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Phylogeography and Antioxidant Activity of Proso Millet (Panicum miliaceum L.)

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[Introduction]

Proso millet (*Panicum miliaceum* L.) or broomcorn millet is among the most important food crops to be domesticated by humans; it is widely distributed in America, Europe, and Asia.

[Materials and Methods]

In this study, we genotyped 578 accessions of *P. miliaceum* using 37 single-sequence repeat (SSR) markers, to study the genetic diversity and population structure of each accession. We also in-vestigated total phenolic content (TPC) and superoxide dismutase (SOD) activity and performed association analysis using SSR markers.

[Results and Discussion]

The results showed that genetic diversity and genetic distance were related to geographic location and the fixation index (Fst). Population structure analysis divided the population into three subpopulations. Based on 3 subpopulations, the population is divided into six clusters in consideration of geographical distribution characteristics and agronomic traits. Based on the genetic diversity, population structure, pairwise Fst, and gene flow analyses, we described the topological structure of the six proso millet subpopulations, and the geographic distribution and migration of each cluster. Comparison of the published cluster (cluster 1) with unique germplasms in Japan and South Korea suggested Turkey as a possible secondary center of origin and domestication (cluster 3) for the cluster. We also discovered a cluster domesticated in Nepal (cluster 6) that is adapted to high-latitude and high-altitude cultivation conditions. Differences in phenotypic characteristics, such as TPC, were observed between the clusters. The association analysis showed that TPC was associated with SSR-31, which explained 7.1% of the total variance, respectively. The development of markers associated with TPC and SOD will provide breeders with new tools to improve the quality of proso millet through marker-assisted selection.

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