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RESEARCH ARTICLE

Dissection of genetic variation and evaluation of yield and key agriculturally important traits in Barnyard millet (*Echinochloa frumentaceae* (Roxb.) Link) under typical sodicity stress

S Muruganantham[1], Kannabiran Sakthivel[1*], Chockalingam Vanniarajan[1*], Paramasiwam Jeyaprakash[1], Thanakkan Ramesh[1], Sadayandi Geethanjali[1], Periasamy Satheeshkumar[1], Selvaraj Rathika[1] & Anandan Annamalai[2]

[1]Tamil Nadu Agricultural University - Anbil Dharmalingam Agricultural College and Research Institute, Tiruchirappalli 620027, Tamil nadu, India

[2] Indian Institute of Seed Science, Regional Station, GKVK campus, Bangalore 560065, Karnataka, India

*Email: sakthivel@tnau.ac.in, vanniarajan.c@tnau.ac.in

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Abstract

Barnyard millet, a climate-resilient small millet, is a valuable feed source for both livestock and humans. Sodicity is an increasingly important soil stress under changing climatic conditions. The present investigation comprised 74 germplasm and three check varieties MDU1, CO(KV)2 and ATL1 evaluated under sodic soil using Augmented Complete Block Design. The analysis of variance revealed the presence of significant differences among the genotypes for all seventeen traits. Genetic variability estimates, such as PCV, GCV, heritability and genetic advance, were high for all the traits except days to maturity. This suggests that these traits are governed by additive gene action, which favours the effective selection of these traits. Association analysis revealed that flag leaf length, days to maturity and single-ear head weight showed significant and positive associations with single plant yield. Therefore, the selection of these traits can improve the yield of barnyard millet under sodic soil. The principal component analysis (PCA) revealed that five significant principal components explained 70.19% of the total variation, with the first two principal components attributed to 48.99% of variation which are majorly attributed to days to 50% flowering, days to maturity, flag leaf length, plant height, single-ear head weight, number of racemes per panicle and number of tillers. Hierarchical cluster analysis grouped the genotypes into five clusters with the accessions in cluster I exhibiting high tillering ability and yield potential. Therefore, the accessions in cluster I can be utilized as parents in the hybridization programme for enhancing the yield of barnyard millet.

Keywords

barnyard millet; genetic parameters; heritability; PCA; sodicity; soil stress

Introduction

By 2050, the global population is expected to reach 9.8 billion. To sustain this rapidly growing population, it is necessary to increase crop production by 60-70% (1). However, biotic and abiotic stresses pose significant challenges to boosting agricultural production. Particularly, soil salinity has been gradually increasing over the recent years with approximately 1128 million hectares affected by salinity and sodicity stresses with the Middle East, Australia and North Africa experiencing high soil salinization followed by India with the least soil salinization (2). Sodic soils are generally characterized by a pH range of 8.5 to 9.0, an exchangeable sodium percentage (ESP) above 15%, a sodium adsorption ratio (SAR) above 13 and electrical conductivity (EC) below 4.0 dS/m which results in nutritional imbalances and ion toxicity in soil (3). These soils have high concentration of sodium ions in their exchange complex which hinders crop growth. Further, sodic soils are poorly structured, with dispersed colloidal clays in the topsoil, resulting in low permeability, poor aeration and surface crusting which hinders root penetration and seed germination ultimately it affects crop growth and development (4). The rise in area under salinity is a major threat to food security. However, millets possess a promising solution due to their remarkable ability to thrive under adverse agro-climatic conditions.

The Indian barnyard millet is renowned for its short growth cycle, ability to thrive in resource-poor and heavy metal accumulated soils and abiotic stress tolerance (5) with better nitrogen use efficiency compared to other cereal crops (6). These features make them an ideal crop to cultivate in arid and semi-arid regions of the world. Barnyard millet is typically cultivated as a rainfed crop during the *kharif* season, commonly at elevations up to 2000 meters above sea level (7). Globally over the past three years, India has emerged as the foremost producer with a net cultivated area of 1.46 lakh hectare, production of 14.7 lakh tones and productivity of 1 t/ha (8).

Apart from their climate resilience traits, their nutritional values are peculiar. For example, barnyard millet has a rich source of iron (9.3-18.6 mg/100 g) and low carbohydrate content (51.5- 62.0 g/100 g) compared to other millets (9). Also, it contains higher crude fiber (8.1-16.3%) compared to other cereals (8). The high crude fiber and low carbohydrate in barnyard millet aid in the gradual release of carbohydrates in the blood which assist in blood sugar regulation and can be recommended as a dietary substitute for rice in patients with type 2 diabetes. Therefore, barnyard millet can be regarded as a versatile crop capable of addressing food security, owing to its exceptional nutritional value and climate resilience. However, a specific barnyard millet variety suited for cultivation in sodic soil has not been developed yet.

Development of sodicity tolerant barnyard millet varieties through conventional crop improvement programs should first aim with an evaluation of germplasm and identification of high-yielding genotype under sodicity stress followed by the study of genetic variability and other parameters underlying such germplasm for determining suitable breeding methods and techniques towards the evolution of superior and stress-tolerant varieties. In the present investigation, various genetic analyses were undertaken (i) to evaluate and identify superior genotypes with yield under sodicity, (ii) to dissect the genetic variability present in the germplasm of barnyard millet, (iii) to elucidate the association and effects among yield contributing traits and (iv) to study the grouping pattern among the germplasm through multivariate approach.

Materials and Methods

Experimental material, site and design

The current study comprised 77 barnyard millet genotypes which include 74 germplasm accessions and three check varieties (Table 1). The germplasm was sourced from GKVK (Gandhi Krishi Vigyana Kendra), UAS, Bangalore and ICAR - Indian Institute of Millets Research (IIMR), Hyderabad. The research was performed in Augmented Complete Block Design along with three check varieties MDU1, CO(KV)2 and ATL1 by adopting 30 × 15 spacing between rows and plants under naturally existing sodic soil characterized by pH of 8.59, ESP of 36.7% and EC of 0.73 dS/m at Anbil Dharmalingam Agricultural College and Research Institute, Tamil Nadu Agricultural University, Tiruchirappalli, Tamil Nadu (10°45’16’’ N, 78°36’12’’ E) during January - May 2024. Standard agronomical practices were adhered to ensure optimal crop growth.

Observation recorded

Biometrical traits were noted on five randomly chosen plants from each accession except for days to maturity and days to fifty per cent flowering. Data for the remaining traits were collected based on *Echinochloa* millet descriptors (10) for the traits *viz*., plant height (cm), length of flag leaf (cm), width of flag leaf (cm), inflorescence length (cm), inflorescence width (cm), number of tillers, lower raceme length (cm), peduncle length (cm), internode length (cm), single-ear head weight(g), number of racemes per panicle, stem diameter (cm), the total number of nodes, single plant yield (g) and thousand-grain weight (g).

Statistical analysis

The recorded data were analysed by using the R software package “augmented RCBD” version 0.1.7 (11) for estimating the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) with adjusted means. The adjusted means were used to compute correlation and path coefficient to dissect the inter-relationship among the yield and its contributing characters by utilizing the R software package “corrplot” (12) v0.92 and “bio tools” (13) v4.2. PCA was performed using the ‘factomineR’ and ‘factoextra’ R packages and cluster analysis was conducted using ‘stats’ R package v4.3.0. The dendrogram was constructed based on Euclidean distance values by using Ward’s method.

