers. In these two Japonica varieties, the single dominant gene controlling low-tillering was confirmed on the basis of segregation analyses in each BC₁F₂ population derived from the crosses with Indica-type varieties IR64 and IR72 as recurrent parents, respectively.

Aikawa 1 and Shuho were found to have the same low-tiller gene based on results of allelism tests in F₂ populations derived from reciprocal crosses between Aikawa 1 and Shuho. Transgressive segregation was not observed in any of the distributions of 378 Aikawa 1/Shuho and 425 Shuho/Aikawa 1 F₂ plants.

The low-tiller gene was mapped between the SSR marker, *RM149*, and the RFLP marker, *XNpb56*, on the long arm of chromosome 8 using DNA markers (Fig. 1). As no gene related to low-tillering has been reported yet in this region, the genes found in Aikawa 1 and Shuho plants were tentatively designated as *Ltn* (t).

The near isogenic line (NIL) that introduced *Ltn* (t) into the elite Indica-type varieties IR64 and IR72 were developed from the advanced recurrent backcrosses of progenies to clarify yield ability of low-tiller plant types and to incorporate more detailed genetic and physiological analyses (Fig. 2). Partial sterility and malformed palea in the panicles of NILs were observed; this may have occurred due to the multiple effects of *Ltn* (t).

Information on genetic mechanisms and mapping of low-tiller genes will be used for breeding programs using marker-aided selection or map-based cloning of *Ltn* (t); NILs will also be useful as breeding materials for Indica-type varieties.

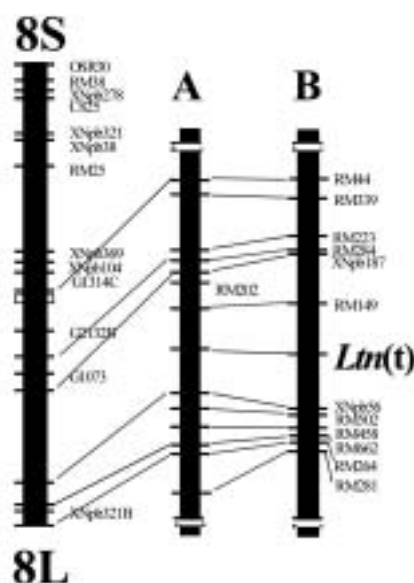


Fig. 1. Identification of *Ltn(t)* locus using DNA markers.
A: BC₁F₂ (IR64/Aikawa1//IR64) family lines (n=33).
B: BC₁F₂ (IR72/Shuho//IR72) family lines (n=74).

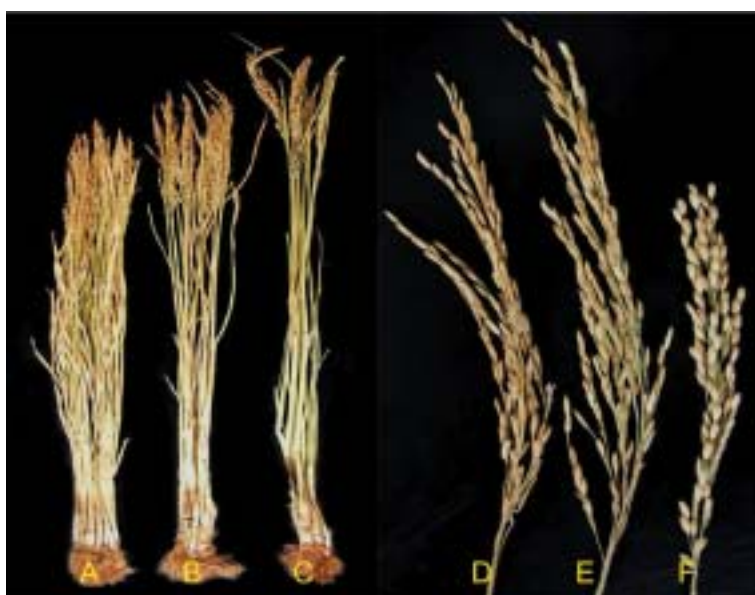


Fig. 2. Near isogenic lines introduced with the low-tiller gene, *Ltn(t)*, into the IR64 and IR72 genetic backgrounds.
A, IR64; B, IR64 NIL (IR64/Aikawa1/5/IR64,BC₆F₃); C, Aikawa 1; D, IR72; E, IR72 NIL (IR72/Shuho/5/IR72, BC₆F₃); F, Shuho.

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