



RESEARCH ARTICLE

Agro-morphological trait diversity of barnyard millet germplasm for utilization in crop genetic improvement

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Abstract

Barnyard millet is a small grain cereal classified as a minor millet, which is highly nutritious and adaptable to various agro-climatic zones and harsh environments. To understand the agro-morphological diversity, a study was conducted using 515 accessions along with three checks: VL 207, DHBM 93-3 and VL 172, employing an augmented block design. Highly significant treatment effects were shown through Analysis of variance (ANOVA) for basal tillers, flowering time and plant height, while block effects were mostly non-significant except for basal tillers. The outcomes from principal component analysis (PCA) stated that 60.1 % of the total variation was explained by the first four principal components. The first principal component traits included days to 50 % flowering, flag leaf blade width, flag leaf blade length, panicle length, peduncle length and panicle width contributed to 29.4 %. Results from the scree plot demonstrated that the majority of the diversity observed in the studied germplasm was from first two components. Out of 515 accessions, 49 accessions were identified for superior performance of multiple traits. The accessions IC0472499 and IC0281471 were identified superior for multiple (five) traits and can be further used as donor parents for specific traits in crop improvement programmes. This study emphasizes that genetic and phenotypic characterization of a large set of germplasm collections helps in identifying trait donors for the improvement of high-yielding, resilient and disease-resistant crops.

Keywords: barnyard millet; genetic diversity; multi-trait specific germplasm; PCA

Introduction

Barnyard millet (*Echinochloa frumentacea* Roxb.) is the fourth most cultivated millet. It is grown in temperate and warm regions globally, with significant cultivation in Asia particularly in India, Japan, China and Korea. It provides multiple securities like food, fodder, feed, health, livelihood and ecology. Worldwide it is cultivated in 0.146 Mha area and 0.147 MT of production, with an average productivity of 1034 kg/ha (1). India occupies the major area of production and largest consumption of barnyard millet (2). Among many species and races in barnyard millet, two species are primarily cultivated *Echinochloa frumentacea* (called as Indian barnyard millet originated from wild progenitor species *E. colona*) and *Echinochloa esculenta* (called as Japanese barnyard millet, originated from a wild progenitor species *E. crus-galli*). It is a hexaploid crop with a basic chromosome number of $n = 9$ ($2n = 6x = 54$). Draft genome sequence information of a line STB08 from the Japanese barnyard millet (*E. crus-galli*) consists about 1.27 Gb of the total genome size which represents 90.7 % of predicted genome of barnyard millet (3). In the direction of generating genome sequence information, Indian barnyard

millet has not yet been sequenced and there exists a strong requirement to comprehend the sequence information, differences and similarities with Japanese barnyard millet.

Patients with dietary based health issues, such as diabetes, heart-related disorders and celiac disease, can benefit greatly from barnyard millet due to its high nutritional profile. When it is compared with wheat and rice it consists of nearly similar values of carbohydrates, protein and fat (4, 5) apart from richness in crude fibre, minerals and vitamins (5). It is also rich in phenolic acids, flavonoids and tannins and considered reliable sources of antioxidants (6).

Genetic diversity and effectiveness decide the progress made in the breeding programs which will further help in the development of crops (7). In barnyard millet, different studies on morphological, physiological and quality characters in Indian and exotic collections were undertaken earlier with a set of germplasm lines (8-13). Research on genetic diversity using EST- SSR molecular markers for 10 morpho nutritional traits in 61 germplasm accessions were conducted and it was found that there is large variability for the traits like flowering, plant height and grain yield (14). Correlation and path coefficient

analysis showed that there is direct effect on grain yield by the traits such as heat units at maturity (HUM), photo-thermal units at 50 % flowering, plant height, panicle weight and days to 50 % flowering and could serve as the potential traits for yield improvement in barnyard millet (10). Another study on diversity was conducted in 194 collections through various eco-geographic regions for quantitative traits and it was revealed that, number of racemes, flag leaf width and internodes length were important while performing selections for grain yield (11). Collection of germplasm lines of barnyard millet from Central Himalayan region was used to perform variability studies. After analysing the reports, it was noticed that for the traits like days to 50 % flowering, days to 80 % maturity, 1000 seed weight and grain yield exhibited significant amount of variability (15).

Multivariate analysis was used as an important statistical tool in breeding studies for deciphering the association of multiple traits from the complex data. Multivariate analysis of global collection of germplasm lines of barnyard millet revealed a high variation for traits days to maturity, five panicle grain weight and other yield related characters. PCA explained 73 % of total variation from the first three PCA categories. The classification on trait morphology resulted in 3 major groups, the lines with origin unknown and with Indian accessions formed a group of *E. frumentacea* and Japanese accession formed a group of *E. esculenta* and the accessions from Russia, Japan, Cameroon and Egypt formed the third group (13). The highest trait variation of 83 % was revealed by first five components of PCA and the characters plant height, ear length, flag leaf length and lower raceme length contributed maximum for variation in barnyard millet (16). Identification of traits specific germplasm lines is a boon to researchers and trait tagged lines serve as ready reckoner for the crop improvement program. Specifically, the lines identified for biotic and abiotic stress tolerance/resistance. However, breeding efforts focused on specific traits identification and improvement of the characters contributing to grain yield are necessary to develop lines with stability and high grain yielding ability (17). In the base material i.e. germplasm, progress in crop improvement relies on the availability of extent of diversity for the desired traits (18). Moreover, the characterization of large set of germplasm in barnyard millet was not undertaken to know the total array of diversity for the economically and agronomically important traits. Identification of germplasm lines with multiple traits specificity is an important aspect yet basic requirement in plant breeding and crop improvement. Barnyard millet being considered as orphan crops, even though rich in nutritional profile and provides food and fodder to the small and marginal farmer's is neglected for basic studies and genetic improvement. Trait specific accessions serve as a donor parent in mapping population development, gene/QTL tagging and main importantly in the grain yield improvement of the crop.

With the above context, the present study on barnyard millet was planned for studying the genetic diversity of 11 agro-morphological traits in large collections of 515 accessions of barnyard millet with trait specific genotypes.

