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Grain Size Related Gene in CNDH, and Identification Of Shape Based on QTL Mapping in Rice

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[Abstract]

Rice is 34% of the world's population used as a staple food. But the world population is increasing. Food security is not well protected. Improving cultivar development can address food security. Quantitative trait locus (QTL) mapping is a statistical analysis using both phenotypic and genotypic dates. The purpose of QTL mapping is to determine a gene. Increasing grain size is a way to increase yield in rice. Grain size-related genes were mapped using CNDH population obtained by cross-breeding Cheongcheong (*Indica*) and Nagdong (*Japonica*) through anther culture. Grain harvested from experimental field of Kyungpook National University in Gunwi in 2021. Genes related to grain length were detected between RM5964-RM12285, RM20924-RM20967 in chromosome 1, 7. LOD score is 5.88 and 5.6. Genes related to grain width was detected between RM289-RM18130 in chromosome 5. LOD score is 4.57. Genes related to grain length/width ratio were detected between RM5459-RM3482, RM5699-RM1211 and RM3838-RM3381 in chromosome 1, 2, 5. LOD score is 3.75, 3.14 and 3.41. 4 genes was detected in chromosome 1 and 2 genes was detected in chromosome 2 and 7 genes was detected in chromosome 5. 2 genes related to grain shape and quality were detected. 4 genes related to grain length were detected. 4 genes related to grain size were detected. 1 gene related to grain size and weight was detected. 2 genes related to grain length and weight were detected. By finding the gene related to grain size, it provides food to people threatened by food security and solves the food shortage.

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