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Cluster and Principle Component Analysis in Maize Hybrids

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Abstract

The present investigation comprised with 11 set of maize hybrids to evaluate the diversity existed suing correlation, principle component and cluster analysis. The correlation coefficient analysis revealed that kernel yield (kg/ha) showed significantly positive correlation with the traits like kernel yield per plot (kg), cob yield per plot (kg), days to 50% silking, number of seeds per cob, number of seed rows per cob and shelling percentage (%). From the cluster analysis and principle component analysis it is clear that the hybrid *i.e.,* PDMH-1449 formed in cluster-3 which showed higher values for the traits like kernel yield (kg/ha), shelling percentage (%), kernel yield per plot (kg), cob yield per plot (kg), number of seeds per cob, number of seed rows per cob, cob girth (cm) and cob length (cm). Out of four components, PC-1, PC-2 and PC-3 showed >1 eigen value which contributed 90.53% of the total variability among the maize hybrids assessed for yield and its associated traits. Out of three components, PC-I contributes the maximum towards the variability (68.42%) followed by PC-II (13.11%) and PC-III (8.99%). From the study it is clear that the traits like plant height (cm), kernel yield (kg/ha), cob yield per plant (kg), days to 50% pollen shed and kernel yield per plot (kg) were the main cause for maximum diversity and also for higher yields.

Key words : *Cluster, principle component analysis, hybrids, maize.*

Introduction

Maize (*Zea mays* L., 2n = 20) a cereal grain first domesticated by indigenos peoples in southern Mexico about 10,000 years ago. Globally maize is the third most important cereal crop after wheat and rice. Many parts in world maize is used as staple food for humans and also used as raw material in different food, medicine and textile industries, to manufacture of corn oil, corn flakes, dextrose, and textile dyes etc (1). It possesses high nutritive values as it contains 72 % starch, 10 % protein, 4.80 % oil, 8.50 % fibre, 3.0 % sugar, and 1.70 % ash (2). Due to its versatile use of almost all parts of the plant, and it grown in vast variety of the environmental conditions it's known as 'queen of the cereal'. Globally maize was cultivated in an area of 19.72 Mha, with a production of 114.85 MMT.

In present scenario Indian maize cultivation increases due to its wider cultivation and adaptability aspects and also its suitability to changing climate resilient agriculture. In present condition Indian maize cultivation is mostly depends on two way hybrid system of developing the high heterotic hybrid combinations. Since several years the production of high yielding hybrids in maize mainly depends on the selection of diverse genotypes used as parents using different morphological and yield traits in association with yield. As we all aware that yield is associated with quantitative trait controlled by polygenic genes and the only way to enhancing the yield trait is through improvement of its attributing traits (3).

Knowledge on association between yield and its attributing traits and also among the other component traits themselves will be the reason to enhance the efficiency of selection in breeding programmes (4). In addition to this it is also important to grouping the similar type genotypes which will similar in different studied traits in direction of enhancing yield trait and also its very important to know the specific components which are closely associate to enhance yield within the available/studied total components. Principal component analysis (PCA) is used to evaluate the magnitude of genetic diversity among the germplasm (5). (6) suggested that first principal component (PC-I) scores as input variables for the clustering process. Similarly hierarchical cluster analysis has been suggested for classifying entries of germplasm collections based on degree of similarity and dissimilarity (7). A combination of cluster analysis and principal component analysis has been used to classify maize accessions by (8).

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Table-1 : Basic statistics of various traits of studied maize hybrids.

