

# ASSESSMENT OF GENETIC DIVERSITY AMONG MAINTAINER (B) LINES OF PEARL MILLET [*Pennisetum glaucum* (L.) R. BR.]

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## ABSTRACT

Genetic diversity is an essential prerequisite for improving the genetic makeup of any cop. Inclusion of genetically diverse parents in hybridization programme helps in isolation of superior recombinants. So, an experiment was conducted to investigate the genetic diversity among 48 maintainer (B) lines of pearl millet for productivity traits. Present study reveals that the clustering pattern based on D<sup>2</sup> statistics grouped 48 genotypes into 7 clusters, out of which cluster I had highest genotypes (26), followed by cluster III (9). Inter cluster distances are higher than the intra cluster distances indicating the presence of wider genetic diversity between the clusters rather than within the clusters. Maximum inter cluster distance (14.50) was observed between cluster I and cluster VIII, while highest intra cluster value (6.67) recorded by cluster VI, indicating there is presence of wide range of genetic diversity among pearl millet maintainer lines. Trait panicle weight contributing highest towards genetic divergence (58.60%) followed by grain yield per plot (12.41 %), such genotypes with wide genetic diversity can be utilized for heterosis breeding programmes.

## INTRODUCTION

Pearl millet [*Pennisetum glaucum* (L.) R. Br.] ranks sixth in global cereal hectareage and the most important coarse-grain cereals in the semi-arid tropical regions of Asia and Africa. Pearl millet displays better adaptation and is grown in relatively more marginal environments. It is originated in central tropical Africa and is widely distributed in the drier tropics and India. It is a highly cross-pollinated crop with protogynous flowering and wind borne pollination mechanism, which fulfils one of the essential biological requirements for hybrid development. Infact, pearl millet is the only suitable and efficient crop for arid and semi arid conditions because of its efficient utilization of soil moisture and higher level of heat tolerance than sorghum and maize. Farmers prefer the crop as low cost, low risk option not only by choice but also by necessity (Harinarayana, 1987).

Pearl millet is being grown in arid and semi arid regions of the world including West Africa, India and Pakistan with the rainfall ranging from 150-700 mm. India is a major pearl millet producing country with 43.3 per cent of the world area and 42 per cent of world production. It is mainly cultivated in the states of Rajasthan, Uttar Pradesh, Gujarat, Haryana, Maharashtra, Madhya Pradesh, Karnataka, Tamil Nadu, Andhra Pradesh and Jammu & Kashmir on a total area of 7.95 million hectare with the production of 8.79 million tones. The national average productivity is 1106 kg/ha during 2013-14 (Anon, 2014).

Pearl millet exhibits tremendous amount of diversity at both phenotypic and genotypic levels (Poncet *et al.*, 1998; Liu *et al.*, 1994) due to its high out-cross breeding behavior, originating from several independent domestication events

and wide range of stressful environmental conditions in which it had been traditionally cultivated.

For the development of effective heterosis breeding programme in pearl millet, one needs to have information about genetic distance and estimated prepotency of parents in hybrid combinations. Selection made on phenotypic performance alone does not lead to expected success in hybrid breeding. Therefore, a study on genetic diversity among parental lines is essential in choosing appropriate parents.

The selection of parental lines plays a vital role in developing ideal combinations. Arunachalam (1981) reported that more diverse the parents, greater the chance of obtaining heterotic F<sub>1</sub>'s. Selection of suitable parental lines (CMS/ maintainer and restorer) to develop heterotic combinations can therefore be facilitated by determining the genetic divergence among them. Careful selection of maintainer lines on the basis of their genetic diversity may lead to the development of hybrids with higher yield potential than parents and standard check varieties (Julfiquar *et al.*, 1985). The present investigation was carried out with an objective to study the diversity level among the parental lines. Identification of diverse parental helps in development of heterotic hybrids.

