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Finger millet germplasm characterization and evaluation using principal component analysis

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Abstract

Finger millet is an important crop in the developing world especially in Africa and Asia. The aim of this study was to characterize 55 finger millet genotypes using multivariate analysis which is an important statistical tool through which we can easily assesses important polygenic characters which are of great importance in a plant breeding programme. The principal component analysis revealed that the first 4 components with Eigen value of greater than 1.33 contributed about 66.54% of total variability. The proportions of the total variance attributable to the first 4 principal components were 33.61, 12.91, 12.14 and 7.87% respectively. The characters including grain yield per plant, 1000-grain weight, productive tillers per plant, days to flowering, days to maturity, finger number per panicle, finger length and finger width were the most important traits contributing for the overall variability. This implied that these traits should be given emphasis in finger millet improvement programme.

Keywords: finger millet, genetic diversity, principal component analysis, quantitative traits, variability

Introduction

Finger millet is one of the most important small millets crop grown in large areas of the developing world especially in Africa and Asia. It has the ability to produce higher yield than other crops under multiple stresses such as drought, soil acidity and land marginality (Barbeau and Hilu, 1993; Upadhyaya *et al*., 2006) [5, 16]. Moreover, it has high nutritional value and excellent storage qualities (Dida *et al*., 2007) [7]. In India, it is cultivated on 1.14 million ha with a production of 1.82 million tons with an average productivity of 1601 kg per ha while in Jharkhand 644 kg/ha only from an area 14.3 thousand ha with a production of 9.2 thousand tons (Anonymous, 2018) [1]. The usefulness of multivariate analysis for the study of morphologically complex individual and for measuring the degree of divergence between biological populations has been shown in different fields of research. Multivariate statistical techniques which simultaneously analyze multiple measurements on each individual under investigation are widely used in analysis of genetic diversity irrespective of whether it is morphological, biochemical or molecular marker-based and subsequently, classification of germplasm collections. Among the multivariate techniques, principal component analysis (PCA) and cluster analysis had been shown to be very useful in selecting genotypes for breeding program that meet the objective of a plant breeder (Mohammadi and Prasanna, 2003) [13]. PCA may be used to reveal patterns and eliminate redundancy in data sets (Adams, 1995) [2] as morphological and physiological variations routinely occur in crop species. Cluster analysis is commonly used to study genetic diversity and for forming core subset for grouping accessions with similar characteristic into one homogenous category. Clustering is also used to summarize information on relationships between objects by grouping similar units so that the relationship may be easily understood and communicated. Multivariate analysis has been used frequently for genetic diversity analysis in many crops such as finger millet (Dagnachew *et al*., 2012) [6] and rice (Gana *et al*., 2013) [9]. The important objective of any plant scientist is to identify an optimum number of plant traits which are sufficient to explain the maximum variability in the crop growth from sowing to harvest. This study was undertaken to run a classification analysis on the finger millet genotypes by means of descriptive statistic and to understand the association of various characters, PCA and cluster analysis which would enable breeders to classify the available germplasm into distinct groups on the basis of their genetic diversity.

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Materials and Methods

A set of 50 germplasm with four checks and one filler germplasm of finger millet obtained from coordinating unit millet, Bengaluru were evaluated in augmented randomized block design at Research Farm, Ranchi Agriculture College, Kanke during *Kharif* 2015. Each germplasm was represented by a single row plot of 3 m length with inter and intra-row spacing of 22.5 cm and 10 cm, respectively. Crop was raised as per the recommended package of practices. Observations recorded on days to 50 per cent flowering, Flag leaf area (sq. cm), Plant height (cm), Effective tillers per plant (number), Ears per plant (number), Fingers per ear (number), Finger length (cm) Days to maturity (days), Grain yield per plant, Grain yield per plot, Biomass yield per plant, Harvest index, 1000 - seed weight, leaf blast, neck blast and finger blast. Days to flowering was noted on single row basis. The data collected for all quantitative characters were subjected to analysis of variance for augmented block design according to the method suggested by Federer and Raghavarao (1975) [8]. The principal component analysis was computed using the software statistical package for the social sciences (SPSS) 16.0 package (Levesque, 2007) [12]. As suggested by Johnson and Wichern (1988) [10], principal components with eigen values less than one was considered.

Results and Discussion

In the present investigation 55 finger millet genotypes were studied to assess their genetic potential. All the genotypes displayed considerable amount of differences in their mean performance with respect to all the characters studied, which indicates that the genotypes under the study were genetically diverse (Table 1).

The principal component analysis is a technique which identifies plant traits that contribute most of the observed variation within a group of genotypes. This tool has a practical application in the selection of best genotypes for breeding purpose. The results of PCA revealed that the first 4 components with eigen value of greater than 0.65 contributed about 87.8% of total variability in 305 genotypes involving all the 13 quantitative traits studied (Table 2). The importance of traits towards the PC could be seen from the corresponding eigen values which are presented in Table 1. The first principal component accounted for 66.7% of the total variation in the population. Grain yield per plant (0.96) contributed more to the variation followed by plant height (0.95), days to flowering (0.92), 1000 grain weight (0.91), productive tillers per plant and flag leaf sheath length (0.90), days to maturity (0.85), flag leaf sheath width, flag leaf blade length (0.84) and finger width (0.34) had the highest loadings in PC1 indicating their significant importance for these components. These traits had the largest participation in the divergence and carried the largest portion of its variability. All other characters contributed negative to the first component.

