# Genetic Diversity for Yield and its Component Traits in Pearl Millet Germplasm

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> One hundred and five genotypes of pearl millet representing different countries were studied for genetic divergence analysis utilizing Mahalanobis D<sup>2</sup> technique. The analysis of data revealed that significant difference was observed among the genotypes for all the traits. Based on the genetic distance ( $D^2$  value), the 105 accessions were grouped into 22 clusters. Of the 22 clusters formed, cluster II was the largest with 63 genotypes followed by cluster III with 10 accessions. Among the twelve characters studied, the most important character contributing to the divergence was days to maturity and the traits like productive tillers/plant, grain yield/ear, peduncle length, grain yield/plant and 1000-seed weight were next in the order. Cluster I and XVII had maximum inter cluster distance suggesting wide diversity and by utilizing these accessions from these clusters desirable segregants may be evolved through hybridization. Maximum diversity was observed between IP-9416 vs. ICTP-8203, IP-5275 vs. IP-14644, IP-8276 vs. IP-18742.

Key Words: Genetic diversity, Cluster, Pearl millet, D<sup>2</sup> technique, Peduncle length

#### Introduction

Pearl millet (Pennisetum glaucum L.) is the fifth most important cereal food crop in India. Information on genetic diversity analysis helps to identify the genetically diverse genotypes for their use in breeding programmes. Choosing genetically diverse parents will enable the expansion of genetic base and development of superior types and greater success can be achieved through judicious choice of parents for hybridization based on genetic divergence. Crosses between divergent parent usually produce greater heterosis than those between closely related ones (Moll and Stuber, 1971). Of the several methods available Mahalanobis's generalized distance estimated by  $D^2$  statistic (Rao, 1952) is a unique tool for discriminating population considering a set of parameters together rather than inferring from indices based on morphological similarities and polygenic relationship.

Mahalanobis's  $D^2$  statistics has been followed by several workers on a wide range of crop species, including pearl millet, to measure the genetic distance among the breeding lines and to identify characters responsible for such divergence. The present investigation aims to determine the genetic diversity among 105 accessions of pearl millet of indigenous and exotic origin using cluster analysis based on morphological traits.

## **Materials and Methods**

The material for the present investigation comprised 105 accessions of pearl millet including 26 lines from India

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and 79 from African countries, viz., Togo, Sudan, Tanzania, Mali, Camerron, Zimbabwe, Namibia, Nigeria, Burkino Faso, Ghana, and nine from ICRISAT, Hyderabad. Thus, the material represented a wide range of geographic diversity. The experiment was carried out in a Randomized Block Design with three replications at Regional Agricultural Research Station, Bijapur (University of Agricultural Sciences, Dharwad) during Kharif, 2004 and 2005. Each accession was grown in two lines of 4 m length. The spacing adopted between rows and between plants with in a row was 50 cm and 15 cm, respectively. The data on days to 50% flowering, days to maturity, plant height, ear length, ear girth, flag leaf area, peduncle length, ear weight, grain yield/ear, grain yield/plant and 1000-seed weight were recorded on five randomenly selected labeled plants for all the entries in each replication All the observations except days to 50% flowering were taken at maturity. The mean data of two seasons was subjected to statistical analysis using Mahalanobis  $D^2$  statistic to assess genetic divergence. The accessions were grouped on the basis of minimum generalized distances using the Tocher's method (Rao, 1952).

# **Results and Discussion**

Analysis of variance revealed significant difference among the accessions for all the characters studied, indicating the existence of wide genetic divergence among them. Based on D<sup>2</sup> values, 105 genotypes were grouped in 22 clusters, indicating the presence of large amount of

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diversity among the genotypes (Table 1). Maximum number of genotypes (63) were in cluster II, ten were grouped in cluster III, four each in cluster I, XV and XVII (Table 1) The dendrogram of 105 pearl millet genotypes depicting the spatial position of each cluster in relation to others is presented in Fig.1. The intra- and inter-cluster  $D^2$  values among the 22 clusters are presented in Table 2. Cluster XV had the maximum intracluster distance of 24.6 followed by cluster II (23.6) and cluster III (22.0). The inter cluster distance ranged between 12.9 minimum (X and XI) and 249.0 maximum (I and XVII). The inter cluster proximity

