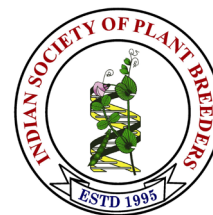


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Research Article

Principal component analysis of foxtail millet accessions under rainfed condition

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Abstract

Foxtail millet (*Setaria italica* (L.) Beauv) is one of the earliest cultivated millet for grain, hay and silage. There is wide genetic diversity available in foxtail millet and characterization of available germplasm is a pre-requisite for the genetic improvement of any crop. Keeping the above fact in view 30 foxtail germplasm lines were evaluated during *kharif* 2020 and 2021 for morphological traits, stover yield, dry fodder yield and seed yield under rainfed conditions of Haryana. The results (based on pooled data of two years) revealed that enough variability was present among germplasm lines for further exploitation. High heritability and positive correlation was reported between traits like plant height, leaf length, leaf stem ratio, stover yield, grain yield etc. Principal component analysis also revealed that PC1, PC2, PC3, PC4 and PC5 contributed for 31.8%, 15.05%, 12.31%, 11.43% and 10.14%, respectively to the total variation. Five foxtail accessions viz., SEA8, SEA12, SEA48, SEJ184 and SEA37 were identified promising for yield and related traits under rainfed conditions of Haryana.

Keywords: Foxtail millet, GCV, PCV, PCA, Correlation

INTRODUCTION

Foxtail millet or *Kangni* is the earliest cultivated cereal grain and world's second largest produced millet after pearl millet. Millets are eco-friendly crops with lower requirements of water, agro-chemicals and management practices for raising the crop (Sukanya *et al.*, 2023). It has multiple uses like food, feed and fodder. It is a diploid ($2n = 18$) crop having genome size of approximately 423 Mbps (Zhang *et al.*, 2012) and belongs to family Poaceae with some closely related tetraploid and polyploid species (Baltensperger and Cai, 2004). It is a self pollinated crop with only four percent out crossing. The primary centre of diversity for foxtail millet is East India, including China and Japan. In Central Europe it is cultivated as a summer crop (Panaud, 2006) for use as hay and silage. The name of this taxon evolved as the panicle shape of this millet has resemblance with the tail of fox in appearance. It is

an annual grass with leafy stem, profuse tillering and plant height ranging from 120-200 cm. It has dense, hairy panicle of 30 cm length. Its seed is small, having huge variation in seed colour. Foxtail millet is a perfect cereal and has an important place in the world agriculture which would help to enhance nutritional and food security in near future (Sharma and Niranjana, 2018). It is very adaptive crop and can grow from sea level up to an altitude of 2000m.

In India, it is mainly grown in the states of Uttar Pradesh, Madhya Pradesh, Bihar, Rajasthan, Andhra Pradesh, Telangana, Maharashtra, Karnataka and Tamil Nadu. The foxtail millet grain is rich in protein (11.2 g) and iron (2.8 mg) per 100 gm, good source of β -carotene (Vitamin A precursor) (Murugan and Nirmalakumari, 2006) and has

low glycemic index (GI). Foxtail millet potential is not yet fully exploited due to main focus on improvement of cash crops. This might be the reason for the non-availability of location/ region specific improved varieties/hybrids of foxtail millet with higher yield and quality. Especially in Northern India productivity of foxtail millet is very low due to the lack of suitable genotypes. Core and mini core collections are reservoirs of diversity for these crops and use of genomic tools help to identify new sources of variation (Vetriventhan *et al.*, 2016)

Since qualitative traits are being more stable over generations (Raut, 2003) they are reliable for characterization of germplasm. Characterization of germplasm is also useful for identification and removal of duplicates. Foxtail millet is a model species to study evolutionary genomics, plant morphological and physiological traits of the C_4 Panicoid crop (Vetriventhan *et al.*, 2016). Local varieties or traditional landraces are still under cultivation which are poor yielders and susceptible to biotic and abiotic stresses. Selection of appropriate parental line is most important for breeding experiments to improve genetic background of any genotype (Singh and Kumar, 2004). Its further evaluation at multi-locations is another pre-requisite for its use in breeding programs.

