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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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Table 1: Grouping of seventy Finger Millet genotypes indifferent Cluster by Tocher Method.

Cluster	No of Genotypes included	Genotypes (I.E No.)
I	38	3317, 4073, 4057,4073,6240,3614,6337,4057,5106,LC5 (PES 110), 121, 5367, 3945, 2572, 518, 2437, 2821, 3475, 5066, 6421, 3721, 5870, 6082, 4497, 5306, 4491, 4671, 3952, 4734, 5201, 4795, LC4 (PR 202), 2710, 3973, 6294, 3392, 2034, 3077.
II	20	2957,5817,3045,4570,4028,4797,6537,4329,5091,4757,2457, LC1 (PES 400), 6154,3391,2872,2619,3470, 2589,4545,6326.
III	6	2606, 6350, 2217, LC2 (HR 374), 2296, 1055.
IV	2	2312, LC3 (RAU 8).
V	1	2430.
VI	1	6473
VII	1	5066
VIII	1	2790

genotypes were also observed by Kempanna and Thirumalacher (1968) and Raut *et al*. (1984) in different clusters respectively.

The intra & inter cluster D^2 values among 70 genotypes (Table 2) revealed that cluster III recorded maximum intra-cluster III values (D = 12) while cluster IV showed minimum intra cluster value (D = 8) This implies that cluster III has the genotype with varied genetic architecture while genotype of cluster IV genetically resembled to each other & might have come from common gene pool. Inter culture difference were maximum between cluster IV and III (D = 31) followed by cluster VII and cluster III (D = 29), cluster VI and cluster III (28.29), cluster V & III (D=26), cluster III and II (26) indicating that the genotype from the these cluster can be selected for hybridization to produce hybrid. The inter cluster difference were minimum between cluster IV and V (D = 17); suggesting that the genetic constitution of these genotypes is one cluster is in close proximity with the genotypes in other cluster of pair.

The Cluster means estimated over genotypes for the fifteen character (Table 3) revealed considerable inter cluster variation. The cluster mean for days to 50 per cent flowering ranged between 80.77 in cluster I to 92.00

Table 2: Average intra- (along diagonal and inter diagonal cluster D^2 /Distance to Finger Millet

Cluster Group	I	II	III	IV	V	VI	VII	VIII
I	114	197	344	417.57	229	172	352.	289
	11	14	19	20	15	13	19	17
II		127	691	316	202	212	271	487
		11	26	178	14	15	16	22
III			397.60	952	671	467	851	359
			12	31	26	22	29	19
IV				64	394	360	403	800
				8	20	19	20	28
V					0	278	331	461
						17	18	21
VI						0	127	432
							11	21
VII							0	705
								27
VIII								0

Table3 : Mean Cluster values For Finger Millet.

Cluster	FLG	PLHT (Cm)	BT	FLBL (Cm)	FLBW (Cm)	FLSL (Cm)	PEDLEN	EXER	INFLL (Cm)	INFW (Cm)	LLF (Cm)	WLF (Cm)	PBN	1000 Wt	YLD/ Plant (Gram)
I	80.77	80.02	4.57	33.50	0.84	10.45	21.56	10.60	6.36	4.36	5.56	0.80	1.22	2.29	4.280
II	83.37	80.03	3.98	31.72	0.81	10.69	22.21	11.96	6.80	4.39	5.72	0.73	1.22	2.04	1.736
III	81.83	81.53	4.28	32.78	0.92	10.33	21.02	9.97	5.48	4.26	5.11	0.77	1.44	2.46	8.580
IV	87.00	82.22	4.83	36.67	0.77	23.83	10.17	7.17	6.50	4.67	7.33	0.73	1.00	2.10	1.033
V	85.00	97.50	12.67	35.67	1.00	10.67	22.33	11.00	7.00	3.67	5.00	0.70	1.00	1.69	2.860
VI	92.00	88.33	3.33	38.33	0.83	9.67	17.67	9.33	11.67	5.67	13.00	0.77	1.00	1.93	4.033
VII	89.00	85.00	4.00	42.33	0.90	11.00	26.67	18.00	8.83	6.33	16.33	0.70	1.00	1.88	2.567
VII	83.00	92.00	6.67	23.00	0.87	14.00	26.33	14.67	8.00	5.64	6.67	0.69	1.00	2.04	6.233