Variable	Mean	Mean SE	CD (5%)	CD (1%)	CV (%)	Range	
						Minimum	Maximum
DFPS	57.12	0.41	1.20	1.64	1.23	52.33	61.67
DFS	59.21	0.41	1.17	1.61	1.17	54.67	64.33
DM	114.42	1.13	16.07	21.92	1.71	111.33	116.33
PH	113.47	4.84	15.94	21.74	7.39	102.60	122.73
EPH	31.88	1.71	5.06	6.89	9.32	25.60	36.40
CL	14.15	0.63	1.99	2.71	7.74	12.89	15.20
CG	11.22	0.53	1.58	2.15	8.25	9.58	12.66
NSRPC	13.36	0.51	1.51	2.06	6.64	11.44	14.47
NSPC	366.03	24.77	73.09	99.69	11.72	271.00	449.33
CYPP	5.37	0.33	0.96	1.31	10.52	4.05	6.24
KYPP	4.62	0.31	0.92	1.26	11.73	3.47	5.57
TW	25.30	0.66	1.94	2.65	4.51	22.59	27.62
SP	85.88	1.74	12.06	16.46	3.50	82.97	89.23
KY	7696.97	521.21	1537.57	2097.33	11.73	5777.78	9277.78

DFPS = Days to 50% pollen shed, DFS = Days to 50% silking, DM = Days to maturity, PH = Plant Height (cm), EPH = Ear placement height (cm), CL = Cob length(cm), CG = Cob girth (cm), NSRPC = Number of seed rows per cob, NSPC = Number of seeds per cob, CYPP = Cob yield per plot (kg), KYPP = Kernel yield per plot (kg), TW = Test weight (g), SP = Shelling percentage (%), KY = Kernel yield (kg/ha).

Keeping the points mentioned above the present investigation is aimed to identify the high yielding maize hybrids among 11 hybrids studied and the groups based on the traits which will the causes for high yielding with the help of association analysis, cluster and Principle component analysis.

Materials and Methods

The experimental material comprising 11 maize hybrids sown in Randomised Block Design with three replications at Research farm, ANGRAU-Maize Research Centre, Agricultural Research Station, Vijayarai. Each entry was sown in three rows of 5 meter length with a spacing of 70 × 25 cm respectively. The entire experiment was conducted with good care followed all package of practices including plant protection measures. Observations were noted on five randomly selected plants for plant height (cm), ear placement height (cm), cob length (cm), cob girth (cm), number of seed rows per cob, number of seeds per cob, test weight (g), shelling percentage (%) and kernel yield (kg/ha). The observations like days to 50% pollen shed, days to 50% silking, days to maturity, cob yield per plot (kg) and kernel yield per plot (kg) will be taken on the basis of plot.

Statistical analysis was subjected to basic statistics methods followed for analysis of variance, coefficient of correlation analysis method developed by (9), cluster analysis as per the method by (10) and principle component analysis or Canonical root analysis (PCA) as per the (11).

Results and Discussion

The basic statistics revealed that significant variability was existed in 11 maize hybrids for studied morphological and yield traits including yield (Table-1). The genotypic coefficient of correlation explained that the kernel yield (kg/ha) showed significantly positive correlation with the traits like kernel yield per plot (kg), cob yield per plot (kg), days to 50% silking, number of seeds per cob, number of seed rows per cob and shelling percentage (%) (Table-2). These findings revealed that higher yields can achieve by selection of these traits in breeding programmes. The similar findings were also reported by the researchers like (12,13,14). Kernel yield (kg/ha) noticed significant negative correlation was noticed for days to 50% pollen shed. This table explained about the positive association of associated traits in improvement of yield. Similar findings have also been reported by (15,16,17).

Cluster analysis was conducted to study the grouping of eleven maize hybrids for 14 morphological and yield traits. The study revealed that the total 11 hybrids were grouped under 3 clusters (Fig-1). Cluster-1 formed by the grouping of 8 hybrids *i.e.,* Kaveri-50, PDMH-1817, PDMH-1829, PDMH-171213, PDMH-153227, PDMH-16921, PDMH-1810 and P-3396 and cluster-2 formed by grouping of 2 hybrids *i.e.,* PDMH-1540 and PDMH-1222 and cluster-3 formed with single hybrid *i.e.,* PDMH-1449 (Table-3). The cluster analysis revealed that out of the three clusters, the cluster-3 registered higher values for the traits like kernel yield (kg/ha), shelling percentage (%), kernel yield per plot (kg),

Table-2 : Simple correlation of various studied traits in maize hybrids.