Materials and Methods

Experimental design and layout

Under the Institute Project (IIMR/CI/2021-2026/150), 515

accessions of barnyard millet germplasm were examined at ICAR-IIMR, Hyderabad during *Kharif* 2021, along with three checks (VL 207, DHBM 93-3 and VL 172), where the checks are the nationally released and are high yielding varieties which were used in the AICRP on small millets system as standard checks. The characterization was done at experimental fields of ICAR- IIMR, Hyderabad with the geographical coordinate of 17.3207° N latitude, 78.3959° E longitude and 476.5 meters above mean sea level (MSL). The augmented block design was used for the experiment including three checks viz., VL 207, DHBM 93-3 and VL 172 which were repeated after every 100 accessions. The plot size maintained was 1 m row length and 45 cm distance between each row. The distance between the plants was maintained at 10 cm after two weeks of thinning. Thinning was followed to maintain the proper plant density in all genotypes. During crop growth, fertilizers were applied @60 kg/ha N and 40 kg/ha P₂O₅ and all necessary packages of practice was followed to maintain good crop stand. Regular irrigation was given to maintain sufficient moisture and the crop were protected from weeds also ensuring that crop is not infested by diseases and pests.

Agro-morphological traits studied

The study included characterization of germplasm for 11 quantitative traits i.e., number of basal tillers, days to 50 % flowering (days), flag leaf blade length (cm), flag leaf blade width (cm), peduncle length (cm), panicle length (cm), panicle width (cm), lowest raceme length (cm), plant height (cm), grain yield (g/plant) and 100 seed weight (g).

Statistical analysis

ANOVA was carried out using augmented RCB (package of R (version 3.4.2) 19). Pearson's correlation coefficient (*r*) was used to indicate the relationship among traits. The factor analysis was based on the Pearson correlation matrix and Euclidean distances. Eigenvalues (latent roots) were calculated for all principal components. Shannon-Weaver diversity index (*H*) and PCA were developed using PAST 4 software (20).

Results

Descriptive statistics and diversity indices for 515 barnyard millet germplasm accessions

The summary statistics of 11 traits were recorded in Table 1 with the help of descriptive statistics like mean, standard error of mean, standard deviation, range and coefficient of variance. Results revealed substantial variation across all studied traits. The number of basal tillers ranged from 1.13 to 17.19 with a mean value of 4.54 whereas for days to 50 % flowering an average of 60.5 days was recorded ranging from 46.5 days to 85.8 days. The flag leaf blade length recorded at the time of flowering varied from 13.16 cm to 40.19 cm while the flag leaf blade width varied from 1.17 cm to 5.5 cm with a mean value of 2.66 cm. Peduncle length exhibited a minimum value of 6.6 cm and a maximum value of 22.23 cm. Panicle characteristics like panicle length (Mean = 19.9 cm; range = 9.9 cm - 32.2 cm) and panicle width (Mean = 3.76 cm; range = 1.5 cm - 7.06 cm) exhibited greater variability with extreme values.

Plant height ranged from 49.7 cm to 299.1 cm, with a mean of 126.4 cm. The main yield and yield attributing trait like

Table 1. Summary statistics and variability parameters of quantitative traits of 515 acc. of Barnyard millet germplasm characterized during Kharif 2021

S. No	Trait	Mean	SE	SD	Range	GCV	PCV	Heritability	CV
1	Number of basal tillers	4.54	0.08	1.78	1.13 - 17.19	36.48	41.72	76.5	16.74
2	Days to 50 % flowering (days)	60.57	0.42	9.43	46.5 - 85.83	15.35	19.24	63.6	3.44
3	Flag leaf blade length (cm)	26.23	0.21	4.7	13.16 - 40.19	16.68	23.71	49.5	16.59
4	Flag leaf blade width (cm)	2.66	0.03	0.68	1.17 - 5.5	23.78	31.15	58.3	19.8
5	Peduncle length (cm)	12.82	0.12	2.83	6.6 - 22.23	20.29	31.39	41.8	24.85
6	Panicle length (cm)	19.94	0.16	3.74	9.9 - 32.44	17.59	23.49	56.1	14.14
7	Panicle width (cm)	3.76	0.03	0.79	1.75 - 7.06	18.61	26.66	48.7	13.45
8	Lowest raceme length (cm)	3.05	0.04	0.83	1.12 - 9.48	25.89	31.99	65.5	18.56
9	Plant height (cm)	126.47	1.72	39.03	49.78 - 299.11	30.41	33.62	81.8	13.1
10	Grain yield (g/plant)	13.73	0.38	8.59	0.36 - 43.3	54.77	73.59	55.4	48.96
11	100-Seed weight (g)	0.28	0.0026	0.06	0.13 - 0.53	16.8	29.56	32.3	21.21

SE: Standard Error of mean; SD: Standard deviation; GCV: Genotypic coefficient of variation ; PCV: phenotypic coefficient of variation; CV: coefficient of variation

seed weight also exhibited variability. An average of 13.7g plant⁻¹ grain yield was recorded as 0.36 g to 43.3 g per plant while 100 seed weight with a mean value of 0.28 g ranged between 0.13g-0.53 g. The frequency distribution of barnyard millet accessions for several studied traits along with the checks was presented in Fig. 1. The mean value of the genotypes under study was found to be around the mean value of the checks. Shannon diversity index for assessed characters ranged from 6.21 for grain yield to a maximum of 8.12 for 100 seed weight, implying the presence of wide range of variations which could be useful for selection (Fig. 2).

Analysis of variance and variability parameters

ANOVA by using augmented design indicated the presence of significant ($P < 0.05$) and non-significant ($P > 0.05$) mean sum of squares for studied traits (Table 2). Block effects after accounting for treatments were non-significant ($P > 0.05$) for almost all traits studied except for number of basal tillers. The treatment effects ignoring blocks were highly significant ($P < 0.01$) for number of basal tillers, days to 50 % flowering, plant height while moderately significant ($P < 0.05$) traits were panicle width and lowest raceme length. The mean sum of squares due to germplasm versus checks was significant ($P < 0.05$) for all traits excluding days to 50 % flowering, lowest raceme length, grain yield and 100 seed weight.

All the traits under study indicated that the traits were influenced by the environment, as the estimates of GCV were lower than PCV. In the present study GCV ranged from 15.35 to 54.77 and PCV ranged from 19.24 to 73.59 respectively. However, high GCV and PCV were recorded for traits such as number of basal tillers, plant height and grain yield per plant. While trait days to 50 % flowering exhibits moderate values of

GCV and PCV. On the other hand, high heritability was recorded for traits such number of basal tillers, days to 50 % flowering, lowest raceme length and plant height, whereas remaining traits were noted for moderate heritability.