FLG = days to 50% flowering
PLHT (Cm) = Plant Height
BT – No. of Basal Tiller
FLBL (Cm) – Flag leaf blade length
FLBW (Cm) = Flag leaf blade width
FLSL (Cm) = Flag leaf sheath length
PEDLEN = Peduncle length
XER – Exertion
INFLL (Cm) – Inflorescence length
INFLW (Cm) = Inflorescence width
LLF (Cm) = Length of longest finger
WLF (Cm) = Width of longest finger
PBN (Cm) – Panicle Branch Number
1000 GRWT – 1000 Grain Weight (G)
YLD = Grain Weight of per plant.

in cluster VI. The cluster mean for basal tiller was ranged between 3.98 in cluster II to 12.67 in cluster V. The cluster means for flag leaf blade length was ranged between 23.00 in cluster VIII to 42.33 in cluster VII. Cluster mean for flag cluster width was ranged between 0.77 in cluster IV to 1.00 in cluster in cluster V. The cluster mean for flag leaf sheath length was 9.67 in cluster VI to 23.83 in cluster IV. The cluster mean for peduncle length was ranged between 10.17 clusters IV to 26.67 in cluster VII. The cluster mean exertion was ranged between 7.17 in cluster IV to 18.00 in cluster VII. The cluster mean for inflorescence length was ranged between 5.48 in cluster III to 11.67 in cluster VI. The mean clusters for inflorescence width was ranged 3.67 in cluster V to 6.33 in cluster VII. The cluster mean for longest length for finger was ranged maximum (16.33) in cluster VII and minimum (5.00) in cluster V. The mean cluster for width of longest finger was maximum (0.80 cm) in cluster I and minimum (0.69 cm) in cluster VIII. The mean cluster for panicle branch was ranged" between 1.00 to 1.22". The cluster mean for 1000 grain weight highest (2.29) was recorded in cluster I while lowest (1.69) in cluster V The cluster mean for grain yield^{-1} (g) plant was highest (8.580) in cluster III while lowest (1.033) in cluster IV. The cluster mean for height and basal tiller were highest in care of cluster V while mean for cluster peduncle length and length of longest finger in ware highest in case of cluster VII and these differ vary much from those of other clusters suggesting quite different make up of genotypes included in these dusters and important role of these characters in the genetic divergence. Taking into account the cluster mean for important seed yield component, the various clusters, which can provide parent for hybridization, in the finger millet.

The clustering pattern observed in the present study reveals that the genetic diversity was not necessarily parallel to the geographic diversity. Genotypes originating in different geographical area cloud form one cluster; white different genotypes evolved in the same area were grouped in to different cluster separated by genetically distance. On the basis of inter cluster distance, cluster means and performance of different genotypes of Eight clusters, Four diverse genotypes were identified

of present parent for crossing Viz. IE No. 2430 (From Cluster V), IE No. 6473 (From Cluster VI), I.E. No.5066 (from cluster VII) I No. 2790 (from cluster VIII) and 1055 (from cluster III) These results were in agreement with Murthy and Arunachalam (1966). Raut *et al.*, (1984) suggested that such pattern of grouping of genotypes together, from distant places indicated that the nature of selection process operating under any geographical region does not seem to be vary dissimilar to that of other region, Murthy and Arunachalam (1966) and Bhatt (1970) stated that the genetic differences and selection in different experiment might cause greater diversity among varieties than their geographical distances. Dhogal and Narsighani (1978) and; Kempanna and Thirumalacher (1968) also obtain similar results.

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