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## QTL Mapping and Candidate Gene Screening Strategy for High Yield Rice Breeding

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### [Introduction]

Rice is the world's most stable food. However, as population growth accelerates with recent rapid climate change, increasing yield is the main goal of rice breeders. Grain size is directly related to grain weight and is the first factor considered for high yield. QTL mapping statistically detects the interaction between phenotype and environment on a genetic map. And screening candidate genes through QTL mapping improves the accuracy of breeding through precision breeding.

### [Materials and Methods]

JJ625LG/Namchan Recombinant Inbred Lines (JNRILs) derived from crossing JJ625LG and Namchan were used as the mapping population. Grain length, width, ratio of grain length to width, and 1000-grain weight, which are traits related to the grain size of each line, were investigated. The correlation of each trait was analyzed, and the QTL region related to grain size was mapped. Then, candidate genes were screened in the mapping region to predict gene homology and protein interaction.

### [Results and Discussion]

For each line of JNRILs, the grain size was investigated. All investigated traits were normally distributed. When performing QTL mapping, *GS3* and *qSW5*, which are major genes for grain size, were identified on chromosomes 3 and 5. And *OsCPq10* was screened on chromosome 10. *OsCPq10* is a sequence coding for cytochrome P450 protein. Cytochrome P450 protein increases yield by positively regulating grain size in *Triticum*, *Hordeum vulgare*, *Zea mays*, and *Sorghum*. Also, when protein interaction is predicted, it interacts with the protein that controls the grain size of rice. We suggest that a strategy for screening candidate genes in QTL mapping can increase precision breeding efficiency.

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