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Genetic variability and multivariate analysis in pearl millet (*Pennisetum glaucum* (L.) R. Br.) germplasm lines

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Abstract

Pearl millet is an imperative cereal crop, where it is a staple food for millions of people in the world. Development of higher yielding cultivars/hybrids is need of day. A set of seventy-five germplasm lines were evaluated in Randomized Complete Block Design during *Kharif* 2021 to study different genetic parameters and associations among different yield accrediting characters. Analysis of variance indicated significant differences for all investigated traits in the experimental materials. The values of PCV were higher than GCV but in a narrow range indicating the least influence of environment on the expression of traits. Estimates of high heritability along with higher genetic advance as a percentage of mean were observed for grain yield plant⁻¹, test weight, harvest index, numbers of productive tillers plant⁻¹ and biological yield indicating the presence of additive gene action signifying for improvement of this trait by applying diverse selection methods. Correlation and path analysis studies revealed that the harvest index, biological yield, and numbers of productive tillers plant⁻¹ could be considered good selection indices for selecting genotypes for yield improvement. The percent contribution of individual characters toward the total divergence was found high for biological yield (g). Based on D² values, 75 genotypes were grouped into five clusters. Intra cluster distance ranged from 0.00 to 67.34. The highest inter-cluster divergence was documented between genotypes of clusters III and V.

Keywords: Genetic variability, correlation, path analysis, pearl millet, PCV (phenotypic coefficient of variance), GCV (genotypic coefficient of variance)

Introduction

Pearl millet [Pennisetum glaucum (L). R. Br] is an important warm-season cereal crop where it was a staple food for millions of people in arid and semiarid tropics (Reddy et al., 2021; Parihar et al, 2022; Rajpoot et al., 2023) [48, 41, 45]. It is a robust, quick-growing, and high tillering capacity with high-yielding potential. Pearl millet crop can able to grow under the adverse agro-climatic condition where other cereal crops like maize and sorghum fail to produce economic yields [Makwana et al., 2021; Patel et al, 2023] [29, 43]. It is the eighth major world cereal and fifth major crop after wheat, rice, maize, and sorghum in India [Singhal et al., 2022] [57]. In African continent, it covers an area of 18.50 million ha by 28 countries which yield 11.36 MT with 30% different region of the continent having diverse Agro-ecologies [Choudhary et al., 2021a] [9]. In India, it covers far-flung area of the country and occupy the fourth position in cereal crop which follows rice, wheat, and maize as first, second and third most producing cereal respectively. It covers an area of 6.93 MHa with a yield of 8.61 MT which possesses a productivity of 1243 kgha⁻¹ (Directorate of Millets Development, 2020). Rajasthan is the largest producing state of India with a yield of 4.283 million tonnes led by Uttar Pradesh (1.302), Haryana (1.079), Gujrat (0.961), Maharashtra (0.66) and Tamil Nādu (0.084). Madhya Pradesh occupies 3.69% area having 7.3% production. It has a productivity of 2458 kgha⁻¹, which is more than the national productivity *i.e.*, 1243 kgha⁻¹.

Pearl millet has a high content of moderate protein, amino acids, carbohydrates, and fats. It has abundant micronutrients such as calcium (Ca), iron (Fe) and zinc (Zn) and does not contain anti-nutrient antagonists such as tannins (Malhotra and Dhindsa, 1984) [30]. Various genetic variants in the Fe (30.1–75.7 mgkg⁻¹) and Zn (24.5–64.8 mgkg⁻¹) genes have been reported in the breeding lines and the necessary plant development measures are also being developed to improve the bio-lines with strong defences.

The past four decades witnessed for improvement in the productivity of major cereal crops achieved through the breeding of high-yielding cultivars with improved agronomic practices. The development of superior varieties/ hybrids mainly depends on the magnitude of variation and heritability present in a base material. Genetic diversity among individuals or populations can be determined by employing morphological (Yadav et al., 2005; Tripathi et al. 2015; Barfa et al., 2017; Choudhary et al., 2021b, Mishra et al., 2021; Shyam et al., 2021; Shyam et al., 2022; Yadav et al., 2022) [71, 63, 4, 10, 35, 54, 53, 72], biochemical (Choudhary et al., 2021c; Sharma et al., 2021) [12, 50] and molecular approaches (Shyam et al., 2020; Mishra et al., 2020; Pramanik et al., 2021; Verma et al., 2021a; and Asati et al., 2022; Mandloi et al., 2022; Mishra et al., 2022a; Mishra et al., 2022b; Parmar et al 2022; Tomar et al., 2022; Tripathi et al., 2022; Tripathi et al., 2023; Yadav et al., 2023) [55, 38, 44, 74, 3, 31, 36-37, 42, 62, 64, 65, 73]

