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SN Jaybhaye
M.Sc. Scholar, Department of Genetics and Plant Breeding, College of Agriculture, Badnapur, Maharashtra, India

AB Bagade
Associate Professor, Department of Plant Breeding, College of Agriculture, Badnapur, Maharashtra, India

SB Pawar
Associate Director of Research, National Agriculture Research Project, Chhatrapati Sambhajinagar, Maharashtra, India

Mahesh D Patil
Ph.D Scholar, Department of Genetics and Plant Breeding, Punjab Agricultural University, Ludhiana, Punjab, India

Corresponding Author:
SN Jaybhaye
M.Sc. Scholar, Department of Genetics and Plant Breeding, College of Agriculture, Badnapur, Maharashtra, India

Genetic diversity analysis of pearl millet (*Pennisetum glaucum* L.) germplasm for yield and yield-contributing traits

SN Jaybhaye, AB Bagade, SB Pawar and Mahesh D Patil

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Abstract

An experiment entitled “Genetic diversity studies in pearl millet [Pennisetum glaucum (L.) R. Br.]”. was carried out during Kharif 2024 at the Research Farm of National Agriculture Research Project, Chhatrapati Sambhajinagar. The experiment was laid out in Randomized Block Design (RBD) with 42 genotypes and two replications to estimate the extent of genetic variability, heritability, genetic advance, correlation coefficient and path coefficient analysis among all the genotypes.

Analysis of Relative contribution of various traits to genetic divergence revealed that the trait panicle girth (cm) as the most substantial contributor, accounting for 29.85%. Following this, days to maturity was identified as the second most influential factor, succeeded by the 1000-Grain Wt. (g), days to 50% flowering, panicle length (cm), number of productive tillers per plant, plant height (cm), Harvest Index, Fodder yield per plot , days of maturity, grain yield per plant. The traits, including the number of productive tillers per plant, panicle girth, 1000-Grain Wt. (g), and Fodder yield per plot, exhibited a strongly positive and statistically significant correlation with grain yield per plant at both genotypic and phenotypic levels. Consequently, these traits can be regarded as pivotal determinants in the effort to enhance overall seed productivity.

Keywords: Genetic diversity, pearl millet, germplasm

Introduction

Pearl millet (*Pennisetum glaucum* L. R. Br.) is an annual, diploid (2n = 14), highly cross-pollinated cereal crop belonging to the family Poaceae, subfamily Panicoideae. Believed to have originated in West Africa (Vavilov, 1950), it is now extensively cultivated in arid and semi-arid regions due to its exceptional drought tolerance, short growth cycle, and high photosynthetic efficiency (Bennett, 2000; Serba & Yadav, 2016) [2, 9]. In India, it is primarily grown during the kharif season, with Rajasthan, Maharashtra, Uttar Pradesh, Gujarat, and Haryana accounting for the majority of production (Directorate of Economics and Statistics, 2024) [4].

The crop thrives under 400-600 mm annual rainfall and temperatures between 15-40°C, with optimum growth at 30-35 °C (Yadav *et al.*, 2021) [14]. It performs well in sandy loam to clay loam soils, tolerates marginal conditions, and is adapted to low-input farming systems (Govindaraj *et al.*, 2020) [5]. Nutritionally, pearl millet surpasses many staple cereals, offering high protein, dietary fiber, essential minerals such as iron and zinc, and health-promoting polyunsaturated fatty acids (Rao *et al.*, 2017; Singh *et al.*, 2018) [8, 10]. Its low glycemic index and high resistant starch content make it beneficial in managing lifestyle-related disorders (Anuradha *et al.*, 2021) [1]. Genetic improvement in pearl millet depends on understanding variability, heritability, and genetic advance for key traits, along with correlations and path coefficient analysis to identify traits with the greatest influence on yield (Johnson *et al.*, 1955; Wright, 1921; Dewey & Lu, 1959) [7, 13, 3]. Estimating genetic diversity within germplasm aids in identifying superior and genetically diverse parents for hybridization, thereby accelerating the development of high-yielding and nutrient-dense cultivars (Gupta *et al.*, 2022; Singh *et al.*, 2023) [6, 12].