Principal component analysis for 515 Barnyard millet germplasm

PCA of the data recorded on characterization of 11 traits from 515 barnyard millet germplasm accessions indicated that 60.1 % of the variation was explained by the first four principal components (Table 3). The total number of principal components is eleven which is also equal to the number of traits studied. The eigenvalue of PC1 was 3.22, while it was 0.35 for PC11 (Table 3), the eigen values of PC 5- PC11 were less than 1 hence, only for the first four PCs were considered for evaluating diversity. The PC1 explained 29.4 % variation followed by PC2 (11.4 %), PC3 (10.1 %) and PC4 (9.2 %). Based on the Eigen values of the first four PCs (>1.0) and the per cent cumulative proportion of each PCs to the total variation (>10 %), first four PCs were considered to measure the variation existing in the genotypes studied for different traits. The non-rotated component loadings for each character of barnyard millet were tabulated in Table 4. Among the traits, days to 50 % flowering (days), flag leaf blade length (cm), flag leaf blade width (cm), peduncle length (cm), panicle length (cm) and panicle width (cm) are important traits as they are related positively and contributing to the variation in first principal component. Grain yield (g/plant) and 100-seed weight (g) are positively related, while traits like panicle length, panicle width, number of basal tillers are negatively related and contributed maximum to the variation explained by PC2, whereas number of basal tillers, plant height and grain yield traits were positively related and contributed to the maximum variability to PC3. The

Table 2. Analysis of variance using augmented block design for 515 Barnyard millet germplasm

Source	Df	NBT	DF	FLL	FLW	Ped L	Pan L	Pan W	LRec L	PH	GY	100S W
Block (eliminating Treatments)	13	1.51*	7.12 ns	7.12 ns	0.22 ns	3.09 ns	11.49 ns	0.51 ns	0.37 ns	338.54 ns	64.11 ns	0.01 ns
Treatment (ignoring Blocks)	514	2.78**	89.03 **	20.3 ns	0.43 ns	7.38 ns	12.39 ns	0.52*	0.62*	1494.74 **	54.53 ns	0.0018 ns
Check	2	1.62 ns	860.17**	116.79**	0.95 ns	30.28 ns	29.93 *	3.59**	0.98 ns	2141.03 **	94.47 ns	0.00087 ns
Germplasm	511	2.76**	86.18 **	19.58 ns	0.41 ns	6.82 ns	12.12 ns	0.5*	0.62*	1489.01 **	54.48 ns	0.0018 ns
Germplasm vs. Check	1	15.66**	0.94 ns	193.7 **	9.68**	247.3 **	115.53**	5.27**	0.17 ns	3126.67 **	1.28 ns	0.01 ns
Error	26	0.57	4.35	19.45	0.29	10.57	7.98	0.26	0.32	269.05	43.18	0.0034
Check vs germplasm CD at 5 %		1.85	5.12	10.84	1.33	7.99	6.94	1.26	1.39	40.3	16.14	0.14

Df: degree of freedom; 100^{SW}: 100 seed weight (g); DF: Days to flowering (days); FLL: Flag Leaf Length (cm); FLW: Flag Leaf Width (cm); GY: Grain Yield (g plant⁻¹); LRecL: Lowest raceme length (cm); NBT: Number of basal tillers; PanL: Panicle Length (cm); PanW: Panicle Width (cm); PedL: Peduncle Length (cm); PH: plant height (cm); ns $P > 0.05$; * $P < 0.05$; ** $P < 0.01$

