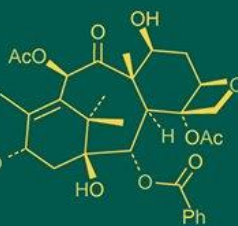
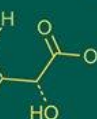
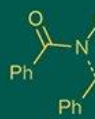


International Journal of Advanced Biochemistry Research



ISSN Print: 2617-4693
ISSN Online: 2617-4707
NAAS Rating (2026): 5.29
IJABR 2026; SP-10(8): 1814-1818
www.biochemjournal.com
Received: 25-05-2026
Accepted: 29-06-2026

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Assessment of phenotypic diversity and cluster analysis in barnyard millet (*Echinochloa frumentacea* (Roxb.) Link) genotypes

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DOI: <https://www.doi.org/10.33545/26174693.2026.v10.i8St.9678>

Abstract

Barnyard millet (*Echinochloa frumentacea* (Roxb.) Link) is a nutrient-dense and climate-hardy cereal with real potential for sustainable farming, though realizing that potential calls for a clear picture of how much genetic variation the crop holds. This study looked at genetic diversity and trait relationships across 200 barnyard millet genotypes raised during *kharif* 2025 in an alpha lattice design with two replications. Ten quantitative traits were recorded and analysed using genotypic and phenotypic correlation coefficients, while Ward's hierarchical clustering based on Euclidean distance was applied to gauge genetic divergence among the genotypes. Grain yield showed a significant, positive correlation with plant height, panicle length, and panicle width, suggesting these traits could serve as useful criteria for selecting higher-yielding lines. The clustering split the genotypes into five distinct groups, pointing to considerable genetic variability within the germplasm, with the widest inter-cluster divergence recorded between Cluster 4 and Cluster 5. Substantial phenotypic variation was evident across traits: Cluster 4 combined the greatest yield potential with late maturity and tall stature, whereas Cluster 5 was made up of early-maturing, short-statured genotypes. Taken together, these results point to the breeding value of this diverse barnyard millet germplasm for parent selection and offer a practical reference for developing high-yielding, nutritionally rich, and climate-resilient cultivars.

Keywords: Barnyard millet, genetic diversity, grain yield, correlation

Introduction

From a taxonomic standpoint, barnyard millet is a self-pollinating allohexaploid ($2n = 6x = 54$) placed within the genus *Echinochloa*, in the family Poaceae and sub-family Panicoideae (Clayton and Renvoize, 2006) [3]. It is raised as a dual-purpose crop valued for both grain and fodder, and two species are cultivated worldwide: *Echinochloa frumentacea*, known as Indian barnyard millet, and *Echinochloa esculenta*, or Japanese barnyard millet (Sood *et al.*, 2015) [15]. These were domesticated respectively from the wild progenitors *Echinochloa colona* and *Echinochloa crus-galli* (Singh *et al.*, 2025) [14]. India is the world's leading producer, growing the crop mainly on marginal, rainfed land where poor soil fertility and cold temperatures at high elevation make rice impractical. Its cultivation stretches across a remarkably wide range of environments, from coastal Andhra Pradesh to the hill districts of Uttarakhand and the higher elevations of the north-eastern states, underlining its broad adaptability (Hasan *et al.*, 2025) [5]. Nutritionally, it compares well with major and minor cereals alike: every 100 g of grain provides roughly 398 kcal, 10.5% protein, 3.6% fat, 68.8% carbohydrates, and 12.6% dietary fibre, and its iron and zinc content exceeds that of major cereals (Ugare *et al.*, 2014; Maurya *et al.*, 2023) [16, 6]. Being gluten-free and low on the glycaemic index, it also helps in managing type 2 diabetes, obesity, and cardiovascular disease (Hasan *et al.*, 2025) [5].

Genetic diversity is the foundation of any crop improvement effort, since it provides the variability that effective selection, parental choice, and the development of better cultivars all depend on (Goron and Raizada, 2015; Bhinda *et al.*, 2023) [4, 2]. Assessing genetic divergence within germplasm collections allows breeders to identify parents distinct enough to generate wide variability and transgressive segregants in later generations (Mehta *et al.*, 2005; Nehru *et al.*, 2023) [7, 9].

