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Research Note

Morphological characterization and multivariate analysis in little millet

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Abstract
One hundred and ten little millet genotypes were evaluated for 12 morphological traits. When the Principal Component Analysis was performed, the first three PCs exhibited 60.74 per cent of the total variation shown by the 12 traits studied. The 110 genotypes were grouped into five basic groups. The results revealed that single plant grain yield, flag leaf length, thousand grain weight, days to 50 per cent flowering and plant height were the major traits contributing for the overall variability implying that these traits would meet the target of little millet improvement programme. Elucidation of morphological data to determine the pattern of variability within 110 little millet genotypes studied led to the recognition of four clusters. Cluster analysis indicated that little millet genotypes from different geographical regions were observed to group together. The reason could be either due to the fact that selection criteria for the specific traits might be similar particularly based on the adaptive nature of the environment or the same type of consumer preference. This approach would help to identify the traits of importance that possessed the maximum variability for evolving high yielding little millet genotypes.

Keywords
Little millet, Morphological traits, Principle Component Analysis, Cluster analysis

The alarming changes occurring in climatic conditions, particularly the erratic rainfall pattern, water scarcity and increasing temperature pose threat to agriculture and food security globally with special reference to arid and sub-arid regions. Small millets offer both nutritional and livelihood security for human beings and also feed and fodder security for poultry and livestock population in dryland regions of rural India (Pradhan *et al.,* 2010). Among the small millets, littlemillet (*Panicum sumatrense* Roth. ex. Roem. and Schultz.) is an important indigenous and drought resistant crop. It is widely grown in the semiarid tropics of Asia and constitutes a vital source of protein, minerals and vitamins for people living in these areas. Littlemillet is also reported to have 38 per cent of dietary fiber and it has fat content which is higher in polyunsaturated fatty acids. It is the primary source of food in situations where other food grains generally could not be raised or unavailable. Being an eco-friendly crop, it is suitable for vulnerable agro-ecosystems and shall be a preferred crop for sustainable and green agriculture.

Principal Component Analysis (PCA) is a valuable technique from applied linear algebra which may be used to classify the relationships between the traits in multi- trait systems and for identifying the patterns of data by reducing the number of dimensions. An insight into the process contributing differences in yield among the genotypes is essential for identification and selection of top ranking genotypes out of diverse germplasm base. Morphological studies provide information which could be used for practical genotype identification and hypothesizing phylogenetic relationships. The limited information available on many important and basic aspects of neglected and under- utilized crops such as littlemillet, hinder their development. Hence, the present study was planned to choose promising genotypes for their specific traits to be evolved as a high yielding variety or used in a crossing programme.

The experimental material consisted of 110 littlemillet genotypes having their origin from different geographical regions maintained at the Small Millets Germplasm Unit of Department of Millets, Tamil Nadu Agricultural University, Coimbatore (Table.1). The 110 genotypes comprised of 105 germplasm accessions and five check varieties *viz.*, CO 2, CO 3, Paiyur 1, CO (Samai) 4 and OLM 203 and the experiment was laid out in Augmented Block Design (ABD) during *kharif*, 2012 at Millets Breeding Station, Tamil Nadu Agricultural University, Coimbatore. Recommended agronomic practices were followed to maintain a good crop stand. Observations on 12 quantitative traits *viz.*, days to 50 per cent flowering (DF), plant height (PH), basal tillers per plant (BT), culm branches per plant (CB), peduncle length (PEL), panicle length (PL), panicle exertion (PE), flag leaf length (FLL), flag leaf width (FLW), thousand grain weight (TGW), single plant dry fodder yield (DFY) and single plant grain yield (SPY) were recorded on five competitive plants in

each entry based on the descriptors for *Panicum sumatrense* (IBPGR, 1985). All the 12 quantitative traits were subjected to Principal Component Analysis using SPSS 16 software to identify the major contributing traits. The multivariate statistic was used for establishing relationships between the genotypes. The data matrix was used to calculate the correlation among various characters. The correlation coefficient matrix was subjected to eigenvector analysis. The eigenvectors derived were used to extract the first three most informative principal components as suggested by Johnson and Wichern (1988). Those three components were plotted in three dimentional mode in various combinations. The Principal Components with eigen values ≥ 1.0 were considered for selection. The observed data on 12 quantitative characters were analysed using NTSYS- Pc (version 2.0) statistical package for UGPMA dendrogram tree construction.

