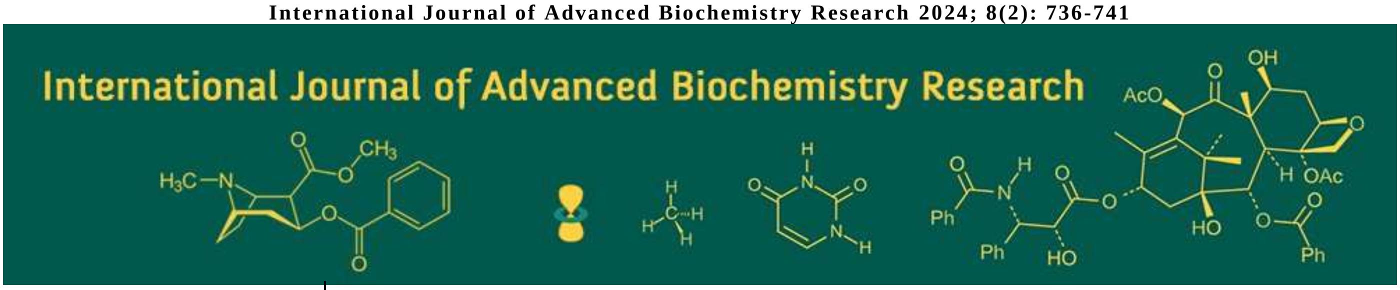

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Multivariate analysis for yield and its component traits in Quality Protein Maize (QPM)

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Abstract

25 genotypes of maize were studied to reveal the genetic relationship between the different accessions. The experiment was laid in randomized complete block design with three replications having plot size of 1.5 x 4.0 = 6 m^2 at TCA, Dholi, Farm. Each plot consisted of 2 rows of 4m length spaced at 75 cm row to row and 20 cm plant to plant, respectively. Recommended agronomic and plant protection measures were followed. The genotypes were observed for 11 quantitative traits from each replication. The traits which were studied include days to 75% tasseling, days to 75% silking, days to 75% brown husk, plant height, ear height, tassel length, cob length, cob diameter, number of kernel rows per cob, Number of kernels per row and grain yield. In this experiment, 5 principal components (PCs) exhibited more than 1.00 eigen value, and showed about 86.62% cumulative variability among the traits studied. The PC1 showed 28.78% while, PC2, PC3, PC4 and PC5 exhibited 26.04%, 11.76%, 10.81% and 9.24% variability respectively among the inbreds**.** In the present study, PCA was done to identify the attributes whose selection would lead to improvement in grain yield of maize. Therefore, an attempt was taken to evaluate the 25 Quality Protein Maize (QPM) genotypes on the basis of PCA before taking up hybridization programme for further maize improvement programme.

Keywords: Quantitative trait, PCA, eigen, inbreds

Introduction

Maize is termed as the queen of cereal crops and is the third most popular cereals grown all over the world after wheat, and rice (Dass, 2012) [4]. It is exploited for various purposes such as animal feed, human food and for a large number of many other industrial products like oil, starch, glucose etc, (Ranum *et al.*, 2014) [13]. India is one of the leading corn producing countries in the world. Production of maize has increased drastically over the last few years and a major breakthrough was noticed at the beginning of the 21st century with the development of new hybrids (Ali *et al.*, 2020) [1]. Estimation of phenotypic and genetic variation among the germplasm is the initial step in maize breeding. Extraction of the maximum genetic variation present in germplasm depends upon the different biometrical techniques used for its estimation and different morphological and physiological traits used for variability estimation (Bajracharya *et al.*, 2006) [3]. Genetic diversity is the foundation of the genetic improvement of crops. The knowledge of the extent and pattern of diversity in the crop species is a prerequisite for any crop improvement as it helps breeders in deciding suitable breeding strategies for their future improvement. Yield and yield contributing parameters are the most widely targeted traits for rice improvement programme worldwide. Yield is a complex trait which is affected by several factors and environment, hence, a well-known technique known as principal component analysis was used to identify and minimize the number of traits for effective selection. PCA is a standard tool in modern data analysis because it is a simple, non-parametric method for extracting relevant information from confusing data sets. It involves a mathematical procedure that transforms a number of (possibly) correlated variables into a (smaller) number of uncorrelated variables called principal components. It reduces the dimensionality of the data, while retaining most of the variation in the data set. Thus, the primary benefit of PCA arises from quantifying the importance of each dimension for describing the variability of a data set. In the present study, we carried out a PCA to identify agronomic attributes whose selection would lead to improvement in grain yield of maize.

