

Principal Component Analysis in Inbreds of Maize (*Zea mays* L.)

S. Sandeep^{1*}, M. Bharathi¹ and V. Narsimha Reddy²

¹ Department of Genetics and Plant Breeding, PJTSAU, Rajendranagar, Hyderabad (500 030) India

² Maize Research Centre, A.R.I, PJTSAU, Rajendranagar, Hyderabad (500 030) India

*Corresponding Author E-mail: siluverusandeep088@gmail.com

Received: 12.07.2017 | Revised: 25.07.2017 | Accepted: 26.07.2017

ABSTRACT

The present study was carried out at college farm, College of Agriculture, PJTSAU, Rajendranagar, Hyderabad during kharif, 2013 with sixty inbreds lines of maize. Principal component analysis revealed that the three vectors accounted for 82.41 per cent of the total variability produced by all the characters under study. The first canonical vector (PC I) accounted for 58.36 percent of the total variability followed by second vector (PC II) accounted for 16.11 percent of total variability and vector III (PC III) which accounted for 7.94 percent total variance. The sixty genotypes were grouped into eight clusters. Cluster I and III were largest comprising of 12 genotypes each followed by cluster IV (11 genotypes), cluster VI (8 genotypes), cluster II (5 genotypes), cluster V (3 genotypes), and cluster VIII (1 genotype). The characters plant height and grain yield per plant and days to 50% tasseling are major contributors to the total divergence.

Key words: Maize, Clusters, Principal component analysis.

INTRODUCTION

Maize is one of the most important cereal crops of the world after wheat and rice. In India it is being cultivated in an area of 8.71 m ha with a production of 22.26 mt, and an average productivity of 2.56 t/ha. (Department of Agriculture and Co-operation, 2014)¹. Maize has myriad of uses in food, feed and industrial segment. Maize has attained a prominent position as an industrial crop because 75% of its produce is used in starch and feed industries. In addition to staple food

for human being and quality feed for animals, maize serves as a basic raw material and ingredient to thousands of industrial products that includes starch, oil, protein, alcoholic beverages, food sweeteners, pharmaceutical, cosmetic, film, textile, gum, package and paper industries etc. In canonical variate analysis, the number of variables is reduced to linear functions called canonical vectors which accounts for most of the variation produced by these characters.

Cite this article: Sandeep, S., Bharathi, M. and Reddy, V.N., Principal Component Analysis in Inbreds of Maize (*Zea mays* L.), *Int. J. Pure App. Biosci.* 5(4): 2008-2013 (2017). doi: <http://dx.doi.org/10.18782/2320-7051.5762>

MATERIALS AND METHODS

The experimental material consisted of sixty inbreds of maize sown in randomized block design with three replications at College of Agriculture, Rajendranagar, PJTSAU, Hyderabad. Each entry was sown as two rows of 4 meter length with row-to-row and plant-to-plant distance of 75 cm and 20 cm respectively. All the recommended package of practices were followed in order to raise a healthy crop. Observations were recorded on five randomly selected plants for plant height, ear height, ear length, ear girth, number of kernel rows per ear, number of kernels per row, 100-kernel weight, grain yield per plant and shelling percentage. However, observations for the characters namely days to 50 per cent tasseling, days to 50 per cent silking, days to maturity were recorded on plot basis. Canonical variate analysis was used to analyze the clustering pattern and canonical roots vectors were calculated to present the genotypes in the graphical form (Rao, 1952)². Statistical analysis was done using Windostat version 9.1

RESULTS AND DISCUSSION

The eigene values, percent variance, per cent cumulative variance and factor loading of different characters studied are given in Table 1. In canonical variate analysis, the number of variables is reduced to linear functions called canonical vectors which accounts for most of the variation produced by these characters. The three vectors accounted for 82.41 per cent of the total variability produced by all the characters under study. The first canonical vector (PC I) accounted for 58.36 percent of the total variability. It could be seen from the first vector that the variables plant height (0.684), grain yield per plant (0.468) and ear length (0.263) had maximum positive contribution towards divergence and the characters days to 50% silking (-0.005) and shelling percentage (-0.248) had negative contribution towards divergence. The second vector (PC II) accounted for 16.11 percent of total variability and the traits like shelling percentage (-0.118), ear girth (-0.137), ear length (-0.158), number of kernels per row (-

0.214), grain yield per plant (-0.215) and 100 seed weight (-0.246) showed maximum negative contribution towards divergence and the character days to 50% tasseling (0.695), days to maturity (0.514), number of kernel rows per ear (0.170), days to 50% silking (0.113), ear height (0.031) and plant height (0.021) contributed positively towards genetic divergence. In vector III (PC III) which accounted for 7.94 percent total variance, the characters number of kernels per row (0.499), ear length (0.204) and grain yield per plant (0.200) had maximum positive contribution, while 100 seed weight (-0.674), plant height (-0.332) and shelling percentage (-0.204) had maximum negative contribution towards genetic diversity.

