

Genetic Diversity for Zinc, Iron and Yield Contributing Characters in Pearl Millet [*Pennisetum glaucum* (L.) R.Br.] Genotypes



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ABSTRACT: The most widely grown drought-tolerant warm-season coarse grain cereal, Pearl Millet [*Pennisetum glaucum* (L.) R.Br.] is grown on almost 26 million ha. Pearl Millet is India's fourth most extensively and widely produced food crop. This study aims for estimation of genetic variability among fifty-two genotypes of Pearl Millet were grown at Bajra Research Scheme, College of Agriculture, Dhule, (MS) during *Kharif*, 2020, in a Randomized Block Design with three replications. The maximum inter-cluster distance (D^2) were observed between clusters VI and VII (23.06) and cluster minimum between II and III (8.23). The significant differences due to genotypes with high range (D^2) value clearly indicated the presence of adequate diversity among genotypes studied. Among the genotypes divergence contributed maximum (41.63%) to iron content, followed by plant height (19.23%), panicle girth (15.16%), test weight (6.86%), days to flowering (5.13%), yield per plant (4.15%), panicle length (4.00%), and zinc content (3.39%) etc. Hence, this traits suggested important indices for selection of superior genotypes of pearl millet in breeding programs.

KEYWORDS: Genetic diversity, Pearl millet.

INTRODUCTION

The pearl millet is most important cereal crop which feeds major group of country. After maize, rice, wheat, barley, and sorghum, Pearl Millet is the world's sixth most significant cereal crop. After rice, wheat, and maize, Pearl Millet is India's fourth most extensively and widely produced food crop. During the 2018-2019 season, it covered an area of around 6.93 million tones and produced 1234 kg/ha. It outperforms all other cereals due to its unique characteristics: a C_4 plant with high photosynthetic efficiency, high dry matter production capacity, and the ability to grow in the harshest agro-climatic conditions, where other crops such as sorghum as well as maize fail to produce economically viable yields. The nutritional values of 100 seeds of pearl are energy 360 calories, moisture 12%, protein 12 %, fat 5 g, mineral 2 g, fiber 1 g, carbohydrates 67 g, calcium 42 mg, phosphorous 242 mg, iron 8 mg, and zinc 3.1 mg respectively. To begin with any crop improvement programme, the information of genetic variability in genetic system of particular crop is sought as pre-requisite. Although increased seed yield is the ultimate aim of the plant breeders, seed yield is a product of interaction of many component traits, which influence it directly or indirectly. Therefore, variability and diversity existing within each component traits must be exploited by selection to realize seed yield. Assessment of genetic diversity is a basic step in any crop improvement programme.

MATERIAL AND METHOD

The 52 genotypes of pearl millet were evaluated in a Randomized Block Design (RBD) with two replications during kharif-2020, at a distance of 50 x 15 cm with two replications. The divergence analysis was carried out by D^2 statistic of Mahalanobis (1936) as described by Rao (1952). Analysis of variance for the individual characters was worked out as per Randomized Block Design to test the significances among the genotypes. The characters exhibited significant differences were only used for further analysis of D^2 statistic. The analysis of covariance for pairs of characters, based on plot averages was carried out.

$$D^2 = \sum_{i,j} \lambda_{ij} \delta_i \delta_j$$

Where,

λ_{ij} = The reciprocal matrix to common dispersion matrix

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δ_i = Difference between the mean values of the two Populations for the *i*th character. ($\mu_{i1} - \mu_{i2}$)

δ_j = Difference between the mean values of the two populations for the *j*th character. ($\mu_{j1} - \mu_{j2}$)

μ = Vector of mean value

RESULTS AND DISCUSSION

The present investigation undertaken with view to genetic diversity and correlation coefficient of fifty-two diverse genotypes in pearl millet. The genetically diverse parents are known to produce high heterotic effects and consequently give desirable recombinants in the breeding material or wide spectrum of transgressive segregants in segregating generations. Multivariate analysis (D2 statistic) measures the genetic variability quantitatively among a set of genotypes. The fifty-two genotypes under study were therefore, assessed for genetic diversity for a set of twelve characters. The fifty-two genotypes were grouped into seven clusters presented in Table No.2. Cluster I had maximum genotypes (28 genotypes) followed by cluster II (12 genotypes), cluster III (8 genotypes) and remaining all other clusters viz., IV, V, VI, and VII containing single genotypes (monogenic).

