Principal Component Analysis for Evaluation of Guinea grass (*Panicum maximum Jacq.*) Germplasm Accessions

P Ramakrishnan¹, C Babu², K Iyanar³

^{1,2,3}Department of Forage Crops, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore - 641 003.

Abstract—The present study was conducted to study the variability among the genotypes by Principal Component Analysis (PCA) in order to select those that are most suitable for breeding programme. This study included ten quantitative traits. The result of principal component analysis showed that the first four principal components with Eigen value greater than 0.88 contributed about 76.10 per cent of total variation in the population. The variability of the genotypes was interpreted based on four principal components, the first principal component described the yield level, the second principal component described the productivity and quality and the last two principal components described the quality of the fodder which indicating that the identified traits within the axes exhibited great influence on the phenotype and this could be effectively used for selection among the tested entries for further development of Guinea grass varieties with improved fodder yield and quality.

Keywords—Principal Component Analysis, Quantitative traits, Variability, Germplasm, Guinea grass.

I. INTRODUCTION

Among the grasses, Guinea grass (*Panicum maximum* Jacq.) is an important forage grass of tropical and semi tropical regions, largely apomictic and predominantly exist in tetraploid form. It is also endowed with virtues like profuse tillering, high leafiness, thin stems, short duration, *etc.*, all of which contributes towards high biomasss production and better palatability. Being tolerance to shade, it is largely cultivated in coconut gardens. It is extensively cultivated under irrigated condition on fairly rich soils and is popular with dairy farmers. At present in India there is a deficit of 64 per cent of green fodder, and hence there is a need of over production of quality fodder especially the range grasses which could rejuvenate the fast degrading grasslands. In order to improve the productivity, adaptability and quality of Guinea grass, it is important to understand the genetic variability that exist in the population which also helps in their conservation and germplasm management (Tiwari and Chandra, 2010).

The major resource of plant breeders is the genetic variability in gene pool accessible to the crop of interest. The successes of crop improvement programs are highly reliant on the efficient manipulation of that genetic variability. Morphological markers have played an essential role in crop improvement since the beginning of modern breeding programs. A large number of variables are often measured by plant breeders, some of which may not be of sufficient discriminatory power for germplasm evaluation, characterization, and management. In such case, Principal Component Analysis (PCA) used to reveal patterns and eliminate redundancy in data sets (Adams, 1995; Amy and Pritts, 1991) as morphological and physiological variations routinely occur in crop. Knowledge of the nature, extent and organization of this variation could be useful for genetic improvement of crop species. Until a collection has been properly evaluated and its attributes become known to breeders, it has little practical use. Therefore, the present investigation was undertaken to study the Principal Component Analysis among 60 germplasm accessions of Guinea grass (*Panicum maximum* Jacq.) for characterization and preliminary evaluation, and also for further evaluation aimed at yield and quality improvement in this crop.

II. MATERIAL AND METHODS

The experimental material consisted of 60 germplasm accessions of Guinea grass (*Panicum maximum* Jacq.) obtained from various countries (**Table 1**) and maintained at Department of Forage Crops, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore, India. The accessions were planted using rooted slips on one side of ridge of 4 metres length, adopting a spacing of 60 x 50 cm in a Randomized Block Design with two replications. All the agronomic practices were followed to maintain the crop stand. The biometrical observations on fodder yield were recorded on single plant basis at the time of harvesting as per descriptors for *Panicum miliaceum* L. (UPOV, 2007), and characterization of perennial *Panicum* species (Wouw *et al.*, 2008). For recording single plant observations, three plants from each entry/replication were randomly selected. Average of these three plants in respect of plant height, number of tillers and leaves

per plant, leaf weight, leaf stem ratio, green fodder yield per plant and dry matter content and the same plants were subjected for the estimation of quality parameters such as crude protein, crude fibre and crude fat content was used for statistical analysis. The Principal Component Analysis was studied to identify plant traits that contribute most of the observed variation within a group of genotypes. Mean values of 60 genotypes for ten quantitative traits were subjected to Principal Component Analysis. PCA calculated by the statistical package NTSYS pcv2.02i (Rholf, 1992).