Canonical graph:

The principal factor scores of the canonical vectors for the first three roots PC I (Z_1), PC II (Z_2) and PC III (Z_3) are presented in Table 2. The mean scores of the first two canonical vectors were used to obtain graphical depiction of the genetic distance of the 60 genotypes. Using these scores, all the genotypes (numbers assigned to them) were plotted for PC I and PC II which cumulatively explained 74.47 percent variability and accounted for the most important yield contributing characters. The scatter plot of PC scores of the first two PC axes is presented in Figures 1 and 2. The canonical root analysis in the present study accounted for 82.41 percent. For getting clear association of two dimensional representation of variation, the first three canonical roots should be more than 95 percent according to Patel *et al.* (1989)³ On the contrary, the three canonical vectors as a whole contributed only for 82.41 percent towards genetic diversity because of which discernible overlapping which was observed in group constellations of canonical vectors. Most of the entries accumulated towards the right side of the PC II axis. Along the PC I axis, most of the entries accumulated towards the middle of the axis which accounts for the traits viz., plant height, grain yield per plant and days to 50% tasseling with positive contribution towards divergence. The plot of PC I - PC II accounting for 74.47

per cent variation showed clear differentiation of genotypes according to their cluster membership. Genotypes belonging to common clusters have fallen nearer to each other and vice versa thereby confirming the results of clustering. The clusters formed by grouping of sixty genotypes by principal component analysis was eight. Regarding clustering pattern, clusters I and III were largest comprising of 12 genotypes each followed by cluster IV (11), cluster VI (8), cluster II (5), cluster V (3), and cluster VIII (1). The clustering pattern of genotypes by Principal component analysis as shown in Table 3. The pattern of distribution of genotypes into different clusters was at random (or independent from their geographic origin). Furthermore, Genetic diversity was the outcome of several factors along with a factor geographic diversity. Hence, the selection for hybridization should be more based on genetic

diversity than geographic diversity. The Principal Component Analysis sorted out the total characters into three main principal components. The contribution of the main characters for variance easily identified by the characters loaded on the PC₁ as it explained maximum variance. By PCA, the in-depth analysis for genetic diversity can be made. In PCA, the characters viz., plant height and grain yield per plant in PC₁ and days to tasseling and maturity were loaded in PC₂, and number of kernels per row and ear length in PC₃ contributing more towards variability. In the present study, principal factor analysis revealed that plant height and grain yield per plant and days to 50% tasseling as major contributors to the total divergence. The results of principal components analysis corroborated with results obtained by solanke *et al*⁴ and Ahmed *et al*⁵.

Table 1: The Eigene values, per cent variance and per cent cumulative variance for three principal components (PCs) and factor loading between PCs and traits studied in maize

	PC1	PC 2	PC 3
Eigene Value (Root)	1276.687	352.430	173.865
% Var. Exp.	58.361	16.111	7.948
Cum. Var. Exp.	58.361	74.471	82.419
Traits	Factor loading		
Days to 50% tasseling	0.083	0.695	0.075
Days to 50% silking	-0.005	0.113	0.082
Days to maturity	0.175	0.514	-0.054
Plant Height (cm)	0.684	0.021	-0.332
Ear Height (cm)	0.208	0.031	-0.142
Ear Length (cm)	0.263	-0.158	0.204
Ear Girth (cm)	0.067	-0.137	0.008
No. of Kernel rows per ear	0.155	0.170	-0.168
No. of Kernels per row	0.263	-0.214	0.499
100 Seed weight (g)	0.064	-0.246	-0.674
Grain yield per plant (g)	0.468	-0.215	0.200
Shelling percentage (%)	-0.248	-0.118	-0.204

