

QUANTITATIVE MORPHOLOGICAL MARKER BASED GENETIC VARIABILITY OF SORGHUM (*SORGHUM BICOLOR*) GERMPLASM ACCESSIONS

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Abstract

Sorghum (*Sorghum bicolor* (L.) Moench) which is belonging to the family Poaceae is considered as the fifth most important cereal crop in the world in terms of production and area planted. Out of all currently cultivated cereals, this can be considered as one of cereals with the best drought tolerance. This study was carried out to assess the genetic diversity of twenty six *ex-situ* conserved sorghum (*Sorghum bicolor*(L.)) germplasm accessions using morphological markers developed for sorghum outlined by the International Plant Genetic Resources Institute (IPGRI). There were significant correlations between pairs of studied quantitative morphological traits including both positive and negative correlations. There was a highly significant, positive correlation between **days to flowering** and **plant height** ($r=0.906$). Three pairs of traits as **days to flowering** and **100 seed – weight** ($r= -0.653$), **plant height** and **100 seed – weight** ($r= -0.616$) and **days to flowering** and **No. of flowering stems** ($r= -0.516$) showed significantly high negative correlations. Cluster analysis based on the studied quantitative traits generated five major clusters. Cluster ‘I’ comprised five Sri Lankan accessions. Cluster ‘II’ comprised of two Italian accessions and two **French** accessions. Cluster ‘III’ composed of one Ethiopian accession and three Sri Lankan accessions. Cluster ‘IV’ consisted of seven accessions including two accessions with unknown origins, four Italian accessions and one Sri Lankan accession. The remaining six Sri Lankan accessions have been grouped together in Cluster ‘V’ at the beginning of clustering. As there is a considerable genetic diversity among the studied germplasm accessions of sorghum, the information obtained from this study will help the breeders in future sorghum breeding programs.

Keywords: *Sorghum bicolor*, germplasm accessions, characterization, genetic diversity, quantitative traits