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Genetic architecture on finger millet (*Eluesine coracana*)

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ABSTRACT

Experiment was carried out with seventy genotypes in Randomized Block Design with three replications at All India Co-ordinated Small Millet Improvement Project, Zonal Agriculture Research Station, Sub-Montane Zone, Shenda Park, Kolhapur during rainy season 2005, to assess the genetic diversity and variability. The mean sum of squares was significant for all the fifteen characters studied indicating presence of variability. The genotypes were grouped into 8 clusters based on D^2 values. There were 4 solitary clusters and in the remaining clusters the genotypes varied from 2 to 4 No. Parallelism was observed between geographical diversity and genetic diversity. Based on D^2. Values and per sent performance, hybridization involving I.E.No.2430 (Cluster V), I.E.No.6473 (Cluster VI), I.E. 5066 (Cluster I), I.E. No. 2790(Cluster VIII), and I.E. No.1055 (Cluster III,) are suggested to obtain superior types to secure yield improvement in Finger Millet.

Key words : *Eluesine coracana* Gaertn, Genetic Architecture, Cluster, Assessment.

INTRODUCTION

In any crop improvement programme assessment of genetic diversity is an essential prerequisite for identifying potential parent for hybridization. Diverse parents are expected to yield higher frequency of heterotic hybrid in addition to generating a broad spectrum at variability in segregating generations. The D^2 statistics is useful on multivariate statistical tool for effective discrimination among various genotypes on the basis of genetic diversity (Murthy and Arunachalam, 1966). Attempt has been made in this study to asses the nature & magnitude of genetic divergence for yield and its component in Finger Millet and also to identify divergent parents from distantly related cluster for suitable hybridization.

MATERIALS AND METHODS

Seventy genotypes of Finger Millet received from ICRISAT, Hyderabad grown at All India Small Millet Improvement Project, Zonal Agricultural Research Project, Shenda Park Kolhapur; farm during *Kharif*, 2005 in completely randomized block design with the three replications. Each entry was grown in a one-metre row with spacing 22.5cm between the rows and 10 cm within row. Five randomly selected plants from each genotypes in each replication were used to record observations on days to 50 per cent flowering, plant height (cm), basal tiller, flag leaf blade length (cm), flag leaf width (cm), flag leaf sheath length (cm), peduncle length (cm), exertion (cm), inflorescence length and width (cm), length of largest finger and width (cm), panicle branch number, 1000 grain weight (gram) grain yield^{-1} (g.) plant. The mean of the five plants was subjected to statistical analysis. Walk's criterion was used to test the significance of difference in mean values for all the fifteen character. Genetic diversity was estimated as Mahalanobis D^2 statistics and clustering of genotypes was done according to Tocher's Method as described by Rao (1952).

RESULTS AND DISCUSSION

The analysis of variance showed highly significant differences among genotypes for all the characters studied, indicating the existence of considerable amount of variability in experimental material. The clustering based D^2 statistics grouped in the genotypes in 8 clusters, indicating the presence of diversity for different traits. (Table1). The cluster I&II were the largest and comprised of 38 & 20 genotypes respectively in the highest group fallowed by cluster III and IV comprised of (6 & 2 respectively) while remaining cluster ware solitary. The genotypes IE Number 6473, 5066 and 2790 were farmed single stocked cluster indicating wide diversity from set, as well as from each other. Presence of variability in the genetic architecture of crop species is basic for their systemic improvement. The plant breeder has always been fascinated by diversity in crop plants. . Mahalanobis (1936) stated D^2 statistics is useful tool and it is now well established and widely used in plant breeding for classifying genetic divergence between populations. Such high amount of diversity between the Finger Millet

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