	DFPS	DFS	DM	PH	EPH	CL	CG	NSRPC	NSPC	CYPP	KYPP	TW	SP	KY
DFPS	1.000													-0.736**
DFS	0.995**	1.000												0.746**
DM	0.514**	0.496**	1.000											-0.301
PH	-0.376*	-0.369*	-0.358*	1.000										0.107
EPH	-0.155	-0.135	-0.166	0.714**	1.000									-0.066
CL	-0.251	-0.256	-0.127	-0.089	-0.387*	1.000								0.326
CG	-0.315	-0.342	-0.136	-0.196	-0.574**	0.824**	1.000							0.334
NSRPC	-0.452**	-0.479**	-0.103	0.076	-0.207	0.377*	0.415*	1.000						0.597**
NSPC	-0.656**	-0.673**	-0.403*	0.210	-0.048	0.242	0.399*	0.697**	1.000					0.619**
CYPP	-0.728**	-0.743**	-0.257	0.044	-0.107	0.330	0.357*	0.580**	0.631**	1.000				0.981**
KYPP	-0.736**	-0.745**	-0.300	0.107	-0.065	0.326	0.333	0.597**	0.618**	0.980**	1.000			0.997**
TW	-0.263	-0.257	-0.194	0.287	0.272	0.244	0.087	0.015	0.026	0.096	0.108	1.000		0.109
SP	-0.96*	-0.381*	-0.307	0.332	0.156	0.160	0.091	0.372*	0.255	0.426*	0.592**	0.147	1.000	0.592**

Note : *significant at 5% level, **significant at 1% level
DFPS = Days to 50% pollen shed, DFS = Days to 50% silking, DM = Days to maturity, PH = Plant Height (cm), EPH = Ear placement height (cm), CL = Cob length(cm), CG = Cob girth (cm), NSRPC = Number of seed rows per cob, NSPC = Number of seeds per cob, CYPP = Cob yield per plot (kg), KYPP = Kernel yield per plot (kg), TW = Test weight (g), SP = Shelling percentage (%), KY = Kernel yield (kg/ha)

Table-3 : Cluster membership of 11 maize hybrids.

Cluster Name	Number of genotypes	Name of genotype in each cluster
Cluster-1	8	Kaveri-50, PDMH-1817, PDMH-1829, PDMH-171213, PDMH-153227, PDMH-16921, PDMH-1810, P-3396
Cluster-2	2	PDMH-1540, PDMH-1222
Cluster-3	1	PDMH-1449

Table-4 : Cluster analysis of various traits in maize hybrids.

Traits studied	Cluster 1	Cluster 2	Cluster 3
Days to 50% pollen shed	56.63	61.50	52.33
Days to 50% silking	58.63	63.83	54.67
Days to maturity	114.63	115.17	111.33
Plant height (cm)	112.88	115.33	114.40
Ear placement height (cm)	31.63	34.07	29.53
Cob length (cm)	14.23	13.28	15.20
Cob girth (cm)	11.36	9.90	12.57
No. of seed rows/cob	13.62	11.83	14.23
No. of seeds/cob	371.71	301.67	449.33
Cob yield/plot (kg)	5.49	4.42	6.23
Kernel yield/plot (kg)	4.71	3.78	5.57
Test weight (g)	25.68	24.43	24.00
Shelling percentage (%)	85.58	85.40	89.23
Kernel yield (kg/ha)	7847.23	6305.57	9277.77

Table-5 : Principle component analysis of different traits in maize.