Table 1. List of barnyard millet germplasm accessions collected

Accessions	Source
GECH-808, GECH-871, GECH-863, GECH-796, GECH-540, GECH- 579, GECH-823, GECH-369, GECH-982, GECH-1084, GECH-600,	GKVK (Gandhi Krishi Vigyana Kendra), UAS, Bengaluru, India
GECH-195, GECH-169, GECH-120, GECH-623, GECH-442, GECH- 896GECH-315, GECH-346, GECH-736, GECH-751, GECH-868, GECH-791, GECH-848, GECH-27, GECH-552, GECH-231, GECH-62, GECH-326, GECH-709, GECH-974, GECH-35, GECH-872, GECH-374, GECH-755, GECH-99	
IC0404540,IC0404294, IC0404549, IC0404326, IC0473117, IC0404347,IC0404395, IC0404413, IC0404416, IC0473006, IC0473062,IC0403063,IC0473077, IC0473109, IC0473115, IC0473125, IC0601270, IC0041785,IC0472864, IC0472927, IC0473075, IC0472732, IC0472748, IC0472735,IC0472954, IC0472971, IC0472985, IC0473005, IC0473049, IC0473054,	Indian Institute of Millet Research, Hyderabad, India
IC0473064, IC0472797, IC0472910, IC0472924, IC0331100,	
MDU 1, CO(KV) 2, ATL 1	Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India

Results and Discussion

The analysis of variance (ANOVA) presented in Table 2 indicates that all the traits studied under a sodic environment show significant differences highlighting the presence of sufficient genetic diversity among germplasm. The computed standard deviation, mean, standard error and range outlined in Table 3 reveal that germplasm, GECH 982 flowered earliest in 34 days while GECH 863 took 68 days to flower. GECH 982 reached maturity in a short span of 72 days, whereas the check CO(KV)2 was found to mature late in 101 days. Plant height ranged from 43.15 cm (IC0473125) to 110.34 cm (GECH 369). The length of the flag leaf ranged from 10.12 cm (IC0473077) to 29.32 cm (GECH 374) regarding the width of fag leaf, GECH 796 was narrow with 1.22 cm while GECH-791 was the broadest (3.37 cm). The longest inflorescence (21.11 cm) was recorded in GECH 35 and the shortest in GECH 982 (6.44 cm). Elevated breadth of inflorescence (5.22 cm) was noted in IC0404294 whereas narrow width (0.92 cm) in IC0473125. Lower raceme length varied from 1.14 cm in GECH 982 to 4.90 cm in GECH 896. The longest peduncle was found in IC0473109 (15.86 cm) whereas GECH 808 recorded the shortest peduncle length of 3.06 cm.

The highest number of tillers was observed in IC0472748 (9.63) and the least in GECH 231 (2.42). More number of nodes (10.66) were noted in the check variety MDU1 and the last one being IC047307 (3.24). The diameter of the stem ranged from 0.32 cm (IC0403063) to 1.23 cm (MDU1). The length of internodes varied from 5.47 cm (GECH 872) to 12.72 cm (GECH 442). More number of racemes per panicle (48.89) was observed in GECH 863 whereas it was least (8.69) in IC0473125. Grain yield per plant varied from 2.5 g to 18.7 g with MDU1 recorded the highest and IC0473125 recorded the lowest yield under a sodic environment. The thousand-grain weight ranged from 1.73 g (IC0473125) to 4.18 g (IC0472748). The weight of a single-ear head ranged from 0.38 g (IC0473125) to 5.44 g (MDU1). Similarly, wide variation for various biometrical traits was reported in barnyard millet under sodic soil (14). The current research observed variation in biometrical traits under sodic stress. However, it was noted that the performance of genotypes showed an overall reduction for various characters such as length of flag leaf, plant height and width of flag leaf due to stress-induced slower cell division and growth (15).

Skewness and kurtosis

The exploration of frequency distribution using skewness (Fig. 1) allows us to infer the mode of gene action whereas examining kurtosis, a fourth-degree statistics, helps us determine the number of genes influencing the traits (16-17). Positive skewness is linked to complementary gene action which requires intense selection for enhancing genetic gain while duplicate gene action is linked to negative skewness which requires mild selection for optimizing genetic gain (18). Significant and positive skewness were expressed for the traits single-ear head weight, days to 50% flowering, lower raceme length, number of tillers and grain yield per plant which displayed complementary nature of gene action (Table 3). The leptokurtic nature of distribution was noted for grain yield per plant and number of tillers suggesting that these

Table 2. ANOVA for biometrical traits in barnyard millet germplasm under sodic soil

Source		Mean Sum of Squares																
		DFF	**DTM**	**PH**	**FL**	**FLW**	**IFL**	**IFW**	**LRL**	**PDL**	**NBT**	**INL**	**TN**	**SD**	**NRP**	**SERHW**	**SPY**	**TGW**
Treatment (Ignoring Blocks)	76	95.55**	64.89*	228.35*	25.47*	0.31*	9.48**	0.99*	0.62*	5.01*	2.1**	4.43**	3.48*	0.08**	92.81**	1.32**	16.48**	0.38*
Treatment: Check	2	10.11^{ns}	19^{ns}	50.92^{ns}	15.42*	0.29*	8.14*	0.94*	0.24^{ns}	0.52^{ns}	0.66*	3.19*	3.02*	0.13**	45.67*	2.43**	22.09**	0.18^{ns}
Treatment: Test	73	53.61*	42.3*	223.36*	19.1*	0.28*	9.55**	0.97*	0.62*	4.93*	2.15**	4.5**	2.71*	0.05*	78.33**	0.66*	3.21**	0.39*
Treatment: Test vs. Check	1	3328.31**	1805.42**	947.45**	511.15**	2.01**	7*	2.21*	1.31*	19.83**	1.88**	2.53*	61.11**	1.91**	1244.47**	47.11**	974.01**	0.23^{ns}
Block (Eliminating Treatments)	2	3.11^{ns}	2.33^{ns}	18.79^{ns}	0.81^{ns}	0^{ns}	5.28*	0.01^{ns}	0.02^{ns}	0.04^{ns}	0.17^{ns}	1.43^{ns}	1.32^{ns}	0^{ns}	13.35^{ns}	0.2^{ns}	19.26**	0^{ns}
Residuals	4	6.94	5.83	27.32	2.09	0.03	0.58	0.12	0.1	0.86	0.06	0.32	0.31	0.01	3.04	0.08	0.23	0.04

