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QTL Analysis of Plant Height in Rice Using CNDH Population

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[Abstract]

Rice is a staple crop used by more than 50% of the world's population. However, in rapidly changing climates such as abnormal high temperatures and typhoons, the food security of rice is greatly threatened. Plant factories have the advantage of being able to grow crops regardless of climate change, so they can be a response to climate change. However, in plant factories, crops are grown by placing the culture bed vertically, so shorter crops are more efficient. Therefore, in order to search for genes related to the height of rice, QTL analysis was performed by investigating the plant height of Cheongcheong/Nagdong doubled haploids from 2017 to 2021. Plant height of rice investigated for five years showed a normal distribution, meaning that genes related to rice height are quantitative traits. As a result of QTL analysis, a total of 12 QTLs were detected, and QTLs overlapped for 5 years in RM12285-RM212 on chromosome 1. Also, The QTLs of plant height detected in 2019 has a LOD score of 17.64 in RM12285-RM212 region of chromosome 1. As a result of QTL analysis, 44 height-related genes were searched from the detected chromosomes, and among them, *Os01g0757200* in RM12285-RM212 on chromosome 1 region, named *OsGA2ox3q1*, were selected as genes related to the height of rice. The relative gene expression level of *OsGA2ox3q1* was highly expressed in cultivar with short culm lines, and was low expressed in cultivar with long culm lines. *OsGA2ox3q1* can be used to breed semi-dwarf cultivar in rice more efficiently.

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