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Genetic dissection and pyramiding of quantitative traits for panicle architecture by using chromosomal segment substitution lines in rice

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The study of rice productivity is vital to ensuring adequate food for all. Rice yield—the total amount of grain harvested—is broadly divided into two components: sink size (panicle architecture or grain size) and source potential (efficiency of photosynthesis). The balance between these two components makes yield one of the most complex traits. The panicle consists of spikelets and rachillae, which are composed of peduncles and primary, secondary, and tertiary branches. In general, elite indica rice cultivars with high yield tend to have more spikelets than japonica cultivars, but this is because they also have longer panicles, longer branches, and more primary and secondary branches. In other words, optimization of the balance of panicle components is also necessary for increasing spikelet numbers, which is the most direct way to increase yield.

To understand the genetic basis of complicated quantitative trait, such as yield-related traits of rice, chromosome segment substitution lines (CSSLs) become a powerful tool for an initial approach. CSSL is a series of experimental lines in which a particular chromosomal segment from a donor line is substituted into the genetic background of the recurrent line. The substituted segments cover all chromosomes in a whole set of lines. We developed CSSLs consisting of 39 lines from a cross between an average-yielding japonica cultivar, Sasanishiki, as the recurrent parent and a high-yielding indica cultivar, Habataki, as the donor (Fig. 1).

By using these plant materials, we mapped quantitative trait loci (QTLs) controlling morphological components of panicle architecture. Five morphological components of panicle architecture—number of spikelets per panicle (SN), number of primary branches per panicle (PBN), average number of secondary branches per primary branch (SBN), panicle length (PL), and primary branch average length (PBL)—in the CSSLs were evaluated in 2 years, and 38 QTLs distributed on 11 chromosomes were detected (Fig. 1). Considerable QTLs were distributed throughout the genome and the effect of each QTL was not so large compared with phenotypic difference between both parents.

To confirm effect of the QTL detected in the CSSL, we developed near-isogenic lines (NILs) for two of the major QTLs for secondary branch number on chromosome 1 (*qSBN1*) and primary branch number on chromosome 6 (*qPBN6*) by marker-assisted selection (Fig. 2), and we analysed the independent and combined phenotypic effects of those QTLs by pyramiding in the Sasanishiki genetic background (Fig. 3). NIL(*PBN6*) and NIL (*SBN1*+*PBN6*) exhibited larger PBNs than that of Sasanishiki. Similarly, NIL(*SBN1*) and NIL (*SBN1*+*PBN6*) exhibited larger SBNs than that of Sasanishiki. On the other hand, all three lines produced more spikelets than Sasanishiki, and NIL(*SBN1*+*PBN6*) produced more spikelets than the other two NILs. These results clearly validate that *qSBN1* and *qPBN6* contributed independently to sink size and that the combined line produced more spikelets. This suggests that the cumulative effects of QTLs distributed throughout the genome form the major genetic basis of panicle architecture in rice.

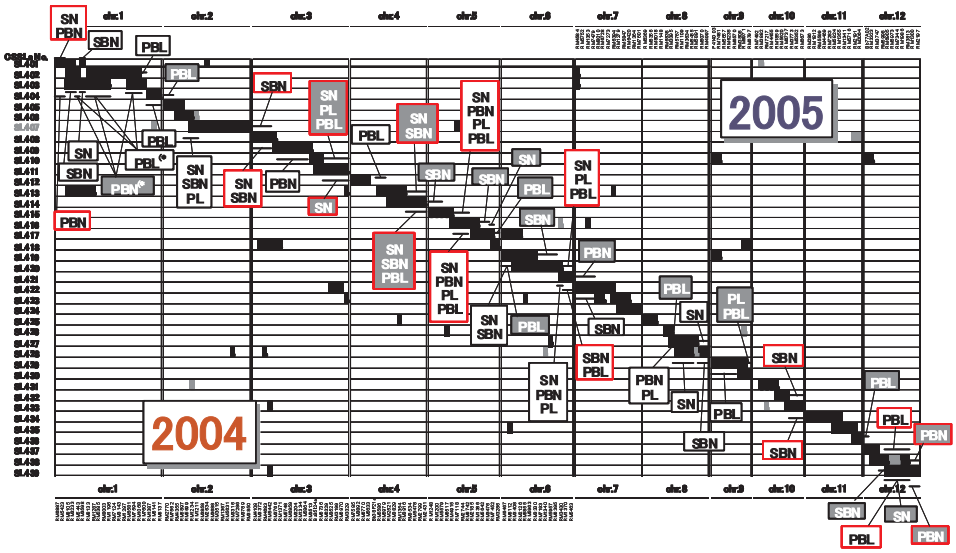

Fig. 1 Chromosomal locations of QTLs for panicle architecture
QTLs detected in 2004 and 2005 are labeled in the lower left and upper right corners, respectively. SN: spikelet number per panicle; PBN: primary branch number per panicle; SBN: secondary branch number per panicle; PL: panicle length; PBL: primary branch length. Black letters on white box indicate traits increased by Habataki allele, and white letters on shaded box indicate traits reduced by Habataki allele. Boxes enclosed with red color indicate the QTLs detected in both years.

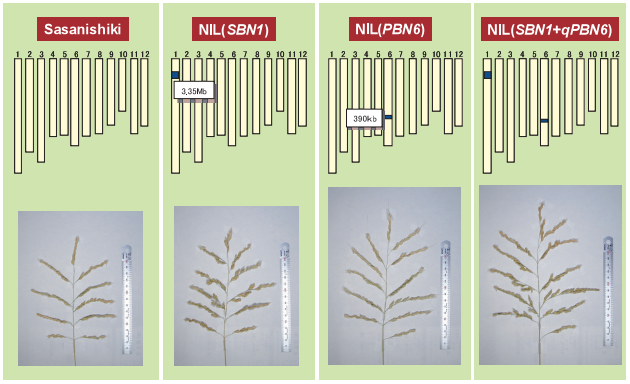

Fig. 2 Graphical genotypes and panicle appearances of Sasanishiki and QTL-NILs developed in the pyramiding experiment
The lengths of the substituted regions were 3.35 Mb in NIL(*SBN1*) and 390 kb in NIL(*PBN6*). Length of ruler in the picture is 15 cm.

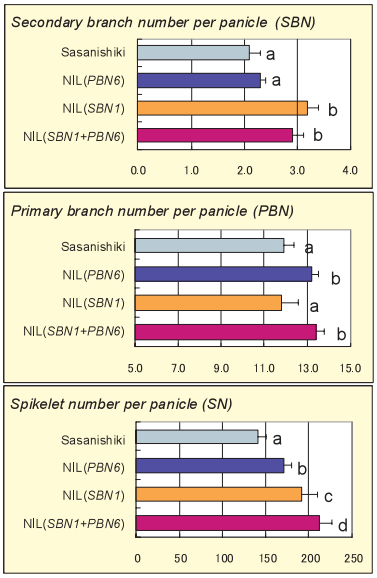

Fig. 3 Phenotypic performances of the QTL-NILs
Bars followed by different letters are significantly different by multiple comparison (Tukey's test).