ns $P > 0.05$; * $P <= 0.05$; ** $P <= 0.01$

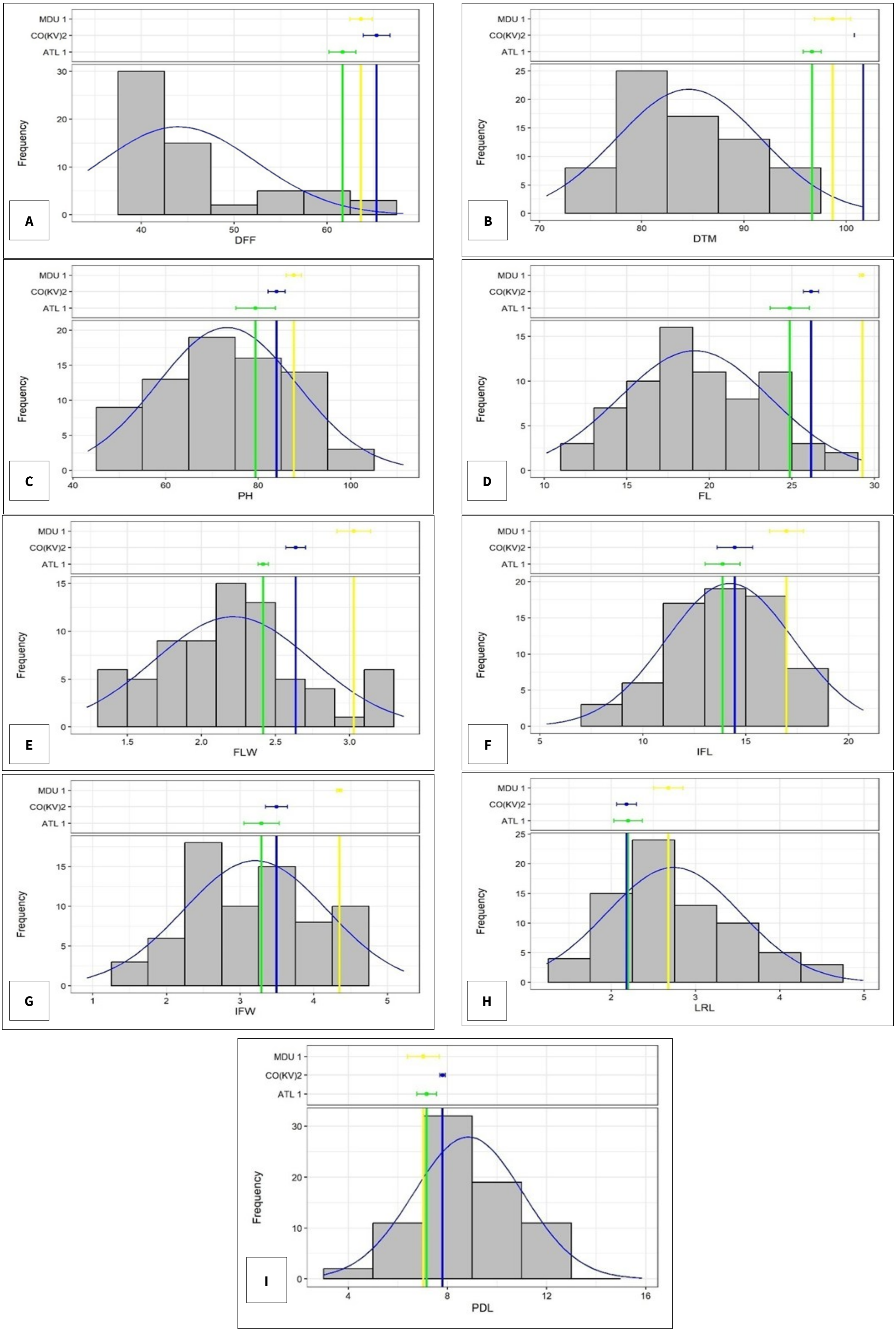
DFF- days to fifty percent flowering, DTM- days to maturity, PH- plant height, LF- flag leaf length, FLW- flag leaf width, IFL- inflorescence length, IFW- inflorescence width, LRL- lower raceme length, PDL- peduncle length, NBT- number of basal tillers, INL- internode length, TN- Total nodes, SD- stem diameter, NRP- number of racemes per panicle. SERHW- single-ear head weight, SPY- single plant yield, TGW- thousand-grain weight

Table 3. Descriptive statistical analysis of biometrical traits under sodic soil

Traits	**Mean**	**Min**	**Max**	**Standard error**	**Standard deviation**	**Skewness**	**Kurtosis**
DFF	43.98	34.00	72.00	0.95	8.34	1.33**	3.78^{ns}
DTM	84.58	75.00	101.00	0.80	7.05	0.46^{ns}	2.47^{ns}
PH	73.24	43.15	110.34	1.72	15.05	0.08^{ns}	2.63^{ns}
FL	19.11	10.12	29.32	0.52	4.58	0.03^{ns}	2.46^{ns}
FLW	2.21	1.2	3.37	0.06	0.53	0.35^{ns}	2.67^{ns}
IFL	14.23	6.44	21.11	0.35	3.11	-0.22^{ns}	2.92^{ns}
IFW	3.21	0.92	5.22	0.11	0.98	-0.04^{ns}	2.34^{ns}
LRL	2.74	1.14	4.90	0.09	0.79	0.57*	3.05^{ns}
PDL	8.84	3.06	15.86	0.25	2.20	0.34^{ns}	3.57^{ns}
NBT	4.38	2.42	9.63	0.16	1.43	1.13**	4.60*
INL	9.69	5.47	16.49	0.25	2.21	0.41^{ns}	3.51^{ns}
TN	6.59	3.24	10.66	0.22	1.89	0.12^{ns}	2.02**
SD	0.75	0.32	1.23	0.03	0.25	0.31^{ns}	2.33^{ns}
NRP	28.45	8.69	48.89	1.00	8.73	0.19^{ns}	2.39^{ns}
SERHW	2.21	0.38	5.44	0.10	0.91	0.60*	4.05^{ns}
SPY	5.39	2.50	18.7	0.36	3.15	1.69**	7.24**
TGW	3.16	1.73	4.18	0.07	0.61	-0.43^{ns}	2.47^{ns}

ns $P > 0.05$; * $P <= 0.05$; ** $P <= 0.01$

DFF- days to fifty percent flowering, DTM- days to maturity, PH- plant height, FL- length of , FLW- flag leaf width, IFL- inflorescence length, IFW- inflorescence width, LRL- lower raceme length, PDL- peduncle length, NBT- number of basal tillers, INL- internode length, TN- Total nodes, SD- stem diameter, NRP- number of racemes per panicle. SERHW- single-ear head weight, SPY- single plant yield, TGW- thousand-grain weight


