

Original Research Article

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## Principal Component Analysis in Genetic Resources of Chinese Millet (*Setaria italica* (L.) Beauv.)

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### ABSTRACT

#### Keywords

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Field experiment was conducted in 50 Chinese millet genetic resources to assess the genetic divergence for 12 metric traits through Principal Component Analysis. The ANOVA revealed existence of highly significant variation for all the traits examined. About 69.15 *per cent* of total variation accrued through Principal component analysis exhibited four Principal components (PC1-29.65%, PC2-16.94%, PC3-12.27% and PC4-10.27%) retained based on the Scree plot and threshold Eigen value greater than one (>1). The PC1 with prime economical traits *viz.*, days to 50% flowering, days to maturity, culm branches, thousand grain weight, number of productive tillers / plant and flag leaf blade length accounted for maximum variance (29.65%) connoting that these traits be given priority in future Chinese millet breeding programmes.

### Introduction

Among the Small millets, Chinese millet popularly known as Foxtail millet, German millet, Italian millet, Red Rala millet and Korra (Andhra Pradesh) ranks second in production next to finger millet in our country. According to Vavilov, China is the considered as the centre of origin for this crop. Post green revolution, the cultivation of this small millet is slowly expanding owing to its distinct nutraceutical properties and ability to withstand biotic and abiotic stresses. In terms of area and turnover, this minor millet accounts for 80 k ha. -900 kg ha<sup>-1</sup> and 51 k ha.

- 945 kg ha<sup>-1</sup> in India and Andhra Pradesh, respectively (Annual report, 2016-17). Wide gene base in Chinese millet provides ample scope for breeders to exploit through various breeding strategies and generate cultigens with promising traits suited to climate resilient agriculture. Moreover, estimates of genetic relationships can be useful for identification of parents for hybridization, and for reducing the number of accessions needed to maintain a broad range of genetic variability (Bezaweletaw, 2011). Principal component analysis (PCA), a multivariate technique is used to classify the genetic relationships between the traits in multi-trait systems and

for identifying the patterns of data by reducing the number of dimensions. It also provides an insight into the process contributing differences in yield among genetic resources, a vital aspect in identification and selection of top ranking genetic resources out of diverse germplasm base. PCA results in generation of a 2D / 3D scatter plot of individuals and characters, whose geometrical distances helps in identification of correlated traits and identification of sets of genetically similar individuals (Mohammadi, 2003).

### **Materials and Methods**

Fifty genetic resources of Chinese millet were raised during *khariif*, 2017 in a completely randomized block design replicated thrice at Regional Agricultural Research Station, Nandyal, Andhra Pradesh, India. Recommended crop production practices and plant protection measures suggested for this crop were scrupulously followed to raise a healthy crop. Inter-Intra row spacing of 22.5 x 10 cm was adopted. Twelve metric traits *viz.*, days to 50 per cent flowering, days to maturity, plant height, flag leaf blade length, flag leaf blade width, peduncle length, peduncle exertion, panicle length, culm branches, number of productive tillers / plant, thousand grain weight and grain yield / plant were recorded on five randomly selected plants in each entry per replication. The data was subjected to statistical analysis for PCA using the software WINDOWSTA of 9.2 version as per the procedure outlined by Rao (1952).

### **Results and Discussion**

The analysis of variance for 12 metric traits in 50 Chinese millet genetic resources (Table 1) revealed existence of ample genetic variation in the material, an important pre-requisite that paved way for further diversity analysis. The canonical root values, *per cent* of variation

and cumulative variation elucidated for 50 Chinese millet genetic resources were presented in Table 2. Through principal component analysis (PCA), the number of variables was reduced to linear functions *viz.*, 'canonical vectors' that accrued for much of the variation exhibited by traits studied. The mean values of canonical variates for three roots X, Y and Z. Two dimensional (2D) and three dimensional (3D) illustrations (Fig. 1 and 2) were constructed by plotting the mean values of vectors. The amount of contribution of various traits in canonical vectors to the total divergence is known. PCA identified four PCs that accounted for 69.15 *per cent* of total divergence (Table 3). The first and second roots contributed 29.65 and 16.94 *per cent* variabilities respectively to total variability. The remaining two PCs *viz.*, third and fourth showed variabilities of 12.27 and 10.27 *per cent* respectively towards the total variability. These four PCs were retained (Fig. 3) based on the Scree plot and threshold eigen value greater than one (>1).

