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Genetic diversity for productivity traits in finger millet

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SUMMARY

A study was conducted to assess extent of genetic diversity involving one seventy-eight genotypes of finger millet for productivity traits. Study revealed that the genetic diversity did not relate to geographic origin. All the genotypes were grouped into ten different clusters. The inter cluster distance revealed that cluster 2 and 5 were found to be highly divergent. Florets number per spikelet contributed maximum to the divergence. Among all the clusters, cluster 7 showed highest cluster mean across the fifteen traits followed by cluster 5, 8 and 4 indicating presence of most promising genotypes in them. Selection of parents for hybridization to get desirable recombinants has been suggested.

Key words : Finger millet, Productivity traits, Diversity, D^2 Analysis, Divergence genotype.

Finger millet (*Eleusine coracona* Gaertn) is one of the important small millet crops in India, grown over an area of 2.15 million hectares with a production of 2.68 million tones (Anon., 2003). Finger millet comes up very well in adverse climatic conditions. It is mainly cultivated for both grain and straw. The adoption of modern genetically uniform varieties in finger millet has resulted in a decline in stability of performance under unfavorable conditions and introduced a greater risk of vulnerability to pests and diseases in more favourable environments. An improvement for yield of any self-pollinated crop is normally achieved by selecting the genotypes with more desirable characters existing in nature or introgressing of important traits by hybridization. Quantification of genetic diversity existing with in and between groups of germplasm for yield components is very important in planning breeding programmes of crop plants. It not only helps in choosing parental combinations to get superior recombinants but also in understanding the pattern of variation for different characters. Hence in the present study an attempt has been made to quantify the magnitude of genetic diversity for yield and its components characters of 178 diverse genotypes of finger millet by Mahalanobis, D^2 stastic.

MATERIALS AND METHODS

The experimental material comprising of 178 genotypes of finger millet, procured from International Crop Research Institute for Semiarid Tropics, Hyderabad, were grown in a randomized block design with two replication at Agricultural Research Station, Hanumanamatti, University of Agricultural Sciences Dharwad, Karnataka, during *kharif* 2002. Each entry in each replication was grown in 2 rows of 3.0-meter length with a spacing of 22.5 x 5 cm.

Five plants were selected randomly in each entry to record the observation on 15 quantitative characters viz, plant height, total number of tillers/plant, productive tillers /plant, days to 50 per cent flowering, days to maturity, number of fingers per ear, length of ear head, length of finger, flag leaf length, florets number/spikelet, spikelet density, ear weight/plant, test weight, straw yield/plant and grain yield/plant. The data were subjected to analysis of variance and multivariate by using Mahalanobis D^2 statistic (1936). The genotypes were grouped in to different clusters by following the Touchers method (Rao, 1952).

RESULTS AND DISCUSSION

Analysis of variance revealed highly significant differences among the genotypes for all the characters studied. Based on D^2 values, 178 genotypes were grouped in to 10 different clusters (Table 1). Twenty-seven genotypes were present in each of cluster 1 to 6, while cluster 7 had 13 genotypes and remaining clusters were solitary with single genotype. The formation of solitary clusters may be due to total isolation preventing gene flow or intensive natural /human selection for diverse adaptive complexes. Genetic diversity has been found to be associated with geographic diversity Shete and Kale (1988). But, Murthy and Arunachalam (1966) have shown that geographic distribution and genetic diversity as estimated by D^2 statistic need not be directly related. In the present study also no close correspondence was evident between geographic distribution and genetic

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