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Identification of Candidate Gene for Tiller Number in the CNDH Population Using QTL Analysis

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[Introduction]
Rice tiller are the one of most important traits for rice yield and development, however although little is known about its mode of inheritance. Therefore, it is important understanding the genetic foundation for control the tiller number to develop ideal rice genotypes using QTL analysis.

[Materials and Methods]
The Cheongcheong/Nagdong Doubled Haploid (CNDH) population used for constructing genetic map were developed from a cross between Cheongcheong and Nagdong. Tiller number was recorded every 7 days for a total of nine times starting at 30 days after transplanting. 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 2.5 after put in all required data.

[Results and Discussion]
A QTL analysis of tiller number detected on RM18130-RM3381 on chromosome 5 has overlap in eight measuring stages and contained 61 tiller number candidate genes. Among the candidate genes, *Os05g0230700*, name *OsIAAq5*, which is similar to Auxin-responsive protein IAA17. Auxin is promoting cell division and meristem maintenance. Auxin as an effective plant regulator that influence plant growth and development through altering various gene expression. *OsIAAq5* opens new possibilities to control tiller number and can be used as a target gene for further studies. Moreover, the newly discovered QTL regulating tiller number might provide a potential new way to develop ideal rice genotypes. These results provide a basis for cloning QTLs that contribute significantly to tiller number in rice.

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