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Establishing a Core Collection of Proso Millet (*Panicum miliaceum*) Germplasm

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The Korean National Agrobiodiversity Center holds the more than 1300 accessions of proso millet, but a large portion of accessions are landrace of Korea that has very similar traits. To comprehend the maximum genetic diversity of this crop, a core collection with minimum number of accessions will facilitate easy access to genetic material. Here we assessed the genetic diversity and population structure in a germplasm collection of 830 accessions by employing EST-SSR markers and morphological traits. A total of 107 alleles were detected with an average allele number of 4.9 per locus among the 830 accessions based on 37 EST-SSR markers. The number of alleles per locus ranged from 2 to 7. Polymorphism information content and expected heterozygosity ranged from 0.06 to 0.68 (mean = 0.21) and 0.06 to 0.73 (mean = 0.23), respectively. The germplasm collection was separated into two groups based on population structure analysis, whereas principal coordinate analysis (PCoA) could not cluster accessions according to their geographic origin. Subsequently, a preliminarily developed core collection with a total of 141 accessions (17%) was selected from the whole set of germplasm by combining allelic variations of EST-SSR markers and eight different phenotypic traits. The core collection optimally represented the whole germplasm collection and displayed a similar level of PCoA value and genetic variation from the initial collection. The results obtained here provide a primary resource for further genetic analysis and establish a reference for further development of appropriate genetic breeding strategies.

Key words: Proso millet, Core collection, EST-SSR, Traits

[This work was supported by a grant (No. PJ013539032020) from the National Institute of Agricultural Sciences, Rural Development Administration, Republic of Korea.]

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