Quantitative assessment of genotypes: Morphological diversity of 110 littlemillet genotypes was studied in this investigation. The findings of quantitative assessment of these genotypes and key morphological variability observed for the 12 traits have been explained. The PCA performed on the 12 quantitative traits confirmed the existence of high genetic diversity in the littlemillet genotypes used for the experiment. The UPGMA dendrogram revealed four major clusters.

Contribution of characters towards principal component factors:The first three components accounted for 31.84, 50.66 and 60.74 per cent of cumulative variation progressively. The proportion of variation contributed by the individual PC1 and PC2 were 31.84 and 18.81 per cent respectively. The PC1, PC2, PC3 and PC4 alone had eigen values greater than one (Table.2 and Fig. 1a). As shown in table 3 the PC1 had high positive loadings for flag leaf width (0.878) followed by plant height (0.865), days to 50 per cent flowering (0.541), single plant dry fodder yield (0.475) and panicle length (0.468). This implied that these five traits were positively correlated with grain yield and selection should be exercised accordingly. On the other hand, it had high negative loading for culm branches per plant (-0.810) and thousand grain weight (-0.771). This in-turn expressed that these two characters were negatively correlated with grain yield. Hence, it is important to select genotypes having optimum plant height, medium duration, high biomass, lengthier panicles and medium test weight with non branching culms for high grain yield. The PC2 axis might be regarded as a yield vector having high factor loadings for single plant grain yield (0.828) along with flag leaf length (0.829), panicle length (0.593) and peduncle length (0.555). The PC3 could be considered as important with reference to selection of plants having more number of basal tillers per plant.

The three dimentional spatial figuration showed six groups of the traits studied (Fig.1b). Group I had two traits *viz*., single plant grain yield and flag leaf length which were confirmed through PC2 also. Group II had three traits (flag leaf width, plant height and days to 50 % flowering) clustered together which were revealed in PC1. Three traits namely, basal tillers per plant, thousand grain weight and peduncle length were found clustered together in group III. The group IV had panicle exertion and single plant dry fodder yield and the group V had panicle length and culm branches per plant together. The trait, flag leaf length contributed more towards single plant grain yield whereas more number of basal tillers per plant contributed towards bold seeds and were clustered together. Several authors indicated that different morphological traits had contributed their role in overall variability observed among the germplasm resources (Lule *et al*., 2011 and Dagnachew Lule *et al*., 2012 in fingermillet).

Grouping of genotypes through Cluster analysis:The UPGMA dendrogram revealed four major clusters (Table 4) and the cluster I consisted 30 genotypes. They were found divided into two separate sub groups. Sub group one comprised of eight genotypes, which had medium duration to flowering, optimum number of basal tillers, multi branched, average single plant grain yield and medium size seeds. The sub group two was composed of 22 genotypes which were characterized by high single plant grain yield. Both the sub groups differed from one another with respect to its single plant grain yield, though the genotypes in cluster I had been collected from Tamil Nadu only.

The cluster II also had 30 genotypes. They in-turn comprised of four sub groups having 4, 6, 4 and 16 genotypes respectively. The sub group one contained the genotypes, TNPsu 10, IPM 59, TNPsu 24/79 and TNPsu 8/78 which were characterized by early flowering duration, dwarf plant stature, average grain yield and medium seed size. Genotypes, CO 2, TNPsu 7, IPM 232, TNPsu 7/ 79, TNPsu 6 and TNPsu 4 were together placed in subgroup two which were characterized by dwarf plant stature, medium flowering duration, average grain yield and medium seed size. Sub group three comprised of genotypes TNPsu 35, TNPsu 31, TNPsu 3 and TNPsu 15 which had dwarf plant stature, late flowering duration, average grain yield and medium seed size. Remaining 16 genotypes were placed together in sub group four and they had late flowering, tall plant stature, average yield and medium size seed characteristics.