Identifying genotypes that pair genetic diversity with sound agronomic performance is therefore essential for broadening the genetic base of breeding populations and accelerating the development of high-yielding, nutrient-rich, climate-resilient barnyard millet cultivars (Bhinda *et al.*, 2023; Singh *et al.*, 2025) [2, 14].

With this context in mind, the present study was designed to assess genetic diversity among 200 barnyard millet genotypes using Ward's hierarchical clustering based on Euclidean distance, aiming to identify genetically divergent parents for future crop improvement programmes.

Materials and Methods

This study evaluated 200 barnyard millet genotypes, including released cultivars, advanced breeding lines, and diverse germplasm accessions, at the research farm of ICAR-Indian Institute of Millets Research, Hyderabad, Telangana, India, during *kharif* 2025. The trial was laid out in an Alpha Lattice Design with two replications, each split into ten blocks, and the crop was managed under recommended agronomic practices to ensure uniform establishment and healthy growth throughout the season. Observations on five randomly selected plants per genotype were used to record ten quantitative traits: seedling height, days to 50% flowering, days to maturity, thousand-seed weight, number of tillers, plant height, panicle length, panicle width, dehulling efficiency, and grain yield, with days to 50% flowering, days to maturity, and grain yield recorded on a plot basis rather than per plant. Trait relationships were examined using Pearson's correlation analysis (Pearson, 1948) [11], and Ward's hierarchical clustering based on genetic distance was used to assess genetic diversity and group the genotypes into distinct clusters.

Results and Discussion

Character association

Grain yield is a complex quantitative trait shaped by the combined influence of several morphological and yield-related characters. Understanding how these traits relate to one another is therefore important for defining effective selection strategies and raising yield potential in breeding programmes. Genotypic and phenotypic correlation coefficients between grain yield and its component traits are presented in Table 1. For most traits, the genotypic correlation coefficients exceeded the corresponding phenotypic values, suggesting that the observed associations are mainly under genetic control, with the environment playing a comparatively minor role in shaping trait expression. At both the phenotypic and genotypic levels, grain yield showed a significant, positive association with days to 50% flowering (0.198**; 0.331**, respectively), plant height (0.270**; 0.275**, respectively), and panicle width (0.207**; 0.2969**, respectively). Because these correlations are positive and significant, the traits concerned could serve as effective selection criteria for raising grain yield in barnyard millet. Similar positive links between grain yield and days to 50% flowering, plant height, and panicle width have previously been reported in barnyard millet by Prakash and Vanniarajan (2014) [13] and Prabu *et al.* (2020) [12], reinforcing the case for these traits as useful indirect selection criteria for improving grain yield. Notably, dehulling efficiency was negatively correlated with thousand seed weight at both the phenotypic and genotypic levels (-0.022^{NS}, -0.0233^{NS}), suggesting that seed size alone does not fully account for variation in dehulling efficiency. This negative association implies that selecting purely for higher thousand-seed weight could inadvertently lower dehulling efficiency, posing a challenge for breeding programmes seeking to improve both traits together.

Table 1: Genotypic and Phenotypic correlations among barnyard millet genotype

Traits		SH	DFF	DM	PH	NOT	PL	PW	TSW	DE	GY
SH	P	1**	0.014 ^{NS}	-0.034 ^{NS}	-0.058 ^{NS}	0.087 ^{NS}	-0.035 ^{NS}	-0.006 ^{NS}	0.010 ^{NS}	-0.098 ^{NS}	0.019 ^{NS}
	G	1**	0.0795 ^{NS}	0.1776 *	-0.2756 **	-0.2178 **	0.2118 **	0.1729 *	0.004 ^{NS}	-0.712 **	0.1779 *
DFF	P		1**	0.570**	0.451**	-0.187**	0.049 ^{NS}	0.240**	0.139**	-0.191**	0.198**
	G		1**	0.8127 **	0.8035 **	-0.1927 **	0.1578 *	0.4534 **	0.2249 **	-0.2247 **	0.3311 **
DM	P			1**	0.229**	-0.178**	0.057 ^{NS}	0.137**	0.012 ^{NS}	-0.012 ^{NS}	0.085 ^{NS}
	G			1**	0.8355 **	-0.1007 ^{NS}	0.3221 **	0.4739 **	0.1219 ^{NS}	-0.0108 ^{NS}	0.2877 **
PH	P				1**	-0.078 ^{NS}	0.463**	0.409**	0.225**	-0.151**	0.270**
	G				1**	-0.3731 **	0.4734 **	0.6522 **	0.2941 **	-0.1947 **	0.275 **
NOT	P					1**	-0.172**	-0.233**	-0.117*	0.056 ^{NS}	-0.019 ^{NS}
	G					1**	-0.451 **	-0.4077 **	-0.1831 **	0.0891 ^{NS}	-0.0585 ^{NS}
PL	P						1**	0.474**	0.211**	-0.158**	0.157**
	G						1**	0.5953 **	0.2285 **	-0.1939 **	0.1686 *
PW	P							1**	0.190**	-0.248**	0.207**
	G							1**	0.2458 **	-0.3394 **	0.2969 **
TSW	P								1**	-0.022 ^{NS}	0.126*
	G								1**	-0.0233 ^{NS}	0.134 ^{NS}
DE	P									1**	-0.126*
	G									1**	-0.1502 *
GY	P										1**
	G										1**