Therefore, an attempt was taken to evaluate the 25 Quality Protein Maize (QPM) genotypes on the basis of PCA before taking up hybridization programme for further maize improvement programme.

Materials and Methods

Twenty-five genotypes of maize were used to reveal the genetic relationship between the different accessions. The experiment was laid in randomized complete block design with three replications having plot size of 1.5 x 4.0 = 6 m^2 at TCA, Dholi, Farm and the list of twenty five genotypes represented in table 1. Each plot consisting of two rows of 4m length spaced at 75 cm row to row and 20 cm plant to plant, respectively. Recommended agronomic and plant protection measures were followed. The field grown 25 genotypes were observed for 11 quantitative traits from each replication. The traits which were studied include days to 75% tasseling, days to 75% silking, days to 75% brown husk, plant height, ear height, tassel length, cob length, cob diameter, number of kernel rows per cob, Number of kernels per row and grain yield. Observations on 11 different quantitative characters were recorded on five randomly selected plants. The average was taken as the mean of the treatment. Out of the 11 quantitative characters, days to 75% tasseling, days to 75% silking and days to 75% brown husk were recorded on plot basis. Rest of the traits were recorded on the basis of five randomly chosen plants at appropriate stage. Data entry and processing was done in Microsoft excel. Principal Components are generally estimated from correlation matrix or covariance matrix. Principal component analysis was done from all the observed data through Minitab 17.

Table 1: Experimental materials:

S. No.	Inbred lines	Abbreviation	Source
1.	[CL-G2501*CML170]-B-2-2-2-B-1-1-BBB-#	CLG-2501-170	AICR, Dholi Centre
2.	CML161*165-18-2-1-2-BBB-#	CML61*65-18	AICR, Dholi Centre
3.	CML161*165-50-1-3-B*4-#	CML61*65-50	AICR, Dholi Centre
4.	(CML161*165)-F2-21-3-1-B*5-#	CML61*65-21	AICRP, Dholi Centre
5.	(CML176*CLG2501)-B-55-1-5-2-BBB-#	CML*CLG-55	AICRP, Dholi Centre
6.	(CML165*CL-02843)-B-12-2-4-B-3-BBB-#	CML*CL02843-12	AICRP, Dholi Centre
7.	(CLQ-6601*CL-02843)-B-23-2-1-B-1-BBB-#	CLQ*CL-23	AICRP, Dholi Centre
8.	(CLQ-6601*CL-02843)-B-26-1-1-BB-1-B*6-#	CLQ*CL-26	AICRP, Dholi Centre
9.	P70C0-BBB-6-B*6-#	P70C0-6	AICRP, Dholi Centre
10.	CLQ-RCYQ28-B-3-B*6-#	CLQ-RCYQ-28	AICRP, Dholi Centre
11.	CLQ-RCYQ41-BB-2-B*6-#	CLQ-RCYQ-41	AICRP, Dholi Centre
12.	CLQ-RCYQ035-B*11-#	CLQ-RCYQ-035	AICRP, Dholi Centre
13.	CLQ-RCYQ12-B-1-B*6-#	CLQ-RCYQ-12	AICRP, Dholi Centre
14.	CML161*165-3-2-3-B*4-#-B1	CML61*65-B*4	AICRP, Dholi Centre
15.	G34QC24-BBB-16-B*8-#-B	G34QC-BB-16	AICRP, Dholi Centre
16.	POO117C8(TEYFQPM)-B-117-B*10	POO-TEYFQM	AICRP, Dholi Centre
17.	CML161*165-16-2-1-B*10	CML61*65-16	AICRP, Dholi Centre
18.	G33QMH103-3-1-5-1-B*14	G33QMH-103	AICRP, Dholi Centre
19.	(CML176*CLG2501)-B-55-1-2-B*4	CML76*CLG-B*4	AICRP, Dholi Centre
20.	CLQRCYQ44-B*4-1-#-B	CLQ-RCYQ-44	AICRP, Dholi Centre
21.	CML161-1-B*8-#-B	CML61-B*8	AICRP, Dholi Centre
22.	CML451Q-B*8	CML451-B*8	AICRP, Dholi Centre
23.	CML165-B*9-#	CML65-B*9	AICRP, Dholi Centre
24.	CML193-B*6-#	CML93-B*6	AICRP, Dholi Centre
25.	(CML161*CLQ-RCYQ31)-B-22-2-B*5	CML61*CLQ-B*5	AICRP, Dholi Centre

