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## Find CNDH Grain Size Relate Gene, and Identification of Shape Based on QTL Mapping in Rice

Ji-Hun Kim<sup>1</sup>, Jae-Ryoung Park<sup>2,3</sup>, Yoon-Hee Jang<sup>3</sup>, Eun-Gyeong Kim<sup>3</sup>, Kyung-Min Kim<sup>1,3\*</sup>

<sup>1</sup>Department of Applied Biosciences, Graduate School, Kyungpook National University, Daegu, 41566, Korea

<sup>2</sup>Crop Breeding Division, National Institute of Crop Science, Rural Development Administration, Wanju, 55365, Republic of Korea

<sup>3</sup>Coastal Agriculture Research Institute, Kyungpook National University, Daegu 41566, Republic of Korea

### [Introduction]

Rice is one of the world's top three crops that 34% of the world's population used as a staple food. But although the world population is increasing, food security is not well protected. Quantitative trait locus (QTL) mapping is a statistical analysis using both phenotypic and genotypic data. The purpose of QTL mapping is to determine a gene. Increasing grain size is a way to increase yield in rice.

### [Materials and Methods]

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. The data were analyzed through QTL. Data analyzed through QTL used RiceXpro and RAP-DB to found candidate genes.

### [Results and Discussion]

Frequency distribution for grain length, grain width, and grain length&width ratio in CNDH lines. Because all traits showed a normal distribution. Genes related to grain length were detected between RM5964-RM12285 and RM20924-RM20967 in Chromosome 1,7. Genes related to grain width was detected between RM289-RM18130 in Chromosome. Genes related to grain length/width ratio were detected between RM5459-RM3482, RM5699-RM1211 and RM3838-RM3381 in Chromosome 1,2,5. Found the candidate gene *Os05g0232500*, *Os05g0235300* associated with the grain width. Though this, we will protect food security by looking for genes related to Grain size.

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\*Corresponding author: E-mail, kkm@knu.ac.kr Tel. +82-053-950-5711