The extent of variation is measured by GCV (Genotypic Coefficient of Variance) and PCV (Phenotypic Coefficient of Variance), which gives information about the variation present in the investigated characters. Heritability along with genetic advance has played a major role in determining the effective selection of experimental material for crop improvement. Selection of material based on yield attributing characters alone is not effective and efficient. So, selection based on its components and secondary characters could be more efficient and beneficial for the development of superior cultivars/hybrids. Therefore, generating information on the association of yield with its accrediting traits may improve the competence of selection in a breeding programme. Several measures have been employed to assess genetic diversity present among plant populations. The multivariate analysis offers the most accurate data of these measures. Among the methods with multiple variables. The generalized distance (D²) introduced by Mahalanobis in 1956 [28] has been widely used. In order to evaluate the variety and diversity existing in pearl millet genotypes for grain yield and its accrediting features, an assessment has been undertaken in the current study.

Material and Methods

Experimental material consisting of 75 pearl millet genotypes was acquired from the All India Coordinated Research Project on Pearl millet, Zonal Agricultural Research Station, Morena, Rajmata Vijayaraje Scindia Agricultural University, College of Agriculture, Gwalior, Madhya Pradesh, India, used for this investigation (Table1). The genotypes were evaluated during *Kharif* 2021 in a randomized block design with two replications. All the recommended agronomic package of practices was adopted properly during crop growth. Observations were recorded for five randomly selected plants from each entry in each replication for ten quantitative characters including plant height (cm), days to 50% flowering, days to maturity, numbers of productive tillers plant⁻¹, panicle length (cm), panicle diameter (cm), test weight (g), biological yield (g), harvest index and yield plant⁻¹

The PCV and GCV in per cent were computed by the following formulae given by Burton (1952) [7]. Heritability in broad sense in per cent was estimated by the following formula given by Singh *et al.* (1977) [75]. Genetic advance was expressed as percentage of mean by using the formula suggested by Johnson *et al.* (1955) [22]. Phenotypic and genotypic correlation coefficient between characters were

computed utilizing respective components of variances and co-variances, by following formula suggested by Miller *et al.* (1958). The estimation of path coefficient analysis as suggested by Wright (1921, 1935) and elaborated by Dewey and Lu (1959). D² values between any two accessions were estimated by multivariate analysis using Mohalanobis (1936) D² statistic as described by Rao (1952) [47]. Based on D² values, accessions were grouped into different clusters according to Tocher's method (Rao, 1952) [47].

Results and Discussion

The genetic characteristics for the characters under study, including mean, range, PCV and GCV, heritability estimates, and anticipated genetic advance as a percentage of mean, are shown in Table 2 and Fig. 1. In the present study, large differences in mean values for all the traits were observed. The trait plant height ranged from 150.50 to 250.50 (cm), days to 50% flowering from 39.00 to 45.50, days to maturity from 79.00 to 85.00, numbers of tillers plant-1 from 1.01 to 2.67 cm, panicle length from 19.05 to 32.25 cm, panicle diameter from 1.85 to 3.06 cm and test weight from 3.07 to 15.39 g, biological yield between 158.02 to 275.50 g harvest index ranged from 14.34 to 39.63 and yield plant⁻¹ from 18.75 to 71.75 g. The experimental material had a wide range of variability and favourable mean performance for most of the traits investigated and these possible combinations could be exploited as potential hybrids aimed for simultaneous improvement of grain yield and other yield-attributing traits. The trait exhibits a more negligible difference between PCV and GCV values, demonstrating a high degree of genetic variability present in these characters and, consequently, greater scope for selection based on those characters. These traits are less influenced by the environment and show high genetic variability. Table 3 provides the estimates of numerous genetic parameters. A higher magnitude as indicated by the high PCV and GCV values for the numbers of productive tillers plant⁻¹, test weight (g), biological yield (g), harvest index, and yield plant⁻¹ (g) indicating the higher magnitude of variability for these traits and consequently more scope for their improvement through selection. Higher estimates of PCV than GCV have also been reported by Manga (2013) [32] and Basavaraj et al. (2017) [5].

