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QTL Mapping of Plant Height of Rice in the CNDH Population

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[Introduction]

Plant factories have been actively studied since they started in Denmark in 1957 with the advantage of being able to produce agricultural products stably regardless of the rapidly changing climate and controlling the growing and harvesting period of agricultural products with a system. The height of a plant is one of the representative agricultural traits, and since the culture bed is arranged vertically in the plant factory, the shorter the plant height, the more efficient the plant can be grown. Therefore, in this study, genes related to the height of rice were searched using quantitative trait loci (QTL) analysis.

[Material and Methods]

To identify genes related to the height of rice, 120 Cheongcheong/Nagdong doubled haploid (CNDH) population were used as materials. Plant height, culm length, and panicle length of the CNDH lines were investigated for five years from 2017 to 2021. For QTL analysis, a genetic map with an average interval of 10.6 cM between the markers made in Mapmaker 3.0 version using Windows QTL Cartographer and 222 SSR markers was used. For QTL analysis, the Threshold LOD score higher than 2.5 was used.

[Result and Discussion]

Plant height, culm length, and panicle length of rice investigated for five years show a normal distribution, meaning that genes related to rice height are quantitative traits. Total twenty-six QTLs related to rice height were detected in the chromosomes except for 4, 9 chromosomes. 9 QTLs were detected in Plant height, culm length, and panicle length for five years in the RM12285-RM212 region of chromosome 1. The QTLs of plant height detected in 2019 has a LOD score of 17.64 in RM12285-RM212 region of chromosome 1. This result can be used to develop dwarf rice suitable for growing in plant factory.

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