A
MDU 1
CO(KV)2
ATL 1
Frequency
0
10
20
30
40
50
60
DFF
B
MDU 1
CO(KV)2
ATL 1
Frequency
0
5
10
15
20
25
70
80
90
100
DTM
C
MDU 1
CO(KV)2
ATL 1
Frequency
0
5
10
15
20
40
60
80
100
PH
D
MDU 1
CO(KV)2
ATL 1
Frequency
0
5
10
15
10
15
20
25
30
FL
E
MDU 1
CO(KV)2
ATL 1
Frequency
0
5
10
15
1.5
2.0
2.5
3.0
FLW
F
MDU 1
CO(KV)2
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Frequency
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I
MDU 1
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Frequency
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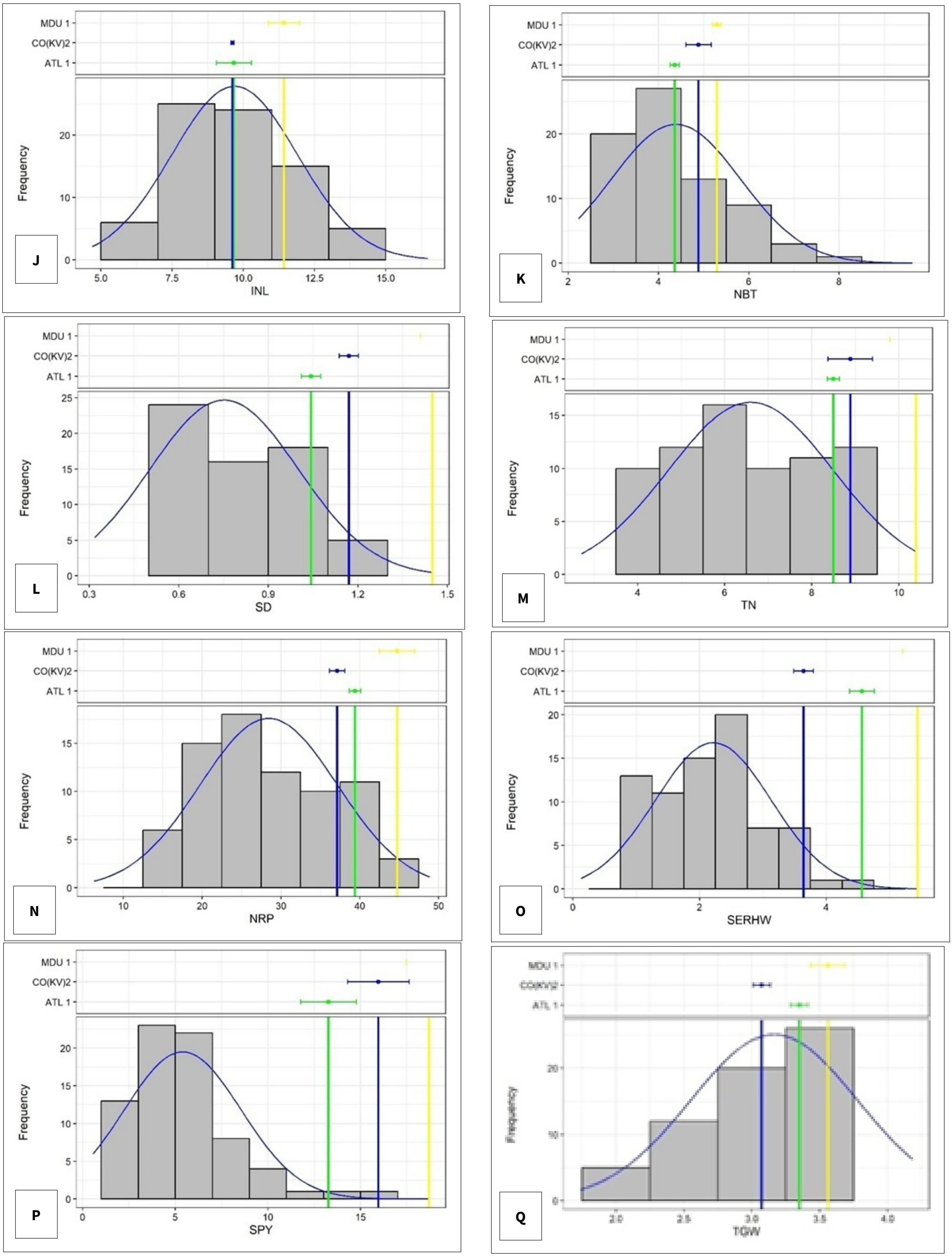
10
20
30
4
8
12
16
PDL



A. DFF- days to 50% flowering, **B**. DTM- days to maturity, **C.** PH- plant height, **D**. FL- flag leaf length, **E**. FLW- flag leaf width, **F**. IFL- inflorescence length, **G.** IFW- inflorescence width, **H.** LRL- lower raceme length, **I.** PDL- peduncle length, **J.** INL- internode length**, K.** NBT- number of basal tillers, **L**. SD- stem diameter, **M.** TN- Total nodes, , **N.** NRP- number of racemes per panicle. **O.** SERHW- single-ear head weight, **P.** SPY- single plant yield, **Q.** TGW- thousand-grain weight

Fig. 1. Frequency distribution of biometrical traits in sodic soil.

traits are governed by fewer genes whereas platykurtic distribution was witnessed for total nodes indicating that these traits are governed by a large number of genes.

Genetic variability parameters

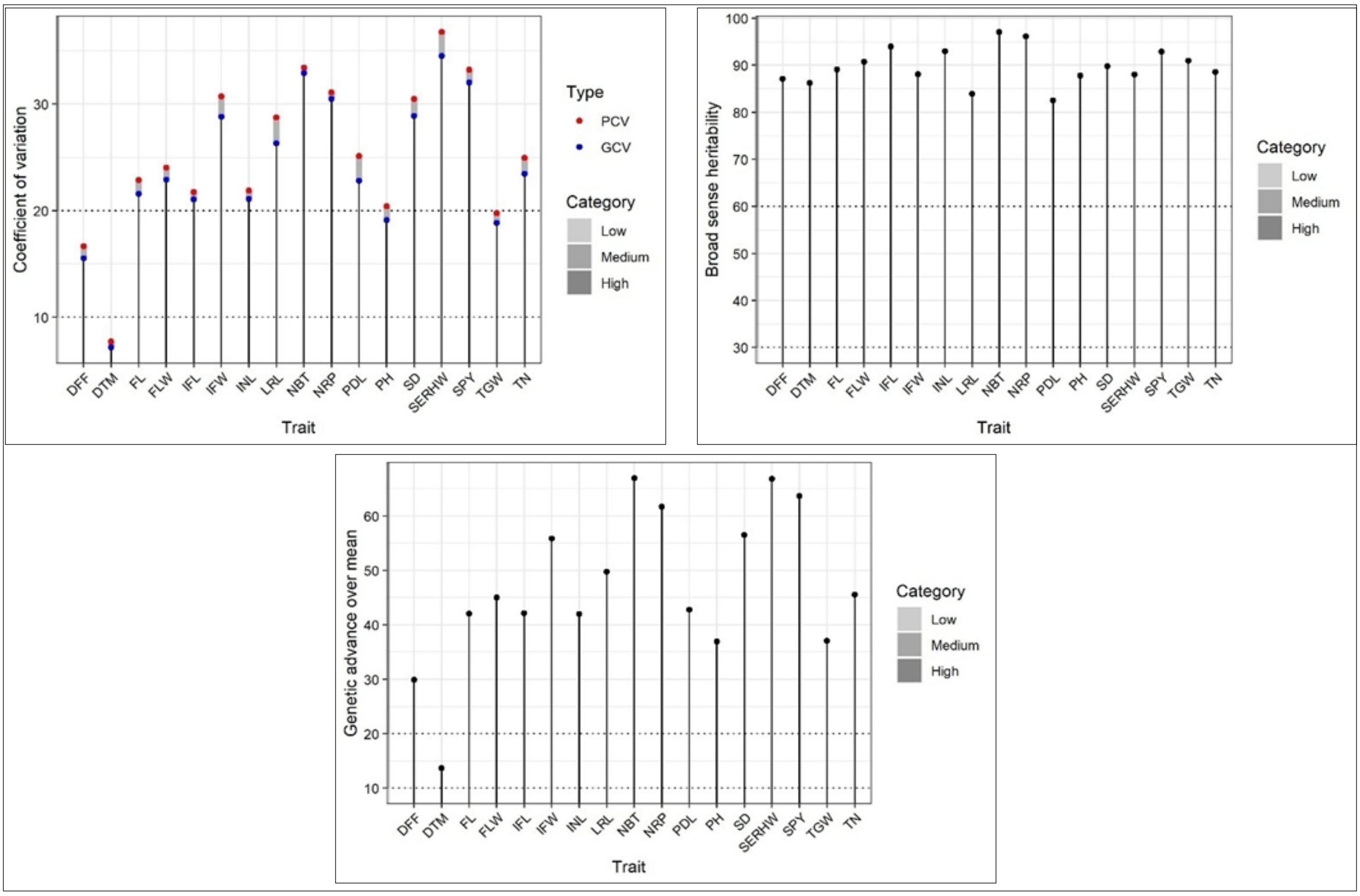
High PCV and GCV values were noted for the length of flag leaf, width of flag leaf, inflorescence length, inflorescence width, peduncle length, length of lower raceme, number of tillers, internode length, total nodes, number of racemes per panicle, stem diameter, single plant yield and single-ear head weight (Fig. 2). It revealed that large amount of variation prevails among germplasm. Similar findings were reported in barnyard millet and little millet earlier (19-20). Low PCV and GCV were noted for days to maturity suggesting that genetic enhancement through trait selection is often ineffective as highlighted by the studies in proso millet (21) and finger millet (22). In the current study, a minimum difference was observed among PCV and GCV indicating that the traits studied are predominantly under genetic control and have minimal environmental impact on their expression. The trait plant height recorded moderate GCV and high PCV which correspond to the results observed in foxtail millet (23). Moderate PCV and GCV are noted for thousand-grain weight and days to fifty per cent flowering which is uniform with the findings of earlier works in barnyard millet (24) and finger millet (25-26). The estimated values of the environmental coefficient of variance (ECV) were less than both PCV and GCV which indicated that there is the least environmental impact on the expression of these traits.