Second principal component contributed 10.7% of the total variation. Characters that contributed to the second component include finger length (0.65), finger number per panicle (0.62), flag leaf blade length (0.26), flag leaf sheath length (0.20), plant height and days to flowering (0.11). The third principal component accounted for 5.5% of the total variation in the population. Finger width contributed the highest (0.69) followed by finger length (0.37) while finger number per panicle contributed less variation. Likewise, the fourth principal component contributed 5.0% of the total variation. The major characters that contributed highly to the variation include flag leaf blade width (0.46), flag leaf sheath width (0.37), days to maturity (0.35), days to flowering (0.27), productive tillers per plant (0.16), finger number per panicle and grain yield per plant (0.15) while 1000-grain weight (0.11) contributed least to the variation. Similar findings with regard to grain yield per plant, plant height, days to flowering and productive tillers per plant were reported by Salini *et al*., (2010) [15] in prosomillet. The traits such as grain yield per plant and plant height as earlier reported by Khavari Khorasani *et al*., (2011) [11] in maize and days to maturity was reported by Azad *et al*., (2012) [4] in maize. Principal component analysis in this study confirmed the first principal components contributed maximum number of characters towards genetic diversity and these traits could be effectively used for further breeding programs to create more variability. Grain yield per plant, plant height, days to flowering, 1000-grain weight, productive tillers per plant, flag leaf sheath length, days to maturity, flag leaf sheath width and flag leaf blade length were the most important traits contributing for the overall variability observed among the genotypes. Characters with high variability are expected to provide high level of transgressive segregation in breeding populations. This is important for breeders to investigate high yielding, early maturing and dwarf varieties through conventional breeding. Several authors indicated that different morphological traits for the different crops have contribution for the overall variability (Negash *et al*., 2005; Assefa *et al*., 2003) [14, 3].

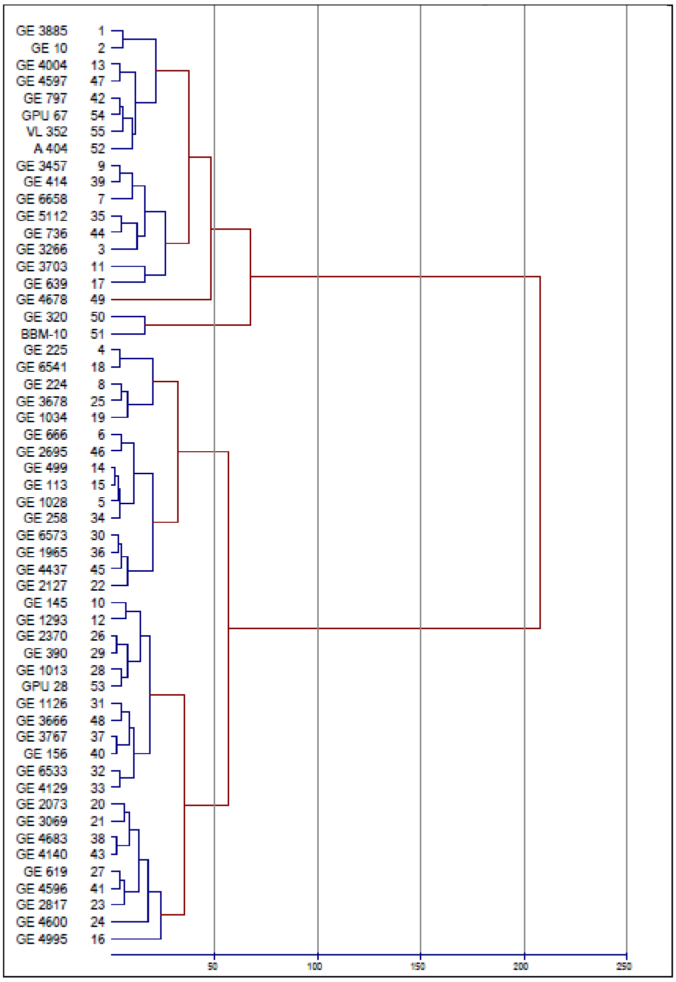

Fig 1: Dendrogram showing clustering of genotypes based on yield attributing traits.