Crop yield is a complex trait which is affected by interaction of genotype and environmental components directly and indirectly (Shi *et al.*, 2009). In conventional plant breeding program, direct selection for yield may be sometimes misleading for crops thus indirect selection may supplement the selection criteria and that would be more reliable. The most widely used approach is use of morphological traits to estimate relationships between genotypes. The genetic variability present among landraces, wild relatives and cultivated species/varieties (Kumari *et al.*, 2016) of a crop forms a potential and continued source of genes for the development of improved varieties/hybrids. A better understanding of genetic diversity in foxtail millet will further facilitate improvement in yield and quality of this crop. Keeping the above facts in view, the present study was carried out to

determine the extent of genetic diversity among foxtail millet germplasm lines for various traits.

MATERIALS AND METHODS

Thirty foxtail germplasm lines procured from IIMR, Hyderabad and ICRISAT, Hyderabad (**Table 1**) were evaluated for biomass yield, grain yield and other morphological traits at the Research Area of Forage Section, CCS HAU, Hisar, Haryana. These germplasm accessions were raised in 2 rows of 2 meter length with 0.25m row to row spacing in RBD design with three replications under rainfed conditions during 2020 and 2021 seasons. No irrigation was given and the crop was totally under rainfed. Weather data for two crop seasons 2020 and 2021 are furnished in **Figs.1 & 2**. Crop was protected from weeds, pests and diseases with appropriate management practices. Data was recorded on five competitive plants in both the years at the stage of 50% flowering from every genotype for plant height (PH; cm), leaf length (LL; cm), leaf breadth (LB; cm), leaf:stem ratio (L/S), number of leaves/plant (NL), number of tillers/plant (NT), panicle length (PL; cm), internode length (IL; cm); stover yield (SY; q/ha) and grain yield (GY; q/ha) was recorded at grain maturity and for estimation of dry fodder yield (DFY; q/ha) 500 g sample of green fodder was taken at the stage of 50% flowering and after sun drying DFY was calculated. Data of both years was pooled and then subjected to ANOVA (analysis of variance) as described by (Panse and Sukhatme, 1967). Genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h^2) and genetic advance was estimated as per Singh and Choudhury (1979). Correlation coefficient analysis and PCA analysis was done using the statistical software (GRAPES) General R-shiny based Analysis Platform Empowered by Statistics.

RESULTS AND DISCUSSION

Germplasm collection and its evaluation for promising traits is the preliminary step for any crop improvement program. In conventional breeding methods morphological markers are used for screening of large number of crop accessions but use of molecular markers is most commonly used