Materials and Methods

In the current study entitled "Genetic Diversity studies in pearl millet germplasm

[*Pennisetum glaucum* (L.) R. Br.].’ ’The experimental material selected from the germplasm of National Agricultural Research Project Chhatrapati Sambhajinagar, were evaluated in a Randomized Block Design (RBD) with two replications during Kharif 2024-2025. Total 42 germplasm including 40 inbred lines and two checks ABPC 4-3 and AIMP 92901 were used.

The fourty two genotypes of pearl millet along with two checks ABPC 4-3 and AIMP 92901 were grown in a randomized block designwith two replications during Kharif 2024-25. Each genotype was sown in a two row of 4 m length with spacing of 45 cm between rows and 15 cm between plants. All cultivation practices viz. weeding, irrigation etc. were carried out regularly as per need and stage of crop growth. The fertilizer application was done as per recommended dose and all activity was carried out as per need.

Experimental material comprising 42 germplasm lines with wider diversity for different characters were selected along with 2 checks.

Table 1: List of Genotypes

Sr. No	Entry	Sr. No	Entry
1	AUBI-15333R	21	AUBI-15280R
2	AUBI-15452R	22	AUBI-15287R
3	AUBI-15313R	23	AUBI-15050R
4	AUBI-15448R	24	AUBI-15309R
5	AUBI-15352R	25	AUBI-15221R
6	AUBI-15387R	26	AUBI-15346R
7	AUBI-15262R	27	AUBI-15286R
8	AUBI-15260R	28	AUBI-15052R
9	AUBI-15279R	29	AUBI-18097R
10	AUBI-15241R	30	AUBI-15022R
11	AUBI-15348R	31	AUBI-15071R
12	AUBI-15245R	32	AUBI-15024R
13	AUBI-15233R	33	AUBI-15415R
14	AUBI-15265R	34	AUBI-16287R
15	AUBI-15385R	35	AUBI-15374R
16	AUBI-15358R	36	AUBI-15184R
17	AUBI-15453R	37	AUBI-15137R
18	AUBI-15468R	38	AUBI-16630R
19	AUBI-15230R	39	AUBI-15043R
20	AUBI-1549R	40	AUBI-18801R
Checks I	ABPC 4-3	Checks II	AIMP-92901

Results and Discussion

Genetic divergence

Forty two bajra genotypes, inclusive of two check varieties, ABPC 4-3 and AIMP 92901, were subjected to quantitative analysis utilizing Mahalanobis's D^2 statistic. The clustering will be executed in accordance with Tocher's method.

Test with Wilk’s criterion and analysis of variance for dispersion of genotype

Wilk’s ‘λ’ statistic was employed as a criterion to assess the statistical significance of differences among genotypes, considering the combined effects of all measured traits. The significance of the ‘λ’ statistic was tested using the χ^2 distribution with 410 degrees of freedom. The computed ‘λ’ value of 0.0000 indicated a highly significant result, suggesting that the genotypes exhibited considerable differentiation when all traits were analyzed collectively.

The analysis of variance for the dispersion of the forty-two genotypes is presented in Table 2 The significant variation observed among genotypes clearly demonstrates substantial diversity across all measured traits. Consequently, further analysis was carried out to estimate the D^2 values.

Table 2: Analysis of variance for dispersion in forty two genotypes in bajra:

Source of variations	Degree of freedom	Mean squares
Varieties	41	1.90
Error	40	5.53
Total	81	9.63

Mahalanobis's D^2 values

The mean values of the forty-two genotypes, along with the two checks $[(X_1)-(X_2)]$, were transformed into standardized, uncorrelated mean values $[(Y_1)-(Y_2)]$. D^2 values were subsequently computed for all possible genotype pairs, yielding a total of 861 pairs, as determined by the formula $n(n-1)/2$, where $n = 42$.

Grouping of genotypes

All forty-two bajra genotypes were grouped into eight distinct clusters using Tocher’s method (Singh and Chaudhary, 1977) [11]. The distribution of genotypes among these clusters, along with their respective geographical areas of adaptation, is presented in Table 3

Cluster I contained the highest number of genotypes (22), followed by Cluster IV (8 genotypes), Cluster II (5 genotypes), and Cluster VIII (3 genotypes). Clusters III, V, VI, and VII were the smallest, each comprising a single genotype.

