

Genetic Diversity and Population Structure of 179 Korean Rice Varieties based on Microsatellite Markers

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[Introduction]

This study was conducted to evaluate genetic diversity and population structure of 179 Korean rice varieties bred by the National Institute of Crop Science, Rural Development Administration of South Korea during 1970 – 2006.

[Materials and Methods]

A total of 179 Korean rice varieties used in this study are composed of 161 *japonica* and 18 Tongil-type varieties. In addition, IR24 and its eight near-isogenic lines carrying different bacterial blight resistance genes were included as controls – IRBB1 (*Xa1*), IRBB3 (*Xa3*), IRBB4 (*Xa4*), IRBB5 (*xa5*), IRBB7 (*Xa7*), IRBB8 (*xa8*), IRBB10 (*Xa10*), and IRBB21 (*Xa21*). A total of 192 polymorphic SSR markers were used to genotype the 188 rice varieties. Genetic diversity and population structure were analyzed using software PowerMarker (v3.25), DARwin (v6.0.017), NTSYSpc (v2.21o), and STRUCTURE (v2.3.4).

[Results and Discussion]

A total of 828 alleles were identified from 192 polymorphic SSRs in 188 rice varieties. In spite of the smaller number of accessions, 18 Tongil-type varieties had higher number of polymorphic markers (189 SSRs) than 161 *japonica* varieties (173 SSRs). Also, both gene diversity and polymorphism information content values were higher in 18 Tongil-type varieties (0.3810 and 0.3410, respectively) than in 161 *japonica* varieties (0.3075 and 0.2703, respectively). This indicated that Korean *japonica* rice varieties have very narrow genetic diversity. Phylogenetic analysis using 192 polymorphic SSRs clearly differentiated the 188 varieties according to their subspecies designations (161 *japonica*, 18 Tongil-type, and nine *indica*). Similar pattern was observed in principal component analysis (PCA), in which most *japonica* varieties formed a very tight cluster that is differentiated from Tongil-type and *indica* varieties. Both phylogenetic analysis and PCA demonstrated that Korean *japonica* rice varieties are genetically very close to each other and thus have limited genetic diversity. To further evaluate subpopulation structure within the *japonica* population, an additional PCA was conducted among 161 Korean *japonica* varieties using 173 polymorphic SSRs. The first principal component explaining 69% of the variance did not classify 161 *japonica* varieties. Although the second principal component divided 161 *japonica* varieties into two potential subpopulations, it explained only 4% of the variance, indicating that the Korean *japonica* varieties used in this study likely belong to a single population.

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