

Genetic Diversity Analysis of Proso millet (*Panicum miliaceum*) Germplasm Using EST-SSR Markers

Myung-Chul Lee, Yu-Mi Choi, Hyemyeong Yun, Myoung-Jae Shin,
Sukyeung Lee and Sejong Oh

National Agrobiodiversity Center, National Institute of Agricultural Sciences, RDA,
Jeonju 54874, Korea

The collection, evaluation and conservation of crop germplasm have been treated as one of the basics to breeding program. An understanding of genetic relationships among germplasm resources is vital for future breeding process like yield, quality, and resistance. In the present study, EST-SSR markers were employed to assess the polymorphism and genetic diversity of 192 accessions of Proso millet preserved in the National Agrobiodiversity Center of RDA. We evaluated the efficiency of EST-SSR markers developed for proso millet species. A total of 98 alleles were detected with an average allele number of 4.5 per locus among 192 proso millet accessions using 22 EST-SSR markers. The averaged values of gene diversity (H_E) and polymorphism information content (PIC) for each EST-SSR marker were 0.362 and 0.404 within populations, respectively. Our results showed the moderate level of the molecular diversity among the proso millet accessions from diverse countries. A phylogenetic tree revealed three major groups of accessions that did not correspond with geographical distribution patterns with a few exceptions. The less correlation between the clusters and their geographic location might be considered due to their type difference. Our study provided a better understanding of genetic relationships among various germplasm collections, and it could contribute to more efficient utilization of valuable genetic resources. The EST-SSR markers developed here will serve as a valuable resource for genetic studies, like linkage mapping, diversity analysis, quantitative trait locus/association mapping, and molecular breeding.

Key words: Proso millet, EST-SSR, Genetic diversity