

PB-19

Identification of Stem Related QTLs Using Milyang23/Gihobyeo Recombination Inbred Lines (MGRILs) in Rice

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[Introduction]

Rice (*Oryza sativa* L.) is one of the most important staple food for more than half the world's population. However, lodging resistance, a major problem in rice breeding, often cause decreases in yield and quality because of severe weather conditions. The objective of this study were to construct the high-resolution genetic map using 'Milyang23' and 'Gihobyeo' recombination inbred lines (MGRILs) and detect highly effective quantitative trait loci (QTLs) related to stems.

[Materials and Methods]

Rice plants were both cultivated in the field and greenhouse, and then investigated the culm length and internode diameters. In genetic analysis, single nucleotide polymorphism (SNP)-based markers from 162 RILs were developed through re-sequencing analysis by next generation sequencing (NGS). Recombination breakpoints were visualized on bin-map and used for the construction of the high-resolution genetic map. This map was applied to QTLs analysis of culm length and internode diameters in rice using Windows QTL Cartographer version 2.5 software.

[Results and Discussion]

In phenotype investigation, normal distributions were shown as the wide variations in all five traits; culm length (CL) and each of four internode diameters (ID1, ID2, ID3 and ID4) from the field and greenhouse, respectively. Significant difference was also shown positively among internode diameters. 2,739 SNP-based markers were developed from re-sequencing, and integrated with 463 PCR-based markers to perform QTL mapping. As a result, 22 QTLs were totally detected for five traits on both the field and greenhouse, and 22 of 10 QTL regions were overlapped with high accuracy. These QTL information will be useful to identify genes related to lodging resistance.

[Acknowledgement]

This research was supported by "National Institute of Agricultural Sciences" (Project No. PJ013442), Rural Development Administration, Republic of Korea.

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