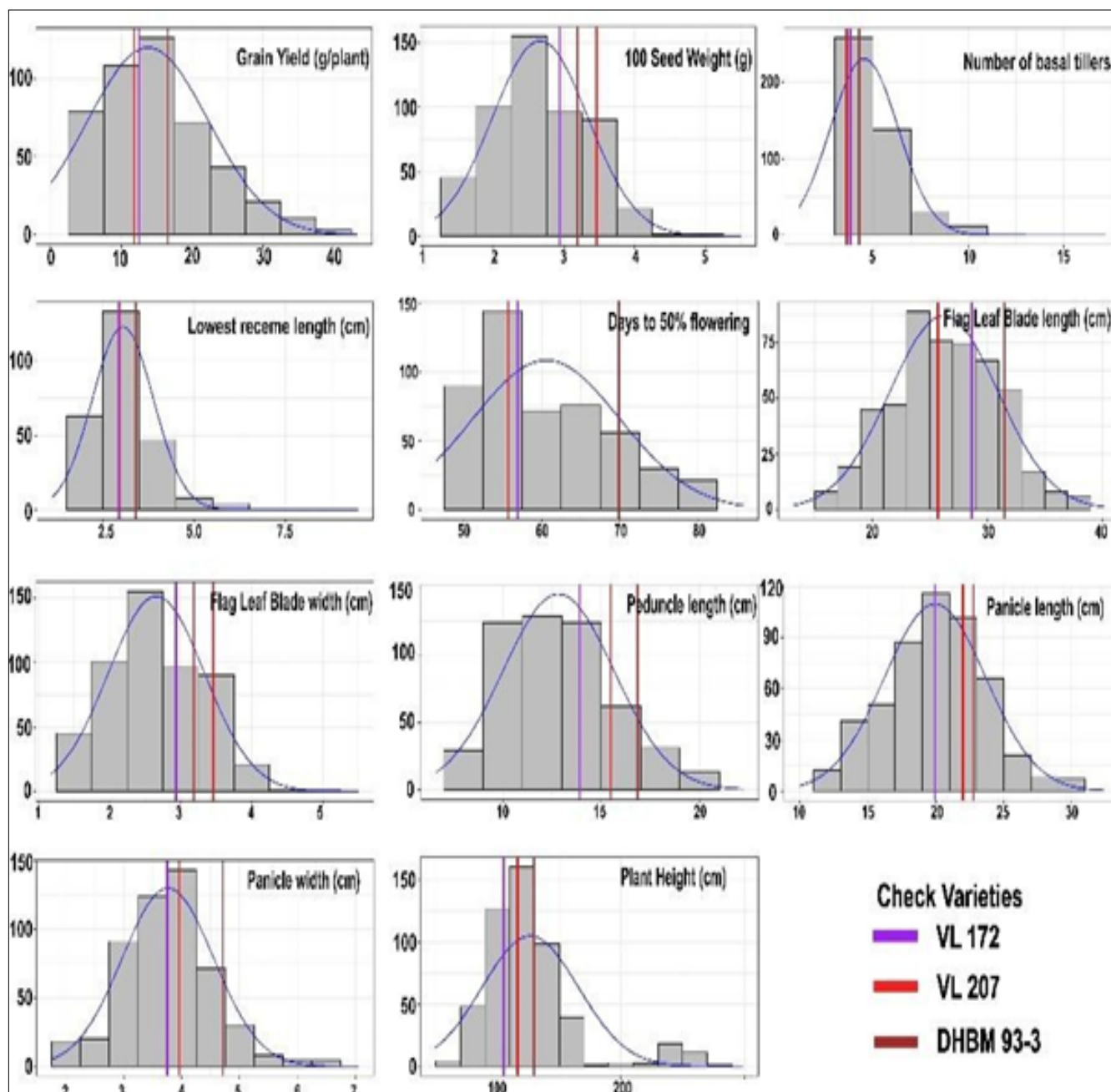


Fig. 1. Histogram showing frequency distribution of quantitative traits studied in 515 Barnyard millet germplasm.

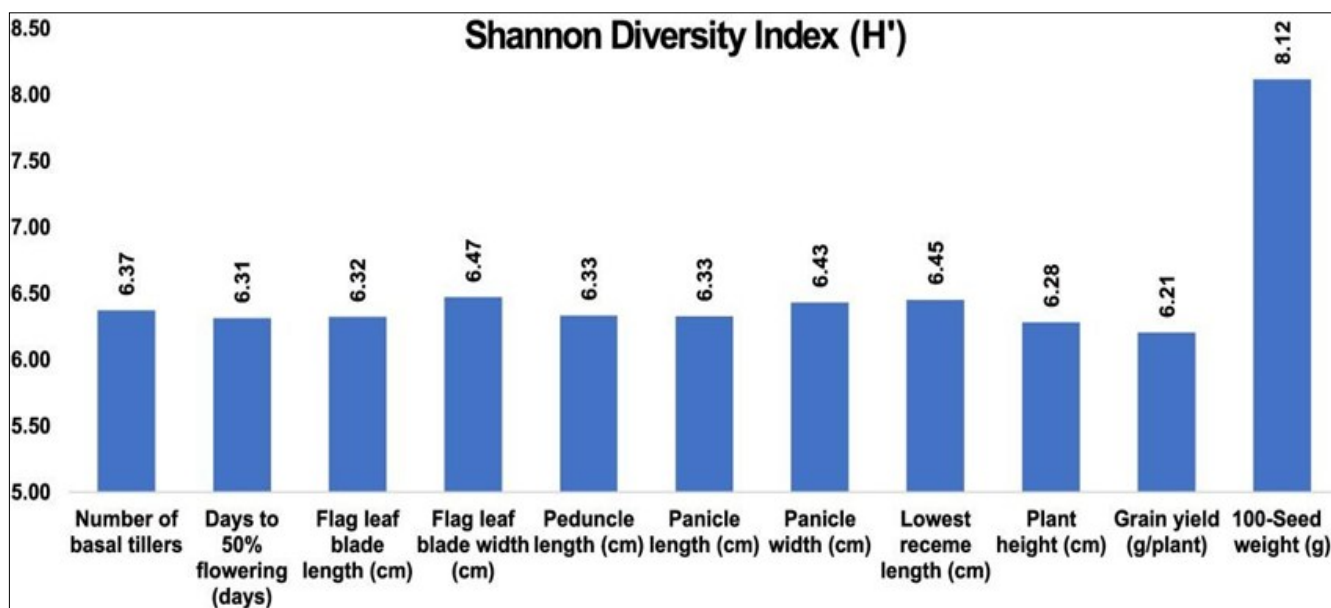


Fig. 2. Diversity among 515 acc. of barnyard millet germplasm based on Shannon diversity index.

Table 3. Eigenvalues (Latent roots) and variability of non-rotated values of principal components

Principle component	Eigenvalue	Proportion of variance explained	Components cumulative proportion (%)
PC1	3.2288	0.294	29.4
PC2	1.2594	0.114	40.8
PC3	1.1071	0.101	50.9
PC4	1.0147	0.092	60.1
PC5	0.9206	0.084	68.5
PC6	0.7945	0.072	75.7
PC7	0.7127	0.065	82.2
PC8	0.6299	0.057	87.9
PC9	0.4948	0.045	92.4
PC10	0.4789	0.044	96.7
PC11	0.3586	0.033	100

Table 4. Non-rotated component loadings (values of principal component traits of Barnyard millet)