## MATERIALS AND METHODS

Experimental material consist of 48 diverse maintainer (B) lines received from ICRISAT, Patancheru, Andhra Pradesh (Table. 1) and were sown during *kharif*, 2014-15 in Randomized Block Design with two replications at Regional Agricultural Research Station, Vijayapur (Karnataka, India). The recommended packages of practices were followed to raise the crop. Each germplasm line was sown in two rows of 4 m.

length with 45 X 15 cm spacing. The observation on days to 50 per cent flowering, plant height (cm), panicle length (cm), panicle girth (cm), panicle weight (g/panicle), grain yield/plot (kg), stover yield/plot (kg), number of productive tillers (No. 's) and 1000 seed weight (g) were recorded on five randomly selected plants for all the lines in each replication. The genetic divergence of those genotypes was studied by employing Mahalanobis' (1936)  $D^2$  technique. The varieties were grouped into a number of clusters with  $D^2$  being treated as the square of generalized distance, according to the method described by Tocher (Rao, 1952).

## RESULTS AND DISCUSSION

The analysis of variance (Table 2) is not a reliable basis for measuring the extent of genetic diversity. In order to overcome this problem and to quantify genetic divergence between any two genotypes or group of genotypes, the numerical measure of diversity was obtained with the help of  $D^2$  – statistics and constellations of genotypes into clusters was done. To start a sound crossing programme, it is necessary that the genotypes should be genetically diverse.

On the basis of  $D^2$  values, all the 48 genotypes were grouped into 7 clusters (Table 3). The maximum number of genotypes were in cluster I (26 genotypes), followed by clusters III (9), IV (4) and cluster VI (4). However, clusters II, V and VII were distinct from the rest with each of them having single genotypes

(CPBLT-110, TPBLT-121 and ICMB94555 respectively) indicating their uniqueness from breeding point of view. Lakshmana (2008) reported 22 clusters for productivity traits in pearl millet restorer and maintainer lines.

The cluster mean values for each character are presented in (Table 4). The cluster VII showed the lowest mean for days to 50 per cent flowering (39). While cluster II had maximum plant height (132.50). Cluster IV exhibited highest panicle length (25.88). With respect to panicle girth (10.09) cluster VI recorded highest mean. Cluster IV showed maximum values for panicle weight (48.92). Regarding stover weight per plot, the genotypes having highest values were grouped into cluster IV. In case of grain yield per plot, cluster means ranged from 0.70 (Cluster VII) to 1.78 (Cluster VII). Highest cluster mean for grain yield per plot recorded in the cluster VI. In case of 1000 seed weight cluster II exhibited higher mean value (13.50). The cluster VII showed highest mean for number of productive tillers (3.25).

The intra and inter cluster divergence among the genotypes was varying in magnitude (Table 5). Inter cluster distances are higher than the intra cluster distances indicating the presence of wider genetic diversity between the clusters rather than within the clusters. It revealed that inter cluster distance ranges between 5.04 (Cluster II and III) to 14.50 (cluster I and VII). Intracluster distance was maximum for cluster VI followed by clusters IV, III, and I. The clusters II, V and VII were having only one genotype and thus had zero value. The maximum inter