Thirty genotypes placed together in cluster III had seven sub groups. Group 1 contained the maximum number of individuals (11) followed by group 4 (7), group 3 (6), group 5(3) and group 2, group 6 and group 7 had a single genotype. Genotypes in sub group one were characterized by tall plant stature, medium flowering duration, non branched culms , broad leaves, average yield and small size seeds. The only one genotype PM 29 in sub group two differed from other genotypes by tall plant stature, late flowering, high yield and bold seeds. Six genotypes *viz.*, IPM 272, MS 3969, TNPsu 18, CO 3, TNPsu 24 and TNPsu 13 together placed in sub group three were characterized by dwarf, early flowering, high yield and bold seeds. The sub group four composed of seven genotypes which had dwarf, early flowering, average yield and bold seeds. Genotypes, MS 662, MS 4700/1 and TNPsu 29 were placed in sub group five which were dwarf in plant stature, early flowering and low yielder with bold seeds while, sub group six had a single genotype, TNPsu 16/78, which was dwarf, early flowering and average yielder with medium seed size. Genotype, TNPsu 14 constituted sub group seven which had dwarf plant stature, medium flowering duration, average yield and small size seeds.

Cluster IV was formed by 20 individuals which were characterized by tall plant stature, late flowering, low tillering capacity, non branching culms, longer flag leaf, broad leaves, average grain yield and small size seeds.

First and second sub groups of cluster I, first, second and third sub groups of cluster II and fifth, sixth and seventh sub groups of cluster III had accessions collected from Tamil Nadu only. These genotypes showed parallelism between geographical origin and genetic diversity. The reason for these accessions from geographical origin grouped into distinct clusters might be due to the identical genetic architecture among them. This is in agreement with the earlier findings of Nagarajan and Prasad (1980) and Manoharan and Sivasubramanian (1988) in prosomillet. Accessions of different geographical origins *viz.*, Karnataka, Andhra Pradesh, Bihar and Madhya Pradesh were grouped together into fifth sub group of cluster II. This would be due to the similarity of objectives and conditions under which these genotypes were bred and domesticated in different localities.

First sub group of cluster III had accessions from Odisha and Andhra Pradesh, which indicated that these genotypes were evolved under similar selection pressure irrespective of their geographic origins. It is due to differential adaptation of various accessions belonging to same eco geographic region. Also the similarity could be either due to the fact that farmer's selection criteria for a given trait might be similar particularly based on the adaptive role of the traits for the environment or the primary parental seed source could be the same. However, early and quick seed exchange might also be an additional reason for grouping of genotypes from different regions into one cluster. Such supportive results were reported by Reddy *et al*. (2009) and Andualem Wolie and Ketema Belete (2013) in fingermillet.

Conclusion: From this experiment, it is observed that the first three principal components contributed the maximum variability by more number of characters to aid selection and this could in-turn be effectively used for further breeding programmes. In addition, the results implied that the important traits such as, single plant grain yield, thousand grain weight, flag leaf length, plant height and panicle length were the important contributors for the variability. Hence, selection should be exercised for grain yield enhancement using these traits.

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Table 1. List of little millet genotypes used for evaluation

