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Population Genetic Structure and Marker - Trait Associations in a Collection of Traditional Rice (*Oryza sativa* L.) from Northern Vietnam

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[Abstract]

Rice is the world's most important food crop and a major source of nutrition for about two thirds of populations. Northern Vietnam is one of the most important centers of genetic diversity for cultivated rice. In this study, we determined the genetic diversity and population structure of 79 rice landraces collected from northern Vietnam and 19 rice accessions collected from different countries. In total, 98 rice accessions could be differentiated into *japonica* and *indica* with moderate genetic diversity and a polymorphism information content of 0.382. We also detected subspecies-specific markers to classify rice (*Oryza sativa* L.) into *indica* and *japonica*. Additionally, we detected five marker-trait associations and rare alleles that can be applied in future breeding programs. Most interestingly, analysis of molecular variance (AMOVA) found genetic differentiation was related to geographical regions with an overall PhiPT (analog of fixation index FST) value of 0.130. More emphasis was given to provide signatures and infer explanations about the role of geographical isolation and environmental heterogeneity in genetic differentiation among regions in landraces from northern Vietnam. Our results suggest that rice landraces in northern Vietnam have a dynamic genetic system that can create different levels of genetic differentiation among regions, but also maintain a balanced genetic diversity between regions.

[Acknowledgement]

This work was carried out with the support of "Cooperative Research Program for Agriculture Science and Technology Development (Project No. PJ015757)" Rural Development Administration, Republic of Korea.

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