In the vector  $Z_1$ , traits contributing towards total divergence positively were 1000 grain weight (0.26), number of productive tillers / plant (0.23), culm branches (0.30), flag leaf blade length (0.22), plant height (0.25), days to 50% flowering (0.47) and days to maturity (0.46). For the vector  $Z_2$ , days to 50% flowering (0.07) and culm branches (0.08) contributed positively to the genetic diversity. In the vector  $Z_3$ , the traits *viz.*, days to 50% flowering (0.09), peduncle length (0.30), peduncle exertion (0.45), flag leaf blade width (0.04) and culm branches (0.06) had contributed positively to diversity. Flag leaf blade length (0.29) and grain yield / plant (0.29) together contributed maximum to the diversity in vector  $Z_4$  followed by days to maturity (0.28), days to 50% flowering (0.27), peduncle exertion (0.12), plant height (0.09), peduncle length (0.07) and flag leaf blade width (0.02) (Table 4).

**Table.1** ANOVA for grain yield and yield attributes in 50 Chinese millet genetic resources

S. No.	Characters	Mean squares		
		Replications (df:2)	Genotypes (df:49)	Error (df:98)
1.	Days to 50% flowering	3.02	35.96**	2.37
2.	Days to maturity	4.53	37.07**	3.09
3.	Plant height	104.27	275.89**	69.31
4.	Peduncle length	11.61	33.63**	4.83
5.	Peduncle exertion	4.61	24.15**	6.15
6.	Panicle length	5.30	15.09**	4.97
7.	Flag leaf blade length	21.33	23.88**	10.30
8.	Flag leaf blade width	0.049	0.056**	0.019
9.	Culm branches	0.002	2.39**	0.06
10.	Number of productive tillers / plant	0.28	0.74**	0.12
11.	1000 grain weight	0.013	0.13**	0.00
12.	Grain yield / plant	0.60	1.60**	0.21

\*\* 1% level of Significance

**Table.2** Canonical root values, per cent of variation and cumulative variation explained for 50 Chinese millet genetic resources

Canonical root	Value of canonical root	percent of variation accounted for	Cumulative total variation accounted for
Z <sub>1</sub>	3.55	29.65	29.65
Z <sub>2</sub>	2.03	16.94	46.59
Z <sub>3</sub>	1.47	12.27	58.87
Z <sub>4</sub>	1.23	10.27	69.15

**Table.3** Canonical vectors for 12 characters in 50 Chinese millet genetic resources

S. No	Character	Z <sub>1</sub>	Z <sub>2</sub>	Z <sub>3</sub>	Z <sub>4</sub>
1.	Days to 50% flowering	0.47	0.07	0.09	0.27
2.	Days to maturity	0.46	-0.01	-0.01	0.28
3.	Plant height	0.26	-0.46	-0.03	0.09
4.	Peduncle length	-0.02	-0.61	0.30	0.07
5.	Peduncle width	-0.22	-0.28	0.45	0.12
6.	Panicle length	-0.19	-0.16	-0.49	-0.30
7.	Flag leaf blade length	0.22	-0.19	-0.36	0.29
8.	Flag leaf blade width	-0.36	-0.28	0.04	0.02
9.	Culm branches	0.30	0.08	0.06	-0.34
10.	No. of productive tillers / plant	0.23	-0.13	0.00	-0.60
11.	1000 grain weight	0.26	-0.38	-0.16	-0.29
12.	Grain yield / plant	-0.18	-0.16	-0.55	0.29
	Eigen Value (Root)	3.56	2.03	1.47	1.23
	Expression of /centage variance	29.65	16.94	12.27	10.27
	Expression of cumulative variance	29.65	46.60	58.87	69.15