	PC 1	PC 2	PC 3	PC 4
Eigen value	9.5728	1.8687	1.1639	0.7887
% of total variance	68.4	13.3	8.3	5.6
Cumulative variance	68.4	81.7	90.0	95.6

cob yield per plot (kg), number of seeds per cob, number of seed rows per cob, cob girth (cm) and cob length (cm) and the cluster-2 showed higher values for ear placement height (cm), plant height (cm), days to maturity, days to 50% silking and days to 50% pollen shed (Table-4). The cluster-1 showed higher values for test weight (g). From the cluster analysis it is clear that the traits associated with the hybrids in cluster-1 followed by cluster-2 are more meaningful to get higher variability due to presence of maximum diversity in those crosses which inferred that selection of these traits would be more successful to get better yields in breeding programmes. The similar findings were also noticed by (18).

The principle component analysis explained that the total components were expressed in four components and in that three components i.e., PC-1, PC-2 and PC-3 showed >1 eigen value which contributed 90.53% of the total variability among the maize hybrids assessed for yield and its associated traits. Out of three components, PC-I contributes the maximum towards the variability (68.42%) followed by PC-II (13.11%) and PC-III (8.99%) (Table-5). If you see the loadings among genotypes due

Table-6 : Factor loadings by morphological and yield traits.

	PC 1	PC 2	PC 3	PC 4
Days to 50% pollen shed	0.302	0.150	0.243	0.118
Days to 50% silking	0.244	-0.046	0.517	-0.347
Days to maturity	0.203	0.435	-0.189	0.454
Plant height (cm)	0.312	-0.009	0.137	-0.130
Ear placement height (cm)	0.239	-0.176	-0.228	0.610
Cob length (cm)	-0.201	0.414	0.395	-0.181
Cob girth (cm)	-0.308	-0.043	0.174	-0.127
No. of seed rows/cob	-0.307	-0.089	-0.221	-0.080
No. of seeds/cob	0.141	-0.575	-0.141	0.193
Cob yield/plot (kg)	0.304	-0.221	-0.028	0.032
Kernel yield/plot (kg)	0.291	-0.110	0.223	0.209
Test weight (g)	0.18	0.374	-0.503	-0.317
Shelling percentage (%)	0.304	0.198	-0.098	-0.124
Kernel yield (kg/ha)	0.318	0.052	0.005	0.131

to traits in view of components, the considerable positive loadings were recorded among genotypes due to the traits like plant height (cm), kernel yield (kg/ha), cob yield per plant (kg), days to 50% pollen shed and kernel yield per plot (kg), while negative loadings were observed for number of seed rows per cob and number of seeds per cob in principle component-I (Table-6). It indicated that the traits plant height (cm), kernel yield (kg/ha), cob yield per plant (kg), days to 50% pollen shed and kernel yield per plot (kg) were showed the prime importance in showing maximum variability to express higher yields.

The maximum diversity was established due to days to maturity, test weight (g) and cob length (cm) and negative expression was noticed for number of seeds per cob in PC-II. In PC-II the variability among the genotypes due to positive loadings of days to 50% silking and cob length (cm) while negative loadings of test weight (g) and number of seeds per cob.

The bi-plot analysis picture (Fig-2 and Fig-3) explained that the hybrids and the variables are super-imposed on the plot as vectors. The distance of each variable with respect to PC-I and PC-II explained about the contribution of the studied variables. In-terms of variation of genotypes studied here. Bi-plot analysis revealed that the traits like plant height (cm), kernel yield (kg/ha), cob yield per plot (kg), cob girth (cm) and number of seed rows per cob contributes the maximum variability in the proposed maize hybrids for study. The data was also supported by the canonical cluster analysis. Hence improvement of a hybrid/genotype in-terms of yield is mainly possible by the traits plant height (cm), kernel yield (kg/ha), cob yield per plot (kg), cob girth (cm) and number