Table 2: The PCA scores for sixty genotypes of maize

S.No.	Genotypes	Z1	Z2	Z3
1.	DHM 107 5-1	25.44	53.75	5.58
2.	(BML8XCM131)-1-2	27.70	52.78	2.51
3.	(BMLL8XCM131)-2-2	30.49	52.74	3.97
4.	(BML8XCM131)-2-3	34.30	48.26	3.90
5.	(CM211XCM131)-3	26.20	49.84	4.31
6.	PVT MH, 08 09 11-1	28.74	51.45	1.92
7.	PVT MH, 08 09 24	28.62	51.41	2.04
8.	3511-2	32.41	54.01	4.55
9.	3530-3	28.40	49.21	6.79
10.	3556-1-1-2	28.53	53.79	5.85
11.	3549 B-2-3-1	39.19	49.97	4.86
12.	3521 A-2-3-1	39.68	47.67	3.07
13.	1013	37.99	49.27	4.38
14.	1014	27.00	54.97	5.54
15.	3544	28.13	50.77	3.11
16.	MS 5-S6	29.79	49.93	4.06
17.	BH 407138-2	28.39	51.88	2.84
18.	BH 4065-2-1	36.52	48.54	6.97
19.	BH 408002-4	30.93	53.27	5.73
20.	BH 40715-3-2	33.52	53.83	5.02
21.	COMMANDO-1-3	33.14	50.39	3.58
22.	COMMANDO-3-3	37.51	49.92	7.57
23.	BH 40707-2	33.31	52.03	6.55
24.	UNKNOWN 3-2	32.54	55.50	4.34
25.	CM118-1	36.46	49.28	0.40
26.	Z-49-102-3	24.24	49.09	1.81
27.	Z-55-6-2	28.01	47.93	2.19
28.	Z-56-2-2	35.58	50.16	4.05
29.	Z-63-45	35.39	52.83	3.16
30.	1669-1	38.55	50.59	4.64
31.	1728-1-2	37.25	51.79	5.99
32.	5063	39.04	56.01	3.27
33.	1219-2	30.77	49.05	3.47
34.	1234-3	30.85	51.50	5.12
35.	3050-1	30.07	46.39	5.10
36.	3125-3	31.84	48.59	4.44
37.	BML 2	35.75	50.75	2.53
38.	BML 5	34.00	55.47	7.01
39.	BML 6	33.72	54.22	4.94
40.	BML 8	33.30	55.07	5.34
41.	BML 10	26.39	49.44	4.67
42.	BML 11	30.12	47.44	5.48
43.	BML 13	29.46	48.66	6.21
44.	BML 20	31.83	52.67	6.14
45.	CM 104	26.00	52.69	4.16
46.	CM 105	26.63	50.84	5.64
47.	CM 114	24.11	47.30	7.28
48.	CM 115	24.12	48.78	5.84
49.	CM 118	25.39	49.65	7.08
50.	CM 119	28.22	49.28	4.17
51.	CM 121	20.66	50.24	3.23
52.	CM 130	22.41	50.62	3.36
53.	CM 133	27.60	51.34	3.35
54.	CM 201	27.66	51.85	6.95
55.	CM 202	28.02	51.73	2.62
56.	CM 206	24.52	57.40	5.29
57.	CM 208	30.82	53.80	-0.56
58.	CM 209	24.07	54.24	4.88
59.	CM 210	24.68	52.01	3.69
60.	CM 211	31.60	52.78	2.22

Table 3: Clustering pattern of maize (*Zea mays* L.) genotypes by PCA

Cluster No	No. of genotypes	Names of the Genotypes
I	12	(BML8XCM131)-1-2, (BMLL8XCM131)-2-2, PVT MH, 08 09 11-1, PVT MH, 08 09 24, 3556-1-1-2, 3544, BH 407138-2, 1234-3, CM 105, CM 133, CM 201, CM 202.
II	5	DHM 107 5-1, 1014, CM 104, CM 209, CM 210.
III	12	3511-2, BH 408002, BH 40715-3-2, BH 40707-2, UNKNOWN-3-2, Z-63-45, BML 5, BML 6, BML 8, BML 20, CM 208, CM 211.
IV	11	3549 B-2-3-1, 3521 A-2-3-1, 1013, BH 4065-2-1, COMMMANDO-3-3, CM 118-1, Z-56-2-2, 1669-1, 1728-1-2, 5063, BML 2.
V	3	(BML8XCM131)-2-3, COMMANDO-1-3, 3125-3.
VI	8	3530-3, MS 5-S6, Z-55-6-2, 1219-2, 3050-1, BML 11, BML 13, CM 119.
VII	8	(CM211XCM131)-3, Z-49-102-3, BML-10, CM 114, CM 115, CM 118, CM 121, CM 130.
VIII	1	CM 206.