Clusters

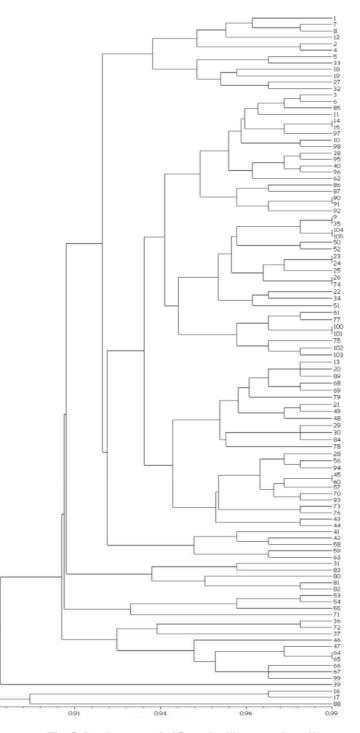


Fig. 5: Dendrogram of 105 pearl millet germplasm lines

0.88

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Cluster number	Total number of genotypes in each cluster	Genotypes included in the clusters	Origin
Ī	4	IP-9140, IP-9286, IP-15857, IP-15899	India=1 Togo=1 Tanzania=2
П	63	IP-11211, ICTP-8203, WC-075, IP-8540, ICMV-221, IP-15355, IP-15256, IP-4759, IP-15257, IP-14942, IP-10394, IP-3150, IP-4169, IP-15220, IP-15273 IP-12779, IP-7838, IP-17978, IP-12682, IP-8276, IP-8069, IP-12768 IP-17566, IP-17753, IP-9301, IP-17493, IP-17690 IP-10761, IP-10914, IP-10839, IP-10945 IP-15817, IP-15710, IP-15681, IP-15829 IP-10085, IP-6451, IP-6417, IP-10186, IP-6460, IP-6545 IP-12901, IP-14497, IP-6125 IP-14028, IP-16911, IP-16449, IP-8818, IP-16402, IP-14026 IP-19246, IP-17144, IP-18657, IP-18742, IP-19388 IP-5275, IP-19067, IP-13137 IP-11503, IP-13840, IP-10339, IP-13875 IP-8416	India=15 ICRISAT=7 Togo=5 Sudan=4 Tanzania=4 Mali=6 Camerron=3 Zimbabwe=6 Namibia=5 Nigeria=3 Burkino Faso=4 Ghana=1
Downloaded From IP - 14, 139.224.50 on dated 10-Feb-2023 XI X XI X XI II. I. A A A A A A A A A A A A A A A A	10	IP-14038 IP-16196, IP-4695, IP-4779 IP-17979 IP-14644, IP-14778 IP-19321 IP-7488 IP-8429	Zimbabwe=1 India=3 ICRISAT-1 Camerron=2 Namibia=1 Tanzania=1 Nigeria=1
VI ge	1	IP-11680	Sudan=1
e V	1	IP-10811	Sudan=1
IV 5	1	IP-15364	India=1
S VII	1	IP-19243	Namibia=1
VIII	1	IP-19361	Namibia=1
IX	1	IP-18800	Namibia=1
Toged From XI XI	1 4	IP-12474 IP-11577, IP-13833 IP-18625 IP-16690	India=1 Burkino Faso=2 Namibia=1 Zimbabwe=1
A XII	1	IP-16197	India=1
XIII	1	IP-13154	Nigeria=1
XIV	1	IP-18389	Namibia=1
XV	4	IP,13645, IP-4331 IP-17144, IP-16638	India=2 Zimbabwe=2
XVI	1	IP-10826	Sudan=1
XVII	4	IP-17028, IP-10488, IP-18621 IP-7440	Zimbabwe=2 Namibia=1 Tanzania=1
XVIII	1	IP-10085	Mali=1
XIX	1	IP-6510	Mali=1
XX	1	IP-8229	ICRISAT=1
XXI	1	IP-3799	India=1
XXII	1	IP-9149	India=1

Table 1. Distribution of 105 pearl millet genotypes into different clusters

seems to be minimum between cluster X and XI as indicated by lowest inter cluster distance of 12.9. Hence, the genotypes included in cluster I and XVII may be selected for more effective crossing programme and should result in wide spectrum of variability to operate selection in segregating population. Presence of diversity among pearl millet genotypes of the present study is in accordance with earlier reports (Yadav, 1994; Hepziba *et al.*, 1995).