Heritability and genetic advance

The estimated heritability combined with genetic advancement provides a potential value for efficient selection. The germplasm showed high heritability for all characters studied including grain yield per plant and thousand-grain weight under a sodic environment and these findings resembled the outcomes of several reports in barnyard millet (19, 24) and finger millet (27) under sodic soil. High heritability suggests that there is a minimum environmental influence on the expression of these traits (28). Broad sense heritability facilitates selection based on phenotypic expression and may involve both additive and non-additive gene effects such as epistasis and dominance. The trait days to maturity recorded moderate genetic advance while the remaining traits exhibited high genetic advance as a percentage of the mean. Similar findings are documented in barnyard millet (19) and finger millet (27). High heritability and high GAM were observed for nearly all the traits examined, except for the trait days to maturity, which exhibits high heritability and moderate GAM. This indicates that the presence of additive gene action favours the efficient selection of traits.

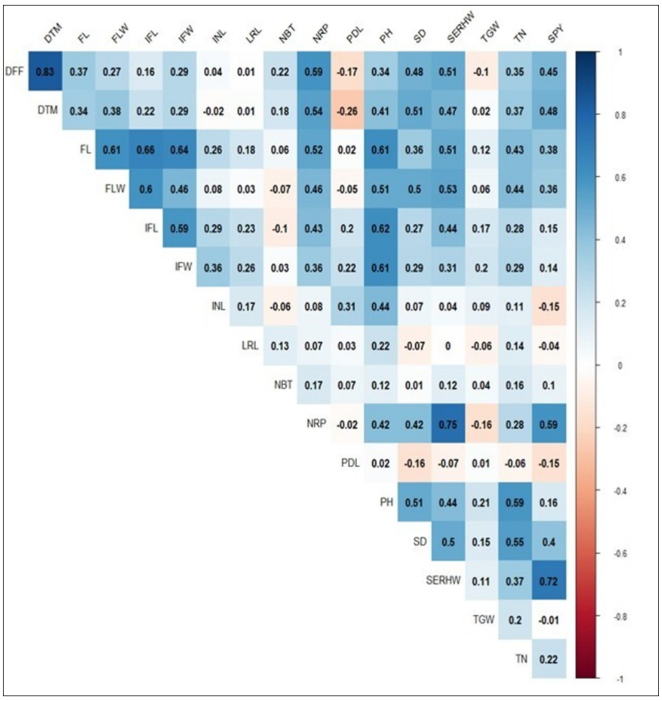
Correlation

Yield, being a complex trait, is influenced by other quantitative traits. Correlation study revealed the inter-relationship between yield and its attributing characters which aid in the improvement of the yield through selection of these attributes. Correlation coefficients for 17 quantitative traits were estimated (Fig. 3). In this study, the grain yield per plant showed a significant and positive correlation with length of flag leaf, days to 50% flowering, width of flag leaf, days to maturity, stem diameter, number of racemes per panicle and single-ear head weight which is identical to the outcome of several researchers in barnyard millet for number of racemes per panicle, stem



PCV- Phenotypic coefficient of variation, GCV- genotypic coefficient of variation

Fig. 2. Genetic variability parameters for biometrical traits in sodic soil.



	DTM	FL	FLW	IFL	IFW	INL	LRL	NBT	NRP	PDL	PH	SD	SERHW	TGW	TN	SPY
DFF	0.83	0.37	0.27	0.16	0.29	0.04	0.01	0.22	0.59	-0.17	0.34	0.48	0.51	-0.1	0.35	0.45
DTM		0.34	0.38	0.22	0.29	-0.02	0.01	0.18	0.54	-0.26	0.41	0.51	0.47	0.02	0.37	0.48
FL			0.61	0.66	0.64	0.26	0.18	0.06	0.52	0.02	0.61	0.36	0.51	0.12	0.43	0.38
FLW				0.6	0.46	0.08	0.03	-0.07	0.46	-0.05	0.51	0.5	0.53	0.06	0.44	0.36
IFL					0.59	0.29	0.23	-0.1	0.43	0.2	0.62	0.27	0.44	0.17	0.28	0.15
IFW						0.36	0.26	0.03	0.36	0.22	0.61	0.29	0.31	0.2	0.29	0.14
INL							0.17	-0.06	0.08	0.31	0.44	0.07	0.04	0.09	0.11	-0.15
LRL								0.13	0.07	0.03	0.22	-0.07	0	-0.06	0.14	-0.04
NBT									0.17	0.07	0.12	0.01	0.12	0.04	0.16	0.1
NRP										-0.02	0.42	0.42	0.75	-0.16	0.28	0.59
PDL											0.02	-0.16	-0.07	0.01	-0.06	-0.15
PH												0.51	0.44	0.21	0.59	0.16
SD													0.5	0.15	0.55	0.4
SERHW														0.11	0.37	0.72
TGW															0.2	-0.01
TN																0.22

DFF- days to 50% flowering, DTM- days to maturity, PH- plant height, FL- flag leaf length, FLW- flag leaf width, IFL- inflorescence length, IFW- inflorescence width, LRL- lower raceme length, PDL- peduncle length, NBT- number of basal tillers, INL- internode length, TN- Total nodes, SD- stem diameter, NRP- number of racemes per panicle. SERHW- single-ear head weight, SPY- single plant yield, TGW- thousand-grain weight

Fig. 3. Correlation coefficient for different biometrical traits under sodic soil.

diameter, days to maturity and single-ear head weight (19, 29). Correlation between days to 50% flowering and days to maturity was found to be significant and positive with each other. The trait number of racemes per panicle showed a significant and strong correlation with single-ear head weight. Identification of the existence of inter-relationships among various traits from the genetic evaluation is expected to devise trait selection strategies for the simultaneous development of traits, particularly under sodicity stress.

