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Research Article

MULTIVARIATE ANALYSIS IN BARNYARD MILLET (*ECHINOCHLOA FRUMENTACEA* (ROXB.) LINK)

Anuradha N., Patro T.S.S.K., *Udaya Bhanu K., Madhuri J. and Sowjanya A.
All India Coordinated Small Millets Improvement Project (AICSMIP)
(Agricultural Research Station, Vizianagaram, Andhra Pradesh, ANGRAU)
**Author for Correspondence*

ABSTRACT

In the present study, an attempt was made to assess the genetic divergence among the 21 germplasm lines using Mahalanobis D^2 statistic collected from different sources including local checks. The observations were recorded on seed yield and its components. The 21 germplasm lines that were grouped into four different clusters based on D^2 analysis revealed that Cluster I was the largest with 11 genotypes followed by cluster II (8). Cluster IV showed the maximum mean value for seed yield per plot. The intra and inter cluster divergence among the genotypes was varying in magnitude. Further it was implied that intra-cluster distance was maximum in cluster II followed by clusters I. The widest inter cluster distance was noted between cluster I and IV giving scope for hybridization programme with improvement of genotypes. The distance between clusters II and III was minimum indicating close relationship between those clusters.

Keywords: *D^2, Genetic Divergence, Barnyard Millet, Multivariate Analysis*

INTRODUCTION

Small millet crops have a long history of cultivation of more than 5000 years and grown in many states, due to their unique adaptation properties for poor degraded lands and ability to tolerate abiotic stress. Six small millets *viz*, finger millet, barnyard millet, foxtail millet, proso millet, kodo millet and little millet are the most important small millet crops of India. Among these, barnyard millet (*Echinochloa frumentacea* (Roxb.) Link) also called as Oodalu, Jhangora, Sawan or Madira (Hindi), has emerged as very important dual purpose feed and fodder crop. It is grown in many countries like, India, China, Japan, Malaysia, East Indies, Africa and United States of America (6). In India, the crop is grown in Andhra Pradesh, Madhya Pradesh, Uttarakhand, Tamil Nadu, Karnataka, Maharashtra and Bihar.

MATERIALS AND METHODS

The present study was carried out with 21 genotypes of barnyard millet (*Echinochloa frumentacea* (Roxb.) Link) obtained from different research centres across the country. The experiment was conducted in randomized block design with three replications at Agricultural Research station, Vizianagaram during 2013-2014. The inter and intra-row spacing adapted was 22.75 x 7.5 cm. Each genotype was sown in ten rows of 3m length and observations were recorded on ten plants from each genotype per replication for characters *viz.*, days to 50% flowering and seed yield per plot. The data were statistically analyzed to study diversity by Mahalanobis' D^2 statistic as per Rao (1952), principal component analysis (PCA) as described by Morrison (1976) and cluster analysis as described by Anderberg (1993). The genetic diversity analysis helps in selecting genetically diverse parents. Genetically diverse parents are likely to produce high heterotic effects and desirable segregants. It is widely accepted that evaluation of genetic resources (GR) is an essential preliminary to utilization and the more information that is available the more valuable will be the collection. By using the diversity analysis tools we can quantify the degree of genetic divergence amongst different populations. There is limited study on diversity in barn yard millet. Therefore, the present investigation is aimed at estimating the nature and magnitude of genetic diversity among different Barnyard germplasm collections.

RESULTS AND DISCUSSION

Mahalanobis D^2 Analysis

On the basis of D^2 values the twenty one genotypes were grouped into four clusters. Based on D^2 values, clustering pattern comprised four clusters, out of which cluster I was the biggest cluster with 11 genotypes followed by clusters II which consisted of eight genotypes followed by cluster III & IV genotype each as shown in Table 1.

Based on D^2 values the maximum inter cluster D^2 value were observed between cluster I and IV followed by cluster IV and III and the least inter-cluster distance was observed between cluster VI and cluster VI. The maximum intra cluster D^2 value for cluster II followed by for cluster I, for cluster IV while it was zero for cluster III, IV (Table 2). The results obtained from the data on cluster means (Table 4) from the different characters based on D^2 statistic revealed that cluster IV had recorded the highest mean value for seed yield per plot, productive tillers per plant, Days to 50% flowering and Days to maturity where as for the plant height it showed less mean. The genotypes fall under this cluster may be tried for direct adaptation for hybridization for improvement of yield.