Note: SH- Seedling height, DFF- days to 50% flowering, DM- days to maturity, TSW- thousand seed weight, NOT-number of tillers, PH- plant height, PL- panicle length, PW-panicle width, DE- dehulling efficiency, GY- grain yield P- phenotypic correlation, G- genotypic correlation

Mean performance of morphological traits

Table 2 presents the mean values recorded for the ten traits: seedling height (14.0 cm), days to 50% flowering (53.2 days), days to maturity (90.4 days), plant height (143.6 cm), number of tillers (3.2), panicle length (21.9 cm), panicle width (3.00 cm), thousand-seed weight (3.80 g), dehulling efficiency (58.4%), and grain yield (398.7 g). Among the genotypes, PRJ-1 flowered and matured earliest, recording the lowest values for both days to 50% flowering (40 days) and days to maturity (79 days). PRJ-1 is normally grown as

a medium-duration, high-yielding variety in the hill regions of Uttarakhand, and the change in altitude and photoperiod under the present trial conditions appears to have brought on shorter stature, earlier flowering and maturity, and lower grain yield than usual. The smallest seeds were produced by BAR 317, with a test weight of 2.63 g, while IIMR-BM-R2425-1411 gave the highest grain yield per plot (868 g), though its dehulling efficiency was comparatively low (23.75%). BAR 211 had the lowest plant height (73.9 cm) together with the shortest panicle length (14.3 cm).

Table 2: Mean performance of agro-morphological traits

Traits	Mean	Max.	Min.
Seedling Height (cm)	14.0	21.8	9.2
Days to 50% Flowering (days)	53.4	68	40
Days to Maturity (days)	90.5	101	79
Plant Height (cm)	143.6	198.1	73.9
Number of Tillers	3.3	7.6	1.8
Panicle Length (cm)	21.9	29.5	14.3
Panicle Width (cm)	3.0	5.1	1.4
Thousand Seed Weight (g)	3.8	4.85	2.63
Dehulling Efficiency (%)	58.4	77.654	23.1
Grain Yield (g)	398.7	868	125

Ward's hierarchical clustering

Ward's hierarchical clustering sorted the 200 genotypes into five distinct clusters (Fig. 1), reflecting substantial genetic diversity within the germplasm. Cluster 3 was the largest group, with 57 genotypes (28.5%), while Cluster 2 was the smallest, with 21 genotypes (10.5%), pointing to a small set of relatively unique, elite genotypes (Table 3). Intra-cluster distances ranged from 3.03 to 3.97, with Cluster 5 showing the greatest internal diversity (3.97), reflecting high heterogeneity among its 32 member genotypes, and Cluster 1 the greatest homogeneity (3.03). Inter-cluster distances varied more widely, from 3.77 to 6.82. Genetic divergence peaked between Cluster 4 and Cluster 5 (5.82), followed

closely by Cluster 2 and Cluster 5 (5.50), while the smallest distance appeared between Cluster 1 and Cluster 3 (3.84), pointing to a relatively close genetic relationship between the two. The genotypes evaluated also showed significant phenotypic variation, as summarised in Table 4, echoing the broad genetic diversity reported earlier in barnyard millet by Mehta *et al.* (2005) [7], Nehru *et al.* (2023) [9], and Arya *et al.* (2018) [1]. Grain yield ranged from a minimum of 131.00 in Cluster 5 to an elite maximum of 796.00 in Cluster 4. Cluster 5 held the earliest-maturing (DFF minimum: 40.00) and shortest (PH minimum: 96.14 cm) genotypes, while Cluster 4 was marked by late maturity and the tallest plants.