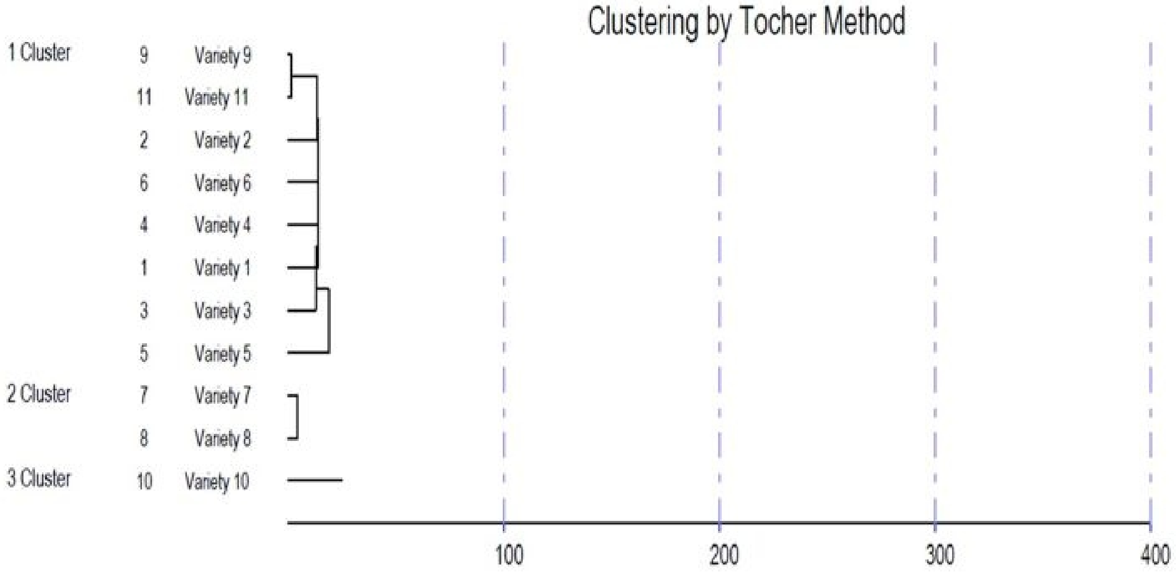

Fig 1: Cluster analysis of 11 maize hybrids for 14 morphological and yield traits