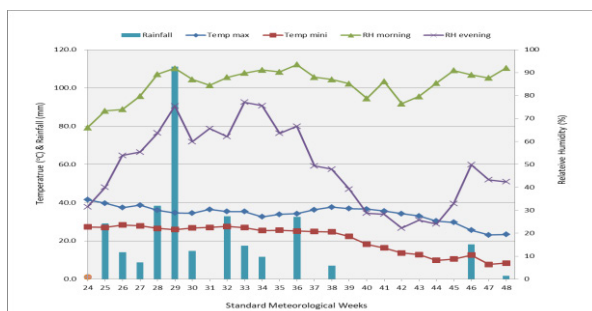


Fig. 1. Weather data for crop season of 2020

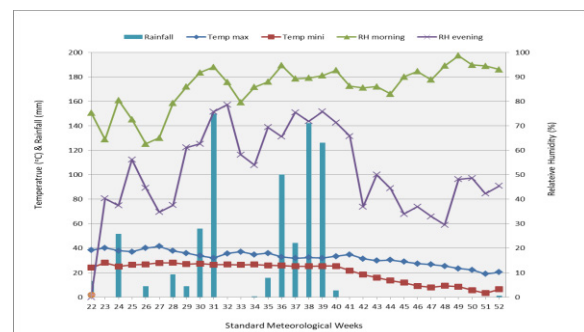


Fig. 2. Weather data for crop season of 2021

Table 1. Pedigree details of genotypes used in study

S. No.	Foxtail germplasm lines	Botanical name	Cultivar/Wild	IC No	District	State
1	SEJ 29	<i>Setaria viridis</i>	Cultivar	IC-0628926	Koraput	Odisha
2	SEJ 47	<i>Setaria italica</i>	Cultivar	IC-0628935	Koraput	Odisha
3	ESJ 166	<i>Eleusine coracana</i>	Cultivar	IC-0628973	Kalahandi	Odisha
4	SEJ 184	<i>Eleusine coracana</i>	Cultivar	IC-0628974	Kalahandi	Odisha
5	SEA 5	<i>Setaria italica</i>	Cultivar	-	Prakasam	Andhra Pradesh
6	SEA 8	<i>Setaria italica</i>	Cultivar	-	Prakasam	Andhra Pradesh
7	SEA 12	<i>Setaria italica</i>	Cultivar	IC-0627116	Prakasam	Andhra Pradesh
8	SEA 15	<i>Setaria italica</i>	Cultivar	IC-0627118	Prakasam	Andhra Pradesh
9	SEA 37	<i>Setaria italica</i>	Cultivar		Prakasam	Andhra Pradesh
10	SEA 41	<i>Setaria italica</i>	Cultivar	IC-0627134	Prakasam	Andhra Pradesh
11	SEA 48	<i>Setaria italica</i>	Cultivar	IC-0627141	Prakasam	Andhra Pradesh
12	SEA 51	<i>Setaria italica</i>	Cultivar	IC-0627144	Prakasam	Andhra Pradesh
13	EN 53	<i>Setaria italica</i>	Cultivar		Thiruvavannamalai	Tamil Nadu
14	EN 101	-	-	-	-	-
15	EN 284	-	-	-	-	-
16	ESD 42	<i>Setaria italica</i>	Landrace	IC 0618630	Nandurbar	Maharashtra
17	ESD 46	<i>Setaria italica</i>	Cultivar	IC 0618634	Nandurbar	Maharashtra
18	ESD 49	<i>Setaria italica</i>	Cultivar	IC 0618636	Nandurbar	Maharashtra
19	ESD 67	<i>Setaria italica</i>	Landrace	IC 0618650	Nandurbar	Maharashtra
20	ESD 71	<i>Setaria italica</i>	Landrace	IC 0618654	Nandurbar	Maharashtra
21	ESD 91	<i>Setaria italica</i>	Landrace	IC 0618672	Nandurbar	Maharashtra
22	ESD 95	<i>Setaria italica</i>	Landrace	IC 0618676	Nandurbar	Maharashtra
23	ESD 100	<i>Setaria italica</i>	Landrace	IC 0618680	Nandurbar	Maharashtra
24	ESD 114	<i>Setaria italica</i>	Primitive cultivar	IC 0618687	Nandurbar	Maharashtra
25	ESD 121	<i>Setaria italica</i>	Landrace	IC 0618693	Dhule	Maharashtra
26	Ise 375	<i>Setaria italica</i>	Landrace	-	-	-
27	Ise1060	<i>Setaria italica</i>	Landrace	-	-	-
28	Ise909	<i>Setaria italica</i>	Landrace	-	-	-
29	Ise869	<i>Setaria italica</i>	Landrace	-	-	-
30	Ise 1468	<i>Setaria italica</i>	Landrace	-	-	-

technique in advance breeding program which gives quick, easy and reliable results. Diverse germplasm accessions give us immense opportunity for selection of trait specific donor lines for genetic improvement of foxtail millet effectively.

For all the accessions, mean sum of squares were highly significant for all the eleven traits under study based on pooled data (Table 2). This indicated that the prevalence of enough genetic variability in the material evaluated for selection and we can use these germplasm accessions in foxtail improvement. This also indicated suitability of data for further statistical analysis for all the characters. Among the eleven traits, the largest variation was observed for number of tillers per plant with the coefficient of variation

17.51 per cent, followed by leaf breadth (8.05%), panicle length (7.59%). Least coefficient of variation (3.56 per cent) was observed for leaf stem ratio. While cataloguing the germplasm lines of foxtail millet, similar results were obtained by Mokkaraj and Geethanjali, 2016.