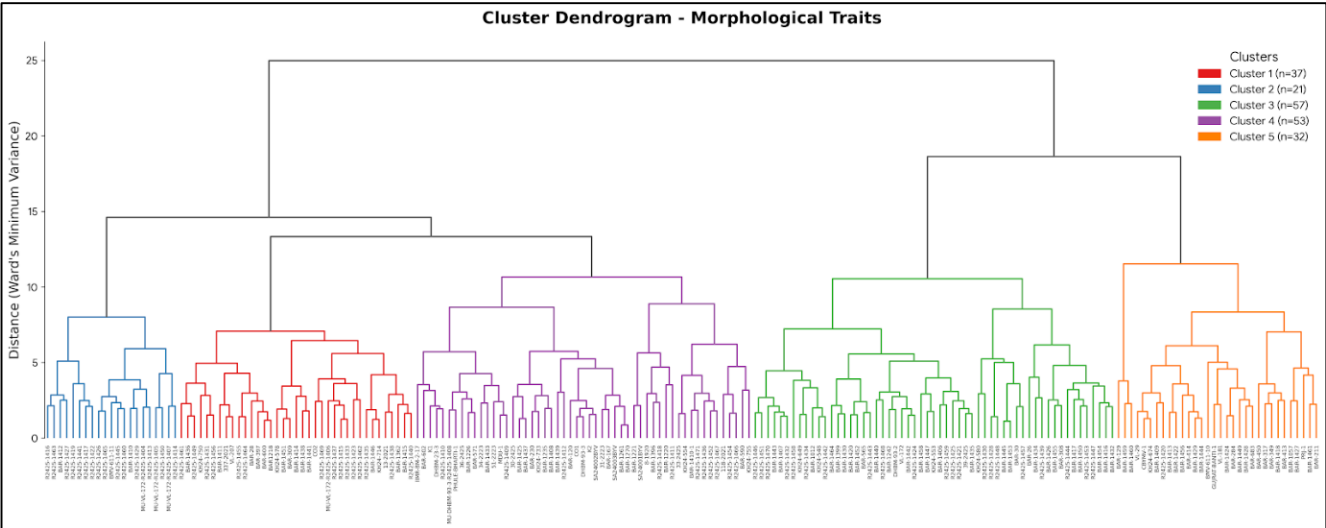


Fig 1: Ward's hierarchical clustering of genotypes

Table 3: Cluster wise grouping of barnyard millet genotypes

Cluster	No. of Genotypes	Name of the Genotypes
I	37	BAR 1362, BAR 1411, BAR 1414, BAR 1415, BAR 1436, BAR 1438, BAR 1441, BAR 1446, BAR 1451, BAR 28, BAR 309, BAR 397, BAR 600, BAR1218, CO2, IIMR-BM-13-2021, IIMR-BM-337-2021, IIMR-BM-Kh24-578, IIMR-BM-Kh24-714, IIMR-BM-Kh24-750, IIMR-BM-R2425-1415, IIMR-BM-R2425-1423, IIMR-BM-R2425-1431, IIMR-BM-R2425-1433, IIMR-BM-R2425-1435, IIMR-BM-R2425-1437, IIMR-BM-R2425-1438, IIMR-BM-R2425-1440, IIMR-BM-R2425-1449, IIMR-BM-R2425-1455, IIMR-BM-R2425-1456, IIMR-BM-R2425-1461, IIMR-BM-R2425-1462, IIMR-BM-R2425-1464, IIMR-BM-R2425-1469, Mu VL 172-R2425-1406, VL 207
II	21	BAR 1410, BAR 1412, BMV 611-11, IIMR-BM-R2425-1413, IIMR-BM-R2425-1414, IIMR-BM-R2425-1416, IIMR-BM-R2425-1417, IIMR-BM-R2425-1419, IIMR-BM-R2425-1422, IIMR-BM-R2425-1426, IIMR-BM-R2425-1427, IIMR-BM-R2425-1429, IIMR-BM-R2425-1441, IIMR-BM-R2425-1445, IIMR-BM-R2425-1450, IIMR-BM-R2425-1460, IIMR-BM-R2425-1463, IIMR-BM-R2425-1465, Mu VL 172-R2425-1404, Mu VL 172-R2425-1405, Mu VL 172-R2425-1407
III	57	BAR 1012, BAR 1242, BAR 1399, BAR 1406, BAR 1407, BAR 1416, BAR 1417, BAR 1420, BAR 1426, BAR 1430, BAR 1432, BAR 1434, BAR 1435, BAR 1440, BAR 1442, BAR 1443, BAR 1445, BAR 1447, BAR 1450, BAR 1452, BAR 1453, BAR 1454, BAR 1455, BAR 1458, BAR 1464, BAR 26, BAR 30, BAR 308, BAR 565, DHBM 93-2, IIMR-BM-39-2425, IIMR-BM-Kh24-548, IIMR-BM-Kh24-553, IIMR-BM-Kh24-580, IIMR-BM-Kh24-649, IIMR-BM-R2425-1421, IIMR-BM-R2425-1424, IIMR-BM-R2425-1425, IIMR-BM-R2425-1428, IIMR-BM-R2425-1430, IIMR-BM-R2425-1432, IIMR-BM-R2425-1434, IIMR-BM-R2425-1439, IIMR-BM-R2425-1442, IIMR-BM-R2425-1443, IIMR-BM-R2425-1444, IIMR-BM-R2425-1446, IIMR-BM-R2425-1447, IIMR-BM-R2425-1448, IIMR-BM-R2425-1451, IIMR-BM-R2425-1453, IIMR-BM-R2425-1457, IIMR-BM-R2425-1458, IIMR-BM-R2425-1459, IIMR-BM-R2425-1468, IIMR-BM-R2425-1470, VL 172
