

A BETTER EARTH IS POSSIBLE

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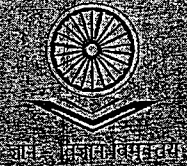
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SSR markerbased genetic diversity of some finger millet germplasm accessions having different geographical origins

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Abstract

Finger millet (*Eleusine coracana* 2n=4x=36) is a cereal staple cultivated in the arid and semi-arid regions of the world. High nutritional value, special qualities like blood glucose and cholesterol lowering and its ability to adapt to a wide range of adverse agro-ecological conditions make finger millet worthy to be focused in large scale in research by which core populations for conservation and parents who give hybrid vigour in crossing programs can be identified. This study was conducted to reveal the genetic diversity of forty eight finger millet germplasm accessions having geographical origins of India, Zimbabwe and Sri Lanka using thirty one SSR (Simple Sequence Repeats) markers published by Dida *et al* 2007.

DNA was extracted from immature leaves, SSR markers were developed for extracted DNA and maker products were separated in 6% polyacrylamide gels, visualized by silver staining. Alleles were scored and the data was analyzed using PowerMarker version 3.25 (Liu and Muse 2006). Shared alleles were calculated and cluster analysis was performed with Neighbor joining method and the Treeview software (TreeView 1.6 version for WXP)

Nine markers were monomorphic, one failed in amplifying the target loci for most of the samples and three were found difficult to score on polyacrylamide gels. Eighteen markers were polymorphic where two of them amplified duplicate loci which were scored as two separate loci. Altogether 20 polymorphic markers were identified and used for the study. Across the 48 accessions, the total number of alleles amplified by 20 markers was 69, ranging from 2 to 8 alleles per locus. Polymorphic information content ranged from 0.04 to 0.80 with a mean of 0.29.

Dendrogram constructed on the basis of SSR polymorphism contained two main clusters leaving one of the accessions of Zimbabwe as an out group. One main cluster comprised of three accessions of India and one of Nuwara Eliya District of Sri Lanka. In the second cluster two sub clusters were identified where one sub cluster contained the remaining three accessions of Zimbabwe, three of India and two accessions of Kurunegala district of Sri Lanka. The rest of the Sri Lankan accessions and five remaining accessions of India were clustered in the second sub cluster. Clustering of accessions of Zimbabwe and India with that of Sri Lanka in the first sub cluster and clustering of Indian accessions with that of Sri Lanka in both the main clusters implies their genetic relatedness irrespective to their geographical origin. The highest distance of 0.70 was observed between one of the accessions of Zimbabwe and one Indian and the accession of Nuwara Eliya District followed by 0.68 between the same accession of Zimbabwe and one of the Indian accessions, 0.65 again between the same accessions of Zimbabwe and one of India, one accession each from Rathnapura and Hambanthota Districts of Sri Lanka. Genetically distinct individuals identified from the study can be used as potential parents in crossing programs. Genetic similarity was observed between four pairs of accessions from different districts of Sri Lanka and between one of the Indian accessions and one accession from Kurunegala District. These data can be used to avoid duplications in conservation programmes.