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Research Article

Diversity study using principal component analysis in barnyard millet (*Echinochloa frumentacea*(Roxb.) Link)

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Abstract
Among nutri-cereals, now-a-days, barnyard millet getting popular among the public for its rich nutritional and cooking qualities. A total of forty genotypes were evaluated in three different environments to study the genetic diversity using Principal Component Analysis.Foremost three components contributed 85.65 % of the total multivariable differences. Germplasm projection delivered four main groups on first two canonical components. Genotypes splitting were on the basis of trait performance. Majority of the traits had explained low to moderate values with negative loadings to PC1, PC2 and PC3 except few traits like thousand grain weight and number of basal tillers, which had positive loadings with high values. Loadings bi-plots of PC1-PC2 and PC1-PC3, classified the groups into two major categories, consisting of late matured –high yielding genotypes on left side and early matured –low to medium yielding genotypes on right side of scattering.

Key words
Barnyard millet, Principal Component Analysis, genetic diversity

INTRODUCTION

Among poor man's cereal, barnyard millet (*Echinochloa frumentacea* (Roxb.) Link) is an under-explored crop which has the cultivation history of long years ago and was major food crop once upon a time.In the present millet cultivation scenario, the area under cultivation of barnyard millet is getting increased and the knowledge about the crop is being disseminated among the public and farmers, along with its health benefits. The grain of barnyard millet consists of 10.8 g of protein, 14.7 g of crude fibre and it has 300 kcal of energy per 100 g of grain. It is also rich in some important micro nutrients with 340 mg of P, 82 mg of Magnesium, 22 mg of Calcium, 18.6 mg of Iron, 2.6 mg of Zinc, 1.30 mg of Cupper and 1.33 mg of Manganese Muthamilarasan *et al.*(2016). Its grains are used just like rice Ruiz-santaell *et al.*(2006). It is being widely cultivated in two diverged ecological environments, of which one is in mid hills area of Himalayas of Uttarakhand in northern India and other is in the plain region of southern IndiaSood *et al*(2015). Particularly, in Tamil Nadu state, it is being majorly cultivated in rain fed areas and hilly region by tribal planters of Theni, Namakkal, Salem, Dindigul, Viluppuram, Coimbatore, Madurai and Erode districts Nirmalakumari *et.al* (2009).

Gathering knowledge about grouping of genotypes and their inheritance pattern is a basic necessity for breeding approaches and to maintain genetic resources since it is handful to plant breeders and farmers Govindaraj *et al* (2015). Canonical analysis is one of the multivariable analyses which provides information on maximum

contribution of vector variation towards the total variance (Rao, 1952).This analysis measures divergence between genotypes in terms of spatial distance rather than quantifying the genotypes as D^2 does. Few studies have been done for exploitation of this crop with reference to collection, documentation, evaluation and utilization of genotypes Sood *et al* (2015); Trivedi *et al* (2018) and Gupta *et al* (2009).Hence, the present study was undertaken to investigate the relative contribution of various traits to the total variability and clustering of genotypes based on PCA bi-plots of barnyard millet using Principal Component Analysis.

MATERIALS AND METHODS

A sum of 40 barnyard millet germplasm were sourced at gene bank, ICRISAT, Hyderabad, India; All India Coordinated Small Millets Improvement Project, Bengaluru, India; Department of millets, Tamil Nadu Agricultural University (TNAU), Coimbatore and Department of Plant Breeding and Genetics, Agricultural College and Research Institute (AC & RI), Madurai. The total germplasm includes two check varieties namely, MDU 1 and CO (Kv) 2 which were released from AC & RI, Madurai in 2015 and Department of millets, TNAU, Coimbatore in 2009, respectively. The experiments

were raised in randomised block design (RBD) with two replications at three different environments.The experiments were laid in three environments , namely Idukki, a hill region of Kerala state, considered as E1, AC&RI, Madurai (E2), a plain region and Theni, a valley region considered as E3.The meteorological data of the distinguished environments is furnished below **Table 1.**

All these experiments were conducted during summer season 2019 and sowing was carried out with two days gap in each location **(Table 1)**.The data on seventeen yield and its contributing traits were recorded on five plants which were selected randomly in each genotype and in each replication. The data were recorded following the barnyard millet descriptor (Bioversity International. 1983). The characters *viz.*, plant height, days to flowering, days to maturity, node number, node length, stem diameter, flag leaf length, flag leaf width, inflorescence length, inflorescence width, lower racemes length, peduncle length, racemes number, thousand grain weight, single ear head weight and grain yield per plant were considered for recording observations. All the agronomic practices were followed on time with proper pest management as recommended by TNAU, Coimbatore.