Clustering pattern in relation to geographical diversity

The genotypes were allocated randomly among all clusters. A correlation was observed between geographic origin and genetic diversity, as genotypes originating from distinct geographic regions were found grouped within the same cluster.

Table 3: Composition of forty two bajra genotypes into different clusters by Tocher’s method.

Cluster Number	No. of Genotypes	List of Genotypes
I	22	AUBI-15333R, AUBI-15360R, AUBI-15313R, AUBI-15241R, AUBI-15262R, AUBI-15233R, AUBI-15348R, AUBI-15489R, ABPC4-3, AUBI-15286R, AUBI-15052R, AUBI-18097R, AUBI-15221R, AUBI-15425R, AUBI-15352R, AUBI-15387R, AUBI-15287R, AIMP92901, AUBI-18801R, AUBI-15358R, AUBI-15280R, AUBI-15309R
II	5	AUBI-15265R, AUBI-15346R, AUBI-15468R, AUBI-15022R, AUBI-15050R
III	1	AUBI-15230R
IV	8	AUBI-15245R, AUBI-15453R, AUBI-15385R, AUBI-15279R, AUBI-15415R, AUBI-16287R, AUBI-16630R, AUBI-15184R
V	1	AUBI-15071R
VI	1	AUBI-15448R
VII	1	AUBI-15374R
VIII	3	AUBI-15137R, AUBI-15043R, AUBI-15024R

Cluster diagram

Using the D² values from Table 3, a cluster diagram was constructed to illustrate the relationships among the different genotypes. The greatest distance between two clusters was observed between Cluster II and Cluster VII (16.86), indicating the highest degree of divergence. This was followed by the distances between Cluster VI and Cluster VII (16.68), Cluster IV and Cluster VI (16.12), Cluster V and Cluster VII (15.99), Cluster II and Cluster VIII (14.89), Cluster IV and Cluster V (14.73), Cluster II and Cluster III (14.55), Cluster II and Cluster IV (13.80), Cluster I and Cluster V (9.09), Cluster III and Cluster IV (9.04) and finally, Cluster I and Cluster III (8.89).

Intra cluster average distance

The average intra-cluster distance D² values for the clusters are provided in Table 4 and illustrated in Figure 1. The intra-cluster distances ranged from 0.00 to 9.50. The highest intra-cluster distance of 9.50was observed in Cluster IV, followed by 7.54 in Cluster VIII and 7.44 in Cluster. Genotypes within these clusters, displaying substantial genetic divergence, represent optimal candidates for hybridization programs. These genotypes are expected to generate superior breeding material, thereby enhancing genetic improvement for targeted traits.