S.No	Genotype	Origin
1	TNPsu 1/79	Tamil Nadu
2	TNPsu 2	Tamil Nadu
3	TNPsu 3	Tamil Nadu
4	TNPsu 4	Tamil Nadu
5	TNPsu 5	Tamil Nadu
6	TNPsu 6	Tamil Nadu
7	TNPsu 7	Tamil Nadu
8	TNPsu 7/79	Tamil Nadu
9	TNPsu 8	Tamil Nadu
10	TNPsu 8/78	Tamil Nadu
11	TNPsu 9	Tamil Nadu
12	TNPsu 10	Tamil Nadu
13	TNPsu 11	Tamil Nadu
14	TNPsu 12	Tamil Nadu
15	TNPsu 13	Tamil Nadu
16	TNPsu 14	Tamil Nadu
17	TNPsu 15	Tamil Nadu
18	TNPsu 16	Tamil Nadu
19	TNPsu 16/78	Tamil Nadu
20	TNPsu 17	Tamil Nadu
21	TNPsu 18	Tamil Nadu
22	TNPsu 19	Tamil Nadu
23	TNPsu 21	Tamil Nadu
24	TNPsu 22	Tamil Nadu
25	TNPsu 23	Tamil Nadu
26	TNPsu 24	Tamil Nadu
27	TNPsu 24/79	Tamil Nadu
28	TNPsu 25	Tamil Nadu
29	TNPsu 26	Tamil Nadu
30	TNPsu 27	Tamil Nadu
31	TNPsu 28	Tamil Nadu
32	TNPsu 29	Tamil Nadu
33	TNPsu 30	Tamil Nadu
34	TNPsu 31	Tamil Nadu
35	TNPsu 32	Tamil Nadu
36	TNPsu 33	Tamil Nadu
37	TNPsu 34	Tamil Nadu
38	TNPsu 35	Tamil Nadu
39	MS 108	Tamil Nadu
40	MS 109	Tamil Nadu
41	MS 110	Tamil Nadu
42	MS 115	Tamil Nadu

Table 1. Contd..

S.No	Genotype	Origin
43	MS 509	Tamil Nadu
44	MS 662	Tamil Nadu
45	MS 1003/1	Tamil Nadu
46	MS 1211	Tamil Nadu
47	MS 1236	Tamil Nadu
48	MS 1826	Tamil Nadu
49	MS 3969	Tamil Nadu
50	MS 4527	Tamil Nadu
51	MS 4684	Tamil Nadu
52	MS 4700	Tamil Nadu
53	MS 4700/1	Tamil Nadu
54	MS 4725	Tamil Nadu
55	MS 4729	Tamil Nadu
56	MS 4735	Tamil Nadu
57	MS 4779	Tamil Nadu
58	MS 4784	Tamil Nadu
59	PM 29	Madhya Pradesh
60	PM 42	Bihar
61	PM 141	Madhya Pradesh
62	PM 143	Karnataka
63	PM 295	Andhra Pradesh
64	PM 295/1	Madhya Pradesh
65	PM 296	Bihar
66	PM 307	Andhra Pradesh
67	PM 410	Karnataka
68	IPM 59	Patancheru, Andhra Pradesh
69	IPM 115	Patancheru, Andhra Pradesh
70	IPM 118	Patancheru, Andhra Pradesh
71	IPM 221	Patancheru, Andhra Pradesh
72	IPM 221/A	Patancheru, Andhra Pradesh
73	IPM 226	Patancheru, Andhra Pradesh
74	IPM 231	Patancheru, Andhra Pradesh
75	IPM 232	Patancheru, Andhra Pradesh
76	IPM 272	Patancheru, Andhra Pradesh
77	IPM 838	Patancheru, Andhra Pradesh
78	IPM 884	Patancheru, Andhra Pradesh
79	IPM 895	Patancheru, Andhra Pradesh
80	IPmr 700	New Delhi
81	IPmr 709	New Delhi
82	IPmr 712	New Delhi
83	IPmr 712/1	New Delhi
84	IPmr 837	New Delhi
85	IPmr 838/1	New Delhi
86	IPmr 839	New Delhi
87	IPmr 841	New Delhi
88	IPmr 857	New Delhi

Table 1. Contd..