PCV and GCV estimates were moderate for panicle length (cm) and panicle diameter (cm). This implied equal importance of additive and non-additive gene action for the traits recorded. Similar results found by Talawar *et al.* (2017) [60] and Anuradha *et al.* (2018) [2]. Low GCV and PCV were recorded for plant height (cm), days to 50% flowering and days to maturity. These results are in conformity with the findings of Kumar *et al.* (2016) [24], Pallavi *et al.* (2020) [40] and Chauhan *et al.* (2020) [8].

Higher heritability was recorded for all the studied characters except days to maturity which showed moderate heritability and days to 50% flowering displayed low heritability (Table 2). Present results are in accordance with the findings of Sumathi *et al.* (2010) ^[59], Kumar *et al.* (2014) ^[25], Singh and Singh (2016) ^[56] and Talawar *et al.* (2017) ^[60]. The expected genetic advance as a percentage of the mean was found to be low for days to 50% flowering and days to maturity. Whilst high heritability coupled with higher genetic advance as percentage of mean were recorded for plant height, test weight, and plant yield whereas several productive tillers plants⁻¹ showed moderate heritability combined with high

GAM, which indicated that additive gene action on the expression of these characters which revealed an effective selection of desirable genotypes. In such cases improvement by the recurrent selection, and development of synthetics and composites may be proved beneficial. Similar results were also reported by Sumathi *et al.* (2010) ^[59], Singh and Singh. (2016) ^[56], Bhasker *et al.* (2017) ^[6], Subbulakshmi *et al.* (2018) ^[58] and Sharma *et al.* (2018) ^[51].

A higher coefficient of variation was present in the present investigation signifying the possibility of improving characters through phenotypic selection (Table 2). Estimates of high coefficient of variation with high heritability and higher genetic advance as percentage of mean were also observed for the numbers of productive tillers plant⁻¹, spike girth and harvest index by Manga (2013) [32] and Mukh *et al.* (2014) [39].

Correlation studies provide a natural relationship between diverse plant characters on yield and its components on the selection of genotypes for genetic improvement in yield. The genotypic and phenotypic correlation between all possible combinations of characters were estimated. Moreover, genotypic correlation coefficient was higher than their phenotypic correlation coefficient for all characters under study (Table 3). Grain yield plant-1 had a positive and significant correlation with days to 50% flowering, days to maturity, biological yield, and harvest index. Similar finding were also observed by Kumar et al. (2014) [25], Singh and Singh (2016) [56] and Talawar et al. (2017) [60] in pearl millet. Plant height showed positive significant correlation with numbers of productive tillers/ plant and test weight (g). Days to 50% flowering exhibited positive correlation with days to maturity, panicle length (cm) and harvest index. Days to maturity displayed positive correlation with numbers of productive tiller plant-1, panicle diameter (cm) and harvest index. Numbers of productive tillers plant⁻¹ expressed positive significant correlation with panicle length (cm), which is like findings of Choudhary et al. (2012) [13] and Dapke et al. (2014) [14]. Biological yield and harvest index are important yield attributing characters disclosed significant and positive correlation towards grain yield plant-1 indicating their contribution towards yield improvements. Abuali et al. (2012) [1], Choudhary et al. (2012) [13], Ezeaku et al. (2015) [20] and Sumathi et al. (2010) [59] also obtained similar results for test weight towards yield.

The Phenotypic correlation of grain yield plant⁻¹ showed positive significant correlation with days to maturity, biological yield (g) and harvest Index (g). While panicle length exhibited positive significant correlation with plant height (cm) and numbers of productive tillers plant⁻¹. Panicle diameter displayed positive significant correlation with days to maturity. Test weight exhibited positive significant correlation with plant height cm (Table 3). The similar results also obtained by Abuali *et al.* (2012) ^[1], Kumar *et al.* (2014) ^[25], Dhedhi *et al.* (2015;2016) ^[16-17] in pearl millet.