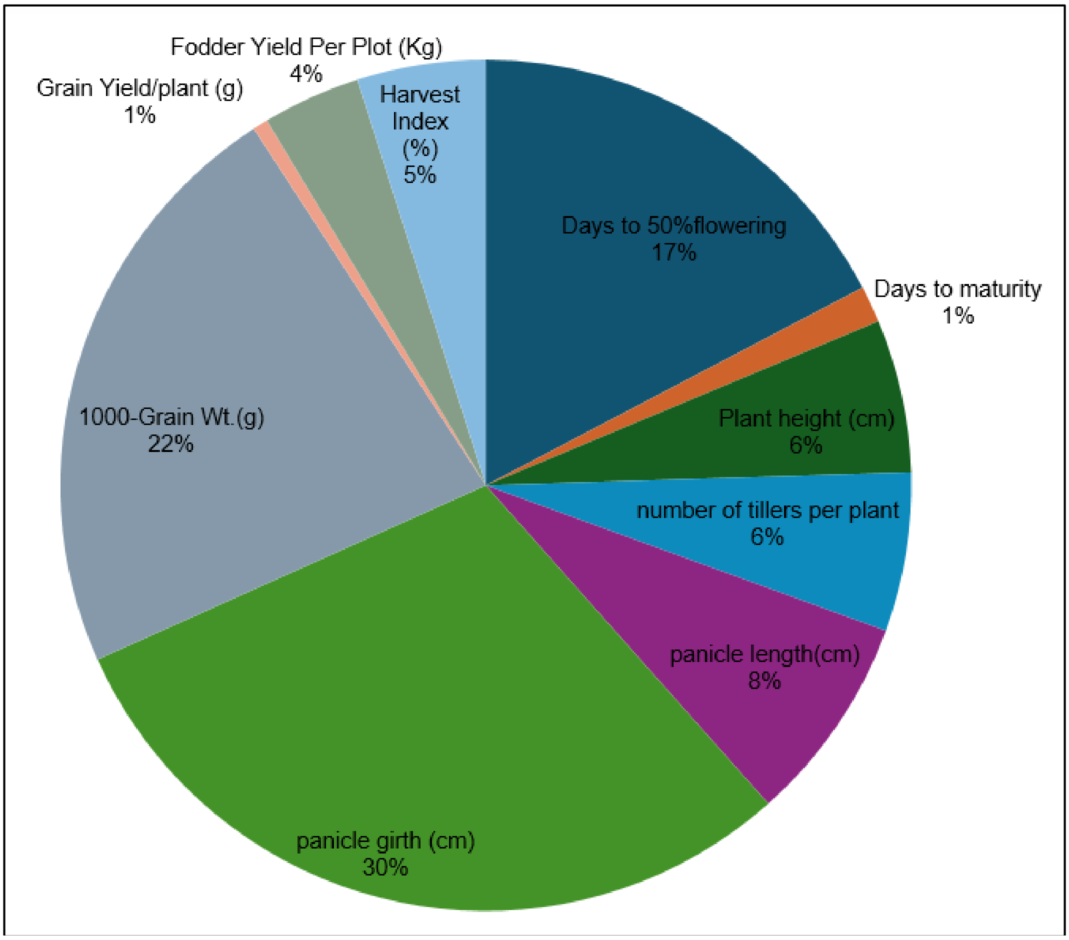


Fig 1: Percent contribution of different characters of bajra to genetic diversity

Table 4: Average intra and inter cluster distance (D^2) values in bajra.

Cluster Number	I	II	III	IV	V	VI	VII	VIII
I	7.44	10.12	8.89	11.19	9.09	9.83	13.20	10.63
II	10.12	4.87	14.55	13.80	10.44	13.15	16.86	14.89
III	8.89	14.55	0.00	9.04	12.54	12.25	11.80	11.56
IV	11.19	13.80	9.04	9.50	14.73	16.12	11.47	13.42
V	9.09	10.44	12.54	14.73	0.00	9.87	15.99	11.57
VI	9.83	13.15	12.25	16.12	9.87	0.00	16.68	11.64
VII	13.20	16.86	11.80	11.47	15.99	16.68	0.00	11.51
VIII	10.63	14.89	11.56	13.42	11.57	11.64	11.51	7.54

Cluster means for various characters

Table 5 presents the cluster means for the nine evaluated traits. Considerable inter-cluster variation was observed for all traits studied, namely days to 50% flowering, days to maturity, plant height (cm), number of tillers per plant, panicle length (cm), panicle girth (cm), 1000-grain weight (g), grain yield per plant (g), fodder yield per plot (kg), and harvest index (%).

The cluster mean for days to 50% flowering ranged from 42.00 in Cluster II to 58.50 in Cluster VI. For days to maturity, the means varied between 83.50 days in Cluster IV and 92.50 days in Cluster VI. Plant height was highest in Cluster VII (178.00 cm) and lowest in Cluster III (141.56 cm). The number of tillers per plant ranged from 1.23 in Cluster III to 2.33 in Cluster VII. Panicle length varied from 17.91 cm in Cluster VII to 23.75 cm in Cluster II. Panicle girth was greatest in Cluster V (2.94 cm) and smallest in Cluster VII (1.46 cm). The highest 1000-grain weight was recorded in Cluster II (13.00 g), whereas Cluster III had the lowest (7.55 g). Grain yield per plant ranged from 25.02 g in Cluster III to 34.06 g in Cluster VI. Fodder yield per plot was lowest in Cluster IV (8.11 kg) and highest in Cluster V (11.00 kg). Harvest index was highest in Cluster VI (36.07%) and lowest in Cluster VII (23.31%).

