

Assessment of genetic diversity among *ex-situ* conserved finger millet (*Eleusine coracana* L.) accessions of Nuwara Eliya district in Sri Lanka

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Finger millet (*Eleusine coracana* L.), commonly known as "kurakkan" in Sri Lanka is a highly nutritious crop which is currently gaining popularity as a diabetic relief food. Even in recent records it is stated as a neglected crop globally and locally due to lack of consideration in research and crop improvement programs. Plant Genetic Resource Center, Gannoruwa has a collection of 249 finger millet germplasm accessions representing 13 districts of Sri Lanka where 20 of the accessions are from Nuwara Eliya District. This study was conducted to assess the genetic diversity of those 20 accessions using 20 SSR (Simple Sequence Repeats) markers. DNA was extracted from 7-10 days old leaves and screened for all 20 SSR markers. Alleles were scored and the data was analyzed using Power Marker version 3.25. Shared alleles were calculated and cluster analysis was performed with UPGMA method and the Treeview software (TreeView 1.6 version for WXP). Six of the markers (UGEP 3.1, UGEP 1, UGEP 18, UGEP 31, UGEP 78 and UGEP 90) were found to be monomorphic and the rest of the 14 markers (UGEP 3.2, UGEP 5, UGEP 10, UGEP 12, UGEP 15, UGEP 21.1, UGEP 21.2, UGEP 24, UGEP 68, UGEP 77, UGEP 81, UGEP 102, UGEP 106 and UGEP 110) were polymorphic. Across the 20 accessions, the number of alleles amplified by 14 markers ranged from 2 to 6 alleles per locus. Polymorphic information content ranged from 0.0476 to 0.6573. Dendrogram constructed on the basis of SSR polymorphism contained one main cluster leaving accession 960: "Kurakkan" as an out group. In the main cluster accession 1556: "Kurakkan" was separated from the remaining 18 accessions out of which three of the accessions 1460 "Sudu Kurakkan", 1457 "Kalu Kurakkan" and 9083 "Kaha Kurakkan" were genetically similar although they are having different accession names. Accessions 491 and 8851 were found to be genetically distant irrespective to their same accession name "Mora kurahan". These findings can be used in fine tuning the conservation programs by avoiding duplications and identifying the core species for conservation. Individuals with highest genetic distances can be used as potential parents in breeding programs.

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