TABLE 1
LIST OF GUINEA GRASS GERMPLASM ACCESSIONS USED FOR THE EXPERIMENT

Sample code	Accessions	Geographic source	Sample code	Accessions	Geographic source
1.	GGLC 1	Coimbatore	31.	FD 661	Punjab
2.	GGLC 2	Coimbatore	32.	FD 662	Punjab
3.	GGLC 3	Coimbatore	33.	FD 663	Punjab
4.	GGLC 4	Rajasthan	34.	FD 667	Punjab
5.	GGLC 5	Punjab	35.	GG09 5	Punjab
6.	GGLC 6	Coimbatore	36.	FD 675	Punjab
7.	GGLC 7	Coimbatore	37.	FD 678	Punjab
8.	GGLC 8	Coimbatore	38.	FD 682	Punjab
9.	GGLC 9	Jhansi	39.	FD 679	Punjab
10.	GGLC 10	Hisar	40.	FD 692	Punjab
11.	GGLC 11	Andhra Pradesh	41.	FD 699	Punjab
12.	GGLC 12	Coimbatore	42.	FD 703	Punjab
13.	GGLC 13	Coimbatore	43.	FD 744	Coimbatore
14.	GGLC 14	Coimbatore	44.	FD 783	Coimbatore
15.	GGLC 15	Coimbatore	45.	FD 786	Coimbatore
16.	GGLC 16	Coimbatore	46.	FD 791	Coimbatore
17.	GGLC 17	Coimbatore	47.	FD 1659	Japan
18.	GGLC 18	Coimbatore	48.	FD 2719	Coimbatore
19.	GGLC 19	Coimbatore	49.	FD 2184	Coimbatore
20.	GGLC 20	Coimbatore	50.	FD 2186	Coimbatore
21.	GGLC 21	Coimbatore	51.	FD 2189	Coimbatore
22.	GGLC 22	Coimbatore	52.	FD 2192	Coimbatore
23.	GGLC 23	Coimbatore	53.	FD 2193	Coimbatore
24.	FD 135	Thailand	54.	FD 2199	Coimbatore
25.	FD 137	Thailand	55.	FD 2206	Coimbatore
26.	GG09 3	Coimbatore	56.	FD 2209	Coimbatore
27.	FD 606	Chengalpet	57.	FD 2214	Coimbatore
28.	FD 637	Madurai	58.	FD 2219	Coimbatore
29.	FD 653	Punjab	59.	GG09 6	Coimbatore
30.	FD 657	Punjab	60.	GG09 7	Coimbatore

III. RESULTS AND DISCUSSION

The analysis of variance revealed highly significant differences among accessions for all the characters under investigation thereby indicating the presence of a considerable magnitude of genetic variability among the experimental material (**Table 2**).

TABLE 2.

ANOVA SHOWING VALUES OF MEAN SQUARES FOR DIFFERENT CHARACTERS IN GUINEA GRASS

S. No	Source of variation	Plant height (cm)	Number of tillers per plant	Number of leaves per plant	Leaf weight (g)	Leaf stem ratio	Green fodder yield per plant (g)	Dry matter conten t (%)	Crue protein (%)	Crude fibre (%)	Crud e fat (%)
1.	Treatment Error	527.18* 332.26	20.45** 10.32	2152.79** 369.01	792.64** 170.12	0.0078** 0.0020	5001.93** 1097.98	19.44* 11.68	2.85** 0.44	8.52** 0.21	0.07**