The pattern of group constellation proved that significant amount of variability existed among the studied genotypes. Mahajan and Wadikar (2012) also observed the wide diversity in the experimental material. The intra and inter-cluster D^2 values among seven clusters are given in Table No. 3. Intra-cluster distance ranged from 6.67 to 7.63. Cluster III had the greatest intra-cluster distance (7.63), followed by Cluster I (7.34), while Cluster II had the smallest intra-cluster distance (6.67). While the clusters IV, V, VI and VII recorded zero values as they include single genotypes in each group of them. Maximum inter-cluster distance were observed between clusters VI and VII (23.06) followed by clusters V and VII (20.81), cluster IV and VII (17.20), cluster I and VII (17.08), cluster III and VI (16.93), cluster III and V (15.79), cluster IV and V (15.63), cluster II and VI (15.25), cluster II and V (13.01), cluster V and VI (12.41), cluster III and IV (11.92), cluster I and III (11.29), cluster II and IV (11.17), cluster I and IV (10.79), cluster I and VI (10.32), cluster III and VII (10.12), cluster I and V (9.72), cluster I and II (9.44), cluster IV and VI (9.44), cluster II and VII (9.41) and cluster II and III (8.23).

The inter-cluster distances were higher than intra-clusters which indicated the existence of substantial diversity among the genotypes. The genotypes in this clusters can be utilized as potential parents and crossing between these genotypes results in high heterotic expression for yield and its components. Among all the characters studied, iron content contributed maximum (41.63%), to diversity by taking first rank in 552 times out of 1326 combinations, followed by plant height (19.23% with 255 ranked first), panicle girth (15.16% with 201 times ranked first), test weight (6.86% with 91 times ranked first), days to flowering (5.13% with 68 times ranked first), yield per plant (4.15% with 55 times ranked first), panicle length (4.00% with 53 times ranked first) and zinc content (3.39% with 45 times ranked first). Higher contribution towards genetic divergence was also observed by Govindraj *et.al.* (2013) for zinc content; Athoni *et.al.* (2016) for seed yield and panicle girth; Basavaraj *et.al.* (2017) for panicle girth and Ramya *et.al.* (2017) for plant height, test weight and productive tillers per plant.

In decreasing order, the characteristics of number of productive tillers per plant and days to maturity contributed 0.30 % and 0.15 % to genetic divergence, respectively.

Table No.1: Analysis of variance for ten characters in Pearl Millet:

Sr.No.	Characters	Mean sum of square		
		Replication	Genotypes	Error
1	Day to flowering	0.8141	21.5633**	0.8663
2	Days to maturity	0.7500	27.25527**	1.37745
3	Plant height	24.6602	992.4032**	24.4903
4	No. of productive tillers per plant	0.2925	0.37494**	0.0726
5	Panicle length	0.8296	12.5462**	0.6105
6	Panicle girth	0.0405	0.359461**	0.0201
7	Test weight	0.2805	6.86185**	0.1827
8	Yield per plant	34.8560	138.7306**	9.3943
9	Iron content	15.9307	815.0834**	7.4122
10	Zinc content	2.0967	150.7717**	6.2947

* and ** indicated significance at 5% and 1% levels, respectively.

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Table No.2: Grouping of fifty-two genotypes of Pearl Millet into different clusters:

Sr. No.	Cluster	No. of genotypes	Name of genotypes
1	Cluster I	28	DHLBI-544, S-73, S-69, DHLBI-549, S-84, DHLBI-1609, DHLBI-535, S-65, S-83, S-82, S-81, DHLBI-534, DHLBI-1035, S-71, DHLBI-543, DHLBI-1013, DHLBI-1103, S-59, S-80, S-68, DHLBI-1708, S-72, S-78, S-66, DHLBI-537, DHLBI-967, S-63, DHLBI-539
2	Cluster II	12	DHLBI-541, S-79, S-56, DHLBI-1822, S-58, DHLBI-502, DHLBI-1603, DHLBI-1201, S-62, DHLBI-103, Dhanshakti, DHLBI-1074
3	Cluster III	8	S-75, S-76, S-61, S-67, DHLBI-104, DHLBI-101, S-70, DHLBI-1806
4	Cluster IV	1	DHLBI-907
5	Cluster V	1	S-77
6	Cluster VI	1	DHLBI- 908
7	Cluster VII	1	S-74