Path coefficient analysis

Path analysis splits the correlation coefficient into indirect and direct effects. It provides information about the relationship between dependent and independent factors and the contribution of independent attributes on single plant yield. The computed coefficients were classified into different categories *viz*., high, moderate, very high, low and negligible based on the scales suggested earlier (30). Among the 17 attributes studied, length of flag leaf, days to maturity and single-ear head weight exhibit high positive direct effects on single plant yield (Table 4). Various studies have reported similar findings regarding days to maturity and single-ear head weight in barnyard millet (19, 31). A negligible negative direct effect was noted for the width of the flag leaf, inflorescence width, plant height, internode length, number of basal tillers, thousand-grain weight and total nodes. Whereas negligible positive direct effect was noted for the length of lower raceme, number of racemes and peduncle length. The trait days to 50% flowering exhibited a moderate negative direct effect towards grain yield per plant. The residual effect was found to be 0.5868 which indicated that 58.68% of variability was unnoticed and this implied that other characters might also play a role in enhancing the yield.

Principal component analysis (PCA)

The PCA is a method used to decrease the dimensionality of a multivariable dataset into a reduced number of principal axes to evaluate the significance and contribution of each factor to the total variation. A scree plot (Fig. 4) was created by plotting the principal components against their corresponding eigenvalues. It revealed that five significant principal components having eigenvalues more than one explained 70.19% of the total variation which is consistent with reports in finger millet (32). The contribution of seventeen biometrical traits to total variation is outlined in Table 5.

Table 4. Path analysis showing direct and indirect effects of yield contributing traits towards single plant yield

Trait	DFF	DTM	FL	FLW	IFL	IFW	INL	LRL	NBT	NRP	PDL	PH	SD	SERHW	TGW	TN	SPY
DFF	**-0.2519**	0.3143	0.1203	-0.0144	-0.0422	-0.0085	-0.0035	0.0002	-0.0088	0.0415	-0.0080	-0.0681	0.0509	0.3426	0.0041	-0.0166	0.452**
DTM	-0.2100	**0.3771**	0.1118	-0.0201	-0.0594	-0.0085	0.0017	0.0005	-0.0073	0.0380	-0.0122	-0.0818	0.0540	0.3137	-0.0009	-0.0176	0.479**
FL	-0.0930	0.1294	**0.3258**	-0.0321	-0.1770	-0.0190	-0.0257	0.0069	-0.0023	0.0367	0.0009	-0.1216	0.0378	0.3407	-0.0050	-0.0207	0.382**
FLW	-0.0689	0.1436	0.1983	**-0.0527**	-0.1600	-0.0135	-0.0078	0.0011	0.0028	0.0323	-0.0023	-0.1012	0.0535	0.3544	-0.0025	-0.0210	0.356**
IFL	-0.0397	0.0837	0.2154	-0.0315	**-0.2677**	-0.0174	-0.0283	0.0087	0.0038	0.0303	0.0092	-0.1232	0.0289	0.2953	-0.0074	-0.0134	0.147
IFW	-0.0722	0.1084	0.2096	-0.0241	-0.1573	**-0.0296**	-0.0356	0.0100	-0.0011	0.0255	0.0103	-0.1214	0.0306	0.2071	-0.0084	-0.0140	0.138
INL	-0.0089	-0.0067	0.0855	-0.0042	-0.0774	-0.0108	**-0.0980**	0.0063	0.0025	0.0056	0.0143	-0.0882	0.0072	0.0302	-0.0039	-0.0054	-0.152
LRL	-0.0015	0.0045	0.0591	-0.0015	-0.0614	-0.0077	-0.0162	**0.0381**	-0.0051	0.0049	0.0014	-0.0435	-0.0075	0.0025	0.0027	-0.0066	-0.038
NBT	-0.0556	0.0695	0.0190	0.0037	0.0259	-0.0008	0.0062	0.0049	**-0.0397**	0.0116	0.0034	-0.0234	0.0011	0.0825	-0.0017	-0.0077	0.099
NRP	-0.1490	0.2042	0.1705	-0.0242	-0.1155	-0.0107	-0.0078	0.0027	-0.0066	**0.0702**	-0.0011	-0.0840	0.0448	0.5056	0.0069	-0.0132	0.593**
PDL	0.0430	-0.0982	0.0063	0.0025	-0.0527	-0.0065	-0.0299	0.0012	-0.0029	-0.0016	**0.0467**	-0.0042	-0.0166	-0.0441	-0.0005	0.0027	-0.155
PH	-0.0863	0.1551	0.1993	-0.0268	-0.1659	-0.0181	-0.0435	0.0083	-0.0047	0.0297	0.0010	**-0.1988**	0.0537	0.2949	-0.0087	-0.0282	0.161
SD	-0.1208	0.1918	0.1160	-0.0266	-0.0727	-0.0085	-0.0066	-0.0027	-0.0004	0.0296	-0.0073	-0.1004	**0.1062**	0.3372	-0.0063	-0.0266	0.402**
SERHW	-0.1281	0.1756	0.1648	-0.0277	-0.1173	-0.0091	-0.0044	0.0001	-0.0049	0.0527	-0.0031	-0.0870	0.0532	**0.6736**	-0.0048	-0.0176	0.716**
TGW	0.0246	0.0080	0.0385	-0.0032	-0.0466	-0.0059	-0.0090	-0.0025	-0.0016	-0.0114	0.0006	-0.0410	0.0159	0.0771	**-0.0423**	-0.0097	-0.008
TN	-0.0872	0.1382	0.1407	-0.0231	-0.0751	-0.0087	-0.0110	0.0053	-0.0064	0.0194	-0.0027	-0.1172	0.0589	0.2469	-0.0085	**-0.0479**	0.222

