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Identification for Genes Related with Methane Emission Based on QTL Mapping and Proposal of Ideal Plant Type of Rice

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[Introduction]

Global warming is accelerating due to greenhouse gases including CH_4 emitted from rice fields. Rice is grown under anaerobic conditions, it induces CH_4 production and is a major source of CH_4 emissions. Therefore, in order to develop rice with reduced methane emission, it is important to identify the mechanism of CH_4 emission and related genes.

[Materials and Methods]

A chamber utilizing a methane detection sensor was designed for CH_4 measurement. As plant material, 120 Cheongcheong/Nagdong double haploid (CNDH) populations were used. CH_4 emissions were measured at the fourth leaf stage. Windows QTL Cartographer 2.5 and the genetic map was used to analyze the QTL. The threshold LOD score 2.0 or higher was used to perform the QTL analysis.

[Results and Discussion]

In chromosomes 1, 3 and 6, QTL related with CH₄ emission with an LOD value of 3.3 was detected. As a result of analyzing the gene expression of 39 candidate genes related to CH₄ emission, there were significant differences in $LOC_Os03g13520$, $LOC_Os03g07480$, and $LOC_Os03g13274$ located in the RM14330-RM7197 region of chromosome 3. Among them, $LOC_Os03g07480$ (*OsSUTq3*) is a gene that plays the role of a sucrose transporter and is expected to be closely related to CH₄ emission. Also, CH₄ emission is closely related to traits such as culm length and seed characteristics. These results can be useful for the development of methane-reducing rice in response to climate change.

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