The estimation of correlation alone may be often misleading to the mutual cancelation of components characters, so it is necessary to study path coefficient analysis which provides a degree of relationship. Path coefficient analysis defines partitioning of the correlation coefficient into direct and indirect effect to know the relative importance of the attributing traits. Genotypic path coefficient analysis reflected that harvest index had considerably higher estimates of positive direct effect on grain yield plant (0.8415) followed

by biological yield (0.6844), test weight (0.0114), days to maturity (0.0164) and panicle length (0.0081). While the numbers of productive tillers plant⁻¹ (-0.0163) tracked by days to 50% flowering (-0.0141) and plant height (-0.0678) displayed negative direct effect on grain yield plant-1 (Table 4, Fig.2). Dapke et al. (2014) [14], Kumar et al. (2014) [25] and Bhasker et al. (2017) [6], reported similar results for numbers of productive tillers plant⁻¹ on plant yield. Phenotypic path coefficient revealed that harvest index (0.8369) has significant and positive direct effect on grain yield plant-1 tracked by biological yield (0.6843), test weight (0.0122), panicle length (0.0089), panicle diameter (0.0075) and days to maturity (0.0073). While the numbers of productive tillers plant⁻¹ (-0.0123) trailed by days to 50% flowering (-0.0010) and plant height (-0.0624) showed negative direct effect on grain yield plant⁻¹. The present findings agreed with earlier reported by Izge et al. (2006) [21] and Ramya et al. (2018) [46].

The percent contribution of individual characters toward the total divergence was found high for biological yield (g) (73.69%) followed by test weight (g) (7.96%), harvest index (6.34%), numbers of productive tillers plant (6.27%), yield plant (g) (5.59%), panicle length (cm) (0.07%) and panicle diameter (cm) (0.07%). However, days to 50% flowering, days to maturity and plant height (cm) showed low percentage of contribution indicating that they had little genetic diversity (Table 5, fig.3). In pearl millet, Shanmuganathan *et al.* (2006) [49] and Kumar *et al.* (2015) [26] reported comparable results.

The genetic diversity prevalent among the pearl millet lines was investigated using cluster analysis and the ward approach. With an average D^2 value of 250.73, the experimental material was divided into five clusters, demonstrating the presence of diversity among the lines for the features under investigation (Fig.4). Cluster I had the most lines, with thirty-eight, followed by cluster II, cluster V, cluster III, and cluster IV, each with thirty-two, three, one and two lines respectively (Table 6; Table 7).

The use of phenotypic data to screen breeding material for effective parents for hybridization programmes is a quick and simple technique to measure genetic diversity among genetically distinct lines. Table 7. shows the average D2 values between (intra cluster) and between (inter cluster) clusters. Cluster V (67.34) had the greatest intra cluster distance, followed by cluster I (50.28), and cluster II (47.00). These findings revealed that pearl millet genotypes may be differentiated clearly. Different researchers also demonstrated the clustering of genetic material in pearl millet, based on quantitative data including Drabo et al. (2013) [19] and Vidhyadhar and Devi (2007) [68]. As a result, within these clusters, selection might be based on the greatest mean for desired qualities. It is possible that heterogeneity, pedigree and the degree of general combining ability are responsible for such intra cluster genetic variability among lines within the same group.

The inter cluster distance (relative divergence among different clusters) revealed a high level of divergence between cluster III and V (250.73) tracked by cluster IV and cluster V (248.03), cluster I and cluster V (194.38), cluster II and cluster IV (150.21), cluster II and cluster III (146.12), cluster II and cluster V (127.58) cluster I and cluster II (92.35), cluster I and cluster IV (81.22) and cluster I and cluster III (73.75). As a result, the parents in these clusters are genetically heterogeneous, and when utilized in a hybridization programme, they may have a high heterotic

response. The specified lines might be inter crossed to create a base population with desirable traits (Vidhyadhar and Devi, 2007) ^[68] research backed up these findings. Cluster III and Cluster IV had slight genetic diversity as they have the shortest inter-cluster distance (52.25).

Table 8 explains the cluster mean and every character contribution to genetic diversity. For most of the traits studied, the cluster mean values showed a broad range of variance. In case of plant height (cm) cluster IV showed maximum value 220.50 days and cluster II showed minimum 194.41 days, while for days to 50% flowering, cluster II (42.03) displayed maximum and cluster III (40.00) had minimum cluster mean values. Days to maturity had maximum in cluster IV (84.50) and minimum in cluster III (81.00) respectively. Numbers of productive tillers plant⁻¹ was found maximum in cluster III (2.32), while minimum value

