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Analysis of Population Structure of *Ex-Situ* Conserved Sorghum (*Sorghum bicolor* (L.) Moench) Germplasm Accessions in Sri Lanka Using SSR Markers

D.V.S. Kaluthanthri¹, P.N. Dasanayaka^{1*} and S.A.C.N. Perera²

¹Department of Botany, Faculty of Applied Sciences, University of Sri Jayewardenepura.

²Department of ²Agricultural Biology, Faculty of Agriculture, University of Peradeniya.

*nilanthiedas@sjp.ac.lk

Sorghum (*Sorghum bicolor* (L.) Moench) is an important cereal crop in many tropical and subtropical areas of the world. The present study was carried out to elucidate the population structure of sixty *ex-situ* conserved sorghum germplasm accessions using sixteen SSR markers. The total genomic DNA was isolated from the ground leaf material using CTAB miniprep DNA extraction protocol. PCR was performed in two steps using a modified M13 tagged forward primer, a pig-tailed reverse primer and M13 oligo labeled primer with one of four fluorescent dyes; 6-HEX, FAM, TAMN or PET. Multiplexed PCR products were separated using capillary electrophoresis. Data analysis was performed using GeneMapper4.0, Structure 2.2 and STRUCTURE HARVESTER software. The admixtures of three subpopulations were observed in two germplasm accessions. The optimum number of subpopulation K which best explained the population structure was 3. The subpopulation 1 was comprised of twenty-eight germplasm accessions while fifteen germplasm accessions were grouped in each of subpopulation 2 and 3. The genetic similarity irrespective of the geographical origin was observed in this study. Fifteen local germplasm accessions in subpopulation 2 indicated their genetic uniqueness. Some local germplasm accessions with different vernacular names which are morphologically different were found in the subpopulation 2. The subpopulation 3 was observed with morphologically different exotic germplasm accessions belonging to different countries. The less genetically distinct nature of some germplasm accessions which are morphologically different could be due to various reasons. Out of them, the narrow genetic basis of the observed morphological differences, the farmer's directional selection for different morphological traits for different purposes and the non-detectable nature of observed morphological differences with neutral genetic markers are the main reasons. The results provide a technical guidance for efficient management of sorghum in breeding programmes and revealed the importance of collection of sorghum from different regions.

Keywords: sorghum, *ex-situ*, Sri Lanka, population structure, subpopulation, genetic similarity