Table 1. Meteorological data of the three environments

Location	Latitude	Longitude	Average Rainfall	Average Temperature	Date of sowing
Idukki	10.01^0N	77.34^0E	1082 mm	21.9^0C	07 th January 2019
Madurai	9.95^0N	78.01^0E	857 mm	28.8^0C	09th January 2019
Theni	9.93^0N	77.47^0E	791 mm	27.2^0C	11th January 2019

The data on quantitative traits were analyzed by utilizing Residual Maximum Likelihood (REML) for all environments separately and combined of all. Patterson and Thompson, (1971) in GenStat 19th edition (http://www.genstst. co.uk) giving consideration to accessions as random and environment as fixed. Principal component analysis or canonical analysis was performed using the PBTolls software (PBTools, 2014).(Patterson, 1971 #248)

RESULTS AND DISCUSSION

The relationships between different components were studied by vector analysis, in which, first three axes contributed an effective cumulative towards the variation and estimated 85.65% of the total variation. Fourth component provided less than 5% (**Table 2**). About 68.07 % of the total variation was recorded for first canonical vector which attributed to peduncle length. Peduncle length is the only character that was found with positive loadings and negative loadings were observed for remaining characters. Moderate values were estimated with negative signs for the traits namely, days to flowering, days to maturity, flag leaf length, inflorescence length, number of nodes, racemes number, plant height, stem diameter, width of flag leaf, width of inflorescence, single ear head weight and grain yield per plant.

PC2 contributed an addition of 10.37 % towards total variation by which, genotypes were diverged with positive loading for days to flowering, thousand grain weight, days to maturity, number of tillers, node numbers, stem diameter and single ear head weight. Like-wise, third PC explained an extra of 7.21 % variance for total variation and found positive signs for number of tillers, days to flowering, days to maturity, lower racemes length, inflorescence length, peduncle length, plant height and thousand grain weight. The maximum traits were placed on left hand side of bi-plot except peduncle length (**Fig. 1 & 2**).

Four types of grouping of genotypes were identified in the primary principal components (**Fig. 1**). Maximum of the genotypes were on the left hand side in the plot. In left hand side centre, the genotypes such as ACM 110, IEc 167, ACM 331, M2P1, M5P1, M12P1, M28P1, M37P1, M38P1, ACM-15-353 and CO (Kv) 2 were distributed whereas, GECH 15, M3P2, ACM 161, ACM 333, M36P1, T 5, GECH 10, IEc 672 and IEc 52 were scattered on left hand top side. Similarly, the genotypes M27P1, ACM-15-343, MDU 1, M1P1, ACM 295, IEc 568 and M18P1 placed on left hand bottom side, while, the genotypes such as IEc 396, IEc 350, IEc 391, IEc 71, IEc 296, IEc 385, IEc 356, IEc 386, IEc 108, IEc 107, IEc 109 and IEc 82 had

Table 2 Component Matrix showing latent vectors associated with the first four principal Components, based on three pooled environments

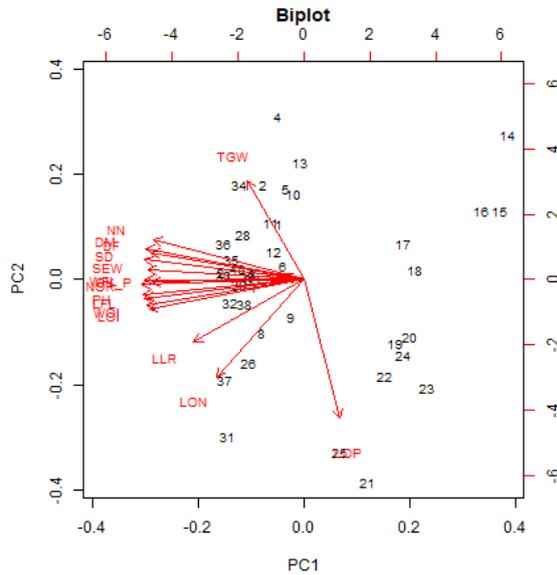| Characters	PC -1	PC- 2	PC- 3	PC - 4
Days to flowering	-0.270	0.125	0.067	-0.157
Days to maturity	-0.279	0.142	0.035	-0.148
Grain yield per plant	-0.268	-0.011	-0.056	-0.115
Flag leaf length	-0.281	-0.084	-0.009	-0.048
Lower racemes length	-0.195	-0.283	0.200	0.376
Inflorescence length	-0.274	-0.133	0.0545	0.116
Node length	-0.155	**-0.444**	-0.284	0.341
Peduncle length	0.064	**-0.630**	0.230	0.007
Number of tillers	-0.034	0.014	**0.853**	-0.198
Node number	-0.266	0.184	-0.071	-0.008
Racemes number	-0.288	-0.020	-0.009	-0.082
Plant height	-0.284	-0.068	0.100	0.071
Stem diameter	-0.282	0.091	-0.126	-0.046
Single ear head weight	-0.275	0.044	-0.041	-0.203
Thousand grain weight	-0.100	**0.449**	0.209	**0.748**
Flag leaf width	-0.281	-0.001	-0.097	-0.114
Inflorescence width	-0.278	-0.119	0.041	0.032
Percentage of total variation (%)	68.07	10.37	7.21	4.33
Cumulative value (%)	68.07	78.44	85.65	89.98
Eigen Values	**11.57**	**1.76**	**1.23**	**0.73**