was noticed for cluster IV (1.36), whilst for panicle length (cm), cluster V (24.41 cm) showed maximum and cluster III (22.20 cm) had minimum cluster mean values. Panicle diameter (cm) exhibited maximum in cluster III (2.45), whereas minimum in cluster IV (1.96). Cluster mean value for test weight (g) revealed maximum in cluster III (10.92) and minimum in cluster IV (3.66). Biological yield (g) recorded maximum mean value in cluster V (249.23) and minimum in cluster IV (92.45). While harvest index (%) recorded maximum mean value in cluster IV (39.27) and minimum of cluster V (19.40). Yield plant-1 (g) was documented in cluster II (54.40g) and minimum in cluster III (28.20g). In order to ensure the effective selection and the selection of parents for hybridization, the features that contribute to most of the divergence should be given more weight (Anuradha et al., 2018) [2].

Table 1: List of pearl millet genotypes used in study

S. No.	Genotype	S. No.	Genotype		
1.	IP-254	39	IP-114		
2.	IP-266	40	IP-119		
3.	IP-261	41	IP-149		
4.	IP-367	42	IP-103		
5.	IP-218	43	IP-227		
6.	IP-271	44	IP-215		
7.	IP-257	45	IP-263		
8.	IP-356	46	IP-242		
9.	IP-279	47	IP-357		
10.	IP-243	48	IP-377		
11.	IP-301	49	IP-335		
12.	IP-226	50	IP-114		
13.	IP-202	51	IP-111		
14.	IP-366	52	IP-353		
15.	IP-201	53	IP-213		
16.	IP-304	54	IP-240		
17.	IP-299	55	IP-317		
18.	IP-256	56	IP-352		
19.	IP-391	57	IP-126		
20.	IP-350	58	IP-205		
21.	IP-354	59	IP-102		
22.	IP-310	60	IP-247		
23.	IP-361	61	IP-386		
24.	IP-298	62	IP-321		
25.	IP-228	63	IP-338		
26.	IP-278	64	IP-208		
27.	IP-362	65	IP-293		
28.	IP-203	66	IP-101		
29.	IP-384	67	IP-210		
30.	IP-259	68	IP-204		
31.	IP-294	69	IP-102		
32.	IP-233	70	IP-376		
33.	IP-258	71	IP-268		
34.	IP-255	72	IP-283		
35.	IP-281	73	IP-107		
36.	IP-241	74	IP-211		
37.	IP-308	75	IP-249		
38.	IP-326				

Table 2: Estimation of range, mean and different genetic parameters for different characters in pearl millet genotypes

S. No.	Characters	Mean	Range		PCV (%)	GCV (%)	Heritability (%)	Genetic advance
S. NO.	Characters	Mean	Min	Max	PCV (%)	GCV (%)	(Broad sense)	as% of mean 5%
1	Plant height (cm)	198.54	150.50	250.50	8.79	8.33	89.7	16.26
2	Days to 50% flowering	41.71	39.00	45.50	3.95	2.49	39.6	3.23
3	Days to maturity	82.70	79.00	88.50	2.41	1.91	63.2	3.14
4	Numbers of productive tillers plant ⁻¹	1.80	1.01	2.67	26.97	26.92	99.6	55.36
5	Panicle length (cm)	23.96	19.05	32.25	11.99	11.78	96.6	23.86
6	Panicle diameter (cm)	2.27	1.85	3.06	11.28	10.91	93.6	21.75
7	Test weight (g)	8.26	3.07	15.39	33.54	33.49	99.7	68.88
8	Biological yield (g)	158.02	92.45	275.50	22.06	22.05	99.1	45.43
9	Harvest index	29.57	14.34	39.63	24.97	24.93	99.7	51.29
10	Yield plant ⁻¹ (g)	46.31	18.75	71.75	29.92	29.89	99.8	61.53

Table 3: Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients between different characters in pearl millet genotypes