* P <= 0.05; ** P <= 0.01 Residual effect: 0.586

Table 5. Contribution of principal components to total variation

Traits	PC1	PC2	PC3	PC4	PC5
DFF	0.663	-0.446	0.225	0.202	-0.059
DTM	0.686	-0.434	0.064	0.224	-0.118
FL	0.781	0.263	0.031	-0.142	-0.049
FLW	0.725	0.094	-0.235	-0.281	-0.108
IFL	0.660	0.487	-0.020	-0.278	-0.039
IFW	0.644	0.488	0.096	-0.003	-0.012
INL	0.237	0.615	0.151	0.091	0.032
LRL	0.157	0.340	0.447	0.248	-0.476
NBT	0.142	-0.163	0.444	0.608	0.378
NRP	0.758	-0.252	0.327	-0.245	0.088
PDL	-0.047	0.527	0.344	-0.128	0.561
PH	0.766	0.367	-0.083	0.230	-0.102
SD	0.681	-0.198	-0.361	0.134	-0.021
SEHW	0.777	-0.254	0.028	-0.226	0.256
TGW	0.139	0.264	-0.580	0.333	0.418
TN	0.617	0.049	-0.270	0.418	-0.073
SPY	0.580	-0.500	0.070	-0.260	0.220
Eigen value	5.97	2.36	1.32	1.26	1.03
% of variance	35.09	13.91	7.75	7.40	6.05
cumulative % of variance	35.09	48.99	56.74	64.14	70.19

DFF- days to 50% flowering, DTM- days to maturity, PH- plant height, FL- flag leaf length, FLW- flag leaf width, IFL- inflorescence length, IFW- inflorescence width, LRL- lower raceme length, PDL- peduncle length, NBT- number of basal tillers, INL- internode length, TN- Total nodes, SD- stem diameter, NRP- number of racemes per panicle. SERHW- single-ear head weight, SPY- single plant yield, TGW- thousand-grain weight

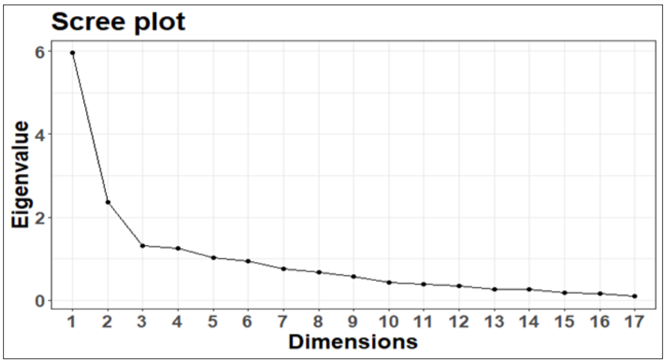


Fig. 4. Scree plot for different principal components in barnyard millet germplasm.

The principal component (PC1) explained 35.08% of the total variation, with the highest factor loading shared by the length of the flag leaf (0.781), followed by plant height (0.766) and single-ear head weight (0.777). Subsequently, the principal components (PC2, PC3, PC4 and PC5) contributed 13.91%, 7.75%, 7.40% and 6.05% to the total variation, respectively. The highest loadings for PC2 (0.527) and PC5 (0.561) were contributed by peduncle length. The trait number of basal tillers contributed the highest loadings for PC3 (0.444) and PC4 (0.608). The principle of factor loading identifies the significant variables that explain the variation captured by each principal component.

Based on five significant principal components the traits *viz*., length of flag leaf (0.781) followed by days to fifty per cent flowering (0.663), width of flag leaf (0.725), single-ear head weight (0.777), number of racemes per panicle (0.758), days to maturity (0.686), number of tillers (0.608), plant height (0.766) and single plant yield (0.582) have contributed more variation to the entire germplasm. Similar trends were reported for days to 50% flowering, width of flag leaf, days to maturity and plant height in barnyard millet (33).

PCA biplot analysis (Fig. 5) indicated that the first two principal axes PC1 (35.1%) and PC2 (13.9%) contributed about 49% of the total variation. The vector (trait) located in the first quadrant exhibits higher positive PC1 and PC2 components revealing that these genotypes have elevated values for plant height, length of flag leaf, inflorescence length, internode length, width of flag leaf, inflorescence width and total nodes. The genotypes located in the second quadrant exhibited positive PC1 values and negative PC2 values with elevated trait vectors for days to 50% flowering, stem diameter, number of racemes per panicle, single-ear head weight, number of tillers, days to maturity and grain yield per plant. The trait peduncle length located in the fourth quadrant has negative PC1 values and positive PC2 values. The results are interpreted from the findings reported in rice (34).

Hierarchical cluster analysis

In the cluster analysis, the genotypes were classified into different groups (Fig. 6). Based on the Wards method, the germplasm was categorized into five clusters (Table 6). Similarly, clustering was reported in barnyard millet (33) and rice (34). Among the five clusters, cluster III is the largest cluster comprising 20 genotypes, while cluster I was the smallest with 7 genotypes.

The computed cluster means and cluster distance were used to analyse the genotypes present in each cluster and their application in the breeding programme. The intra-cluster distance value ranged from 6.69 to 7.34 (Table 7). The cluster III (7.34) and cluster IV (6.69) exhibited maximum and minimum distance, respectively. In the case of inter-cluster distance, the maximum distance (14.42) was noted between clusters I and V while the minimum distance (7.59) was noted between clusters II and III. Crossing between the genotypes of diverse clusters leads to the production of beneficial transgressive segregants with high tolerance to sodicity coupled with better yield.

Cluster I recorded maximum cluster means (Table 8) for yield attributing traits such as day to maturity (96.95), number of tillers (4.99), number of racemes per panicle (42.25), days to fifty per cent flowering (61.22) and single plant yield (12.64). The accessions of cluster I *viz*., GECH 863, IC0404347, IC0404395, IC0404413 and check varieties MDU1, ATL1, CO(KV)2 were of late maturing with more tillers and high yield. Hence, this high-performing germplasm can be used as a potential parent in the hybridization programme for enhancing the yield of barnyard millet under sodic soil. A similar trend was reported for a number of tillers in barnyard millet (32). Subsequently, cluster V recorded the lowest cluster mean for day to fifty per cent flowering suggesting the possibility of developing early maturing