**Table.4** Mean values of canonical vectors for 50 Chinese millet genetic resources

S. No.	Genotype	X Vector	Y Vector	Z Vector
1.	SiA-3347	38.374	-14.128	3.615
2.	SiA-3340	38.982	-15.310	4.548
3.	SiA-3355	35.068	-17.795	2.966
4.	SiA-3382	35.774	-16.441	3.641
5.	SiA-3085	35.383	-14.389	2.304
6.	SiA-3383	35.543	-15.908	1.593
7.	SiA-3398	38.320	-17.800	3.042
8.	SiA-3327	33.638	-17.171	3.185
9.	SiA-3407	36.585	-16.922	2.462
10.	SiA-3376	36.337	-17.026	3.859
11.	SiA-3403	36.383	-16.804	3.190
12.	SiA-3222	25.337	-15.157	2.107
13.	SiA-3318	33.574	-14.772	3.804
14.	SiA-3381	32.675	-18.136	2.381
15.	SiA-3377	35.184	-14.051	2.966
16.	KDR	34.492	-15.806	2.671
17.	SiA-3447	37.012	-15.093	2.843
18.	SiA-3399	36.752	-15.522	2.885
19.	SiA-3395	36.224	-16.324	2.361
20.	Narasimharaya	35.830	-16.761	1.956
21.	SiA-3335	34.169	-16.162	1.240
22.	Prasad	35.436	-16.195	3.991
23.	SiA-3386	35.083	-17.501	2.181
24.	SiA-3363	35.765	-18.063	4.018
25.	SiA-3354	33.891	-16.661	2.782
26.	SiA-3375	34.579	-16.530	4.088
27.	SiA-3333	35.101	-16.376	2.763
28.	SiA-3369	37.262	-13.026	3.383
29.	SiA-3378	35.305	-18.832	3.203
30.	SiA-3328	36.604	-14.473	3.318
31.	SiA-3346	36.666	-16.980	1.408
32.	SiA-3392	36.588	-18.226	2.367
33.	SiA-3156	35.475	-16.484	0.936
34.	Suryanandi	34.984	-16.844	3.297
35.	ISC-379	35.390	-15.948	4.040
36.	SiA-3397	38.245	-17.332	3.609
37.	SiA-3390	36.007	-17.747	3.038
38.	SiA-3393	34.261	-13.040	4.299
39.	SiA-3396	37.737	-15.525	3.466
40.	SiA-3364	35.142	-17.973	3.327
41.	SiA-3405	35.940	-15.525	5.053
42.	SiA-3322	32.858	-17.280	5.295
43.	SiA-3367	36.024	-15.247	3.188
44.	SiA-3394	33.545	-15.247	2.738
45.	SiA-3384	38.991	-16.041	3.336
46.	SiA-3400	37.291	-16.986	3.118
47.	SiA-3404	36.799	-17.077	1.852
48.	SiA-3401	36.401	-13.953	2.765
49.	Sri lakshmi	36.420	-16.354	1.890
50.	SiA-3389	36.532	-15.295	3.553