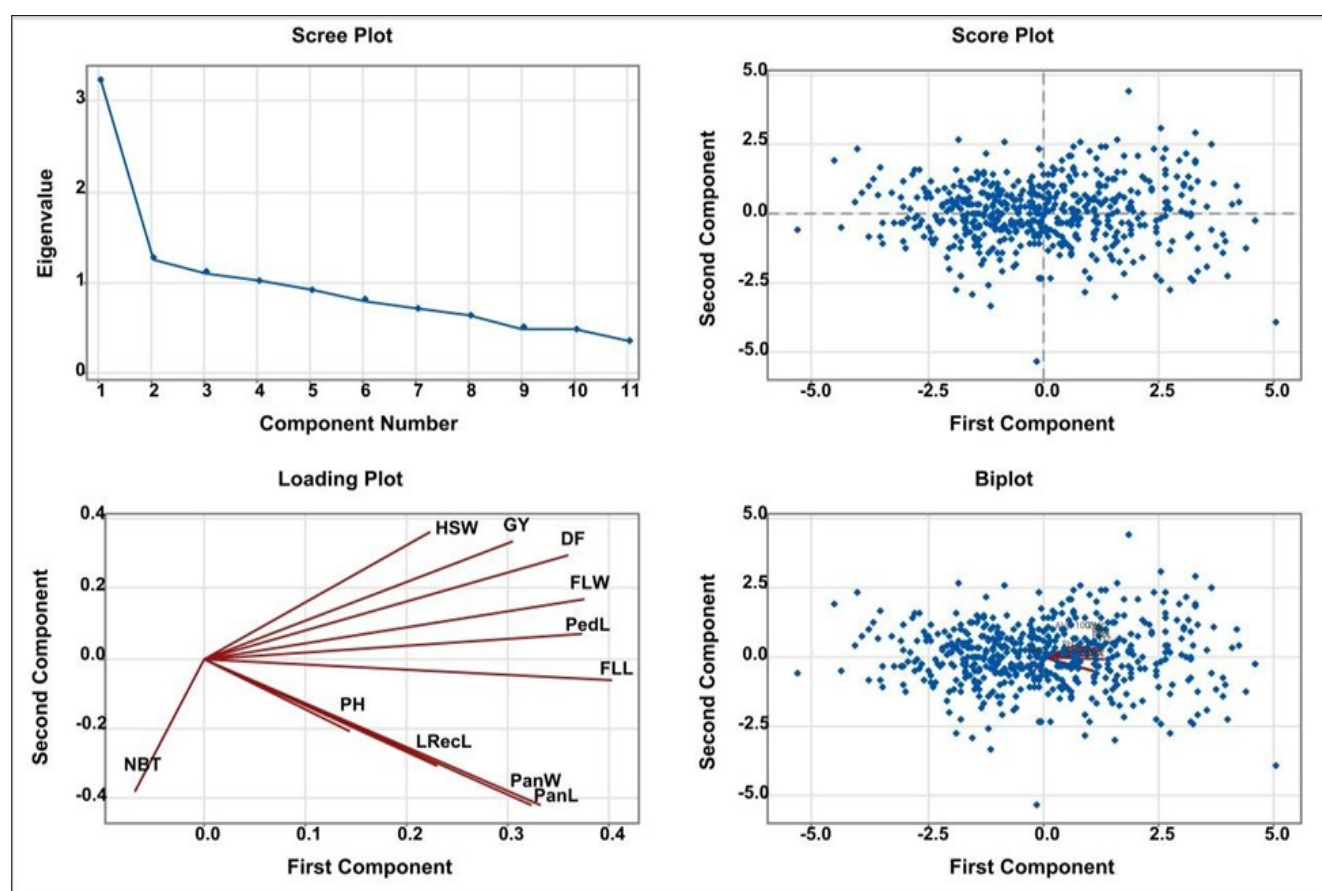
Trait/Variable	PC1	PC2	PC3	PC4	PC5
1. Number of basal tillers	-0.07	-0.38	0.46	0.61	0.20
2. Days to 50 % flowering (days)	0.36	0.29	0.12	0.43	0.12
3. Flag leaf blade length (cm)	0.40	-0.06	-0.19	0.27	-0.17
4. Flag leaf blade width (cm)	0.38	0.17	-0.21	0.11	-0.32
5. Peduncle length (cm)	0.37	0.07	-0.20	0.10	-0.01
6. Panicle length (cm)	0.33	-0.42	-0.18	-0.20	0.21
7. Panicle width (cm)	0.32	-0.42	-0.16	-0.19	0.15
8. Lowest raceme length (cm)	0.23	-0.31	0.35	-0.16	0.23
9. Plant height (cm)	0.14	-0.21	0.48	-0.22	-0.76
10. Grain yield (g/plant)	0.30	0.34	0.38	-0.02	0.08
11. 100-Seed weight (g)	0.22	0.36	0.31	-0.44	0.34

Bold values indicate the traits which contributed maximum to principal component

distribution of traits among the principal components explains the existence of greater variability among the studied accessions. The scree plot, score plot, loading plot and biplot of PCA of 515 accessions of Barnyard millet was shown in Fig. 3. From the scree plot it was noticed that only first two components explained maximum of diversity existed in the studied germplasm lines.

Potential germplasm identified

Multiple superior accessions across traits were identified and are listed in Table 5. The accessions IC0472499 and IC0281471 were identified for five specific traits each. The traits longer peduncle (> 18.00 cm), longer panicle (> 25.00 cm), wider panicle (> 5.00 cm), longer lowest raceme length (> 4.50 cm) were related to panicle traits and contribute to high grain yield

**Fig. 3.** Scree plot, Score plot, Loading plot and biplot of PCA of 515 accessions of Barnyard millet.

100^{SW}:100 seed weight (g); DF: Days flowering (days); FLL: Flag leaf length (cm); FLW: Flag leaf width (cm); GY: Grain yield (g plant⁻¹); LRecL: Lowest raceme length (cm); NBT: Number of basal tillers; PanL: Panicle length (cm); PanW: Panicle width (cm); PedL: Peduncle length (cm); PH: plant height (cm).

(IC0472499) and the traits early flowering (< 50 days), early maturity (< 80 days) along with taller plant (> 200.00 cm) and longer panicle (>25.00 cm) (IC0281471) are useful to develop lines with earliness and high grain yielding ability. Similarly, the lines recognized with more than one trait related to panicle length, raceme length, seed weight and panicle width (IC0404471, IC0404478, CB-EF-97, CB-TNAU-9, CB-Co-2, IC0601269, IC0473007, IC0404463, IC0404480, IC0404485,

IC0425735, IC0097046, CB-EF-32, CB-EF-124, CB-TNAU-23, CB-IEC-629, CB-Co-1) directly can be used for the development of cultivars with high grain yield. The lines identified with earliness in flowering, maturity and taller plant height are suitable for breeding of early maturing varieties. Additionally, cultivars such as IC0404531, IC0313564, IC0589361, IC0404303, IC0473031, IC0473051, IC0472899, IC0404508, IC0404509, IC0404551, IC0280648, IC0280652, IC0280656, IC0280662, IC0280665,

Table 5. Multi-trait specific barnyard millet germplasm identified from 515 acc.