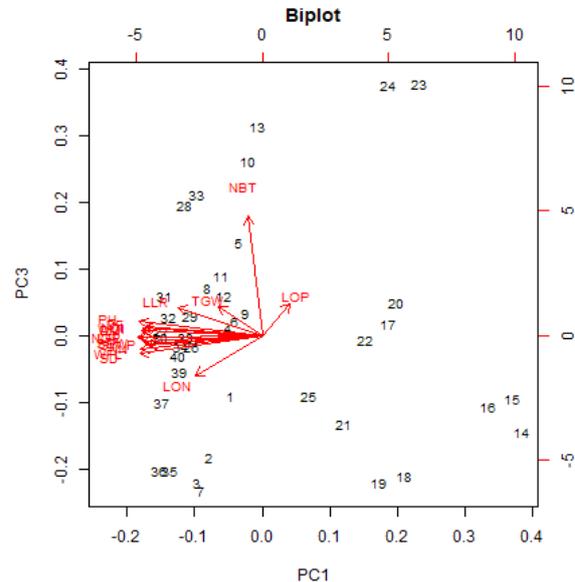**Fig.1.Bi-plots of PC1 and PC2 for 40 barnyard millet genotypes** **Fig.2. Bi-plots of PC 1and PC 3 for 40 barnyard millet genotypes**

DF- Days to flowering; DM – Days to maturity; GY_P – Grain yield per plant; LFL – Length of flag leaf; LLR- Length of inflorescence; LON – Length of node; LOP – Length of peduncle; NBT- Number of basal tiller; NN – Number of nodes; NOR- Number of racemes; PH – Plant height; SD – Stem diameter; SW – Single ear head weight; TGW – Thousand grain weight; WFL – Width of flag leaf ; WOI – Width of inflorescence.

grouped to right hand side.In PC 1-PC 3 biplot, three types of grouping were observed based on germplasm projections (Figure 2). Majority of the genotypes were scattered on the left hand side which further divided into left hand side bottom and top. The left hand bottom side comprised of ACM 161, T 5, ACM 110, ACM 331, M1P1, M2P1, M12P1, M36P1, M37P1, M38P1, MDU 1, ACM-15-343, ACM-15-353 and CO (Kv) 2. In case of left hand top side, the genotype such as IEc 52, M5P1, M27P1, IEc 167, IEc 568, GECH 15, ACM 295, M18P1, ACM 333, GECH 10, M3P2, M28P1, IEc 166 and IEc 672. By contrast, the accessions like IEc 385, IEc 386, IEc 82, IEc 109, IEc 107, IEc 350, IEc 396, IEc 391 and IEc 108 had occupied right hand bottom side. Few genotypes such as IEc 356, IEc 296 and IEc 71 were placed on the right hand top side of biplot. Principal component analysis revealed that basal tiller number, node length, peduncle length, lower racemes length and thousand grain weight provided maximum contribution to genetic divergence. The biplots of PC1 and PC2 exhibited protruding most of the genotypes were late maturing, high yielding accessions, which are positioned in the left hand top, centre and bottom side groups. By contrast, the right hand side group is comprised of 12 accessions which are all early maturing, low to medium yielding accessions. These findings match with the findings of Sood *et al.*(2015); Wallace *et al.*(2015); Anuradha *et al* (2014); Gupta *et al.*(2009) in barnyard millet.Accordingly, these early maturing accessions would be handful to develop extra early maturing cultivars through hybridization breeding approaches as donors.

From the experimental results, it is evident that there is existence of genotypic divergence on biometric traits of barnyard millet accessions. Some of the early maturing genotypes (64-84 days) irrespective of good grain yield,thatcan be implemented for an effective breeding programme for developing early maturity cultivars for drought escape were identified. Therefore, selection of parents by differentiating the genotypes both genetically and phenotypically would pave way for succeeding breeding objectives.

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