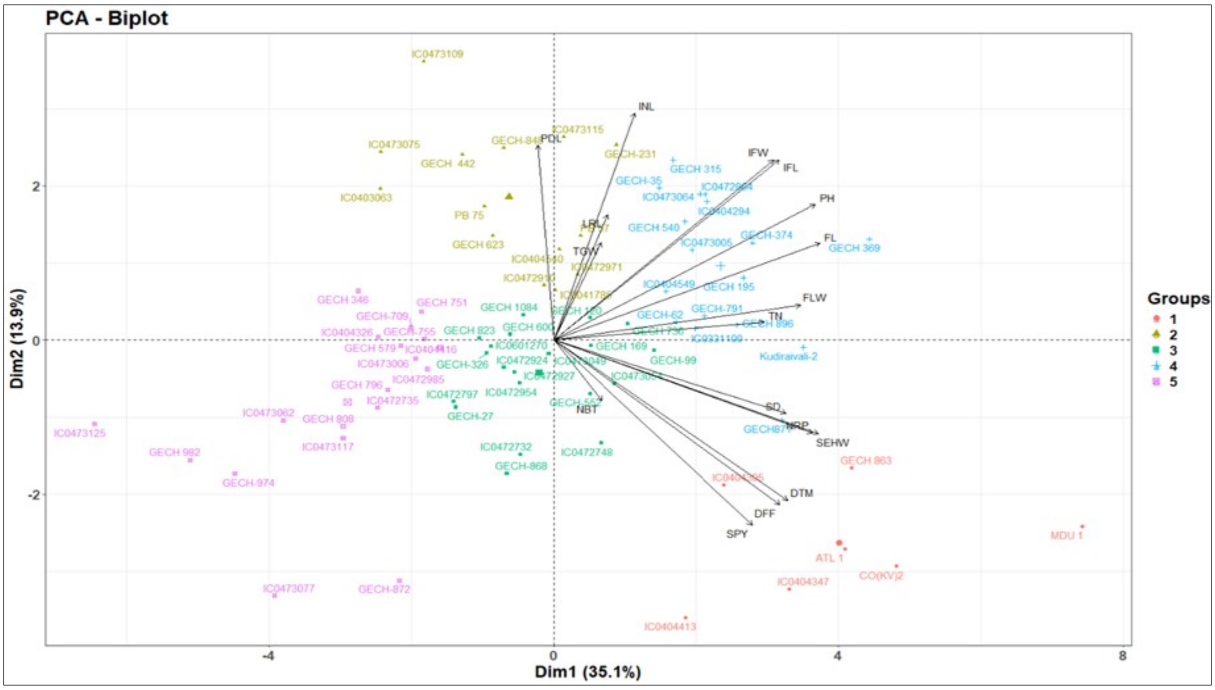


Fig. 5. PCA biplot of variables showing the contribution of various traits to variation in PC1 and PC2.

Table 6. Clustering of barnyard millet genotypes into five clusters based on wards method

Clusters	No. of. genotypes	Accessions
I	7	ATL 1, CO(KV)2, GECH 863, IC0404347, IC0404395, IC0404413, MDU 1
II	14	GECH-231, GECH-848, GECH 442, GECH 623, IC0041785, IC0403063, IC0404540, IC0472910, IC0472971, IC0473075, IC0473109, IC0473115, PB 57, PB 75
III	20	GECH-27, GECH-326, GECH-552, GECH-868, GECH-99, GECH 1084, GECH 120, GECH 169, GECH 600, GECH 736, GECH 823, IC0472732, IC0472748, IC0472797, IC0472924, IC0472927, IC0472954, IC0473049, IC0473054, IC0601270
IV	17	GECH-35, GECH-374, GECH-62, GECH-791, GECH 195, GECH 315, GECH 369, GECH 540, GECH 896, GECH871, IC0331100, IC0404294, IC0404549, IC0472864, IC0473005, IC0473064, Kudiraivali-2
V	19	GECH-709, GECH-755, GECH-872, GECH-974, GECH 346, GECH 579, GECH 751, GECH 796, GECH 808, GECH 982, IC0404326, IC0404416, IC0472735, IC0472985, IC0473006, IC0473062, IC0473077, IC0473117, IC0473125

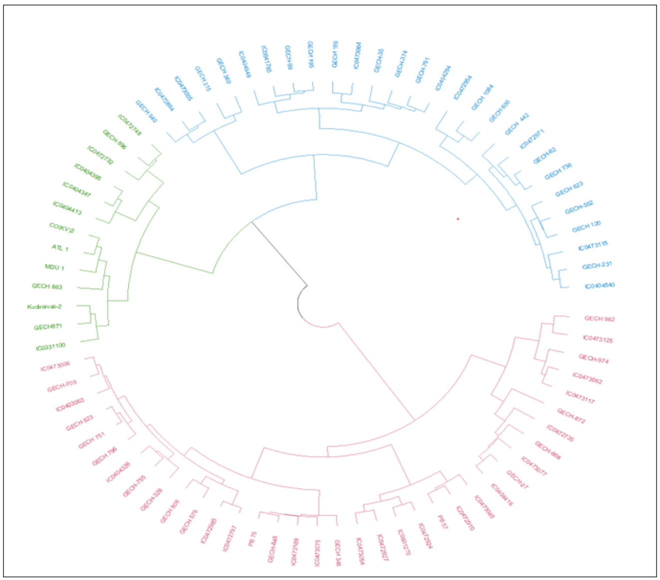


Fig. 6. Dendrogram depicting different clusters of barnyard millet germplasm based on hierarchical cluster analysis.

Table 7. Mean intra- and inter-cluster Euclidean distances among various barnyard millet genotypes

Clusters	I	II	III	IV	V
I	**6.87**				
II	11.60	**6.89**			
III	10.10	7.57	**7.34**		
IV	8.53	8.22	7.59	**6.69**	
V	14.42	9.48	9.21	11.45	**7.27**

Table 8. Cluster means for seventeen metric traits in barnyard millet germplasm

Character	I	II	III	IV	V
DFF	61.22	40.38	43.40	46.32	38.78
DTM	96.95	79.42	84.75	88.19	80.38
FL	22.57	19.67	18.17	23.33	14.60
FLW	2.60	2.05	2.28	2.66	1.71
IFL	14.80	15.46	13.86	17.14	10.87
IFW	3.29	3.70	2.95	4.21	2.16
INL	9.23	11.85	8.93	10.62	8.23
LRL	2.50	3.03	2.53	3.04	2.58
NBT	4.99	4.04	4.36	4.56	4.26
NRP	42.25	26.03	28.98	32.61	20.84
PDL	7.41	11.29	8.23	8.77	8.22
PH	80.50	72.26	72.14	90.79	56.72
SD	1.08	0.61	0.79	0.88	0.57
SEHW	3.85	1.92	2.38	2.46	1.42
TGW	3.03	3.22	3.20	3.24	3.04
TN	8.57	5.89	6.06	8.11	5.58
SPY	12.64	3.71	4.73	5.43	4.61

DFF- days to 50% flowering, DTM- days to maturity, PH- plant height, FL- flag leaf length, FLW- flag leaf width, IFL- inflorescence length, IFW- inflorescence width, LRL- lower raceme length, PDL- peduncle length, NBT- number of basal tillers, INL- internode length, TN- Total nodes, SD- stem diameter, NRP- number of racemes per panicle. SERHW- single-ear head weight, SPY- single plant yield, TGW- thousand-grain weight genotypes. Meanwhile, cluster IV has the highest cluster mean for the thousand-grain weight (3.24) with the added advantage of further improvement in grain yield.

Conclusion

In conclusion, the selection of traits such as single-ear head weight, days to maturity, days to 50% flowering and number of racemes per panicle can contribute to yield improvement in barnyard millet under sodic soil. Three genotypes namely GECH 863, IC0404347 and IC0473049 stand out as the best performing in terms of single plant yield and tillering ability. Hence, these best-performing genotypes can be utilized as parents in plant breeding programmes for developing sodicity-tolerant cultivars.

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Authors' contributions

SM carried out the experiments, analysed the data and wrote the draft manuscript; SK conceived the idea and designed the experiment and revised the draft; CV and PJ designed experimental analysis, data representation, manuscript correction; TR, SG, PS, SR guided the lab and fieldwork, data visualization and data analysis. AA designed experiments and arranged seed material. All authors read and approved the final manuscript.

Compliance with ethical standards

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

Ethical issues: None

Declaration of generative AI and AI-assisted technologies in the writing process

During the preparation of this manuscript, the authors used Grammarly and ChatGpt to improve the language and readability of the text and not for content writing and interpretation of results in the manuscript. After using these tools, the authors reviewed and edited the content as needed and take full responsibility for the content of the publication.

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