Association Analysis of Heading Time, Culm Length, Amylose and Protein Contents in Korean *japonica* Rice Varieties

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[Introduction]

Association mapping is widely used in rice to identify genes or quantitative trait loci controlling agriculturally important traits. Populations composed of landraces or varieties with various geographical origins are popularly used in association mapping to maximize genotypic and phenotypic diversity. While being less frequently used due to limited genetic diversity, association mapping with elite varieties can provide more practical value by mining alleles that can be directly applied in breeding programs.

[Materials and Methods]

A total of 161 Korean elite *japonica* rice varieties were genotyped with 173 polymorphic SSRs and phenotyped for days to heading, culm length, amylose and protein contents. Marker-trait association analysis was conducted with four different models: the simple model (single-locus ANOVA) carried out using SAS (v9.2), the Q model considering population structure, the K model considering familial relatedness, and the Q + K model conducted using TASSEL (v3.0).

[Results and Discussion]

Abundant phenotypic variation was observed in days to heading (74 − 122 days), culm length (55 − 96 cm), amylose content (6.3 − 25.9%) and protein content (5.7 − 9.2%) among 161 Korean *japonica* rice varieties. The quantile-quantile plots of observed and expected P-values from the four models (simple, Q, K, Q + K) indicated that adding the kinship (K) matrix in the model controls spurious associations effectively. Therefore, the K model was selected to identify significant marker-trait associations. At the threshold of $P < 0.01$, six, seven, and ten significant loci were identified for days to heading, culm length, and amylose content, respectively. As only one significant locus was detected for protein content at $P < 0.01$, four loci at $P < 0.02$ were selected for further analysis. Additive effects of the significant loci were tested by analyzing correlation between observed phenotypic values and the sums of allelic effects of the significant loci for each trait. Highly significant positive correlations were observed for days to heading ($r = 0.6119$; $P < 0.0001$), culm length ($r = 0.5765$; $P < 0.0001$), amylose content ($r = 0.6301$; $P < 0.0001$), and protein content ($r = 0.4954$; $P < 0.0001$).

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