SN	IC/EC No	Multi-trait
Five traits		
1	IC0472499	Longer flag leaf blade (> 35.00 cm) and Longer peduncle (> 18.00 cm), Longer panicle (> 25.00 cm), Wider panicle (> 5.00 cm) and Longer lowest raceme (> 4.50 cm)
2	IC0281471	Early flowering (< 50.00 days), Longer panicle (> 25.00 cm), Longer lowest raceme (> 4.50 cm), Taller plant (> 200.00 cm) and Early maturing (< 80.00 days)
Four traits		
3	IC0404531	Number of basal tillers (> 10.00), Early flowering (< 50.00 days), Taller plant (> 200.0 cm) and Early maturing (< 80.00 days)
4	IC0404471	Wider flag leaf blade (> 3.50 cm), Longer panicle (> 25.00 cm), Wider panicle (> 5.00 and Longer lowest raceme (> 4.50 cm)
5	IC0404478	Longer flag leaf blade (> 35.00 cm), Wider panicle (> 5.00 cm), Longer lowest raceme (> 4.50 cm) and 100 Seed weight (> 0.35g)
6	IC0313564	Early flowering (< 50.00 days), Longer lowest raceme (> 4.50 cm), Taller plant (> 200. cm) and Early maturing (< 80.00 days)
7	IC0589361	Early flowering (< 50.00 days), Wider panicle (> 5.00 cm), Taller plant (> 200.00 cm) Early maturing (< 80.00 days)
8	CB-EF-97	Longer peduncle (> 18.00 cm), Longer panicle (> 25.00 cm), Higher grain yield (> 25.00g/plant) and 100 Seed weight (> 0.35g)
9	CB-TNAU-	Longer flag leaf blade (> 35.00 cm), Longer peduncle (> 18.00 cm), Longer panicle (> 25.00 cm) and Wider panicle (> 5.00 cm)
10	CB-Co-2	Longer flag leaf blade (> 35.00 cm), Wider flag leaf blade (> 3.50 cm), Longer panicle (> 25.00 cm) and Wider panicle (> 5.00 cm)
Three traits		
11	IC0404303	Early flowering (< 50.00 days), Taller plant (> 200.00 cm) and Early maturing (< 80.00days)
12	IC0601269	Number of basal tillers (> 10.00), Longer panicle (> 25.00 cm) and Wider panicle (> 5cm)
13	IC0473031	Early flowering (< 50.00 days), Taller plant (> 200.00 cm) and Early maturing (< 80.00days)
14	IC0473051	Early flowering (< 50.00 days), Taller plant (> 200.00 cm) and Early maturing (< 80.00days)
15	IC0472899	Early flowering (< 50.00 days), Taller plant (> 200.00 cm) and Early maturing (< 80.00days)
16	IC0473007	Longer flag leaf blade (> 35.00 cm), Longer panicle (> 25.00 cm) and Wider panicle (> 5.00 cm)
17	IC0404463	Longer flag leaf blade (> 35.00 cm), Wider panicle (> 5.00 cm) and Higher grain yield (> 25.00g/plant)
18	IC0404480	Wider panicle (> 5.00 cm), Higher grain yield (> 25.00g/plant) and 100 Seed weight (> 0.35g)
19	IC0404485	Longer peduncle (> 18.00 cm), Wider panicle (> 5.00 cm) and Higher grain yield (> 25.00g/plant)
20	IC0404508	Early flowering (< 50.00 days), Taller plant (> 200.00 cm) and Early maturing (< 80.00days)
21	IC0404509	Early flowering (< 50.00 days), Taller plant (> 200.00 cm) and Early maturing (< 80.00days)
22	IC0404551	Early flowering (< 50.00 days), Taller plant (> 200.00 cm) and Early maturing (< 80.00days)
23	IC0280648	Early flowering (< 50.00 days), Taller plant (> 200.00 cm) and Early maturing (< 80.00days)
24	IC0280652	Early flowering (< 50.00 days), Taller plant (> 200.00 cm) and Early maturing (< 80.00days)
25	IC0280656	Early flowering (< 50.00 days), Taller plant (> 200.00 cm) and Early maturing (< 80.00days)
26	IC0280662	Early flowering (< 50.00 days), Taller plant (> 200.00 cm) and Early maturing (< 80.00days)
27	IC0280665	Early flowering (< 50.00 days), Taller plant (> 200.00 cm) and Early maturing (< 80.00days)
28	IC0372751	Early flowering (< 50.00 days), Taller plant (> 200.00 cm) and Early maturing (< 80.00days)
29	IC0372754	Early flowering (< 50.00 days), Taller plant (> 200.00 cm) and Early maturing (< 80.00days)
30	IC0372777	Early flowering (< 50.00 days), Taller plant (> 200.00 cm), Early maturing (< 80.00 da
31	IC0372781	Early flowering (< 50.00 days), Taller plant (> 200.00 cm) and Early maturing (< 80.00days)
32	IC0372797	Early flowering (< 50.00 days), Taller plant (> 200.00 cm) and Early maturing (< 80.00days)
33	IC0334008	Early flowering (< 50.00 days), Taller plant (> 200.00 cm) and Early maturing (< 80.00days)
34	IC0334012	Early flowering (< 50.00 days), Taller plant (> 200.00 cm) and Early maturing (< 80.00days)
35	IC0334027	Early flowering (< 50.00 days), Taller plant (> 200.00 cm) and Early maturing (< 80.00days)
36	IC0334039	Early flowering (< 50.00 days), Taller plant (> 200.00 cm) and Early maturing (< 80.00days)
37	IC0334092	Early flowering (< 50.00 days), Taller plant (> 200.00 cm) and Early maturing (< 80.00days)
38	IC0425735	Longer panicle (> 25.00 cm), Wider panicle (> 5.00 cm) and 100 Seed weight (> 0.35g)
39	IC0259309	Early flowering (< 50.00 days), Taller plant (> 200.00 cm) and Early maturing (< 80.00days)
40	IC0097046	Wider flag leaf blade (> 3.50 cm), Longer peduncle (> 18.00 cm) and Higher grain yie(> 25.00g/plant)
41	IC0406615	Early flowering (< 50.00 days), Taller plant (> 200.00 cm) and Early maturing (< 80.00days)
42	IC0589364	Early flowering (< 50.00 days), Taller plant (> 200.00 cm) and Early maturing (< 80.00days)
43	IC0589376	Early flowering (< 50.00 days), Taller plant (> 200.00 cm) and Early maturing (< 80.00days)
44	IC0612220	Early flowering (< 50.00 days), Longer panicle (> 25.00 cm) and Wider panicle (> 5.00cm)
45	CB-EF-32	Longer flag leaf blade (> 35.00 cm), Longer panicle (> 25.00 cm) and Higher grain yie(> 25.00g/plant)
46	CB-EF-124	Wider flag leaf blade (> 3.50 cm), Higher grain yield (> 25.00g/plant) and 100 Seedweight (> 0.35g)
47	CB-TNAU-	Wider flag leaf blade (> 3.50 cm), Longer peduncle (> 18.00 cm) and Higher grain yie(> 25.00g/plant)
48	CB-IEC-629	Longer panicle (> 25.00 cm), Wider panicle (> 5.00 cm) and 100 Seed weight (> 0.35 g
49	CB-Co-1	Wider panicle (> 5.00 cm) and Longer lowest raceme (> 4.50 cm) and Higher grain yie(> 25.00g/plant)

IC0372751, IC0372754, IC0372777, IC0372781, IC0372797, IC0334008, IC0334012, IC0334027, IC0334039, IC0334092, IC0259309, IC0406615, IC0589364, IC058937 and IC0612220 were identified as promising cultivars to escape biotic and abiotic stresses which could be further useful for crop improvement.