High PCV was observed for plant height, leaf length, leaf breadth, number of leaves per plant, number of tillers per plant, panicle length, internode length, stover yield, dry fodder yield and grain yield while leaf stem ratio recorded moderate PCV (Table 3). High GCV was reported for plant height, leaf length, number of tillers/plant, panicle length, internodes length, dry fodder yield, stover yield and grain yield. Moderate GCV was reported for leaf stem ratio, number of leaves and leaf breadth. High heritability values 0.829-1.00 was reported for all the traits related to

Table 2. Analysis of variance (pooled data)

SV	DF	PH	LL	LB	PL	NT	NL	L/S	IL	SY	DFY	GY
Replication	2	101.956	220.82	0.177	19.821	11.356	40.267	0.044	2.778	1,541.27	2,073.09	964.289
Treatment	29	39,965.8*	6,620.49*	17.801*	1,673.54**	1100.622*	1072.23* 0.16*		783.242**	2,08,846.77*	1,85,008.46*	29,048.99*
Error	58	1,128.71	395.84	2.236	121.865	141.311	92.4	0.015	38.822	3,312.07	2,416.24	992.378
Total	89	41,196.4	7,237.1	20.214	1,815.23	1253.28	1204.9	0.219	824.84	2,13,700.10	1,89,497.79	31,005.66

*significant at 5% level; ** significant at 1% level

DF: degree of freedom; PH: plant height; LL: leaf length; LB: leaf breadth; PL: panicle length; NT: number of tillers; NL: number of leaves; L/S: leaf stem ratio; IL: internode length; SY: stover yield; DFY: dry fodder yield; GY: grain yield

Table 3. Estimates for GCV, PCV, heritability and genetic advance (% of mean) for various characters (pooled data)

Traits	PCV (%)	GCV (%)	Heritability (h ²)	Genetic advance GAM (%) (i=5%)
PH	26.411	25.862	0.959	52.166
LL	22.551	21.576	0.915	42.524
LB	19.692	17.951	0.831	33.708
PL	23.813	22.568	0.898	44.061
NT	42.399	38.612	0.829	72.436
NL	19.993	18.766	0.881	36.285
L/S	10.020	10.020	1.000	20.641
IL	29.677	28.607	0.929	56.806
SY	22.321	22.058	0.977	44.905
DFY	33.014	32.694	0.981	66.694
GY	21.280	20.746	0.950	41.665

DF: degree of freedom; PH: plant height; LL: leaf length; LB: leaf breadth; PL: panicle length; NT: number of tillers; NL: number of leaves; L/S: leaf stem ratio; IL: internode length; SY: stover yield; DFY: dry fodder yield; GY: grain yield

fodder yield and seed yield. High genetic advance was reported for number of tillers per plant (72.43), dry fodder yield (66.69), internode length (56.80) and plant height (52.16) whereas rest of the traits exhibited moderate genetic advance. High genetic advance coupled with high heritability for the above traits indicates that variation observed for most of the traits was heritable and greater chances of inheritance of these traits from parents to offspring and selection would be effective for improvement of these traits (Singh *et al.*, 2023). This is conformity with the findings of Reddy *et al.* (2015) and Ramesh *et al.* (2017).

Strong positive and significant correlation was observed between stover yield and dry fodder yield. Plant height was positively correlated with leaf length (0.65*), leaf breadth (0.46*), panicle length (0.40*), stover yield (0.36*), dry fodder yield (0.36*) and grain yield (0.27*) (Figure 1). Leaf length was positively correlated with leaf breadth (0.53*), panicle length (0.38*), stover yield (0.30*), dry fodder yield (0.30*) and grain yield (0.52*). Panicle length was positively correlated with internode length (0.41*), stover yield (0.37*) and dry fodder yield (0.37*) (Fig. 3).

The positive correlation of yield and its traits indicates that these characters are governed by additive gene action and could be improved simultaneously and increase in any one of them would lead to improvement of other related trait directly. Results obtained by Nandini *et al.* (2018) and Shingane *et al.* (2016) were also in agreement with the findings of present investigation. However for plant height with L/S ratio (-0.17), no. of tillers with leaf breadth (-0.19) significant negative correlations were also observed. Similar negative correlations have also been reported by Thippeswamy *et al.* (2017).

