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Development of EST-SSR Markers for Evaluation of Genetic Diversity and Population Structure in Finger Millet (*Eleusine coracana* (L.) Gaertn.)

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Finger millet, *Eleusine coracana* Gaertn., is more nutritious than other cereals and millets and widely cultivate in tropical regions of the world. However, status of its genetic diversity remained concealed due to lack of research work in this species. In recent years, microsatellites have become the most used markers for studying population genetic diversity. In present study, genetic diversity and structure of different populations of finger millet from Africa and South Asia was examined at molecular level using newly developed EST-Simple Sequence Repeat (EST-SSR) markers using a total of 1,927 ESTs of *Eleusine coracana* available in the NCBI database. In total, 46 primers produced 292 alleles in a size range of 100-500 bp and mean Polymorphism Information Content (PIC) and Marker Index (MI) were 0.372 and 1.04, respectively. 46 primers showed polymorphism and 21 primers were identified as having a PIC value above 0.5. Principal coordinates analysis and the dendrogram constructed out of combined data of both markers showed grouping of finger millet accessions to their respective area of collection. The 156 accessions was classified into four groups, such as three groups of Africa collection and one group of Asia. Results of present study can be useful in identifying diverse accessions and management of this plant resource. Moreover, the novel SSR markers developed can be utilized for various genetic analyses in this species in future.

Key words: EST-SSRs, Genetic diversity, Finger millet