Characters	Plant height (cm)	Days to 50% flowering	Days to maturity	Numbers of productive tillers plant ⁻¹		Panicle diameter (cm)		Biological yield (g)	Harvest index	Yield plant ⁻¹ (g)
Plant height (cm)	1.0000	-0.0363	0.1186	0.2346*	0.2713*	0.0173	-0.2673*	-0.0573	0.2131	0.0703
Days to 50% flowering	0.0342	1.0000	0.3521**	-0.1783	-0.2389*	0.0169	0.1172	0.1004	0.3417**	0.3528**
Days to maturity	0.0870	0.2093	1.0000	0.2625*	0.0610	0.3714**	-0.1243	0.1544	0.2439*	0.3113**
Numbers of productive tillers plant ⁻¹	0.2212	-0.1155	0.2003	1.0000	0.2995*	0.1305	-0.1282	-0.0602	0.1705	0.0787
Panicle length (cm)	0.2658*	-0.1538	0.0565	0.2930*	1.0000	0.0840	-0.0671	0.0227	0.0240	0.0247
Panicle diameter (cm)	0.0037	0.0150	0.3202**	0.1252	0.0744	1.0000	0.1055	-0.2063	0.0237	-0.1110
Test weight (g)	-0.2515*	0.0708	-0.1033	-0.1276	-0.0664	0.0978	1.0000	0.0438	0.1887	0.2167
Biological yield (g)	-0.0548	0.0623	0.1234	-0.0599	0.0216	-0.1990	0.0437	1.0000	-0.1669	0.5494**
Harvest index	0.2010	0.2099	0.1952	0.1698	0.0236	0.0254	0.1879	-0.1667	1.0000	0.7116**
Yield plant ⁻¹ (g)	0.0654	0.2177	0.2487*	0.0786	0.0235	-0.1050	0.2160	0.5490**	0.7121**	1.0000

^{**} Correlation is significant at the 0.01 level, * Correlation is significant at the 0.05 level

Table 4: Genotypic and phenotypic path coefficients for yield and its attributing traits of pearl millet genotypes

Characters		Plant height (cm)	Days to 50% flowering	Days to maturity	Numbers of productive tillers plant ⁻¹	Panicle length (cm)	Panicle diameter (cm)	Test weight (g)	Biological yield (g)	Harvest index	Yield plant ⁻¹ (g)
Plant height (cm)	G	-0.0678	0.0025	-0.0080	-0.0159	-0.0184	-0.0012	0.0181	0.0039	-0.0145	0.0703
Fiant height (cm)	P	-0.0624	-0.0021	-0.0054	-0.0138	-0.0166	-0.0002	0.0157	0.0034	-0.0125	0.0654
Days to 50% flowering	G	0.0005	-0.0141	-0.0050	0.0025	0.0034	-0.0002	-0.0017	-0.0014	-0.0048	0.3528
Days to 30% Howering	P	0.0000	-0.0010	-0.0002	0.0001	0.0002	0.0000	-0.0001	-0.0001	-0.0002	0.2177
Days to moturity	G	0.0019	0.0058	0.0164	0.0043	0.0010	0.0061	-0.0020	0.0025	0.0040	0.3113
Days to maturity	P	0.0006	0.0015	0.0073	0.0015	0.0004	0.0023	-0.0008	0.0009	0.0014	0.2487
Numbers of productive	G	-0.0038	0.0029	-0.0043	-0.0163	-0.0049	-0.0021	0.0021	0.0010	-0.0028	0.0787
tillers plant ⁻¹	P	-0.0027	0.0014	-0.0025	-0.0123	-0.0036	-0.0015	0.0016	0.0007	-0.0021	0.0786
Panicle length (cm)	G	0.0022	-0.0019	0.0005	0.0024	0.0081	0.0007	-0.0005	0.0002	0.0002	0.0247
Famcie length (cm)	P	0.0024	-0.0014	0.0005	0.0026	0.0089	0.0007	-0.0006	0.0002	0.0002	0.0235
Panicle diameter (cm)	G	0.0001	0.0001	0.0022	0.0008	0.0005	0.0058	0.0006	-0.0012	0.0001	-0.1110
Famcie diameter (cm)	P	0.0000	0.0001	0.0024	0.0009	0.0006	0.0075	0.0007	-0.0015	0.0002	-0.1050
Test weight (a)	G	-0.0030	0.0013	-0.0014	-0.0015	-0.0008	0.0012	0.0114	0.0005	0.0021	0.2167
Test weight (g)	P	-0.0031	0.0009	-0.0013	-0.0016	-0.0008	0.0012	0.0122	0.0005	0.0023	0.2160
Biological yield (g)	G	-0.0392	0.0687	0.1057	-0.0412	0.0155	-0.1412	0.0300	0.6844	-0.1143	0.5494
	P	-0.0375	0.0426	0.0845	-0.0410	0.0148	-0.1362	0.0299	0.6843	-0.1141	0.5490
Harvest index	G	0.1794	0.2876	0.2053	0.1435	0.0202	0.0200	0.1588	-0.1405	0.8415	0.7116
nai vest ilidex	P	0.1682	0.1757	0.1634	0.1421	0.0197	0.0213	0.1573	-0.1395	0.8369	0.7121

