

Assessment of genetic diversity in little millet (*Panicum sumatrense*) germplasm using EST-SSR

Myung-Chul Lee^{1*}, Yu-Mi Choi¹, Do-Yoon Hyun¹, Sukyeung Lee¹ and Sejong Oh¹

¹National Agrobiodiversity Center, National Institute of Agricultural Sciences, RDA, Jeonju 54874, Republic of Korea

[Introduction]

Little millet (*Panicum sumatrense*) is well known for its salt and drought stress tolerance and high nutritional value, but very limited knowledge of genetic variation and genomic information is available.

[Materials and Methods]

This study was to develop highly polymorphic EST-SSR markers based on cross-species transferability of derived SSRs from switchgrass EST databases and characterize newly developed EST-SSRs to better understand the genetic diversity of collected 37 germplasm accessions of little millet.

[Results and Discussions]

In this study, a total of 779 primer pairs were designed from the 22,961 EST sequences of switchgrass (*Panicum virgatum*), of which 48 EST-SSR markers were developed based on the trials of transferability of these primers in little millet. The EST-SSR amplicons showed reproducible single band polymorphism and produced a total of 160 alleles with an average of 3.3 alleles per locus in 37 accessions of little millet. The average values of expected and observed heterozygosities were 0.266 and 0.123, respectively. The polymorphic information content (PIC) values were observed in range of 0.026 to 0.549 with an average of 0.240. The genetic relatedness among the little millet accessions was evaluated by neighbor-joining dendrogram, which grouped all accessions into two distinct groups. The validation thus demonstrated the utility of the switchgrass EST-SSR markers in assessing genomic relationships in little millet. The findings from this study could be useful for designing strategies for the identification of diverse germplasm for conservation and future molecular breeding programs for little millet.

[Acknowledgements]

This work was supported by a grant (No. PJ013083) from the National Institute of Agricultural Sciences, Rural Development Administration, Republic of Korea.

*Corresponding author: Tel. 063-2239-4900, E-mail. mcleekor@korea.kr