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Development of SSR markers and analysis of genetic diversity and population structure in Finger millet (*Eleusine coracana* L. Gaertn)

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Statement of the Problem: Micronutrient deficiency has been recognized as a serious human health problem worldwide. Finger millet (*Eleusine coracana* L. Gaertn.), highly self-pollinating crop, is a good source of micronutrients like, iron and zinc. Genetic diversity of finger millet has been assessed using different molecular markers, but these studies are limited and more and more germplasm needs to be characterized at molecular level for identification of diverse germplasm links/subpopulations to use in crop improvement.

Methodology & Theoretical Orientation: In this study, we analyzed the genome-wide distribution of microsatellites in finger millet. By sequencing 815 clones from an SSR-enriched genomic DNA library, we obtained 12 polymorphic SSR markers, which also revealed successful amplicons in finger millet accessions.

Findings: Using the developed SSR markers, we estimated genetic diversity and population structure among 76 finger millet accessions in Asia, Africa, and unknown origin. The number of alleles ranged from 2 to 9, with an average of 3.3 alleles. The mean values of observed heterozygosity and expected heterozygosity were 0.27 and 0.35, respectively. The average polymorphism information content was 0.301 in all 76 finger millet accessions. AMOVA analysis showed that the percentage of molecular variance among the populations was 1%, among individuals was 5%, and within individuals was 94%. In STRUCTURE analysis, 76 finger millet accessions were divided into two subpopulations and it revealed that two subpopulations had an admixture of alleles. There was correspondence among PCoA, AMOVA, and population structure.

Conclusion & Significance: In this study, we have developed the 12 SSR markers in finger millet and confirmed that all 76 finger millet accessions were genetically diverse and were clustered into two subpopulations. Data generated through this study may be utilized for mapping of any important agronomical trait for breeding programs to improve the finger millet.

Biography

Mun-Sup Yoon is working as a Senior Scientist in National Agro Biodiversity Center, Republic of Korea. He is now responsible for Deputy Director of Planning and Cooperation team in NAC. He has performed the research mainly for the diversity of soybean germplasm using molecular marker as SSR, SNP and AFLP. He made core collection for Korean soybean landraces using morphological and chemical characteristics. He contributed in making soybean molecular map developing the soybean SNP marker during postdoctoral course in Soybean Improvement Lab, of USDA-ARS.

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