Discussion

Genetic characterization of a large set of available germplasm accessions conserved across the global gene banks were used by researchers worldwide (11). Phenotypic characterization aids breeders, geneticists and botanists in identifying promising trait donors for developing high yielding, climate resilient and pest and disease resistant cultivars (16). In the present study, existence of great amount of variability for traits was observed. Since, traits such as number of basal tillers, plant height and grain yield per plant were recorded for high GCV and PCV these traits are significant through selection for crop genetic improvement. In contrast high heritability was also recorded for number of basal tillers, days to 50 % flowering, lowest raceme length and plant height indicating that variation is due to genetic factors and these traits will aid the breeders for further improvement of crops. Additionally, trait specific germplasm lines were found for potential application in the future use for improvement of cultivars with increased grain yield and also, for earliness. Earlier researchers reported higher variability in barnyard millet germplasm for morpho-agronomic traits (11, 13, 16, 21). High coefficient variation was observed within the studied accessions for few traits and it explained the presence of high variability (22). Significant variations were also reported in previous research for the traits studied in barnyard millet like days to flowering, days to maturity, ear length, panicle weight and grain yield (10).

As documented by previous research, PCA was performed to study the accessions with specific traits contributing maximum towards the variability and to identify traits correlated with the variability components (23). In this study, 60.1 % of the total variation across 11 quantitative traits was captured by the first four principal components (PCs) with eigenvalues greater than one. The 11 quantitative traits showed the inherent uniqueness among the studied barnyard millet accessions. The first two components explained the maximum variation and the traits with good correlation. The scree plot explained that the diversity contribution was by first two components of PCA and consideration may be restricted to PC1 and PC2 for the selection of germplasm for improvement program. However, prior research also reported that first four PCs contributed majorly to diversity in the studied accessions of barnyard millet (15). In the current study, traits including days to 50 % flowering (days), flag leaf blade length (cm), flag leaf blade width (cm), peduncle length (cm), panicle length (cm) and panicle width (cm) were the important traits contributing to variability as explained by the PC1. However, PC1 stating that the accessions which fall under this region of the score plot of PCA could be utilized as potential donors of these traits. In contrast, the traits such as grain yield and 100 seed weight which is consisting of economic importance were mainly contributing to PC2 and hence the accessions falling in this region may be used for the development of the varieties with increased grain yield in

barnyard millet. Although similar kind of study was performed for same traits but the results were noted distinct for traits like flag leaf length, plant height and ear length as they were negatively related to PC1 and the traits like lower raceme length, plant height and ear length was positively related to PC2 (16). The distinctly identified accessions through the PCA may be either used for hybridization programmes as parents or could be released for commercial cultivation directly after multi-location evaluation for stability of the genotype (21, 23).

Identification of the germplasm accessions by tagging traits will be of great advantage to researchers in tailoring the new cultivars with increased performance for grain yield and utilization in breeding programs to dissect the traits at genetic level/molecular level. The current study has identified 49 potential accessions tagged with superior performance for multiple traits. The accessions IC0472499 and IC0281471 were identified for five specific traits each. The traits longer peduncle, longer panicle, wider peduncle, longer lowest raceme length are related to panicle traits and contribute to high grain yield and the traits early flowering, early maturity, along with taller plant and longer panicle (IC0281471) are useful to develop lines with earliness and good grain and fodder yielding ability. It was suggested that trait specific germplasm lines for crops improvement could be the useful genetic material, climate resilience breeding and improving food and nutritional security in a sustainable way (15). In a similar way the trait specific accessions identified with two/three/four traits in the present study will serve as ready reckoner for the improvement of targeted traits in the crop improvement programs of barnyard millet as potential donor parents specifically for the traits like earliness and high grain yielding ability. Similar kind of results were reported in foxtail millet, where 26 accessions with three desirable trait combinations were identified and could be further used as donor lines for grain yield, early flowering, high Fe, Zn and Ca contents (24). Furthermore, another study recognized trait specific lines for vigour, extra early flowering, early maturity, plant height, high productive tillers, long panicle, thick panicle and high grain yield. The study also noted that the developed trait specific gene pools will serve as a storehouse for future breeding programs in pearl millet (25). Although, in the current study molecular work is not performed but from the obtained trait specific germplasms of barnyard millet it is believed that these accessions can be efficiently utilized as trait specific donors for developing mapping populations and qtls. Further, these tagged traits will aid breeders a path for marker assisted breeding programmes.

Conclusion

The present study has identified potential and trait specific germplasm accessions of barnyard millet along with the extent of diversity existing in the large number of lines. The identified 49 accessions were found superior in multiple traits. This provides an added advantage for experiments on grain yield improvement of barnyard millet. The diversity analysis with significant ANOVA values, Shannon's diversity index score, scree plot and PCA, confirmed variability observed in the set of 515 accessions. Utilization of this broad genetic diversity for traits such as days to maturity, panicle length and width, 100

seed weight and grain yield, offers significant potential in crop improvement programs. Diversity studies along with utilization of molecular markers (SSR/SNP) act as the future line of work to correlate the phenotypic variability existing in barnyard millet for better understanding of the diverse traits and their utilization for grain yield enhancement to break the yield stagnation. The trait specific donor germplasm lines can be effectively utilized for development of mapping populations to identify and tag the genes/qtls associated with the trait specificity. The linked marker to specific traits provides a way for Marker assisted breeding (MAS) in barnyard millet improvement programs. Generation of genetic and genomic resources in barnyard millet are lacking. The present study will serve as an excellent source of genotypes identified with specific traits for molecular studies and crop improvement.

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Authors' contributions

BA and KV carried out the characterization experiment in the field, BA, AVU, LC and NK taken the observations on the different traits at different stages. BA, KV, LC were involved in field management and maintenance of the crop in good condition. S, CD and DR analysed the data for various parameters. The manuscript was prepared by BA, LC, S and NK and the manuscript was corrected and revised by AVU, NK and DR. All authors read and approved the final manuscript.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interest to declare.

