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Development of KASP Markers by Genome Re-sequencing of Korean *japonica* Rice Varieties

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[Introduction]

Korean *japonica* rice varieties exhibit remarkable phenotypic variation in important agronomic traits such as disease resistance and yield, despite narrow genetic diversity. However, high-through molecular markers have been required to analyze quantitative trait locus (QTL) in Korean *japonica* rice varieties. Therefore, to develop DNA markers within closely-related Korean *japonica* rice varieties, data obtained from genome re-sequencing 13 Korean *japonica* rice varieties were analyzed to detect single nucleotide polymorphisms (SNPs) among these varieties, and the detected SNPs were converted to kompetitive allele-specific PCR (KASP) markers.

[Materials and Methods]

gDNAs of 13 Korean *japonica* rice varieties were extracted from young leaves, and Illumina HiSeq2000 and CLC Assembly Cell (ver.3.2.2) were used to analyze SNPs of 13 Korean *japonica* rice varieties with reference genome Nipponbare. Polymorphism information content (PIC) values of SNPs were calculated for the design of KASP assays. The PCR profile and composition of KASP reactions were described at <https://www.lgcgroup.com>.

[Results and Discussion]

740,566 SNPs were discovered through re-sequencing of the 13 rice varieties. As a result of annotation of the 740,566 SNPs detected, 572,691 SNPs and 167,875 SNPs were located in the intergenic (77.3%) and genic (22.7%) regions, respectively. Of the genic region SNPs, 86,863, 48,044, 20,714, 10,314, and 1,940 SNPs were detected in introns (51.7%), coding sequences (28.6%), 3' untranslated region (UTR) (12.3%), 5'UTR (6.1%), and non-coding exon (1.2%), respectively. The SNP sites which were selected on the basis of PIC value higher than 0.4 per 200-kbp interval among 740,566 SNPs have been being converted to KASP markers. These KASP markers will be utilized in QTL mapping, marker-assisted selection, and other strategies relevant to crop improvement.

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