IV	53	Mu VL 172-R2425-1404, IIMR-BM-R2425-1460, IIMR-BM-R2425-1423M, BAR 1220, BAR 1410, IIMR-BM-R2425-1413, BMV 611-11, Mu VL 172-R2425-1407, IIMR-BM-R2425-1450, IIMR-BM-R2425-1427, IIMR-BM-R2425-1419, IIMR-BM-R2425-1462, IIMR-BM-R2425-1422, IIMR-BM-R2425-1418, BAR 1396, IIMR-BM-R2425-1441, IIMR-BM-R2425-1417, IIMR-BM-R2425-1463, Mu VL 172-R2425-1405, IIMR-BM-R2425-1445, IIMR-BM-R2425-1414, IIMR-BM-R2425-1411
V	32	BAR 1057, BAR 129, BAR 1409, BAR 1413, BAR 1418, BAR 1422, BAR 1424, BAR 1427, BAR 1428, BAR 1429, BAR 1444, BAR 1449, BAR 1456, BAR 1459, BAR 1460, BAR 1461, BAR 211, BAR 284, BAR 317, BAR 349, BAR 413, BAR 414, BAR 450, BAR 683, BMV 611-10, CBYMV-1, Gujrat Banti-1, IIMR-BM-Kh24-674, IIMR-BM-R2425-1420, PRJ 1, VL 181, VL 29

Table 4: Inter and Intra cluster distances among five clusters of 200 genotypes

Cluster	I	II	III	IV	V
I	3.03	4.07	3.84	3.90	4.57
II	4.07	3.41	4.37	4.46	5.50
III	3.84	4.37	3.47	4.48	4.63
IV	3.90	4.46	4.48	3.72	5.82
V	4.57	5.50	4.63	5.82	3.97

Note: SH-Seedling height, DFF- days to 50% flowering, DM- days to maturity, TSW- thousand seed weight, NOT-number of tillers, PH-plant height, PL- panicle length, PW-panicle width, DE-dehulling efficiency, GY- grain yield

Conclusion

Overall, this study points to considerable genetic variability across the 200 barnyard millet genotypes evaluated, confirming that the germplasm holds valuable resources for crop improvement. The significant, positive associations of grain yield with days to 50% flowering, plant height, and panicle width indicate that these traits can act as reliable indirect selection criteria in breeding programmes aimed at raising productivity. Ward's hierarchical clustering successfully resolved the germplasm into five genetically distinct groups, highlighting the extent of genetic divergence within the collection. Taken together, these findings provide a solid foundation for the strategic use of barnyard millet germplasm in future breeding work, supporting the development of high-yielding, nutritionally enhanced, and climate-resilient cultivars for sustainable millet production.