Hierarchical Cluster Analyses

Based on Ward minimum variance dendrogram, the clustering pattern revealed that Cluster V with 11 genotypes followed by cluster II with four genotypes followed by cluster IV comprising three genotypes followed by Cluster I with two genotypes and cluster III with one genotypes as shown in Table1 and dendrogram. The genotypes falling in the same cluster are more closely related and hence the clusters having the maximum number of genotypes, reflected narrow genetic diversity.

While the grouping based on the cluster analysis resulted in five clusters. The maximum inter cluster Eucledian^2 value were observed between cluster IV and III followed by cluster V and I and the least inter-cluster distance was observed between cluster VI and cluster VI. The maximum intra cluster D^2 value for cluster II followed by for cluster and whiles it was zero for cluster III.

Table 1: Genotypes included in each cluster based on Mahalanobis' D^2 analysis and Ward's minimum variance method

Based on D^2 value (Mahalanobis' analysis)			Based on cluster analysis (Ward's minimum variance method)	
Cluster No.	**No. of genotypes**	**Name of the genotypes**	**No. of genotypes**	**Name of the genotypes**
I	11	VL 244, Check *, VL 207, VL 172, VL 239, VL 245, DHBMV 93-3, TNAU 151, VL 234, VMBC 331, VL 243	2	ACM 10-082,ACM 10-145
II	8	TNAU 155, TNAU 157, TNEF 153, DHBMV 36-8, DHBMV 56-6, TNAU 160, ACM 10-145, ACM 10-082	4	TNAU 155,TNAU 157,TNEF 153,TNAU 160
III	1	DHBMV 83-3	1	KOPBM 46
IV	1	KOPBM 46	3	DHBMV 36-8,DHBMV 56-6,DHBMV 83-3
V	-----	-----------------	11	VL 234,VL 243,VL 245,VL 239,DHBMV 93-3,TNAU 151,VMBC 331,VL 207,VL 172,VL 244,Check *

Table 2: Average intra-and inter-cluster D^2 values among nine clusters based on Mahalanobis' D^2 values

Cluster No	I	II	III	IV
I	**8.500**	70.460	28.544	137.103
II		**11.714**	25.770	33.297
III			**0.000**	92.621
IV				**0.000**

Note: Bold and diagonal values indicate intra-cluster D^2 distance

Table 3: Average intra- and inter-cluster Eucledian^2 values among eight clusters based on cluster analysis

Cluster No.	I	II	III	IV	V
I	**9.53**	44.055	89.205	76.956	290.759
II		**25.973**	81.866	46.424	214.100
III			**0**	190.375	411.309
IV				**21.95**	112.914
V					**25.499**

Note: Bold and diagonal values indicate intra-cluster distance

Table 4: Mean values of clusters estimated from 21 genotypes of barnyard millet (*Echinochloa frumentacea* (Roxb.) Link.) based on D^2 analysis

S No	Days to 50 % flowering	Days to maturity	Plant height	Productive tillers/ plant	Seed yield/ plot
I	46.364	77.909	156.697	2.433	0.757
II	59.167	87.917	158.283	2.688	0.977
III	53.667	81.667	158.467	2.067	0.537
IV	63.333	94.333	150.933	**3.433**	**1.602**

Table 5: Mean values of clusters estimated from 21 genotypes of barnyard millet (*Echinochloa frumentacea* (Roxb.) Link.) based on cluster analysis

S.No	Days to 50 % flowering	Days to maturity	Plant height	Productive tillers/ plant	Seed yield/ plot
I	62.167	92.667	160.267	2.550	0.840
II	59.167	87.250	156.650	2.825	1.088
III	63.333	94.333	150.933	3.433	1.602
IV	55.333	83.556	159.200	2.389	0.774
V	46.364	77.909	156.697	2.433	0.757

Table 6: Eigen values, proportion of the total variance represented by first three principal components, cumulative per cent variance and component loading of different characters in barnyard millet (*Echinochloa frumentacea* (Roxb.) Link.)