S.No	Genotype	Origin
89	IPmr 859	New Delhi
90	IPmr 861	New Delhi
91	IPmr 862	New Delhi
92	IPmr 886	New Delhi
93	IPmr 889	New Delhi
94	IPmr 891	New Delhi
95	IPmr 1018	New Delhi
96	IPmr 1046	New Delhi
97	IPmr 1061	New Delhi
98	PMR 762	Banglore, Karnataka
99	RPM 8-1	Madhya Pradesh
100	RPM 11	Madhya Pradesh
101	ARP 9	Tamil Nadu
102	OLM 112	Odisha
103	OLM 114	Odisha
104	OLM 115	Odisha
105	TNPsu 141	Tamil Nadu
106	Paiyur 1	Tamil Nadu
107	CO 2	Tamil Nadu
108	CO 3	Tamil Nadu
109	CO(Samai) 4	Tamil Nadu
110	OLM 203	Odisha

Table. 2 Eigen values and the proportion of total variability among little millet genotypes as explained by the Principal Components

Principal Component	Eigen value	Proportion of variation (%)	Total variation explained across axis (%)
1	3.82	31.84	31.85
2	2.26	18.81	50.66
3	1.21	10.08	60.74
4	1.03	8.56	69.30
5	0.93	7.71	77.01
6	0.74	6.19	83.20
7	0.58	4.88	88.08
8	0.45	3.76	91.84
9	0.37	3.11	94.95
10	0.23	1.92	96.87
11	0.21	1.80	98.67
12	0.16	1.33	100 .00

Table 3. Eigen value, factor scores and contribution of the first five principal component axes to variation in littlemillet genotypes

Characters	Principal components				
	PC1	PC2	PC3	PC4	PC5
Plant height (cm)	0.865	0.200	0.056	0.026	0.140
Days to 50 % flowering	0.541	-0.135	-0.463	-0.342	0.076
Basal tillers per plant	-0.368	0.216	0.622	-0.238	0.273
Culm branches per plant	-0.810	-0.061	-0.116	0.122	0.081
Peduncle length (cm)	-0.118	0.555	-0.429	0.503	0.221
Panicle length (cm)	0.468	0.593	-0.176	0.103	0.446
Panicle exertion (cm)	0.338	-0.091	0.408	0.715	-0.240
Flag leaf length (cm)	-0.157	0.829	-0.008	-0.090	-0.397
Flag leaf width (cm)	0.878	-0.023	0.030	-0.016	-0.177
Single plant dry fodder yield (g)	0.475	0.296	0.455	-0.104	0.336
Thousand grain weight (g)	-0.771	0.140	0.008	0.052	0.288
Single plant grain yield (g)	-0.162	0.828	0.043	-0.205	-0.358

Table 4. Grouping of little millet genotypes based on quantitative characters

Cluster	Sub group	Number of genotypes	Genotypes
I	1	8	MS 4779,IPM 118, OLM 114, TNPsu 16, ARP 9, MS 4527, MS 108, TNPsu 2
	2	22	TNPsu 17, MS 4729, MS 509, TNPsu 23, TNPsu 25, TNPsu 19, TNPsu 22, CO (Samai)4, TNPsu 21, TNPsu 12, MS 4684, MS 1826, MS 110, MS 4700, TNPsu 27, MS 4784, MS 1236, TNPsu 9, TNPsu 28, MS 1003/1, MS 1211 and TNPsu 1/79
II	1	4	TNPsu 10, IPM 59,TNPsu 24/79, TNPsu 8/78
	2	6	CO2, TNPsu 7, IPM 232, TNPsu 7/79, TNPsu 6, TNPsu 4
	3	4	TNPsu35, TNPsu 31, TNPsu 15, TNPsu 3
	4	16	PM 42, PM 307, IPM 221, PM 141, IPM 115, PM 410, PM 143, TNPsu 33, RPM8-1, TNPsu 34, TNPsu 32, IPM 221/A, MS 109, PM 295/1,PM 295,TNPsu 11
III	1	11	IPmr 861,IPmr 889, IPmr 884, IPM 226, IPmr 891, IPmr 1046, OLM 115, IPmr 1061, OLM 112, IPmr 862, TNPsu 26
	2	1	PM 29
	3	6	IPM 272, MS 3969, TNPsu18, CO 3, TNPsu 24, TNPsu 13
	4	7	Paiyur 1, MS 4725, MS 115, TNPsu 30, RPM 11, PMR 762, TNPsu 5
	5	3	MS 662, MS 4700/1, TNPsu 29
	6	1	TNPsu 16/78
	7	1	TNPsu 14
IV	1	20	TNPsu 8, TNPsu 141, OLM 203, IPmr 886, IPM 838, PM 296, IPmr 1018, MS 4735, IPmr 700, IPmr 857, IPmr 859, IPmr 841, IPmr 839, IPmr 838/1, IPM 895, IPmr 837, IPmr 712/1, IPmr 712, IPmr 709, IPM 231