Table 1: Analysis of variance (mean sum squares) for thirteen yield attributing characters and disease reaction

Source of variation	**d.f**	**Days to 50% flowering**	**Flag Leaf Area**	**Plant Height**	**Effective tillers/plant**	**Ears / Plant**	**Fingers/ Ear**	**Finger length**	**Days to maturity**	**Grain yield/plant**	**Grain yield/plot**	**Biomass of plant**	**Harvest index%**	**1000seed weight**	**Leaf blast**	**Neck blast**	**Finger blast**
Block (ignoring Treatments)	2	19.87**	13.25*	777.68**	0.07	0.09*	0.05	7.24**	152.49**	0.37	4365.66**	269.54**	242.47**	0.036**	2.87**	816.99	805.94
Treatment (eliminating Blocks)	54	199.02**	56.25**	88.57**	0.11*	0.10**	1.77**	1.43**	199.36**	2.46**	4311.46**	23.42**	44.29**	0.21**	0.65**	191.67	193.25
Checks	3	154.08**	58.32**	102.27**	0.23**	0.13**	1.11*	2.6**	76.30**	5.43***	5751.67**	17.20**	109.53*	0.08**	0.69	121.14	128.99
Checks+Var vs. Var.	51	201.67**	56.13**	87.76**	0.10*	0.10**	1.81**	1.36*	206.60**	2.29**	4226.67**	23.79**	40.45**	0.22**	0.03**	195.82	197.03
EERROR	6	1.083	1.47	0.98	0.01	0.01	0.15	0.19	0.64	0.20	2.10	2.54	5.45	0.00	0.00	166.05	158.50
Block (eliminating Check+V ar.)	2	0.75	1.53	1.05	0.00	0.01	0.16	1.27	1.07	0.01	0.58	0.32	1.38	0.00	0.76	0.03	0.00
Entries (ignoring Blocks)	54	199.73**	56.69**	117.33**	0.11*	0.10**	1.79**	1.65*	204.97**	2.47**	4473.13**	33.39**	53.22**	0.21**	0.77**	221.93	223.10
Checks	3	154.08**	58.32**	102.27**	0.23**	0.13**	1.11**	2.60**	76.30**	5.43**	5751.67**	17.20**	109.53*	0.08**	2.52	121.14	128.99
Varieties	50	199.80**	57.71**	116.92**	0.10*	0.10**	1.86**	1.61**	215.42**	1.93**	4000.61**	34.35**	47.39**	0.18**	0.03**	192.24	191.32
Checks vs. Varieties	1	333.33**	0.76**	182.78**	0.24**	0.15*	0	0.87**	68.32**	20.77***	24263.44***	33.78**	175.82*	2.03**	0.36**	2009.00*	2094.41*
ERROR	6	1.08	1.47	0.98	0.01	0.01	0.15	0.19	0.64	0.20	2.10	2.54	5.45	0.00	0.63	166.05	158.50

*, ** = significant at p = 0.05 & 0.01 respectively

Table 2: Principal components showing the Eigen values, proportion of variation and total variation across axis.

Components	**Vector 1**	**Vector 2**	**Vector 3**	**Vector 4**	**Vector 5**	**Vector 6**	**Vector 7**
Days to 50% flowering	0.01	0.04	0.61	0.10	0.24	0.11	0.17
Flag leaf area(cm)	-0.09	0.24	-0.18	0.07	-0.11	-0.19	0.84
Plant height (cm)	0.01	0.04	0.10	0.62	-0.22	-0.32	-0.18
Effective tillers/plant	-0.20	0.44	-0.20	0.20	0.30	0.04	-0.21
Ears/plant	-0.18	0.48	-0.19	0.20	0.25	0.06	-0.19
Fingers/ear	-0.05	-0.01	-0.05	0.26	-0.04	0.72	0.16
Finger length (cm)	-0.13	-0.23	0.03	0.57	-0.27	-0.00	0.07
Days to maturity	-0.07	0.08	0.60	0.06	0.30	0.02	0.08
Grain yield/plant(g)	-0.30	0.29	0.11	-0.17	-0.12	-0.02	0.06
Grain yield/plot	-0.38	-0.05	-0.00	-0.00	-0.18	0.00	-0.01
Biomass yield/plant(g)	-0.21	-0.19	-0.19	0.04	0.47	-0.15	0.23
Harvest index%	-0.07	0.44	0.22	-0.21	-0.51	0.05	-0.04
1000-seed weight	-0.16	0.01	0.12	-0.02	0.05	-0.51	-0.07
Leaf Blast	0.34	0.18	-0.02	0.01	0.01	-0.07	0.12
Neck Blast (ASIN)	0.39	0.13	-0.01	0.07	0.02	-0.05	0.05
Finger Blast (ASIN)	0.39	0.13	-0.01	0.07	0.02	-0.05	0.05
Eigene valve (root)	5.71	2.19	2.06	1.33	1.25	1.12	0.86
%Var. Exp	33.61	12.91	12.14	7.87	7.40	6.60	5.10
Cum. Var. Exp	33.61	46.52	58.66	66.54	73.94	80.54	85.64

Conclusion

The study also revealed that the inter cluster distance were higher than the intra cluster distance, which indicate wide genetic diversity among the germplasm of the different group than those of same group. The least intra distance among the cluster VII. In, cluster VII, there is lack of variation among the germplasm. The principal component analysis revealed that first four vectors accounts 66.66% of total variation and the traits such Fingers per ear, days to maturity, finger length, ears per plant, biomass yield per plant, effective tillers per plant, harvest index, and grain yield per plant has maximum contribution towards genetic divergence.

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