Based on  $D^2$  values, per cent contribution of different characters towards divergence was obtained. Among the twelve quantitative characters studied the most important

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	D							-		, D											
Clusters				;	;				;	;											
			IV			ΠΛ	VIII	X	×	XI	XII	XIII	XIV	XV	XVI	XVII	XVIII	XIX	XX	XXI	XXII
I <u>6.0</u> 2	231.8 253	253.0 21	218.6 2	239.9	227.8	232.4	221.9	218.6	218.8	229.2	225.4	221.8	225.0	242.1	236.9	249.0	242.7	231.6	198.3	220.0	141.8
Π	23.6 33	33.5 3	31.6	31.9	34.4	29.7	30.7	28.3	33.0	28.5	30.5	39.2	31.7	36.7	29.4	33.3	42.4	34.6	57.8	73.5	218.0
II	2	22.0 5	51.4	35.0	48.4	32.9	41.3	47.9	51.8	44.1	41.6	50.1	49.7	35.0	35.2	32.5	41.2	42.1	74.0	89.9	235.3
IV		J	0.00	43.8	30.0	46.6	40.3	14.0	14.7	14.8	41.1	47.4	14.6	52.0	35.4	39.7	57.1	45.0	59.1	67.8	210.2
Λ				0.00	23.1	42.3	48.6	37.3	36.3	33.4	45.5	57.5	40.4	48.5	44.3	31.6	18.3	22.0	61.2	71.1	226.9
ΙΛ					0.00	51.8	51.3	24.0	20.4	21.9	48.3	59.6	28.9	55.9	47.7	36.8	34.7	26.9	56.9	62.8	219.3
ΠΛ						0.00	20.3	43.8	49.2	45.3	23.4	27.9	46.3	32.0	29.6	44.0	49.2	43.8	58.5	80.2	215.5
ΛIII							0.00	38.0	45.9	44.0	14.4	17.6	45.1	28.9	35.7	51.0	54.9	43.6	48.5	78.1	206.8
IX								0.00	15.0	18.0	38.6	46.4	16.8	48.9	35.3	38.1	49.6	37.7	55.0	66.3	211.8
Х									0.00	12.9	46.5	55.2	16.9	57.3	40.0	37.7	49.8	40.3	58.6	64.3	213.4
IX										0.00	43.7	52.8	14.8	51.5	34.0	29.2	47.7	39.3	63.4	69.2	220.7
IIX											0.00	13.8	45.3	26.7	40.1	51.5	50.4	37.1	42.8	71.1	205.7
XIII												0.00	51.7	31.9	43.2	60.3	63.2	50.0	48.1	76.2	200.4
XIV													0.00	55.2	30.2	33.9	56.1	46.9	66.3	66.1	218.0
XV														<u>24.6</u>	43.3	50.5	51.9	43.3	60.9	87.3	219.9
IVX															0.00	30.5	58.4	53.6	75.1	82.6	224.8
IIVX																21.9	45.3	45.8	79.5	84.0	237.2
IIIVX																	0.00	19.6	59.3	78.4	227.4
XIX																		0.00	43.8	6.99	215.1
XX																			0.00	63.2	181.9
IXX																				0.00	200.8
IIXX																					0.00
Underlined figures indicates intra-cluster distance	gures indica	ates intr	a-cluster	· distanc	Ð																
	, see	4	Ć	ç	Dlone		t contrib	ution of	each chi	Percent contribution of each character towards genetic divergence in pearl millet	ards genet	tic diverge	nce in pe	arl millet		ć	bloin ai		L loine	1000	
Cliaracters	50%	g _	to	×.	height		rrouucuve tillers/		rtaut length	girth	riag ic area	riag icai area	length	th	weight	p d	per ear	per	per plant	we	weight
% Contribution	flowering 0.13	ing	maturity 32.58	nity 8	(cm) 0.09		ear 36.23		(cm) 0.42	(cm) 0 35	$(cm^2)$	n <sup>2</sup> ) )()	(cm) 0.48	(- ×	(g) 0.04	-	(g) 0.31	)00	(g) 20.26	ం	(g) 9 12
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Table 2. Average intra-cluster inter-cluster distances for 22 clusters in 105 pearl millet genotypes