References

1. Arya R, Bhatt A, Kumar V. Study of genetic divergence in barnyard millet (*Echinochloa frumentacea* (Roxb.)

Link) germplasm. International Journal of Bio-resource and Stress Management. 2018;9(2):192-196.

2. Bhinda MS, Joshi DC, Parihar M, Meena RP, Joshi P, Gupta A, et al. Genetics, breeding, and genomics of Indian barnyard millet (*Echinochloa frumentacea*): status and perspectives. In: Neglected and underutilized crops. 2023. p. 115-135.
3. Clayton WD, Renvoize SA. Genera graminum. Grasses of the world. 2006.
4. Goron TL, Raizada MN. Genetic diversity and genomic resources available for the small millet crops to accelerate a New Green Revolution. Frontiers in Plant Science. 2015;6:157.
5. Hasan N, Budakoti M, Meena RP, Bhinda MS, Rani V, Nandini C, et al. Barnyard millet. In: Millets: Crops for climate resilience and for food and nutritional security. 2025. p. 67-91.
6. Maurya NK, Singh J, Gupta E. Barnyard millet's health and nutritional significance. International Journal of Agriculture Innovation. 2023;8(2):156-160.
7. Mehta H, Tyagi PC, Mohapatra KP. Genetic diversity in barnyard millet (*Echinochloa frumentacea* Roxb.). Indian Journal of Genetics and Plant Breeding. 2005;65(4):293-295.
8. Mohammadi SA, Prasanna BM. Analysis of genetic diversity in crop plants—salient statistical tools and considerations. Crop Science. 2003;43(4):1235-1248.
9. Nehru G, Reddy AT, Reddy CV, Sreenivasulu KN. Study of genetic diversity in Indian barnyard millet genetic resources [*Echinochloa frumentacea* (L.)]. International Journal of Environment and Climate Change. 2023;13(10):3094-3110.

10. Rao CR. Advanced statistical methods in biometrical research. New York: John Wiley & Sons; 1952.
11. Pearson K. Early statistical papers. Cambridge: University Press; 1948.
12. Prabu R, Vanniarajan C, Vetriventhan M, Gnanamalar RP, Shanmughasundaram R, Ramalingam J. Association studies in barnyard millet (*Echinochloa frumentacea* (Roxb.) Link) for early maturity and yield contributing traits at high altitude region. Electronic Journal of Plant Breeding. 2020;11(1):192-196.
13. Prakash R, Vanniarajan C. Correlation analysis in barnyard millet [*Echinochloa frumentacea* (Roxb.) Link]. Trends in Biosciences. 2014;7(20):3255-3257.
14. Singh B, Pandey S, Nivedhitha S, Shekhawat N, Singh M, Jat B, et al. Comprehensive phenotyping of 1,807 Indian barnyard millet (*Echinochloa frumentacea* Link) accessions from Indian national genebank: unlocking diversity for core set development. Frontiers in Plant Science. 2025;16:1644491.
15. Sood S, Khulbe RK, Gupta AK, Agrawal PK, Upadhyaya HD, Bhatt JC. Barnyard millet—a potential food and feed crop of future. Plant Breeding. 2015;134(2):135-147.
16. Ugare R, Chimmad B, Naik R, Bharati P, Itagi S. Glycemic index and significance of barnyard millet (*Echinochloa frumentaceae*) in type II diabetics. Journal of Food Science and Technology. 2014;51(2):392-395.
17. Vanniarajan C, Prabu R, Vetriventhan M, Gnanamalar RP, Shanmughasundaram R, Ramalingam J. Association studies in barnyard millet (*Echinochloa frumentacea* (Roxb.) Link) for early maturity and yield contributing traits at high altitude region. Electronic Journal of Plant Breeding. 2020;11(1):192-196.