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References

- Indian Institute of Millets Research (IIMR). Annual report 2017–18. Hyderabad: Indian Institute of Millets Research; 2018.
- Renganathan VG, Vanniarajan C, Karthikeyan A, Ramalingam J. Barnyard millet for food and nutritional security: current status and future research direction. *Front Genet.* 2020;11:500. <https://doi.org/10.3389/fgene.2020.00500>
- Guo L, Qiu J, Ye C, Jin G, Mao L, Zhang H, et al. *Echinochloa crus-galli* genome analysis provides insight into its adaptation and invasiveness as a weed. *Nat Commun.* 2017;8(1):1031. <https://doi.org/10.1038/s41467-017-01067-5>
- Kumar KK, Parameswaran KP. Characterisation of storage protein from selected varieties of foxtail millet (*Setaria italica* (L.) Beauv). *J Sci Food Agric.* 1998;77(4):535–42.
- Veena B, Chimmad BV, Naik RK, Shanthakumar G. Physico-chemical and nutritional studies in barnyard millet. *Karnataka J Agric Sci.* 2005;18(1):101–5.
- Kulkarni LR, Naik RK, Katarki PA. Chemical composition of minor millets. *Karnataka J Agric Sci.* 1997;10(2):470–2.
- Asghar MJ, Mehdi SS. Selection indices for yield and quality traits in sweet corn. *Pak J Bot.* 2010;42(2):775–89.
- Halaswamy BH, Srinivas GV, Ramakrishna BM, Magar VK, Krishnappa M, Gowda J. Characterization and preliminary evaluation of national collections of barnyard millet (*Echinochloa* species) germplasm. *Indian J Plant Genet Resour.* 2001;14(2):213–6.
- Mehta H, Tyagi PC, Mohapatra KP. Genetic diversity in barnyard millet (*Echinochloa frumentacea* Roxb.). *Indian J Genet Plant Breed.* 2005;65(4):293–5.
- Mehta H, Tyagi PC, Mohapatra KP. Genetic analysis of morphophysiological and yield component traits in barnyard millet (I). *Crop Improv.* 2007;34(1):82–5.
- Gupta A, Mahajan V, Kumar M, Gupta HS. Biodiversity in the barnyard millet (*Echinochloa frumentacea* Link, Poaceae) germplasm in India. *Genet Resour Crop Evol.* 2009;56:883–9. <https://doi.org/10.1007/s10722-009-9462-y>
- Gowda J, Bharathi S, Somu G, Krishnappa M, Rekha D. Formation of core set in barnyard millet [*Echinochloa frumentacea* (Roxb.) Link] germplasm using data on twenty-four morpho-agronomic traits. *Int J Plant Sci.* 2009;4(1):1.
- Sood S, Khulbe RK, Kumar A, Agrawal PK, Upadhyaya HD. Barnyard millet global core collection evaluation in the submontane Himalayan region of India using multivariate analysis. *Crop J.* 2015;3(6):517–25. <https://doi.org/10.1016/j.cj.2015.07.005>
- Manimekalai M, Dhasarathan M, Karthikeyan A, Murukarthick J, Renganathan VG, Thangaraj K, et al. Genetic diversity in the barnyard millet (*Echinochloa frumentacea*) germplasms revealed by morphological traits and simple sequence repeat markers. *Curr Plant Biol.* 2018;14:71–8. <https://doi.org/10.1016/j.cpb.2018.09.006>
- Trivedi AK, Arya L, Verma SK, Tyagi RK, Hemantaranjan A. Evaluation of barnyard millet diversity in central Himalayan region for environmental stress tolerance. *J Agric Sci.* 2017;155(10):1497–507. <https://doi.org/10.1017/S0021859617000545>
- Dhanalakshmi R, Subramanian A, Thirumurugan T, Elangovan M, Kalaimagal T. Genetic diversity study in barnyard millet (*Echinochloa frumentacea* (Roxb.) Link) germplasm under sodic soil condition. *Plant Arch.* 2019;19(2). <https://doi.org/10.5958/0975-928X.2019.00055.3>
- Arunachalam P, Vanniarajan C, Nirmalakumari A. Consistency of barnyard millet (*Echinochloa frumentacea*) genotypes for plant height, duration and grain yield over environments. *Madras Agric J.* 2012;99(1–3):11–3. <https://doi.org/10.29321/MAJ.10.100004>
- Sharma KC, Sharma RK, Singhania DL, Singh D. Variation and character association in fodder yield and related traits in pearl millet [*Pennisetum glaucum* (L.) R. Sr.]. *Indian J Genet Plant Breed.* 2003;63(2):115–8.
- Aravind J, Mukesh Sankar S, Wankhede DP, Kaur V. Augmented RCBD: analysis of augmented randomised complete block designs. *R Package Version.* 2020;0.1.2.
- Hammer Ø, Harper DA. PAST: Paleontological statistics software package for education and data analysis. *Palaeontol Electron.* 2001;4(1):1.
- Prabu R, Vanniarajan C, Vetrivanthan M, Gnanamalar RP, Shanmughasundaram R, Ramalingam J. Diversity study using principal component analysis in barnyard millet (*Echinochloa frumentacea* (Roxb.) Link). *Electron J Plant Breed.* 2020;11(2):606–9. <https://doi.org/10.37992/2020.1102.099>
- Furman BJ, Qualset CO, Skovmand B, Heaton JH, Corke H, Wesenberg DM. Characterization and analysis of North American triticale genetic resources. *Crop Sci.* 1997;37(6):1951–9. <https://doi.org/10.2135/cropsci1997.0011183X0037000600046x>
- Shitta NS, Abteu WG, Ndlovu N, Oselebe HO, Edemodu AC, Abebe AT. Morphological characterization and genotypic identity of African yam bean (*Sphenostylis stenocarpa* Hochst ex. A. Rich. Harms) germplasm from diverse ecological zones. *Plant Genet Resour.* 2021;19(1):58–66. <https://doi.org/10.1017/S1479262121000095>

24. Upadhyaya HD, Ravishankar CR, Narasimhudu Y, Sarma ND, Singh SK, Varshney SK, et al. Identification of trait-specific germplasm and developing a mini core collection for efficient use of foxtail millet genetic resources in crop improvement. *Field Crops Res.* 2011;124(3):459–67. <https://doi.org/10.1016/j.fcr.2011.08.004>
25. Khairwal IS, Yadav SK, Rai KN, Upadhyaya HD, Kachhawa D, Nirwan B, et al. Evaluation and identification of promising pearl millet germplasm for grain and fodder traits. *J SAT Agric Res.* 2007;5(1):1–6.

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