Table No.3: Average intra and inter-cluster distance (D^2) value for ten characters in Pearl Millet:

Sr. No.	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	7.34	9.44	11.29	10.79	9.72	10.32	17.08
Cluster II	9.44	6.67	8.23	11.17	13.01	15.25	9.41
Cluster III	11.29	8.23	7.63	11.92	15.79	16.93	10.12
Cluster IV	10.79	11.17	11.92	0.00	15.63	9.44	17.20
Cluster V	9.72	13.01	15.79	15.63	0.00	12.41	20.81
Cluster VI	10.32	15.25	16.93	9.44	12.41	0.00	23.06
Cluster VII	17.08	9.41	10.12	17.20	20.81	23.06	0.00

➤ Bold values indicates the intra-cluster distance

Table No. 4.: Relative per cent contribution of different characters towards total genetic divergence in Pearl Millet.

Sr. No.	Characters	No. of times ranked first	Per cent contribution
1	Days to flowering	68	5.13
2	Days to maturity	2	0.15
3	Plant height	255	19.23
4	Number of productive tillers/plant	4	0.30
5	Test weight	91	6.86
6	Panicle length	53	4.00
7	Panicle girth	201	15.16
8	Yield per plant	55	4.15
9	Iron content	552	41.63
10	Zinc content	45	3.39

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The success of any crop improvement program involves selection of best parent having high potential for the economically important characters. Among different approaches for selection of parents, selection based on diversity has its own significance, as diversity is a basic need of crop improvement. Therefore, in the present investigation diversity among different genotypes was studied, which yielded valuable information that could be useful in selection of potent parent for hybridization.

In the present study, an attempt was made to classify the cluster combination into four divergence classes by following the above procedure suggested by Arunachalam and Bandyopadhyay (1984). The statistical distance (D^2) given in Table No. 3, represents the index of genetic diversity among the clusters. The mean of seven cluster and three intra clusters (as monogenotypic clusters IV, V, VI and VII had no intra-cluster distance) was 12.44 and standard deviation 3.17. The minimum (X) and maximum (Y) values among these distances were 6.67 and 23.06 respectively.

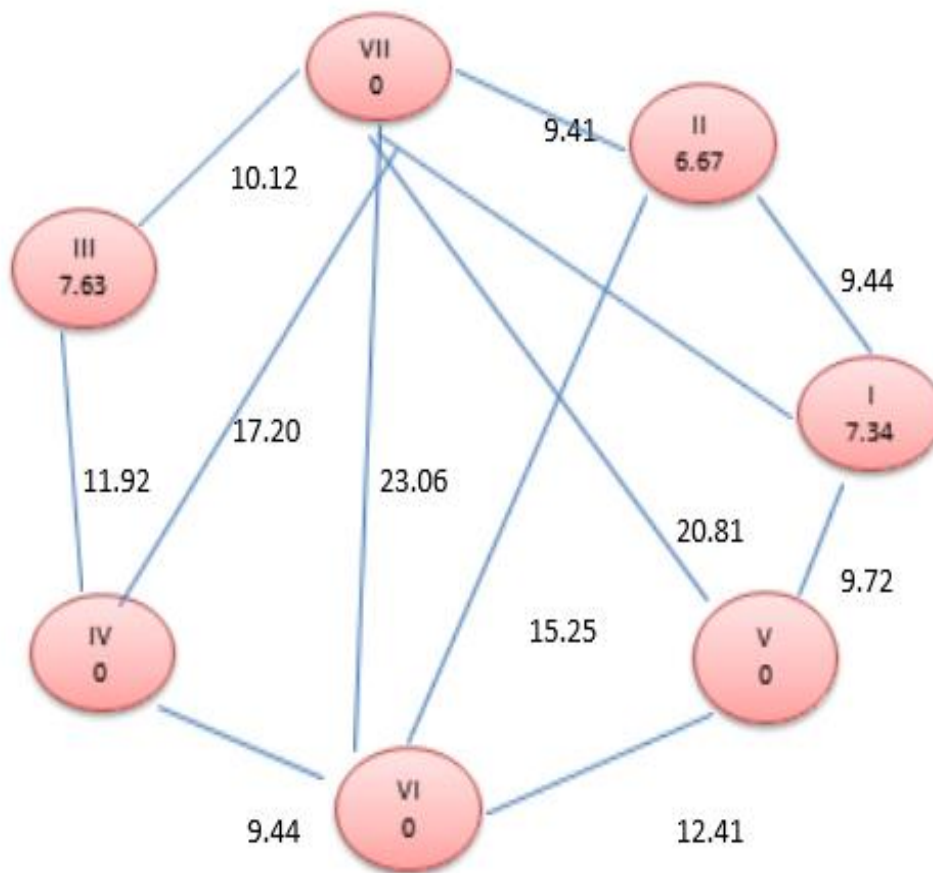
	DC4	DC3	DC2	DC1
	↓	↓	↓	↓
X	m-s	M	m+s	Y
(6.67)	(9.27)	(12.44)	(15.61)	(23.06)