Table 5: Contribution of different characters toward clustering of pearl millet genotypes

Source	Contribution%
Plant height (cm)	0
Days to 50% flowering	0
Days to maturity	0
Numbers of productive tillers plant ⁻¹	6.27
Panicle length (cm)	0.07
Panicle diameter (cm)	0.07
Test weight (g)	7.96
Biological yield (g)	73.69
Harvest index	6.34
Yield plant ⁻¹ (g)	5.59

Table 6: Inter and intra cluster D² values for different clusters of pearl millet genotypes

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	50.28	92.35	73.75	81.22	194.38
Cluster II		47.00	146.12	150.21	127.58
Cluster III			0.00	52.25	250.73
Cluster IV				0.00	248.03
Cluster V					67.34

Table 7: Distribution of pearl millet genotypes in different clusters by Tocher's Method

Cluster Number	Numbers of genotypes	Name of the genotypes
I	38	IP-266, IP-261, IP-367, IP-218, IP-271, IP-257, IP-356, IP-243, IP-301, IP-226, IP-202, IP-366, IP-201, IP-304, IP-299, IP-391, IP-354, IP-310, IP-361 IP-298, IP-228, IP-278, IP-362, IP-203, IP-384, IP-259, IP-294, IP-233, IP-258, IP-255, IP-281, IP-241, IP-308, IP-326, IP-114, IP-119, IP-149, IP-103
II	32	IP-227, IP-215, IP-263, IP-242, IP-357, IP-377, IP-335, IP-114, IP-111, IP-353, IP-213, IP-240, IP-317, IP-352, IP-126, IP-205, IP-102, IP-247, IP-386, IP-321, IP-338, IP-208, IP-101, IP-210, IP-204, IP-102, IP-376, IP-268, IP-283, IP-107, IP-211, IP-249
III	01	IP-350
IV	01	IP-256
V	03	IP-254, IP-293, IP-279

Table 8: Cluster mean for yield and its attributing traits of pearl millet genotypes

	Plant height (cm)	Days to 50% flowering	Days to maturity	Numbers of productive tillers plant ¹	Panicle length (cm)	Panicle diameter (cm)	Test weight (g)	Biological yield (g)	Harvest index (%)	Yield plant ⁻¹ (g)
Cluster I	200.18	41.61	82.46	1.86	24.04	2.32	8.08	133.53	29.95	40.03
Cluster II	194.41	42.03	82.89	1.71	23.89	2.25	8.67	182.52	29.80	54.40
Cluster III	196.00	40.00	81.00	2.32	22.20	2.45	10.92	96.70	29.17	28.20
Cluster IV	220.50	41.00	84.50	1.36	23.65	1.96	3.66	92.45	39.27	36.30
Cluster V	215.50	40.50	83.67	1.98	24.41	2.05	6.97	249.23	19.40	49.03

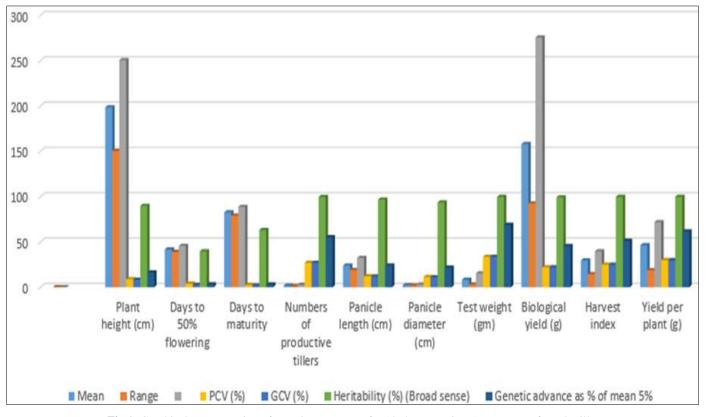
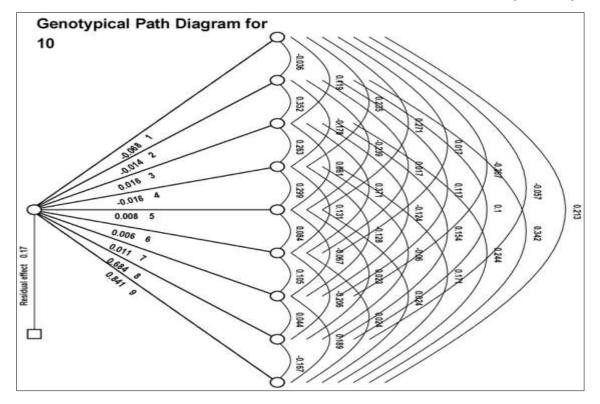