Characters	Davs to	Davs	Plant	rcent contributio Productive	n of each cha Plant	tracter towar Far	ds genetic diverg Flag leaf	Percent contribution of each character towards genetic divergence in pearl millet Productive Plant Ear Flav leaf Pednucle	let Far	Grain vield	Grain vield
	50 % flowering	to maturity	height (cm)	tillers/ ear	length (cm)	girth (cm)	area (cm <sup>2</sup> )	length (cm)	weight (g)	per ear (g)	per plant (g)
	51.33	86.83	182.24	2.58	20.98	7.51	85.36	21.10	35.02	22.18	
П	50.22	86.66	172.97	2.13	23.52	7.68	81.21	21.97	49.80	26.72	
III	51.17	87.80	176.89	2.07	25.18	7.63	79.03	21.54	48.26	26.00	
IV	51.67	90.33	168.00	1.93	19.10	7.50	93.00	19.83	47.87	20.20	
~	50.33	85.00	185.63	2.63	24.23	6.00	87.60	22.43	53.40	30.70	
Ν	51.33	87.67	190.67	2.07	29.80	5.73	99.40	23.37	43.33	20.23	
ΝII	50.00	83.33	171.57	2.47	23.23	8.23	92.13	23.27	48.67	23.30	
VIII	50.00	85.00	170.10	1.97	21.63	8.10	81.03	21.33	42.33	21.73	
IX	48.67	86.67	160.47	2.00	28.73	8.37	71.50	20.70	43.00	19.83	
X	46.67	84.67	171.83	2.13	23.83	6.93	73.33	22.37	44.17	21.57	
IX	48.25	86.00	174.00	2.60	25.20	6.10	78.00	22.20	46.50	24.80	
ШX	51.33	89.00	171.23	2.23	29.17	8.23	67.93	19.03	53.07	21.43	
XIII	45.00	83.67	190.83	1.57	19.27	6.97	88.17	24.00	60.97	34.67	
XIV	47.67	86.67	171.00	2.67	23.37	8.07	75.00	20.17	42.03	21.50	
XV	48.83	84.75	171.47	2.00	24.13	7.00	84.15	19.43	48.69	22.05	
ХVI	46.33	85.00	170.60	2.47	20.87	8.83	69.50	25.33	51.23	25.33	
ПЛХ	50.33	86.83	176.21	2.08	26.79	9.20	83.13	23.65	49.73	26.73	
ШЛХ	52.67	89.00	188.67	2.90	24.83	6.73	99.83	26.63	53.57	27.77	
XIX	54.00	92.00	203.03	1.93	20.67	9.17	71.13	27.93	42.67	20.20	
XX	50.67	86.33	189.83	2.30	20.60	8.63	79.50	21.47	51.77	28.67	
XXI	10.00										

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6.70 11.07 9.03 10.27

63.37

27.30

40.50

20.10

91.27

9.03

15.67

2.20

189.50

87.33

47.00

IIXX

8.73 7.70 10.20 8.83 8.83 9.00 9.00 9.00 10.80 6.80 6.80 13.70 8.88 8.02 8.03 10.13

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1000-grain weight (g)

11.28 9.63 character contributing to the divergence was days to maturity. The traits like productive tillers/ plant, grain yield per ear, peduncle length, grain yield per plant, 1000-seed weight were next in the order. These characters can be given greater importance in selection of potential parents for hybridization. These observations are in line with the observations of earlier workers (Hepziba *et al.*, 1995; Quendeba *et al.*, 1995).

The existence of diversity among the genotypes was also assessed by the considerable amount of variation in cluster means for different characters (Table 3). Genotypes in cluster VII, XIII, X, XV and VIII were the early maturing. The genotypes in clusters XIX, XIII and VI were tallest, and cluster IX had the dwarf genotype. The cluster mean for ear length ranged from 15.67 cm to 29.80 cm, which were attained by group XXII and VI, respectively. The maximum ear girth was noticed in cluster XVII (9.20) while minimum was observed in cluster V (6.0). Less number of productive tillers per plant was recorded by the individuals in the cluster XIII (1.57), while more number was seen in cluster XVIII (2.90). Regarding peduncle length, cluster XIX had the highest mean value (27.93 cm), while cluster means for flag leaf area was in the range of 54.97 (cluster XXI) to 99.40 cm<sup>2</sup> (cluster VI). The mean values for ear head weight per ear was in the range of 35.02 (cluster I) to 60.97 g (cluster XIII). The maximum grain yield per ear head was produced by genotypes in cluster XIII (34.67 g). The minimum grain yield per ear head was recorded by genotypes in cluster IX (19.83 g). The higher mean grain yield per plant was recorded by the genotypes in cluster XIII (86.00 g), while lower grain yield was noticed in cluster IV (32.67 g). With respect to 1000grain weight, cluster XIII had highest mean value (13.70 g) followed by cluster X (12.63 g) and cluster I

(11.28 g). Cluster XIX had very low mean values for grain weight (6.70 g).

Maximum diversity was observed between IP-9416 vs. ICTP-8203 followed by IP-5275 vs. IP-14644 and IP-8276 vs. IP-18742. These divergent pairs will make 'B' and 'R' line combinations at least on any one of the CMS sources. If such hybrids are good, the corresponding cytoplasmic sources can be used for developing male sterile version and utilized in hybridization programme for developing hybrids or can be involved in crossing programme (B x R) for creating variability to isolate superior 'B' and 'R' lines on one or two cytoplasm.

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