Principal component analysis is an important approach to study the importance and contribution of each component to total variability and every coefficient of eigen vectors which helps to study the degree of contribution of original variable to each principal component. It retains all crucial information from the original data set and helps to reduce duplication in experimental data (Amy and Pritts, 1991). The principal components and eigen values of 30 genotypes were estimated and PC1 was the largest contributing principal component, followed by PC 2 to PC 11. Principal component analysis indicated that

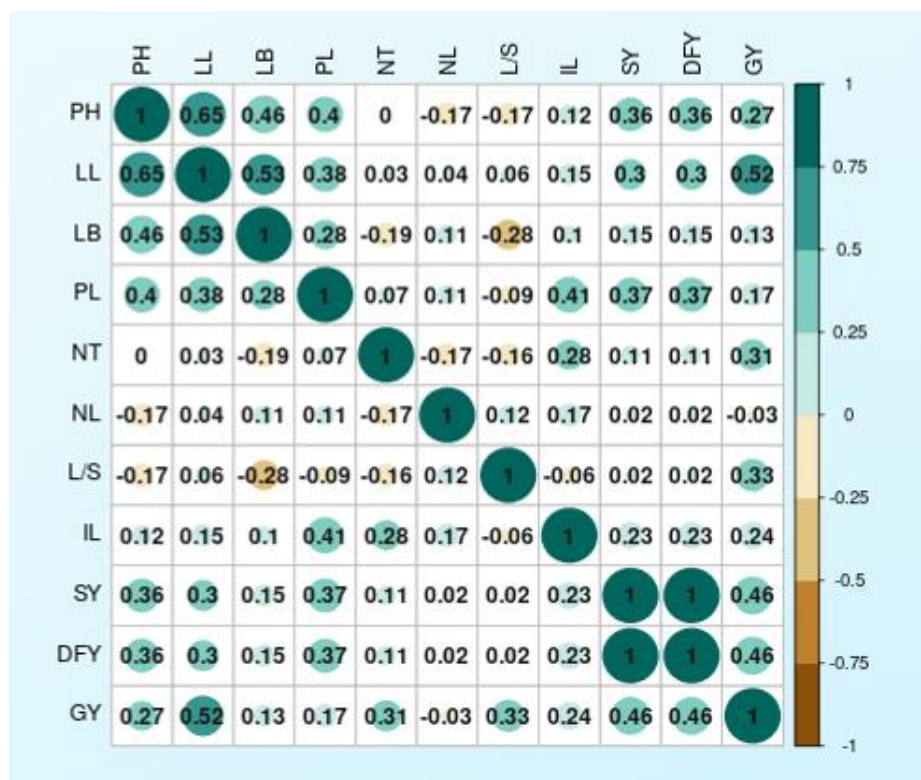


Fig. 3. Phenotypic Correlation among various traits in foxtail germplasm lines (pooled data)

almost 80.8% of the total variation for eleven quantitative characters responsible for fodder and grain yield in foxtail millet genotypes was up to first five principal components which are having eigen values more than one. The principal components PC1, PC2, PC3, PC4 and PC5 contributed 31.88%, 15.05%, 12.31%, 11.43% and 10.14%, respectively to the total variation which indicated their importance for the foxtail millet germplasm characterization. PC1 was the most important contributing

component with the eigen value of 3.058, PC2 had an eigen value of 1.656, PC3 had an eigen value of 1.355, PC4 had an eigen value of 1.257 and PC5 had an eigen value of 1.115 (Table 4). In the scree plot the black line represents the cumulative variability percentage with respect to PC1 to PC10 (Fig. 4). In biplot graph, the PCA in general confirmed the groupings of the genotypes based on PC1 and PC2 (Fig. 5). The accessions SEA 5, SEA 12, SEA 48, SEA 37, SEA 8 and SEJ 184 were grouped

Table 4. Principal components, eigen value, percentage of variance and cumulative percentage of variance (pooled data)

Principal Components	Eigen value	Percentage of variance	Cumulative percentage of variance
PC1	3.508	31.889	31.889
PC2	1.656	15.052	46.941
PC3	1.355	12.317	59.258
PC4	1.257	11.431	70.689
PC5	1.115	10.14	80.829
PC6	0.724	6.586	87.415
PC7	0.515	4.677	92.093
PC8	0.401	3.646	95.739
PC9	0.258	2.343	98.082
PC10	0.211	1.918	100
PC11	0	0	100

