

Gene discovery of *SPIKE*

-A unique gene from a rice landrace increases grain yield of *Indica*-type cultivars-

Increasing crop production is essential for securing the future food supply in developing countries. Total spikelet number per panicle (TSN) is one of the most important traits to increase grain productivity in rice (*Oryza sativa* L.). We previously reported the detection of *qTSN4*, a QTL for increasing TSN on the long arm of chromosome 4 derived from new plant type (NPT) cultivars with the genetic background of IR64 (Refer the Research Highlight in 2012). In this study, we attempted to clone the gene for *qTSN4*. We further conducted characterization of agronomic traits of a near isogenic line (NIL) with the gene. To understand the effect of the gene in different genetic backgrounds, we introduced it into six *indica* cultivars popular in South and Southeast Asian countries by marker assisted selection.

We successfully identified a causative gene for *qTSN4*, designated here as *SPIKE* (*SPIKELET NUMBER*) by map based cloning using 7996 BC₄F₃ plants of an NPT cultivar as a donor and IR64 as a recurrent parent (Fig. 1A). NIL for *SPIKE* had higher TSN (Fig. 1B), wider flag leaf (Fig. 1C) and heavier root dry weight (Fig. 1D) than those of IR64. Rate of filled grain were also higher, but panicle number per plant and 1000-grain weight were lower in the NIL (data not shown). Notably, the grain appearance of the NIL was significantly improved (Fig. 2A), presumably owing to a strengthening of assimilate supply to the larger number of spikelets by an increase in vascular bundle number (Fig. 2B). Consequently, the grain yield of the NIL was consistently higher by 13-36% than that of IR64 over four cropping seasons, significantly so in three of the four seasons (Fig. 2C). *SPIKE* also increased TSN in six cultivars popular in South and Southeast Asia (Fig. 3), confirming its effectiveness in various genetic backgrounds.

SPIKE would be a unique gene to increase grain yields of *indica* cultivars in South and Southeast Asia through molecular marker-assisted breeding, thus contributing to food security in these regions.

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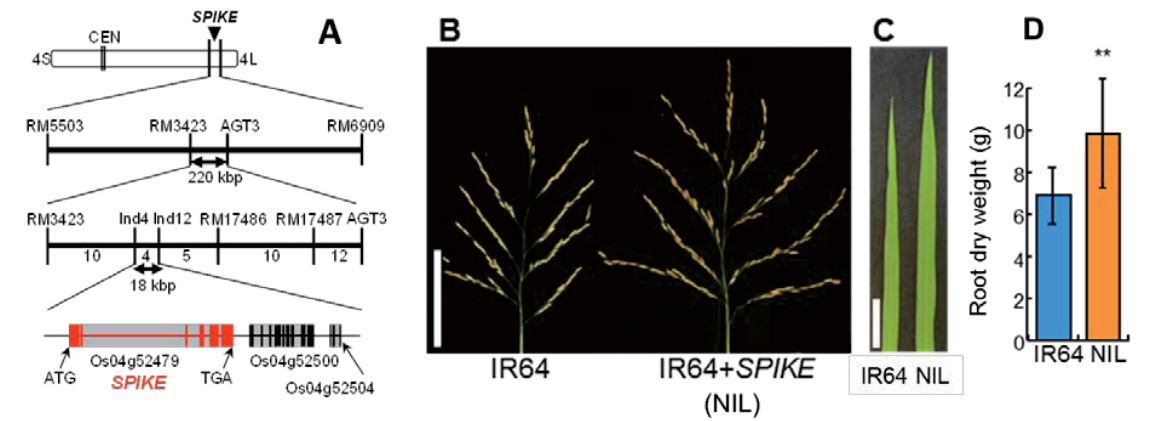


Fig. 1 Chromosomal location of *SPIKE* (A), panicle architecture (B), flag leaf width (C) and root dry weight (D). Values are mean \pm SD. **Significant at 1% level by *t*-test.

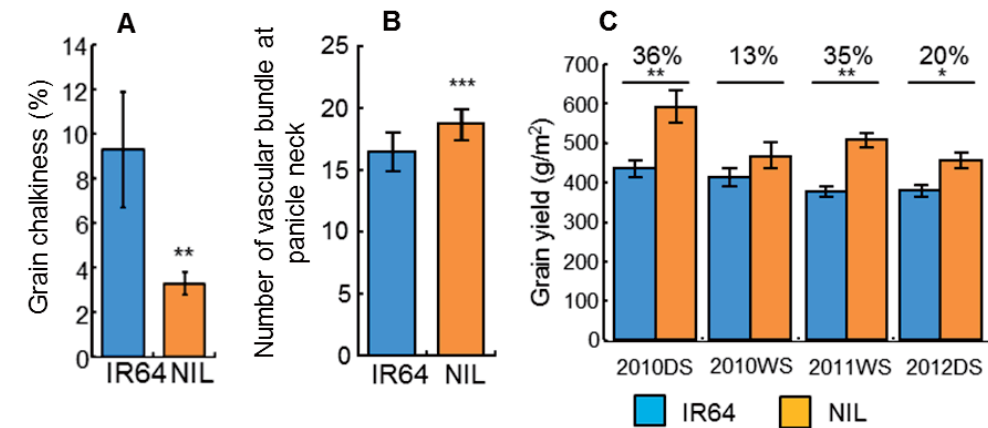


Fig. 2 Percentages of grain chalkiness (A), number of vascular bundle at panicle neck (B) and grain yield (C). Values are mean \pm SD (A, B) or SE (C). Significant at ***0.1%, **1% and *5% level by *t*-test.

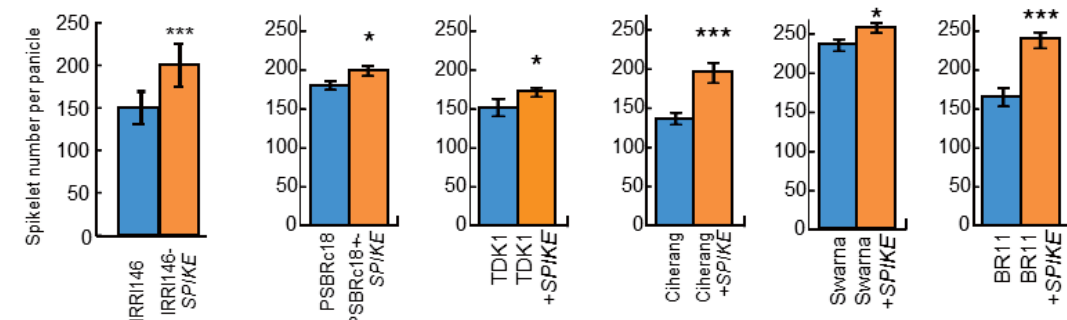


Fig. 3 Total spikelet number per panicle between *Indica*-type cultivars with and without *SPIKE*. Values are mean \pm SE. Significant at ***0.1%, **1% and *5% level by *t*-test.