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## Correlation and cluster analysis in phenotypic diversity studies of barnyard millet (*Echinochloa frumentacea* Roxb. L.)

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### Abstract

A set of 75 genotypes of barnyard millet including germplasm accessions, released cultivars and advanced genetic material were assessed for character associations and Ward's hierarchal clustering with Euclidian distance using 11 agro-morphological traits during studied kharif 2023 in an Alpha Lattice Design with two replications. The analysis of variance shown the presence of significant variations among the genotypes for all the traits evaluated. In correlation studies, grain yield exhibited significant and positive association with days to maturity, plant height and panicle length at both genotypic and phenotypic levels. The traits which are exhibiting positive significant correlation on grain yield can be considered as important traits to be included in the selection to achieve genetic improvement of grain yield in barnyard millet. The Ward's hierarchal clustering of genotypes with Euclidian distance has generated four main clusters separated at similarity index of 300 Euclidian distances. Similarly, K-means analysis generated four clusters containing 21, 31, 13 and 10 genotypes in respective clusters I, II, III and IV. Cluster II has maximum number of genotypes followed by Cluster I, Cluster III and Cluster IV.

**Keywords:** Barnyard millet, correlation, Euclidian and alpha lattice

### Introduction

Barnyard millet (*Echinochloa frumentacea* L.) a small seeded millet crop, is an hexaploid species ( $2n=6x=54$ ) belongs to Poaceae family, is an ancient millet crop which can be grown in warm and temperate regions of the world and it is widely cultivated in Asia. India occupies the major area of cultivation. Whereas, in China, Japan and Korea the area under barnyard millet has reduced drastically and replaced by rice crop. In addition to being a climate resilient crop, it has very high nutritive value and lower outlay when compared to major cereals (Renganathan *et al.* 2020) [1]. The major cultivated species of barnyard millet are Indian species (*Echinochloa frumentacea*), and the Japanese species (*Echinochloa esculenta*) (Rawat *et al.* 2020) [2]. In India, it is widely cultivated in Himalayan region of Uttarakhand in the north and in Deccan plateau region in Tamil Nadu (Sood *et al.* 2015) [3]. In addition to its high nutritive value, it is highly useful to diabetic patients as it contains high amount of dietary fibre which leads to slow digestion and low glycemic index (Ugare *et al.* 2014) [4].

It is essential to understand the genetic variability available within breeding populations or germplasm accessions, as this knowledge is crucial for the success of any crop improvement programme (Allard 1960). Genetic variability is rapidly diminishing due to the destruction of natural habitats, eradication of wild and cultivated species and the replacement of traditional cultivars with modern ones with narrow genetic base. Consequently, to identify elite accessions, it is essential to characterize crop germplasm (Abdulhakeem *et al.* 2019) [6]. Therefore, evaluating variability, heritability and genetic advance in breeding materials will determine the true potential of genotypes for their usage in breeding programmes. Additionally, a thorough understanding of character associations will enhance selection efficiency in any crop breeding programme. Identifying traits contributing to grain yield is crucial for crop improvement, as grain yield is a complex trait influenced by multiple factors. Moreover, information on the direct and indirect effects of various component traits on grain

yield, obtained through path coefficient analysis will aid in establishing effective selection criteria for the genetic improvement of grain yield.

The present study is conducted to understand character association studies as well as diversity among set of 75 genotypes of barnyard millet, which will aid in the pointing out of elite genotypes and deciding effective selection criteria to achieve grain improvement in barnyard millet.

### Materials and Methods

A set of 75 genotypes of barnyard millet comprising of germplasm accessions, released cultivars and advanced genetic material were grown in the research farm at the ICAR - Indian Institute of Millets Research, Hyderabad, Telangana, India during kharif 2023 in Alpha Lattice design with two replications. A healthy and sound crop was raised by following the recommended package of practices. The observations were recorded on five randomly chosen plants for 8 characters, viz, plant height, peduncle length, panicle length, panicle width, number of tillers, number of racemes, dry fodder yield, and test weight from both replications, except for 3 traits viz, days to 50% flowering, days to maturity and grain yield, which were recorded on a plot basis. The data collected was subjected to correlation analysis as suggested by Pearson (1948) [7] and Ward's hierarchal clustering analysis was also performed to know the distance and diversity.

### Results and Discussion

#### Character association

Grain yield is a multifaceted trait, influenced by several distinct component traits. Therefore, understanding the relationship between grain yield and its component traits is crucial for crop breeders. The genotypic and phenotypic correlations among grain yield and its component traits are presented in (Table 3). The genotypic correlation coefficients exceeded the phenotypic correlation coefficients for the majority of the traits studied, indicating a strong genetic association between these traits and a limited influence of environmental factors on their phenotypic expression. At the genotypic and phenotypic levels, grain yield exhibited significant and positive association with days to maturity (0.7458\*\*; 0.2166\*\* respectively), plant height (0.4633\*\*; 0.2666\*\* respectively) and panicle length (0.6503\*\*; 0.2578\*\* respectively). The traits viz., days to maturity, plant height and panicle length could be utilised in the genetic improvement of grain yield due to their positive and significant correlation with grain yield. Similar to the results obtained in this study, significant and positive correlations of grain yield with its component traits such as days to maturity, plant height and panicle length were reported earlier in this crop (Prabhu *et al.* 2020) [8]. Days to maturity and plant height

results were identical to the results of (Monika *et al.* 2021) [9] in barnyard millet.