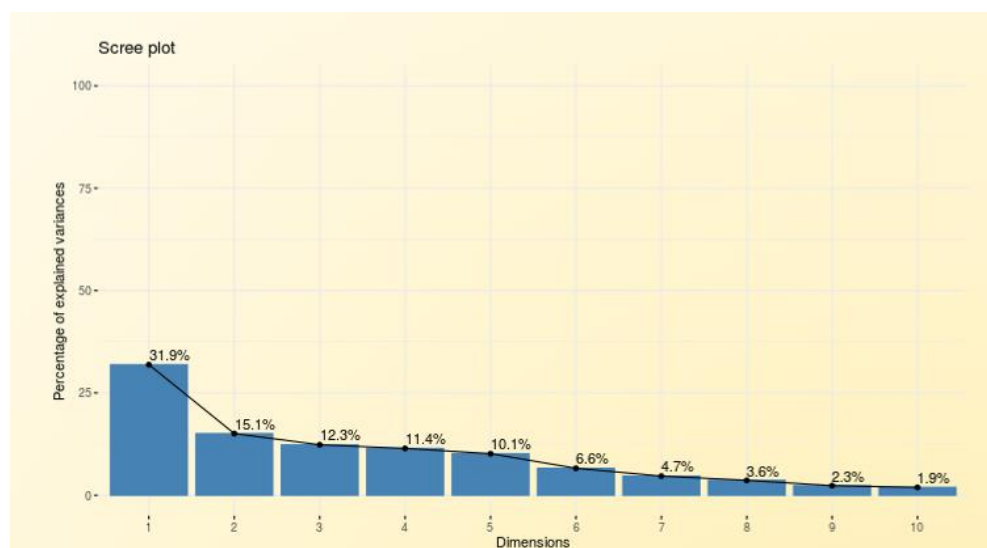


Fig. 4. Scree Plot (pooled data)

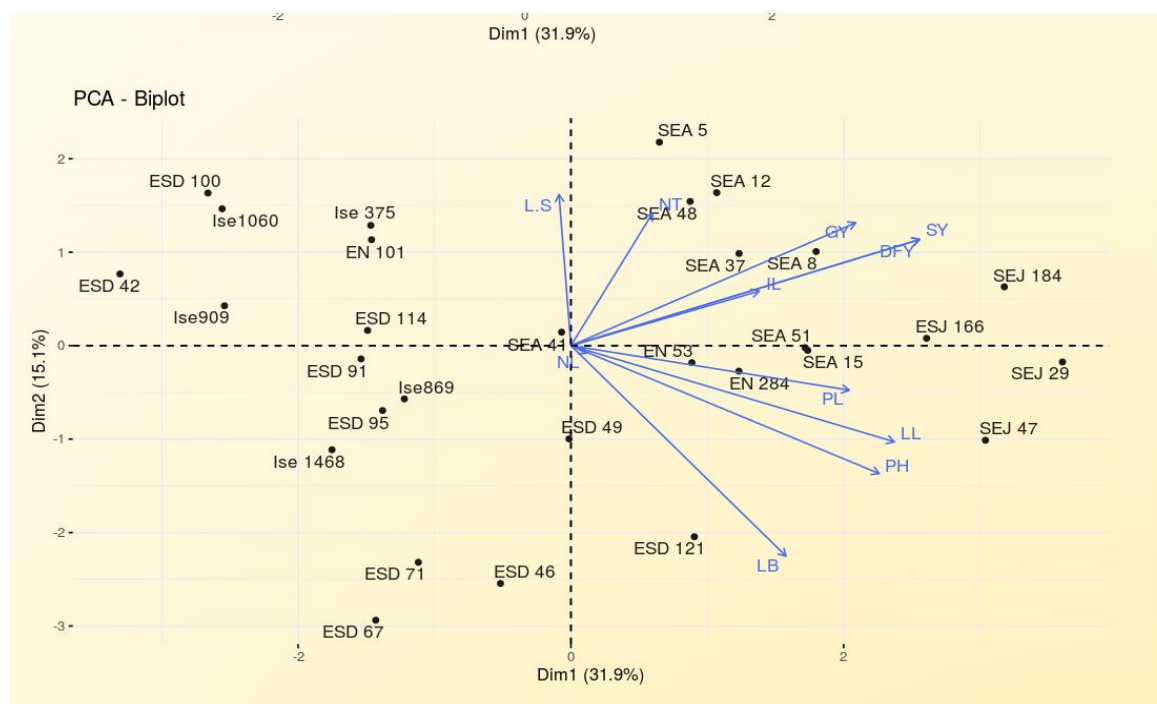


Fig. 5. PCA biplot based on PC 1 and PC 2 (pooled data)

for high dry fodder yield, stover yield and grain yield. All these accessions are released cultivars from Prakasam District of Andhra Pradesh except SEJ 184 which belongs to Kalahandi district. This clearly indicates that genotypes belonging to Andhra Pradesh district were having dual purpose potential as compared to those released from other states used in the study.