^{**} Significant at 1% level

The principal component with eigen value and percentage contribution of each component to the total variations are presented in **Table 3** and the same depicted in **Figure 1**. The number of Principal Components calculated from correlation matrix is ten. It is similar to the number of observed traits. The Principal Component one (PC 1) with eigen value of 3.48 contributed 34.80 per cent of the total variability, PC 2 with eigen value of 2.02 accounted for 20.20 per cent and PC 3 had eigen value of 1.17 and contributed 11.70 per cent, and, PC4 had eigen value of 0.94 and accounted for 9.40 per cent of total variability, while the remaining Principal Components (*i.e.* PC 5 - PC 10) had weak or no discriminatory power. Thus, the most important descriptors were those associated with first four principal components. Similarity indices and pattern of relationships among the germplasm collections, the principal component analysis are useful in evaluating the potential breeding value of the lines. Germplasm evaluation and characterization is a routine endeavour for plant breeders, and application of PCA tool, provide a useful means for estimating morphological variability within and between germplasm collections. This tool useful for the evaluation of potential breeding value and were used to detect significant differences between germplasm and magnitude of deviation among crop species.

TABLE 3.
EIGEN VALUES AND VARIABILITY OF NON-ROTATED VALUES OF PRINCIPAL COMPONENTS

Principal Component	Eigen value	Per cent variation	Cumulative variation
1.	3.48	34.80	34.80
2.	2.02	20.20	55.00
3.	1.17	11.70	66.70
4.	0.94	9.40	76.10
5.	0.79	7.90	84.00
6.	0.62	6.20	90.20
7.	0.52	5.20	95.40
8.	0.30	3.00	98.40
9.	0.15	1.50	99.90
10.	0.01	0.10	100.00

^{*} Significant at 5% level

Scree Plot

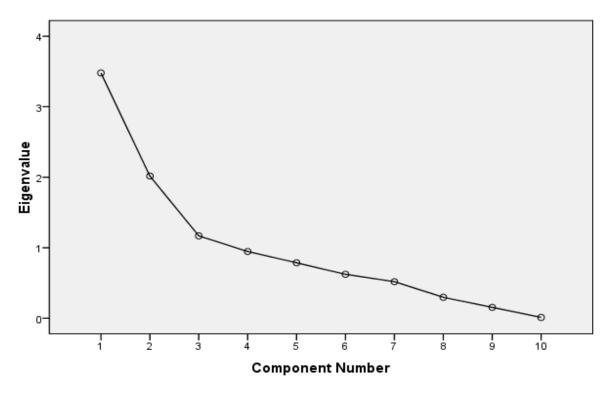


FIG. 1. SCREE PLOT FOR EIGEN VALUE AND TEN PRINCIPAL COMPONENTS OF GUINEA GRASS GERMPLASM ACCESSIONS

The first four PCs (Principal Components) based on non-rotated values accounted for most of the variability among the Guinea grass germplasm collections from different locations are presented in **Table 4**. Principal Component one (PC 1) accounted for 34.80 per cent of the morphological variation in the Guinea grass germplasm collections and was positively loaded on number of tillers per plant (0.715), number of leaves per plant (0.877), leaf weight (0.816), leaf stem ratio (0.731) and green fodder yield per plant (0.454). Thus, this component was the weighted average of the characters which determine the yield level. These traits have the largest participation in the divergence and carry the largest portion of its variability. Using this principal component for genotype differentiation, could distinguished between yielding genotypes with large number of leaves per plant and greatest leaf weight. Similar findings with regard to number of tillers per plant were reported by Salini *et al.* (2010) in *Panicum miliaceum*. Crude protein content (0.271) and crude fat content (0.138) contributed low to the variation, while plant height (-0.634), dry matter content (-0.047) and crude fibre content (-0.544) contributed negatively to the first component.

The second principal component (PC 2) contributed 20.20 per cent of the total variation. The characters that contributed to this component include plant height (0.417), number of tillers per plant (0.130), number of leaves per plant (0.040), leaf weight (0.334), dry matter content (0.798), crude protein content (0.158), crude fibre content (0.413), green fodder yield per plant (0.754). Thus, this component weighted by both productivity and fodder quality characteristics. Hence, the traits green fodder yield per plant as an important productivity factor, as well as dry mater content which is fodder quality determining trait. Similar finding with respect to quality were reported by Mirjana *et al.* (2008) in dry bean.

