Analysis of Molecular Diversity of Selected Foxtail Millet (*Setaria italica*) Germplasm in Sri Lanka Using Microsatellite Markers

Tharindi P.W.M.[1 *], Bandara P.K.G.S.S.[2], Karunaratne P.M.A.S.[1], and Wimalasiri G.E.M.[1]

[1]*Department of Export Agriculture, Faculty of Agricultural Sciences, Sabaragamuwa University of Sri Lanka*
[2]*Department of Biosystems Technology, Faculty of Technology, Sabaragamuwa University of Sri Lanka*
[*]*malitha@agri.sab.ac.lk*

In Sri Lanka, foxtail millet, a nutritionally rich and climate-resilient cereal, remains as an underutilized crop. To ensure its future breeding and conservation, understanding its genetic diversity is essential. A modified DNA extraction protocol and optimized PCR protocols allowed the screening of 24 SSR primers for further studies. From 29 diverse genotypes collected across Sri Lanka, 10 were selected for preliminary diversity analysis using 5 SSR markers after three generations of self-pollination. Products were analyzed on a 2% agarose gel and further assessed using Power Marker V3.25 software. The results underscored significant insights. Major Allele Frequency ranged from 0.3 to 0.6 with an average of 0.46 per SSR locus. The allele number per locus varied from 4 to 5, with a mean of 4.6. The polymorphic information content (PIC) of the 5 SSR markers ranged from 0.54 to 0.72, with an average of 0.64 indicating their informativeness for genetic diversity analysis. A complete absence of heterozygosity in the studied markers indicates a potential homozygosity. Further, the developed dendrogram revealed two primary clusters at the highest level of dissimilarity (0.48). Among the genotypes, KCFM 013-3 and 0415PGRC displayed the closest genetic affinity. Despite being in the same cluster, genotypes, Panamure and 341 PGRC, exhibited a broader distance of approximately 0.36. The clustering patterns suggest distinct genetic groupings among the selected genotypes. This research lays the groundwork for exploring the genetic potential of foxtail millet germplasm in Sri Lanka for future breeding and conservation endeavours.

Keywords: *Allelic distribution, Genetic diversity, Germplasm characterization, Polymorphic chain reaction, SSR markers*