Fig.1 Two dimensional (2D) plot of canonical analysis

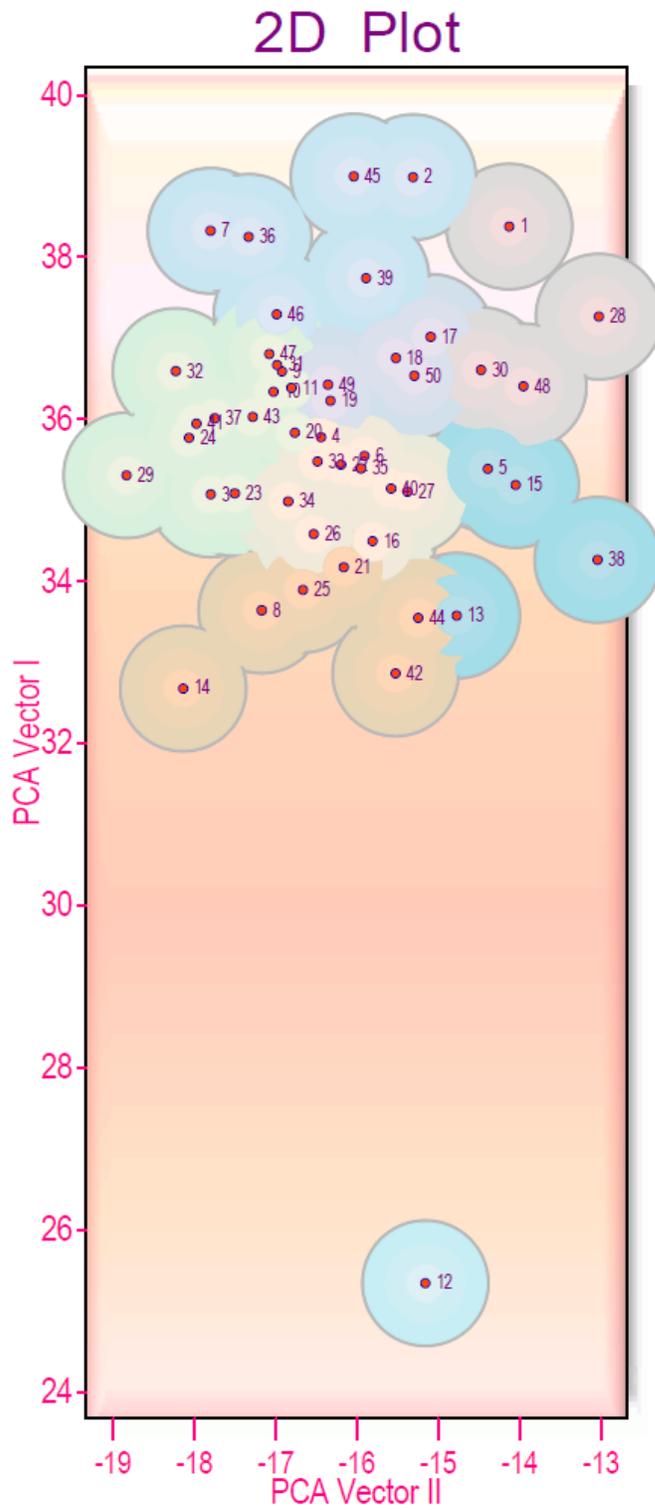
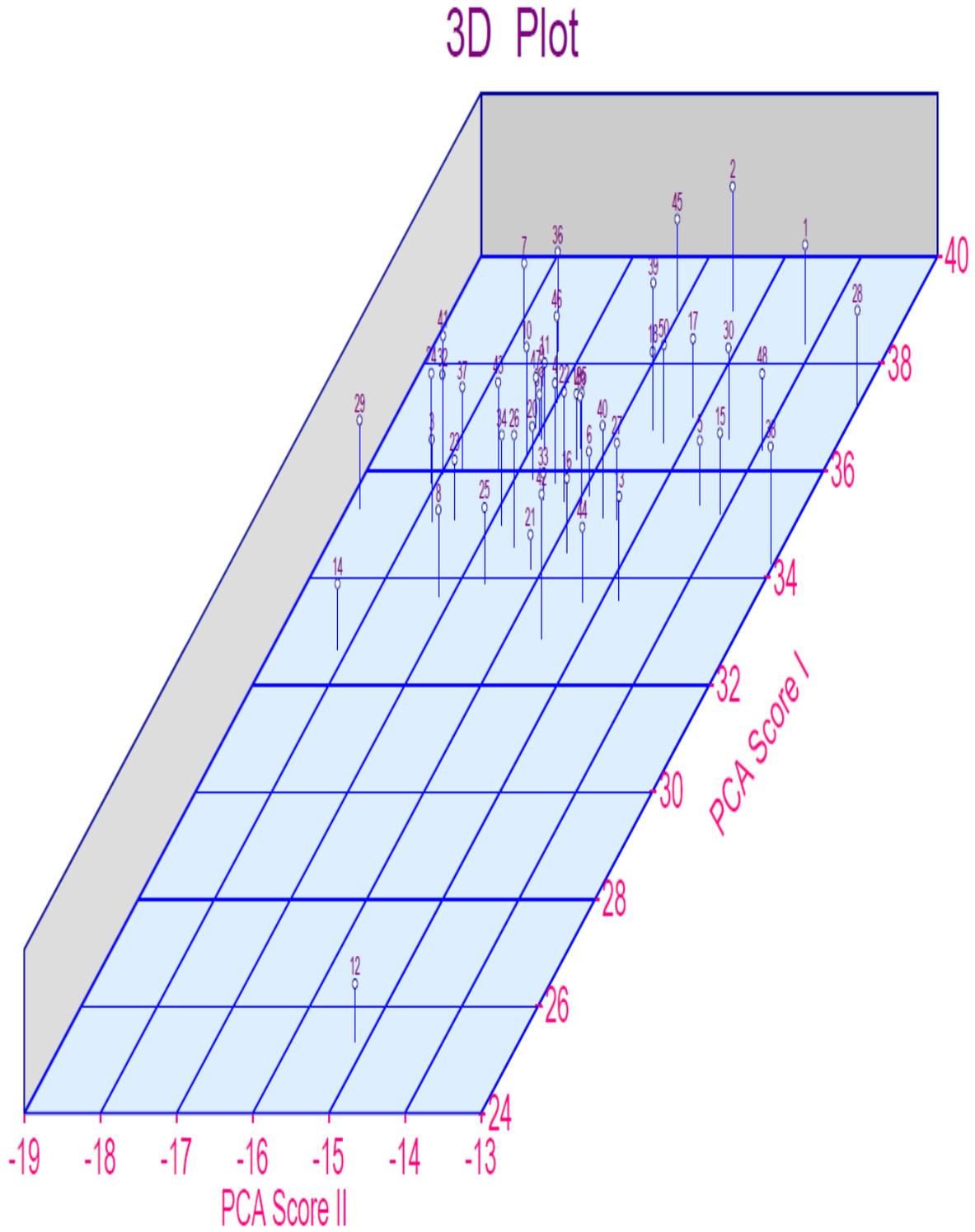
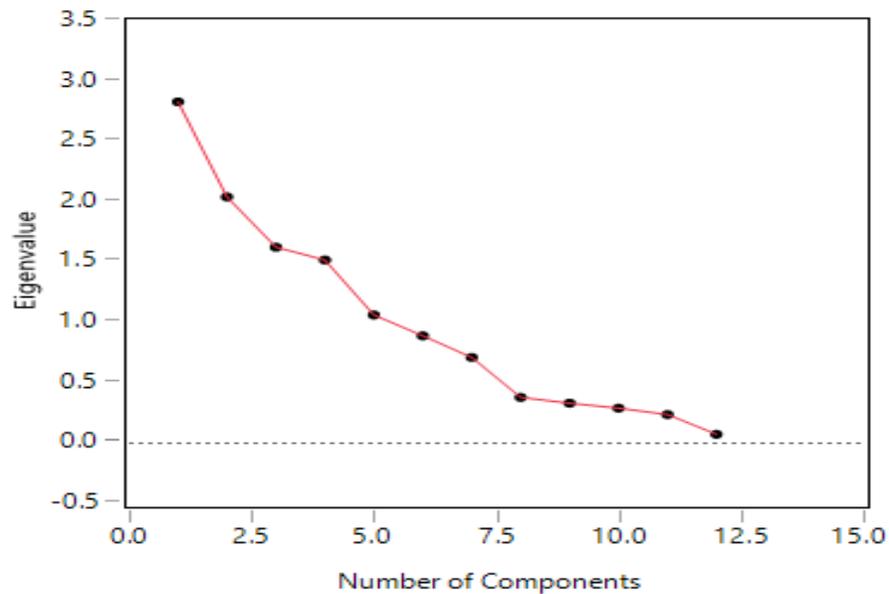


Fig.2 Three dimensional (3D) plot of principal component analysis



**Fig.3** Scree plot showing the Eigen value variation for 12 quantitative traits in 50 Chinese millet genetic resources



In a nut shell, the PCA results of the present study revealed that four PCs retained based on the Scree plot and threshold Eigen value greater than one (>1) contributed much (69.15 per cent) of total genetic divergence.

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