Percent contribution of various characters for divergence

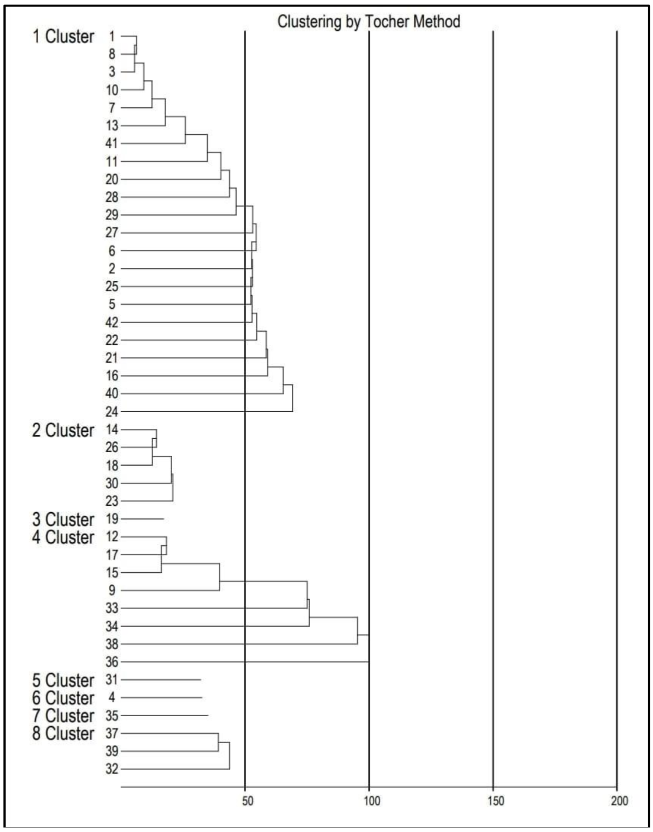
The utility of D² analysis was further enhanced by using it to estimate the relative contribution of various plant characters to genetic divergence. The percentage contribution of the nine traits studied to the total divergence is presented in Table 6 Panicle girth (cm) contributed the most to genetic divergence, accounting for 29.85%, followed by 1000-grain weight (g) at 22.53%, and days to 50% flowering at 17.31%. Panicle length (cm) contributed 7.90%, the number of productive tillers per plant 6.04%, plant height (cm) 5.81%, and harvest index (%) 4.88%. Contributions from days to maturity were 1.39%, while fodder yield per plot (kg) and grain yield per plant (g) contributed 3.72% and 0.58%, respectively.

Table 5: Cluster means for seed yield and its components in bajra.

	Days to 50% Flowering	Days to Maturity	Plant Height (cm)	No. of Tillers/Plant	Panicle Length (cm)	Panicle Girth (cm)	1000-GrainWt. (g)	Grain Yield/plant (g)	Fodder Yield per Plot (kg)	Harvest Index (%)
Cluster 1	50.98	85.11	150.91	1.77	21.54	2.52	10.86	28.39	9.04	32.90
Cluster 2	42.00	85.50	138.58	2.22	23.75	2.90	13.00	32.57	10.95	31.77
Cluster 3	55.50	88.50	141.56	1.23	20.75	2.19	7.55	25.02	8.82	31.04
Cluster 4	49.63	83.50	144.65	1.77	22.92	2.00	8.22	27.66	8.11	28.53
Cluster 5	53.00	87.00	174.00	1.60	22.10	2.94	12.15	30.35	11.00	25.40
Cluster 6	58.50	92.50	146.27	2.18	19.71	2.82	12.04	34.06	9.81	36.07
Cluster 7	45.50	87.50	178.00	2.33	17.91	1.46	8.06	32.40	10.19	23.31
Cluster 8	53.17	84.17	161.01	1.87	20.47	1.79	12.39	26.71	8.83	23.83

Table 6: Percent contribution of different characters of bajra to genetic diversity.

Sr. No	Characters	No. of times appearing I in ranking	% Contribution
1	Days to 50%flowering	149	17.31%
2	Days to maturity	12	1.39%
3	Plant height (cm)	50	5.81%
4	number of tillers per plant	52	6.04%
5	panicle length(cm)	68	7.90%
6	panicle girth (cm)	257	29.85%
7	1000-Grain Wt.(g)	194	22.53%
8	Grain Yield/plant (g)	5	0.58%
9	Fodder Yield Per Plot (Kg)	32	3.72%
10	Harvest Index (%)	42	4.88%
	Total	861	100%



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