**Table 1: List and pedigree details of maintainer (B) lines of pearl millet used in the study**

B lines Sl.No.	Genotype	Pedigree
1	CPBLT-101	(ICMB 0133 X HHVDBC HS-10-1-2-1-1-3-B)-2-1-3-2-1
2	CPBLT-102	[[[ICMV 88908-11-12-3-2-B x B-bulk)-8-B-3]]843B x ICMP5 900-9-3-2-2)-41-2-5-5 S2 -34-1-2-1-1 X B-bulk]-5-B-B]-11-1-1-B-B X ICMB 04111]-54-2-3-5
3	CPBLT-103	(SRC II C3 S1-19-3-2 X HHVBC)-12-4-1-3-2-1-B-5-B-3-B-B
4	CPBLT-104	(ICMB 01888 X ICMB 01222)-16-1-2-2-1-B-B
5	CPBLT-105	(SRC II C3 S1-19-3-2 X HHVBC)-3-5-1-1-2-B
6	CPBLT-106	[(SRC II C3 S1-103-1-1 X HHVBC)-20X (81B X ICMP 451)-5-4-2]-3-2-3-1-B-B
7	CPBLT-107	[(SRC II C3 S1-1-1-2 X HHVBC)-2-2-1-1-1-B-B X (81B X 4017-5-4-B)-12-3-1-3]-2-3-1-2-2
8	CPBLT-108	(NC D2 S1-2-2-2-3-3-4-B X ICMB 97333)-1-2-3-3
9	CPBLT-109	(ICMB 93333 X ICMB 01222)-20-2-B-5-B-1-B
10	CPBLT-110	[(DMR 133 x HTBC 48-B-1-1-1-5)-19-2-B-B x ICMB 04111]-145-6-2-4
11	CPBLT-111	[(81B X 4017-6-1-1)-3-1-3-3-1-1-B-B X ICMB 04111]-86-4-4
12	CPBLT-112	9ICMB 94333 X ICMB 01222)-47-1-B-B-B
13	CPBLT-113	(ICMB 01888 X ICMB 01222)-4-4-B-B-B-1
14	CPBLT-114	{[(843B X ICTP 8202-161-5)-20-3-B-B-3 X B-bulk]-2-B-9 X [(ICMB 96555 X LaGrap C2 S1-32-1)-10 X IP 14758-2-1]-8-2]-1-1-1-2
15	CPBLT-115	(ICMB 96555 X IP 10437)-9-2-2-5-1-B-1-B-1-3-B
16	CPBLT-116	(EBC-Gen-S1-40-2-2-1 X B-bulk)-28-B-B-3-B-B-3
17	CPBLT-117	[[[ICMV 88908-11-12-3-2-B X B-bulk)-8-B-3 X {(843B X ICMP5 900-9-3-2-2)-41-2-5-5 S2-34-1-2-1-1-1 X B-bulk)-5-B-B]-11-1-1- B-B X ICMB 04111]-67-5-2-1
18	CPBLT-118	[(SRC II C3 S1-1-1-2 X HHVBC)-2-2-1-1-1-B-B X (81B X 4017-5-4-B0-12-3-1-3)-2-3-1-2-3
19	CPBLT-119	ICMB 93333
20	CPBLT-120	ICMB 01666
21	CPBLT-121	JMSB-101
22	CPBLT-122	JMSB-2007
23	CPBLT-123	JMSB-20082
24	TPBLT -101	(HHVDBC HS-246-1-2-1-1-2 X ICMB 98444)-4-3-2-1
25	TPBLT -102	(ICMB 01666 X ICMB 01222)-49-1-2-B-2
26	TPBLT -103	(B X B) F2 S1 109-2-3-3-1-4-2
27	TPBLT -104	(HHVDBC HS-246-1-2-1-2 X ICMB 01222)-4-2-1-1
28	TPBLT -105	(ICMB 01333 X HHVDBC HS-10-1-2-1-1-3-B)-2-1-3-2-4

Table 1: Cont.....