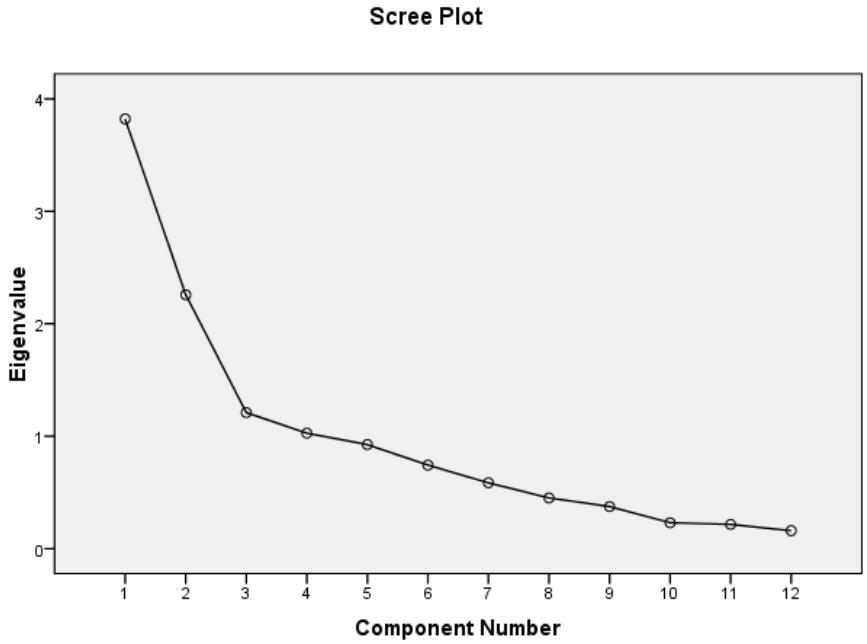

Fig. 1(a) Scree plot for 12 quantitative traits in 110 littlemillet genotypes

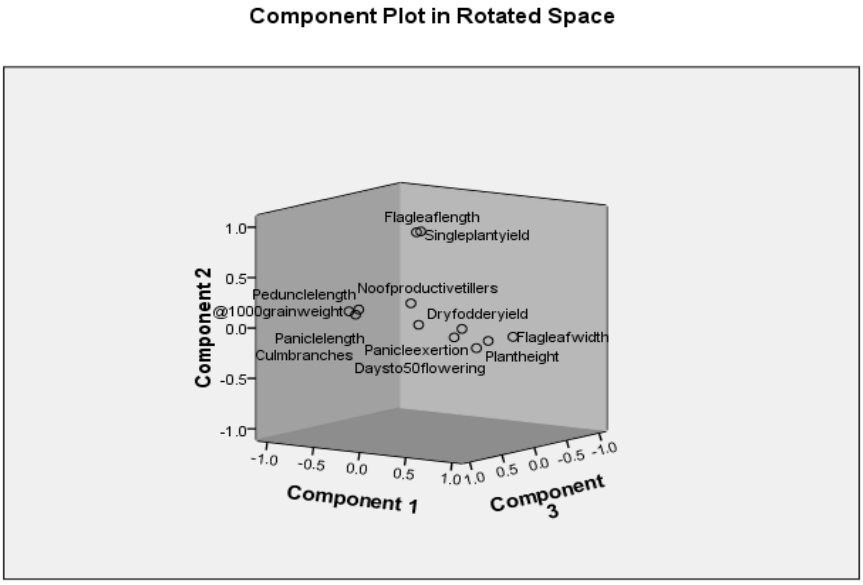

Fig. 1(b) Three dimentional plot for 12 quantitative traits in 110 littlemillet genotypes