#### Mean performance of morphological traits

The mean performance data of morphological traits was presented in (table 2). In the present study the mean values recorded for the traits viz., days to 50% flowering (61.9 days), days to maturity (104.1 days), thousand seed weight (2.9 g), number of tillers (3.9), number of racemes (37.8), plant height (124.3 cm), panicle length (20.7 cm), panicle width (2.8 cm), peduncle length (14.3 cm), dry fodder weight (926.6 g) and grain yield (406.5 g). The genotype KOPBM-9 was recorded highest DFF (84 days), which can be grouped in late flowering in turn late maturing group. The genotype IEc566 was recorded highest thousand seed weight (4.1 g), plant height (207 cm), peduncle length (46.5 cm) and dry fodder weight (2650.0 g) with lowest number of racemes (10.1). The genotype PRJ-1 has shown lowest days to 50% flowering (40 days) and days to maturity (81.5), which indicates it as an early maturing variety. The earlier reports from Uttarakhand state of India shows that PRJ-1 is medium maturing variety with good grain yielding ability. Its phenotypic expression and earliness in flowering and maturity indicates its photosensitivity in hill cultivation areas and plain cultivation areas with changing altitude and whether conditions. The genotype BAR 317 has shown lowest thousand seed weight of 2.2 g with very small seed size.

#### Ward's hierarchal clustering

The Ward's hierarchal clustering of genotypes with Euclidian distance has generated four main clusters separated at similarity index of 300 Euclidian distance. Similarly, K-means analysis generated four clusters containing 21 genotypes in cluster I, 31 genotypes in cluster II, 13 genotypes in cluster III and 10 genotypes in cluster IV. Cluster II has maximum number of genotypes followed by Cluster I, Cluster III and Cluster IV. From the clustering data we have found that Cluster II is more diverse as it grouped the various genotypes which are having extreme values for the different traits viz., KOPBM 9 for the days to 50% flowering, number of racemes, panicle width, peduncle length has recorded high mean values, BAR 397 has recorded high mean value for days to maturity, KOPBM 43 for plant height. The genotype CO-2, which has recorded high grain yield was grouped in Cluster III. The genotype IEc566 is found superior to other varieties in plant height trait, is grouped in Cluster I. The genotype PRJ-1 which is found as an early flowering variety is grouped in Cluster IV. Similar results were observed by (Trivedi *et al.* 2017) [10]. These results clearly indicate that there is high level of diversity is existing among the genotypes studied.

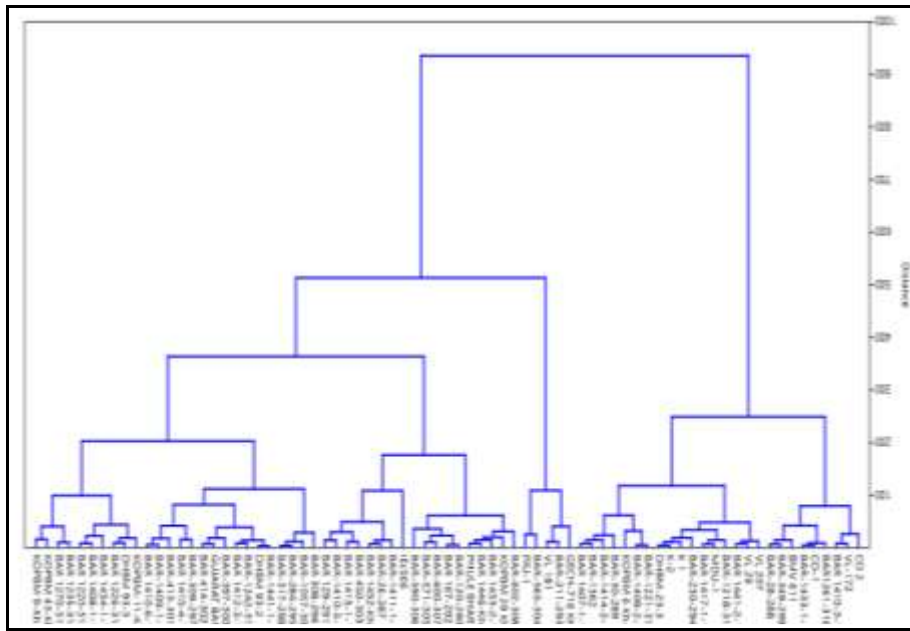
**Table 1:** Cluster wise grouping of barnyard millet genotypes