29	TPBLT -106	(ICMB 01888 X ICMB 01222)-16-1-2-B-1-3
30	TPBLT -107	([ICMB 95111 X (ICMB 96555 X IP 10437)-3] X B-bulk (3981-3989/S06 G1))-3-2-4-B X ICMB 08999-13
31	TPBLT -108	{[78-7088/3/SER3 AD//B282/(3/4)EB X PBLN/S95-359]-7-4-B-B-2-B-B X HHVDBC HS-10-1-2-1-1-1-4-1-1-1-1-4-1-1-1-16-2-1-2
32	TPBLT -109	(ICMB 04888 X HHVDBC HS-10-1-21-1-1-2-B)-1-2-3-2
33	TPBLT -110	([ICMB 95111 X (ICMB 96555 X IP 10437)-3]-7-2-1-B-2-15-1]X B-bulk(3981-3989/S06 G1))-3-2-1-B X HHVDBC HS-10-1-2-1-1-1-3-B)-14-1-5-1
34	TPBLT -111	(ICMB 04888 X HHVDBC HS-120-1-2-1-2-B-2-B)-5-5-2-2
35	TPBLT -112	NC D2 S1-20-2-2-1-1-5-3-B
36	TPBLT -113	(HHVDBC HS-10-1-2-1-1-1-4 X [ICMB 99555 X {78-7088/3/SER3 AD//B2A2/(3/4)EB X PBLN/S95-359} -19-5-B-B]-13-2-B-B-B)-22-1-4-2-2
37	TPBLT -114	{(MC 94 S1-81-1-B X HHVDBC)-4-4-1 X (MC 94 S1-81-1-B X HHVBC)-4-2-4-7-1-1-B X ICMB 02777}-8-1-B-4-1
38	TPBLT -115	{(ICMB 96555 X IP 10437)-3-4-1-2-8 X [(ICMB 96555 X LaGrap C2 S1-32-1)-10 X IP 14758-2-1]-8-3-2-4-1-2
39	TPBLT -116	[(MC 94 S1-34-1-B X HHVBC)-10-4-32-2-B-B-2 X (ICMR 312 S1-1-5-3-B X HHVBC)-7-1-1-1-B-B-B]-21-B-1-4-1-2-1-3
40	TPBLT -117	{[78-7088/3/SER3 AD//B282/(3/4)EB X PBLN/S95-359]-7-4-B-B-2-B-B X HHVDBC HS-10-1-2-1-1-1-4-1-3}-17-1-2
41	TPBLT -118	{[78-7088/3/SER3 AD//B282/(3/4)EB X PBLN /S95-359] -7-4-B-B-2-B-B X HHVDBC HS-10-1-2-1-1-1-4-1-2}-8-1-5
42	TPBLT -119	ICMB 00555
43	TPBLT -120	ICMB 01777
44	TPBLT -121	JSMB-200042
45	TPBLT -122	JSMB-20091
46	TPBLT -123	JSMB-20101
47	TPBLT -124	ICMB 02333 B
48	TPBLT -125	ICMB 263 B

Table 2: ANOVA, Mean sum of squares for yield and its component traits in 48 pearl millet maintainer lines (B).

Sl. No.	Character	Replication	Treatment	Error	S. Em. ±	C.V. (%)	C.D. @5%	C.D. @1%
1	Days to 50 per cent flowering	0.09	40.85**	7.79	1.95	5.97	3.93	5.24
2	Plant height (cm)	642.57	826.14**	318.86	12.49	15.09	25.13	33.54
3	Panicle girth (cm)	0.33	2.21**	0.33	0.4	6.18	0.81	1.08
4	Panicle length (cm)	26.07	59.69**	6.49	1.78	10.66	3.58	4.78
5	Panicle weight (g)	7.88	211.32**	3.88	1.37	5.41	2.77	3.7
6	Stover weight per plot (kg)	0.03	0.89**	0.27	0.36	29.01	0.74	0.99
7	Grain yield per plot (kg)	0.01	0.25**	0.03	0.12	12.51	0.25	0.33
8	1000-grain weight (g)	0.09	6.06**	2.09	1.01	12.66	2.03	2.71
9	Number of productive tillers	1.89	0.49**	0.13	0.25	17.09	0.51	0.69

Note: \* Indicates significance at 5per cent probability level;\*\* Indicates significance at 1per cent probability level.

Table 3: The cluster means in respect of a total of nine characters and overall character wise score

Clusters	DFL	PH	PL	Characters					Productivity traits		
				PG	PW	SW	GY	TSW	PD	Total score	Rank
I	45.63 (4)	122.61 (3)	25.03 (4)	9.45 (3)	40.31 (2)	1.83 (2)	1.51 (3)	11.46 (5)	2.12 (4)	30	3
II	44.00 (3)	132.50 (1)	26.40 (1)	8.92 (4)	28.94 (5)	1.60 (5)	1.60 (2)	13.50 (1)	1.75 (7)	29	2
III	46.72 (5)	109.83 (5)	20.07 (5)	8.60 (5)	22.68 (6)	1.77 (3)	1.24 (5)	10.72 (6)	1.97 (5)	45	4
IV	51.08 (6)	124.95 (2)	25.88 (2)	9.82 (2)	48.92 (1)	2.21 (1)	1.41 (4)	11.58 (4)	2.46 (2)	26	1
V	42.00 (2)	93.13 (6)	18.45 (6)	7.95 (7)	36.75 (3)	1.20 (6)	0.95 (6)	12.50 (2)	1.88 (6)	48	5
VI	51.25 (7)	119.03 (4)	25.24 (3)	10.09 (1)	32.20 (4)	1.76 (4)	1.78 (1)	12.25 (3)	2.22 (3)	30	3
VII	39.00 (1)	49.13 (7)	14.30 (7)	8.34 (6)	7.00 (7)	0.65 (7)	0.70 (7)	9.50 (7)	3.25 (1)	50	6