	PC_1	PC_2	PC_3
Eigene Value (Root)	2.629	1.324	0.819
% Var. Exp.	52.572	26.471	16.377
Cum. Var. Exp.	52.572	79.043	95.421
Days to 50% Flowering	0.566	0.238	0.032
Days to Maturity	0.019	-0.629	0.757
Plant Height cm	0.402	0.468	0.515
Productive Tillers/ Plant	0.595	-0.145	-0.150
Grain Yield/ plot	0.404	-0.555	-0.372

PC= Principal component

Table 7: Characters contribution towards divergence by D^2 analyses

Source	Times Ranked 1st	Contribution %
Days to 50% Flowering	154	73.33
Days to Maturity	15	7.14
Plant Height cm	3	1.43
Productive Tillers/ Plant	1	0.48
Grain Yield/ plot	37	17.62

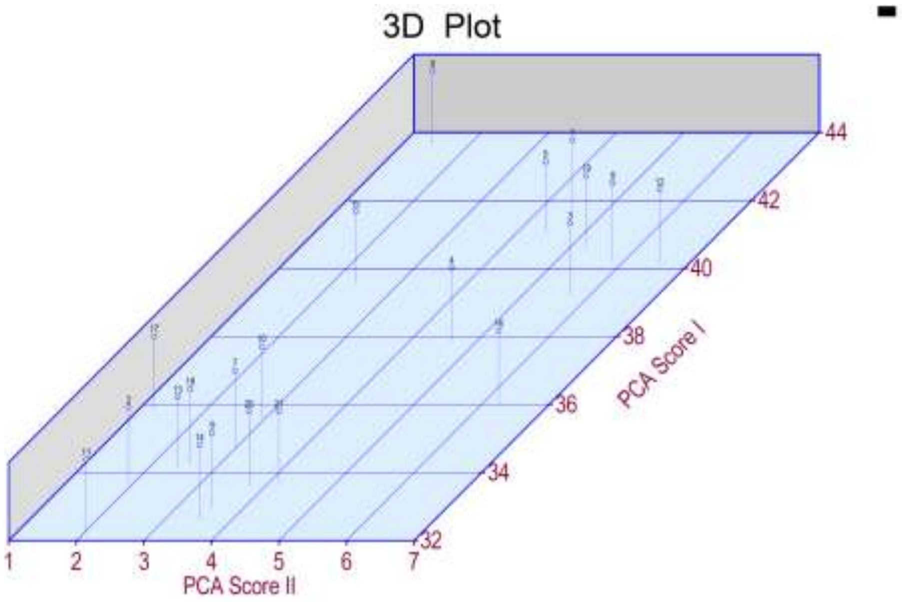

Figure 1: Dendrogram showing relationship of 21 Barnyard millet () genotypes in five clusters