In the last two principal components (*i.e.* PC 3 and PC 4) fodder quality content is dominant. Correlation of crude protein content with the third principal component is high, as well as crude fat content with the fourth principal component is high. Similar finding with regard to quality were also reported by Mirjana *et al.* (2008) in dry bean.

TABLE 4.

EIGENVECTOR ("WEIGHT") AND EIGEN VALUE ("LOAD") OF THE CORRELATION MATRIX AND THEIR CONTRIBUTION TO TOTAL VARIATION OF GUINEA GERMPLASM COLLECTIONS

S. No.	Variables	PC1	PC2	PC3	PC4
1.	Plant height (cm)	-0.634	0.417	-0.042	-0.268
2.	Number of tillers per plant	0.715	0.130	0.323	-0.375
3.	Number of leaves per plant	0.877	0.040	0.079	0.255
4.	Leaf weight (g)	0.816	0.334	0.086	0.383
5.	Leaf stem ratio	0.731	-0.262	0.078	0.326
6.	Dry matter content (%)	-0.047	0.798	-0.037	-0.087
7.	Crude protein content (%)	0.271	0.158	0.863	-0.150
8.	Crude fibre content (%)	-0.544	0.413	0.498	-0.185
9.	Crude fat content (%)	0.138	-0.493	0.216	0.558
10.	Green fodder yield per plant (g)	0.454	0.754	0.041	0.198
	Eigen value	3.48	2.02	1.17	0.94
	Per cent variation	34.80	20.20	11.70	9.40
	Cumulative variation	34.80	55.00	66.70	76.10

Extraction method: Principal Component Analysis - non rotated values

IV. CONCLUSION

In the present study, Principal Component Analysis showed that cumulative variance of 76.10 per cent by the first four axes with eigen value of greater than 0.88 indicates that the identified traits within the axes exhibited great influence on the phenotype of the tested entries. The variability of the genotypes was interpreted based on four principal components, the first one described the yield level, the second described the productivity and quality level and the last two principal components described the quality of the fodder which indicating that the identified traits within the axes exhibited great influence on the phenotype and this could be effectively used for selection among the tested entries for suitable breeding programme. The variability that are strongly associated in the component traits may share some underlying biological relationship, and these associations are often useful for generating hypothesis for better understanding of behaviour of complex traits that would allow breeders to maximize their knowledge.

REFERENCES

- [1] Adams, M.W. 1995. An estimate of homogeneity in crop plants with special reference to genetic vulnerability in dry season. *Phseolus vulgaris*. **Ephytica**, **26**: 665-679.
- [2] Amy, E.L., Pritts, M.P. 1991. Application of principal component analysis to horticultural research. Hortscience, 26(4): 334-338.
- [3] Mirjana, V., V. Jelica and C. Janko. 2008. Divergence in the dry bean collection by principal component analysis (PCA). **Genetika**, **40** (1): 23 -30.
- [4] Rohlf, F. J., 1998. NTSYS-pc. Numerical taxonomy and multivariate analysis system, version 2.02. Exter Software, Setauket, NY.
- [5] Salini, K., A. Nirmalakumari, AR. Muthiah and N. Senthil. 2010. Evaluation of proso millet (*Panicum miliaceum L.*) germplasm collections. **Electronic Journal of Plant Breeding, 1 (4)**: 489 499.
- [6] Tiwari, K.K. and A. Chandra. 2010. Use of degenerate primers in rapid generation of microsatellite markers in *Panicum maximum*. J. Envir. biol., 31: 965-968.
- [7] UPOV, 2007. TG/248/1 Common millet. 1-37.
- [8] Wouw, M.V.D., M.A. Jorge, J. Bierwirth and J. Hanson. 2008. Characterization of a collection of perennial *Panicum* species. **Tropical Grasslands**, **42**: 40–53.