

Study of the genetic diversity of Moringa germplasm accessions using Simple Sequence Repeat markers for diverse ecosystems of Telangana State

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In the present study, 20 Moringa genotypes collected from diverse ecosystems of Telangana were evaluated for genetic diversity using Simple Sequence Repeat (SSR) markers. Genetic diversity at molecular level was also analyzed using simple sequence repeat (SSR) markers. Though 20 SSR markers were employed, only 13 SSR profiles for all the 20 moringa accessions were generated. On an average, two bands per SSR marker were produced. In contrary to morphological cluster analysis, only two distinct clusters were found since high levels of genetic similarity were estimated from the dendrogram generated through SSR marker data. The Jaccard's similarity coefficient ranged from 0.08 to 1.00. Among the two clusters, cluster I was the smallest with 4 accessions and cluster II had 16 accessions, grouped under two major sub cluster (II a and II b). The 4 accessions under cluster I are MO 1, MO 3, MO 19, MO 6. Cluster IIa contained MO 7, MO 10, MO 14, MO 15 and rest of the accessions were grouped in cluster IIb in two minor clusters. Thus this study helped to identify agronomically superior and genetically diverse novel moringa germplasm accessions that can be utilized in moringa breeding for enhancement of pod yield and leaf protein.