Fig 1: Graphical representation of genetic parameters for 10 characters in 75 genotypes of pearl millet



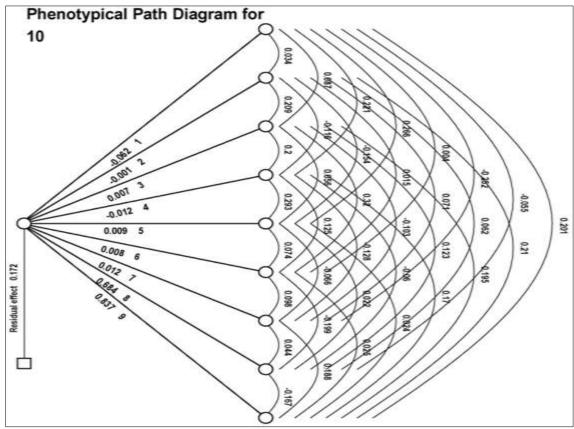


Fig 2: Path Diagram at genotypic and phenotypic level in Pearl millet

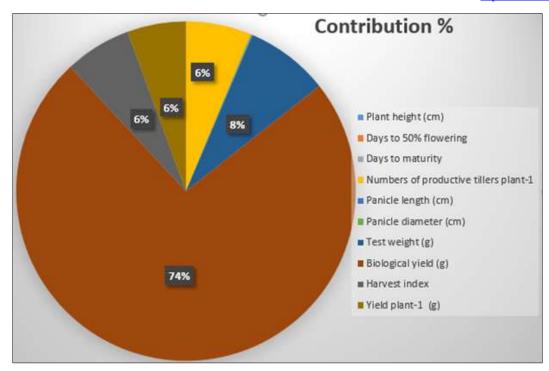


Fig 3: Contribution of different characters toward clustering of pearl millet genotypes

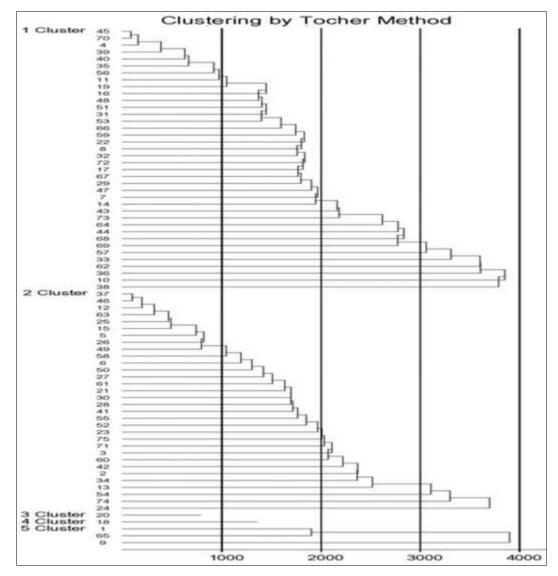


Fig 4: Cluster Diagram in Pearl millet

Conclusion

Based on the present investigation, it can be concluded that the values of PCV were higher than GCV but in a narrow range for almost all the studied characters indicating the least influence of the environment. The characters viz., numbers of productive tillers plant⁻¹, test weight, biological yield, harvest index and grain yield plant-1 exhibited high heritability coupled with higher genetic advance as a percentage of mean. Association studies revealed that numbers of productive tillers plant⁻¹, biological yield, plant height and test weight should be considered as major characters while selecting the genotype (s) for yield improvement because it expressed high positive significant correlation with yield. Path analysis also revealed that biological yield and harvest index had a high positive direct effect on yield and a high indirect effect through most of the other characters. Correlation and path analysis revealed that biological yield and harvest index could be considered as good selection indices for selecting genotype (s) for yield improvement. In accordance with current findings, it is suggested that genotypes fall in cluster III and IV has wider diversity may fruitful for further breeding improvement programme.

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