The first principal component exhibited high positive loading for stover yield, dry fodder yield and leaf length and it was responsible for largest portion of the variability. The second principal component had shown high loading for leaf breadth and PC3, PC4 and PC5 showed high loadings for leaf:stem ratio, number of leaves and stover yield, respectively (Fig. 6). Rao and Chaturvedi, 2022

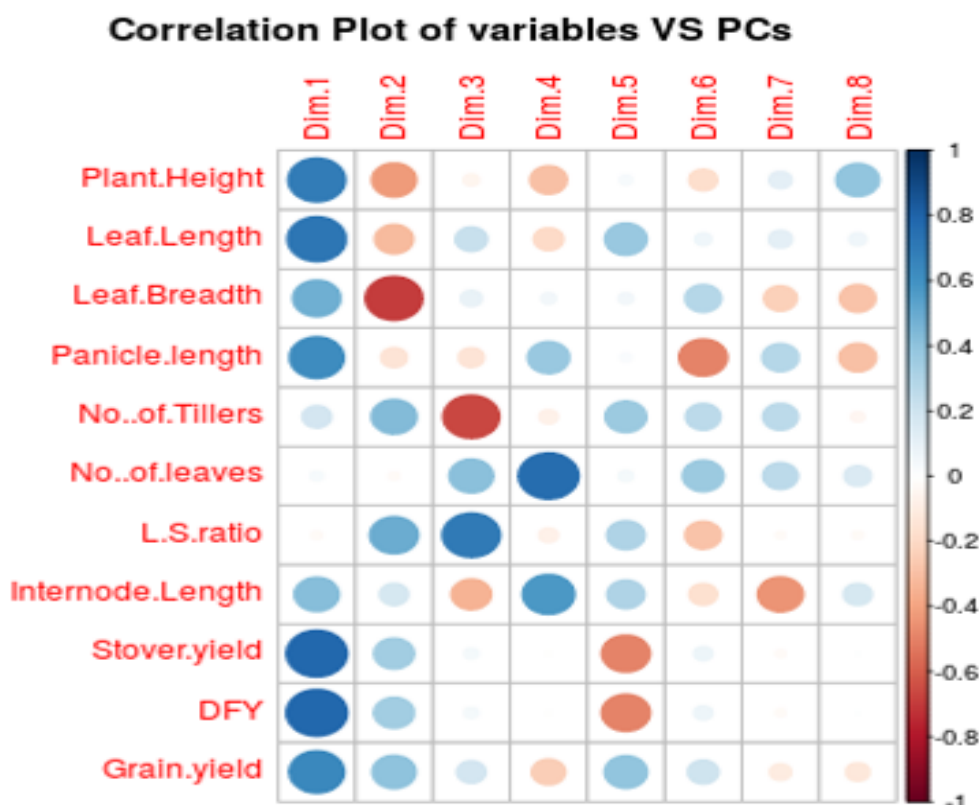


Fig. 6. Correlation plot of variables and principal components (pooled data)

also reported that first five PCs had contributed 82% of total variation among foxtail germplasm lines for different agro-morphological traits based on the scree plot and threshold eigen value greater than 1. Similarly, Nandini *et al.* (2018) also reported that first five principal components contributed about 72.87% of the total variability among germplasm lines. Singh *et al.* (2023) based on PCA analysis identified few promising foxtail accessions which could be utilized to improve various morphological traits based on direct and indirect selection.

The present investigation for evaluation of genetic diversity among foxtail accessions was helpful in identifying the variability contributing traits and in the identification of potential genotypes with high grain and fodder yield viz., SEA8, SEA12, SEA48, SEJ184 and SEA37 which could be incorporated in foxtail millet improvement program and at the same time they will also aid in broadening the gene pool of foxtail millet for development of dual purpose foxtail millet varieties to combat with climate change.

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