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Screening QTLs for Lodging Resistance in Rice, Using Cheongcheong/Nagdong Doubled Haploid Population

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[Introduction]

Lodging is the most common factor that affects crop productivity, gain quality, harvesting efficiency, and reducing yield. One of the most common difficulties in developing high-yield varieties is lodging. Therefore, it is important to develop rice variety that are lodging resistance and to found the possible gene responsible to improve plant resistance against lodging.

[Materials and Methods]

The Cheongcheong/Nagdong Doubled Haploid (CNDH) population used for constructing genetic map were developed from a cross between Cheongcheong and Nagdong. Pushing strength of the lower stem before the heading date (PSLSB) and pushing strength of the lower stem after the heading date (PSLSA) were measured when plants were bent to 45º using the digital force gauge (IMADA, Japan). To identify the putative QTLs (Quantitative trait loci), WinQTLcart 2.5 and genetic map that the average interval of markers is 10.6 cM made by Mapmaker version 3.0 using 222 SSR markers. Composite interval mapping (CIM) was operated for the entire genome at a threshold of LOD 3.0 after put in all required data.

[Results and Discussion]

A QTL analysis of PSLSA and PSLSB detected on RM439-RM20318 on chromosome 6 has overlap in three consecutive years and contained 15 lodging resistance candidate genes. Among the candidate genes, *Os06g0623200*, name *OsPSLSq6*, which is similar to *Cinnamoyl-CoA reductase*, involved lignin biosynthesis in defense responses. Lignin is the main structual component of vascular plants' secndary cell wall, which is not only related to plant growth and development but also to mechanical strength. *OsPSLSq6* opens new possibilities to control lignin synthesis to improve lodging resistance and can be used as a target gene for further studies.

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