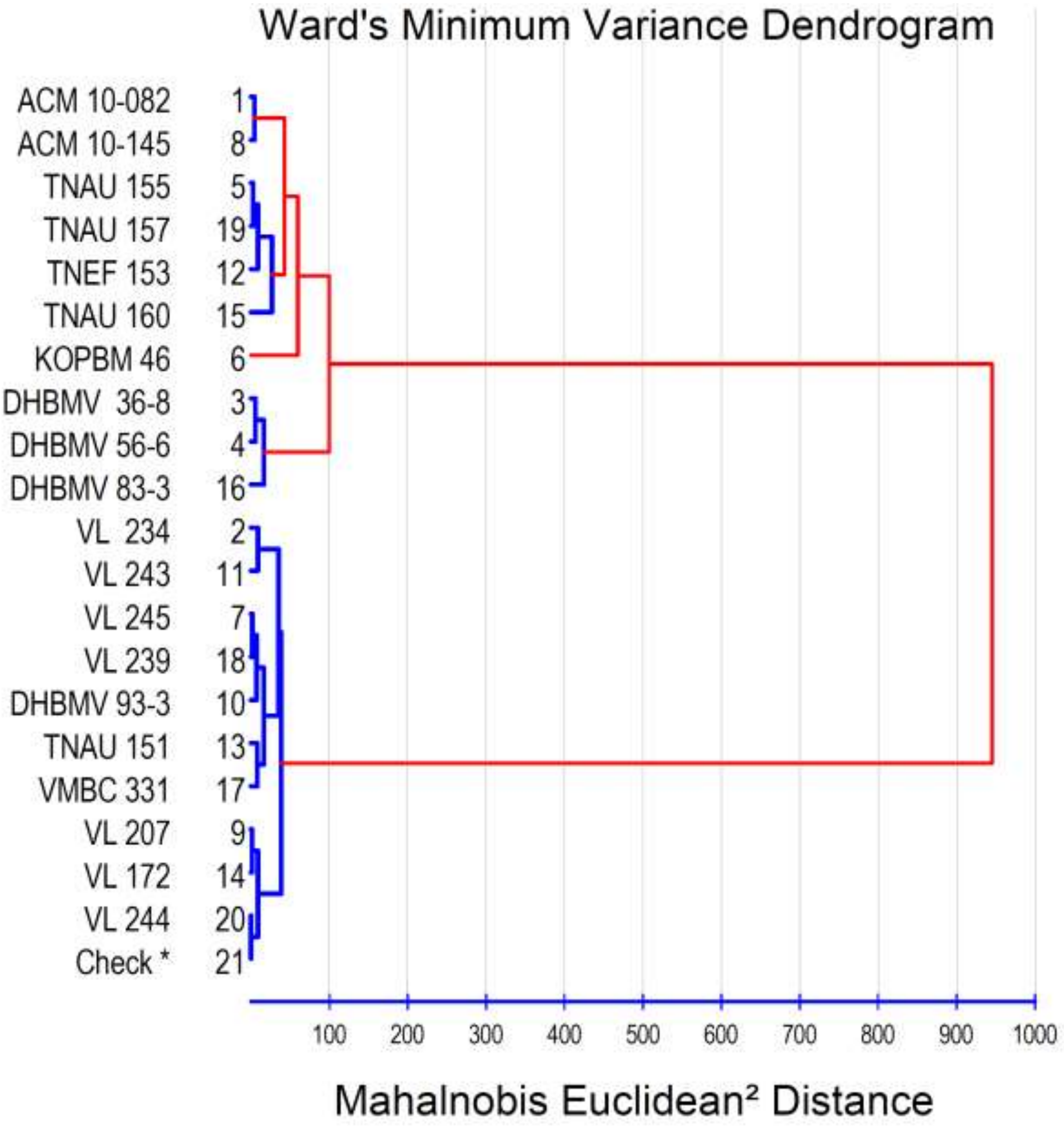

Figure 2: Three dimensional graph showing relative position of 21 of Barnyard millet (.) genotypes based of PCA scores

The results obtained from the data on cluster means (Table 5) from the different characters based on Eucledian^2 statistic revealed that cluster III had recorded the highest mean value for seed yield per plot, productive tillers per plant and less mean for plant height. The genotypes fall under this cluster may be tried for direct adaptation for hybridization for improvement of yield.

Principle Component Analyses

Based on the three principal components, a cumulative of 90.83% of variation formed the basis meant for the divergence into different clusters. A variance of 52.72, 26.47 and 16.37 % were extracted from the first to third components respectively. The variation in the first principle component is due to productive tillers per plant. The variation in the second principle component is due to days to maturity and seed yield per plot and the variation in the third principle component is due to days to maturity and plant height. Main principal components were given in Table 6. D^2 statistic showed that the characters contributing towards divergence in Table 7 revealed that the maximum contribution towards divergence is by days to 50 % flowering, seed yield per plot.

Several authors indicated that different agronomic and phenotypic traits for the different crops have contributed for the overall variability observed between study germplasms and geo-ecological zones of origin (Assefa *et al*., 1999; Ayana and Bekele, 1998; Quendeba *et al*., 1995).

The distribution of genotypes based on PCA values were shown in 2D plot and 3D plot where the genotypes VL 243 and TNEF 153 were away from the genotypes from other genotypes on the basis of PCAI and PCA II scores.

As per the mean values of different characters for different clusters, it can be said that genotypes belonging to these clusters can be used in breeding program for improvement of various yield. Hence these genotypes could be used in crossing program. Thus an improvement program involving patterns of different clusters may yield transgressive and heterotic segregants.

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