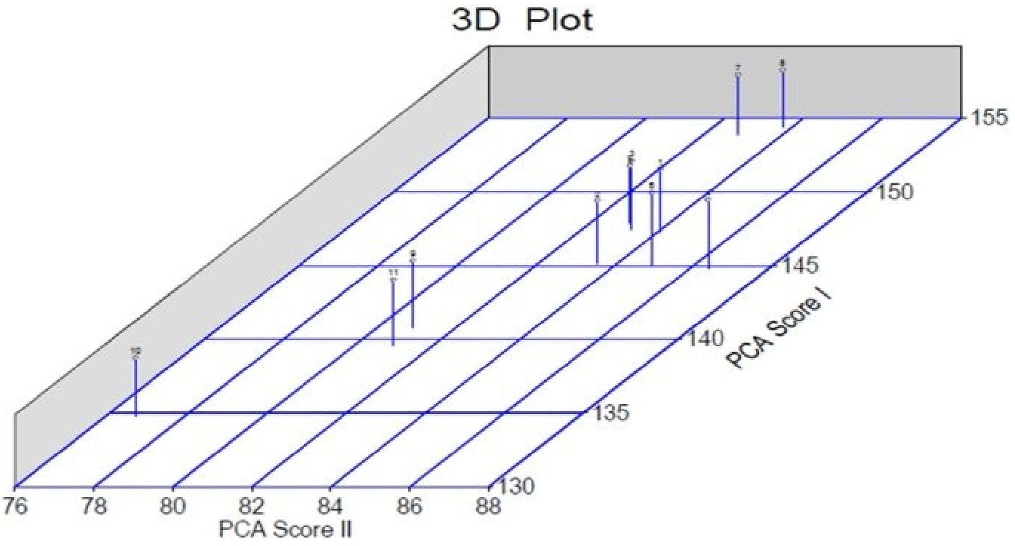

Fig 2: Bi-plot analysis of PC-I and PC-II

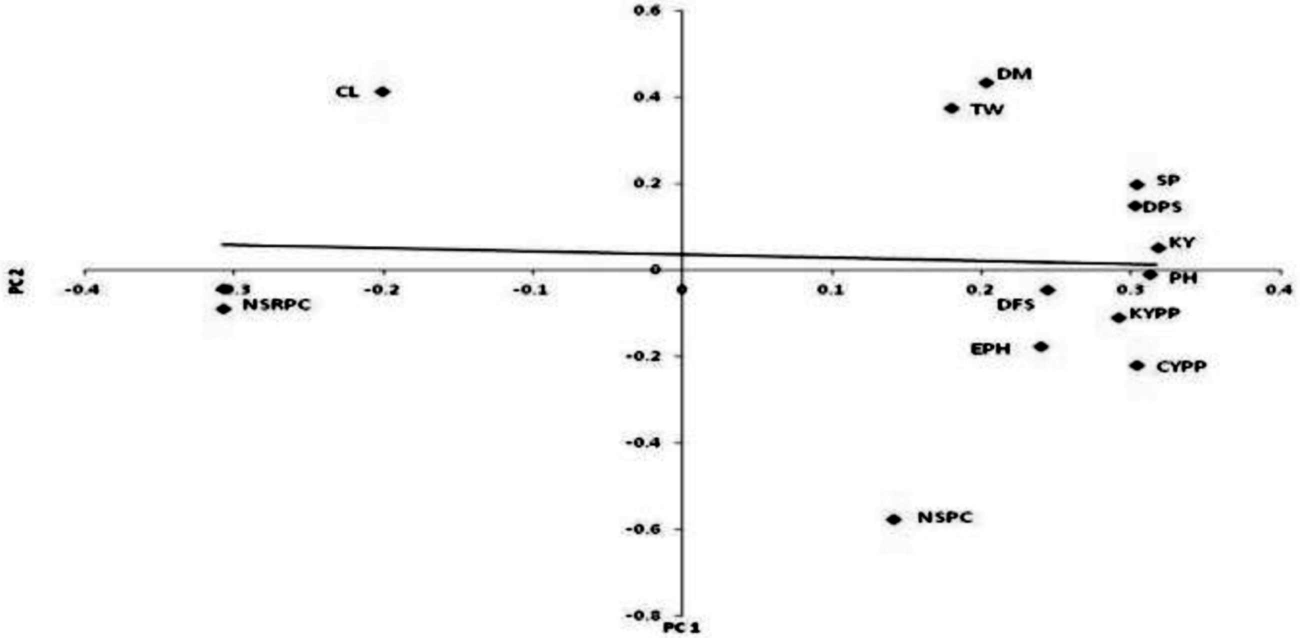

Fig.-3 : Bi-plot analysis between principle component-1 and principle component-2.

of seed rows per cob which showed the maximum variability in the study. The results of principal components analysis corroborated with results obtained by (19,20,21).

Conclusion

The PCA, Cluster and Correlation analysis in present investigation have provided the information in classification of studied maize hybrids and also provided the information on subset of core hybrids which are the high yielders. The information from the cumulative of the PCA, Cluster and Correlation analysis will yields the information about the grouping of good combination of genotypes and also about the studied traits which are useful in further breeding programmes.

Authors Contribution

Conceptualization of research (KMVV); Designing of the experiments (KMVV, KMDM, KPK, KMR); Contribution of experimental materials (KMVV); Execution of field/lab experiments and data collection (KMVV, KMDM, KPK, KMR); Analysis of data and interpretation (KMVV, MSD); Preparation of the manuscript (KMVV, YSSK).

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