Note: DFL: Days to 50% flowering (days), PH: Plant height (cm), PL: Panicle length (cm), PG: Panicle girth (cm), PW: Panicle weight (g/panicle), SW: Stover weight per plot (kg), GY: Grain yield per plot (kg), TSW: 1000 seed weight (g), PD: Number of productive tillers. Figures in the parenthesis, indicate the ranks based on cluster mean. Total score is the summation of rank numbers for all characters, based on which final rank is indicated.

cluster distance suggests that the genotypes belonging to these clusters if chosen for hybridization programme, give highly heterotic hybrids and broad spectrum of variability in subsequent segregating generations.

The characters contribution in cluster divergence (Table 6) revealed that the maximum contribution in cluster formation

was attributed by panicle weight (58.60) followed by grain yield per plot (12.41), panicle girth (8.69) and number of productive tillers (7.62). Whereas, remaining traits played minor role in cluster divergence as attributed by present pearl millet materials. Lakshmana (2008) observed maximum contribution of days to maturity to genetic diversity in pearl millet restorers

**Table 4: Average intra and inter cluster D<sup>2</sup> values of pearl millet genotypes**

Clusters	I	II	III	IV	V	VI	VII
I	4.50	5.69	8.49	6.46	5.74	6.60	14.50
II		0.00	5.04	9.47	5.35	5.75	11.10
III			5.30	11.94	6.90	8.00	9.02
IV				5.86	8.65	8.83	18.09
V					0.00	8.28	11.70
VI						6.67	13.56
VII							0.00

Note: 1. Above diagonal values are inter-cluster D<sup>2</sup> Values; 2. Diagonal values are intra cluster D<sup>2</sup> Values

**Table 6: Per cent contribution of characters towards divergence in pearl millet genotypes**

Sl. No	Character	Times ranked 1 <sup>st</sup>	Contribution %
1	Days to 50 per cent flowering	40	3.55
2	Plant height (cm)	14	1.24
3	Panicle length (cm)	36	3.19
4	Panicle girth (cm)	98	8.69
5	Panicle weight (g/panicle)	661	58.60
6	Stover weight per plot (kg)	36	3.19
7	Grain yield per plot (kg)	140	12.41
8	1000-grain weight (g)	17	1.51
9	Number of productive tillers	86	7.62
	Total		100

**Table 7: Pair wise combination (BxB) of genotypes with maximum diversity among 48 maintainer lines used in pearl millet**

Rankings	Distance between B lines		
	D <sup>2</sup> Values	B line 1	B line 2
1	13640.54	ICMB94555	CPBLT-118
2	11550.02	ICMB94555	CPBLT-106
3	10774.07	ICMB94555	CPBLT-109
4	10700.37	ICMB94555	CPBLT-103
5	9871.25	ICMB94555	CPBLT-104
6	9859.21	ICMB94555	CPBLT-113
7	9779.55	ICMB94555	CPBLT-114
8	9614.25	ICMB94555	CPBLT-102
9	9022.92	ICMB94555	TPBLT-102
10	8988.76	ICMB94555	CPBLT-111

and maintainers. Vijayakumar *et al.* (2016) reported maximum contribution of number of pods per plant in Mothbean, Sachin *et al.* (2014) in Chickpea and Brijendra *et al.* (2014) in wheat. The top ten pair wise combination of genotypes B vs B, with

maximum D<sup>2</sup> values among 48 maintainer lines given in (Table 7). In the B vs B combinations, the line ICMB94555 belongs to cluster VII showed maximum D<sup>2</sup> values with line CPBLT-118, followed by lines CPBLT-106 of cluster IV, CPBLT-109, CPBLT-103, CPBLT-104 of cluster I. CPBLT-113, CPBLT-114, CPBLT-102, TPBLT-102, and CPBLT-111. These lines in top ten B vs B pairwise combinations may be useful in development of trait specific heterotic pool of B lines.

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