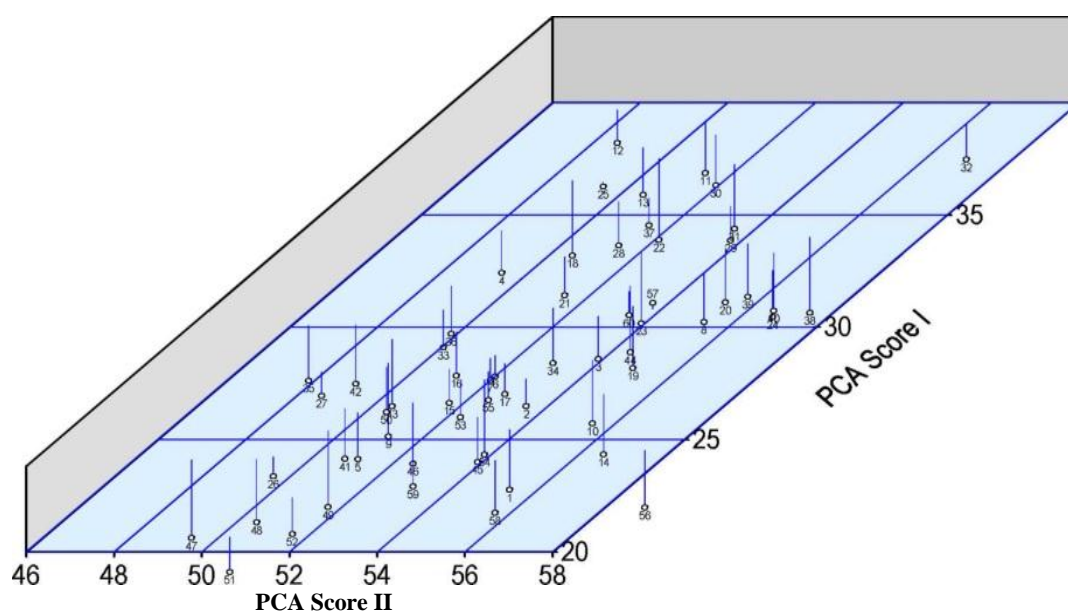


Fig. 1: Three dimensional principal component scatter plot

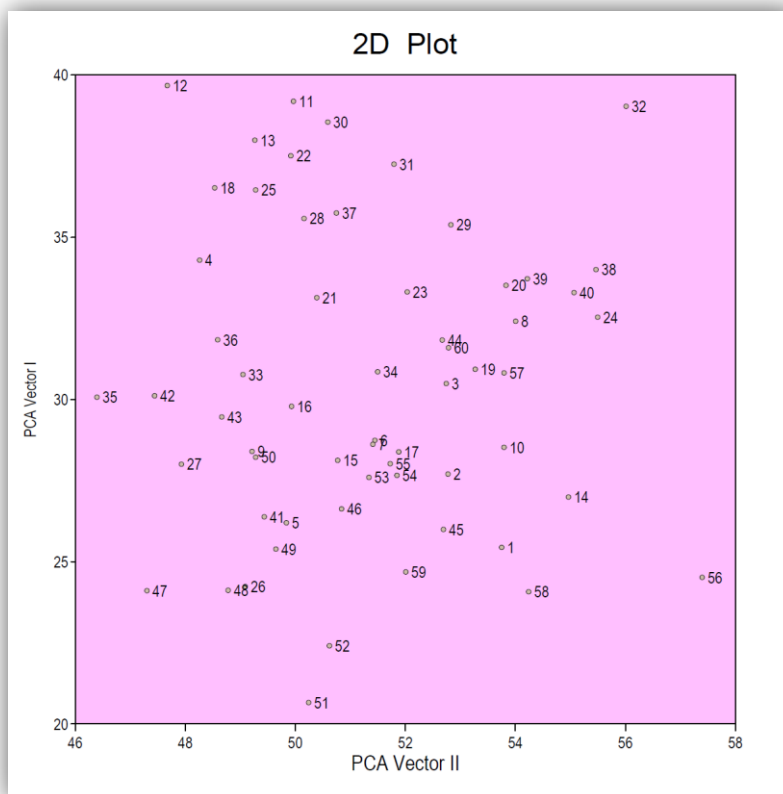


Fig. 2: Two dimensional scatter plot of Principal Component Analysis showing positions of sixty genotypes of maize

REFERENCES

1. Department of Agriculture and Co-operation. Normal estimates. (2014).
2. Rao, C.R. *Advanced statistical methods in biometrical research*. John Wiley and Sons Inc., New York. pp. 236-272 (1952).
3. Patel, M.Z., Reddi, M.V., Rana, B.S and Reddy, B.J. Genetic divergence in safflower (*Carthamus tinctorius* L.) *Indian Journal of Genetics and Plant Breeding*. **49**: 113-118 (1989).
4. Solanke, P.D., Charjan, S.U., Patil, S.R., Palkar, A.B., Khillari, A.V., Tele, R.B and Shinde, A.V. Genetic divergence for selection of parents for hybridization in maize. *Journal of Soils and Crops*. **23 (1)**: 140-150 (2013).
5. Ahmed, S., Malaviya, R and Majumdar, A.B. Genetic divergence and variability in fodder maize. *Forage Research*. **35 (4)**: 223-226 (2010).