Cluster	No. of Genotypes	Name of the Genotypes
I	21	K2, BAR 230, BAR 30, BAR 1218, IEc566, DHBM-23-3, BAR-1410-5, BAR-26, BAR-1411, K 1, BAR 129, BAR 590, BAR 1221, VL 29, MDU-1, BAR 1408-2, BAR 1417, BAR 1441-2, BAR 145, KOPBM 6, VL 207,
II	31	BAR 1242, BAR 602, BAR 1409, BAR 397, BAR 1235, BAR 600, KOPBM 43, GUJARAT BANTI-1, BAR 1415, BAR 1441-1, BAR 571, KOPBM 9, BAR 1433, BAR 1412, BAR 284, BAR 413, BAR 309, BAR 317, BAR 1270, BAR 1057, BAR 120, KOPBM 29, BAR 1410-4, BAR 1408-1, DHBM 93-2, BAR 1410-6, BAR 1220, BAR 167, BAR 1446, PHULE BHARTI-1 (KOPBM 46), BAR 414
III	13	BAR 1414, CO 1, BAR 450, VL 172, BAR 1261, BAR 1362, BAR 1433-1, CO 2, BMV 611, BAR 349, BAR 28, BAR 1410-3, BAR 1407,
IV	10	DHBM 93-3, KOPBM-11, BAR 308, BAR 565, BAR 211, PRJ-1, GECH 716, VL 181, BAR 1434, BAR 1226

**Table 2:** Mean performance of the barnyard millet genotypes for morpho-agronomic traits

Traits	Mean	Max.	Min.
DFF	61.9	84	40
DTM	104.1	113	81.5
TSW	2.9	4.1	2.2
NOR	37.8	69.8	10.1
NOT	3.9	6	2.4
PH	124.3	207	75.2
PaL	20.7	27.8	11
PaW	2.8	4.9	1.7
PedL	14.3	46.6	6.8
DFW	926.6	2650	187.5
GY	406.5	624.5	140

DFF- days to 50% flowering, DTM- days to maturity, TSW- thousand seed weight, NOR- number of racemes, NOT- number of tillers, PH- plant height, PaL- panicle length, PaW- panicle width, PedL- peduncle length, GY- grain yield. Max- maximum, Min- minimum.



**Fig 1:** Ward's hierarchial clustering of genotypes

**Table 3:** Genotypic and Phenotypic correlations among barnyard millet genotype

Traits		DFF	DTM	TSW	NOR	NOT	PH	PaL	PaW	PedL	DFW	GY
DFF	G	1**	0.4064**	0.0598NS	0.7062**	0.0764NS	0.7229**	0.6177**	0.755**	0.1351NS	0.4134**	0.1413NS
	P	1**	0.3118**	0.0067NS	0.6569**	0.0588NS	0.6067**	0.4751**	0.5627**	0.1226NS	0.3755**	0.0216NS
DTM	G		1**	-0.1086NS	0.2137NS	0.3216**	0.4512**	0.6396**	0.1929NS	-0.0113NS	0.4896**	0.7458**
	P		1**	-0.0984NS	0.167*	0.2326**	0.2956**	0.3772**	0.0625NS	-0.0154NS	0.3708**	0.2166**
TSW	G			1**	-0.127NS	0.1384NS	0.4028*	0.0484NS	0.0312NS	0.4007**	0.1597NS	0.0522NS
	P			1**	-0.1011NS	0.1061NS	0.2774**	-0.0219NS	-0.0131NS	0.3308**	0.0845NS	0.0216NS
NOR	G				1**	-0.081NS	0.5467**	0.7049**	0.8457**	-0.1916NS	0.2462*	0.2037NS
	P				1**	-0.0566NS	0.5127**	0.586**	0.6968**	-0.1838*	0.219**	0.1014NS
NOT	G					1**	0.0839NS	-0.0812NS	-0.2557*	0.0412NS	0.1032NS	0.2284*
	P					1**	0.0611NS	0.0909NS	-0.154NS	0.0336NS	0.105NS	0.0454NS
PH	G						1**	0.7352**	0.4941**	0.4979**	0.4566**	0.4633**
	P						1**	0.658**	0.4491**	0.4574**	0.412**	0.2666**
PaL	G							1**	0.4403**	0.0953NS	0.4506**	0.6503**
	P							1**	0.4281**	0.1006NS	0.3934**	0.2578**
PaW	G								1**	-0.0025NS	0.0879NS	-0.0335NS
	P								1**	-0.0152NS	0.0857NS	0.0194NS
PedL	G									1**	0.1253NS	0.0042NS
	P									1**	0.1172NS	0.0095NS
DFW	G										1**	0.6561**
	P										1**	0.2557NS
GY	G											1**
	P											1**

DFF- days to 50% flowering, DTM- days to maturity, TSW- thousand seed weight, NOR- number of racemes, NOT- number of tillers, PH- plant height, PaL- panicle length, PaW- panicle width, PedL- peduncle length, GY- grain yield. P- phenotypic correlation, G- genotypic correlation

## Conclusion

The identification of diversity existing in the studied 11 traits in 75 genotypes and clustering them in different groups based on Euclidian hierarchical clustering method greatly helps to identify the genotype selection for utilization in the breeding program. The genotype IEC566 exhibits photosensitive and the flowering and maturity values are differing greatly from the earlier reported values. Correlation studies have depicted the significant positive correlation of traits to grain yield and selection can be relied on those traits to improve the barnyard millet genotypes for higher grain yield production.

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