Grouping of cluster pairs into the divergence class (DC) are presented in Table No. 5. Following the debate, the initial selection of parents should be selected from cluster combinations in the DC2 and DC3 divergence classes. When crossing genotypes within a cluster, the genotypes' individual performance for characters such as earliness (days to flowering and maturity), plant height, number of productive tillers per plant, panicle length, panicle girth, test weight, grain yield per plant, iron and zinc content, and so on should be considered. So, the desirable transgressive segregants would be obtained after hybridization.

Table No.5: Distribution of different clusters combination into four divergence classes based on D^2 values between them. (Cluster combination)

DC1	Y (23.06) (VI, VII), (I, VII), (III, V), (III, VI), (IV, V), (IV, VII), (V, VII) (7)
DC2	(m+s) (15.61) (II, V), (II, VI) (2)
DC3	M (12.44) (I, II), (I, III), (I, IV), (I,V), (I, VI), (II, IV), (II, VII), (III, IV), (III,VII) (IV, VI), (V, VI) (11)
DC4	(m-s) (9.27) (I, I), (II, III) (2) X (6.67) (II, II) (1)

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lists the various clusters that can provide desirable parents for hybridization programmes to improve the characters shown against them, based on the cluster mean presented in Table No.6

Table no: 6: Character improvement on the basis of source clusters:

Sr. No.	Characters	Source clusters
1	Days after flowering (Early)	VII, III, II, V, I
2	Days to maturity (Early)	II, III, V, VII, I
3	Plant height (cm) (Tall)	VI, IV, VII, V
4	No. of productive tillers per plant (Maximum)	V, VII, VI
5	Test weight (Maximum)	IV, V, VI, III
6	Panicle length(cm) (Maximum)	IV, III, VI
7	Panicle girth(Maximum)	III, VI, I
8	Yield per plant (Maximum)	III, VI, IV, I
9	Iron content (Maximum)	VII, III, II, IV
10	Zinc content (Maximum)	III, VII, IV, II

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Keeping in view all the above aspects the following genotypes in the present studies, deserve to be considered as potent parents for future crossing programme for improvement of seed yield and yield contributing traits in Pearl Millet.

- | | |
|---------------|---------------|
| 1. DHLBI- 907 | 5. DHLBI-1201 |
| 2. DHLBI- 908 | 6. Dhanshakti |
| 3. S-74 | 7. DHLBI-1806 |
| 4. S-75 | 8. S-77 |

Taking into account the inter-cluster distance, cluster means, genotype per se performance, and divergence class, the above genotypes may be used in future breeding programmes to create a broad spectrum of variability for different yield contributing characters, allowing for the development of superior genotypes for multiple characters and the improvement of multiple characters simultaneously.

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