Results and Discussions

Principal component analysis is a simple nonparametric method for extracting relevant information from confusing data sets. With minimum efforts, this provide a road map for how to reduce a complex data set to a lower dimension to sometimes hidden, simplified structures that often underlines it. PC is a statistical procedure that uses an orthogonal transformation to convert a set of observations of possibly correlated variables into a set of values of linearly uncorrelated variables called principal components the number of principal components is less than or equal to the number of original variables. This transformation is defined in such a way that the first principal component has the largest possible variance (that is accounts for as much of the variability in the data as possible) and each succeeding component in turn has the highest variance possible under the constraint that it is orthogonal to the proceeding components. The resulting vectors are an uncorrelated orthogonal basis set. The principal components are orthogonal because they are the Eigen vectors of the covariance matrix, which is symmetric. In present investigation principal component analysis was performed for yield and yield contributing traits of maize. Minimum, maximum, mean and standard deviation were calculated for all the genotypes, as the main indicators of variability (Table- 2).

In principal component (PC) analysis, the number of variables was reduced to linear functions called canonical vectors which accounted for most of the variation produced by the characters under study. The eigen values, per cent variance, per cent cumulative variance and factor loading of different characters studied are presented in Table 3a & 3b. In this experiment, Out of 11, 5 principal components (PCs) exhibited more than 1.00 eigen value, and showed about 86.62% cumulative variability among the traits studied. Hence, these 5 PCs were given due importance for further explanation. Eigen values of three principal component axes and percentage of variation accounting for them obtained from the principal component analysis are presented in Table 3a. The PC1 showed 28.78% while, PC2, PC3, PC4 and PC5 exhibited 26.04%, 11.76%, 10.81% and 9.24% variability respectively among the inbreds**.** These results were in accordance with those of Jinju *et al.*, (2009) [7], Muhammad *et al.*, (2012) [9], Sandeep *et al.*, (2015) [14], (Gour *et al.*, 2017) [5] and Shrestha *et al.*, (2016) [15] in maize**.**

Table 2: Basic statistics for various characters of Maize genotypes.

Parameters	Minimum	Maximum	Mean	Standard deviation
Plant height (PH)	93.33	145.17	121.43	15.73
Ear height (EH)	32.5	77.5	55.39	10.22
Days to 75% tasseling (PT)	49.33	60.67	56.16	3.15
Days to 75% silking (PS)	53.67	63.67	59.3	2.88
Days to 75% brown husk (BH)	90	97	93.77	1.73
Tassel length (TL)	24.03	32.53	28.87	2.49
Cob length (EL))	13.43	22.58	17.3	2.28
Cob girth (EG)	11.23	15.78	12.73	1.1
Number of kernel rows per cob (KE)	12	16.23	13.63	1.1
Number of kernels per row (KR)	24.17	35.67	29.28	2.97
Grain yield (GY)	1211.75	3081.56	2100.42	517.98

Further, the scree plot is also shown in Fig. 1 This exhibit plots of 11 Principal Components used in this study. Starting with the first PC, the plot slopes steeply downward initially and then slowly become an approximately horizontal line. The point at which the curve first begins to straighten out is considered to indicate the maximum number of components to extract. As seen in this Fig. 1, 3 Principal Components were considered. Therefore, these results illustrate the need for multiple decision criteria in deciding the number of components to be retained.

Table 3 (a): Eigen values and contribution of variability for various principal components of maize inbreds.

Statistics	PC1	PC2	PC3	PC4	PC5
Eigen Values	3.166	2.865	1.294	1.189	1.016
% Variance explained	28.780	26.040	11.760	10.810	9.240
Cumulative% Variance	28.780	54.820	66.580	77.390	86.620

Table 3 (b): Principal component scores of different characters in maize inbreds

	PH	EH	PT	PS	BH	TL	EL	EG	KE	KR	GY
PC1	-0.008	-0.063	-0.532	-0.541	-0.513	-0.162	0.116	-0.067	0.088	0.246	0.212
PC2	0.427	0.393	0.097	0.101	0.095	0.047	0.406	0.434	0.072	0.317	0.418
PC3	-0.513	-0.571	0.098	0.114	0.093	-0.027	0.398	0.207	0.120	-0.042	0.401
PC4	0.079	0.113	-0.044	-0.004	-0.116	0.431	0.177	-0.162	0.750	-0.398	-0.030
PC5	0.010	0.083	0.194	0.085	0.167	-0.679	-0.190	-0.341	0.483	0.168	0.213

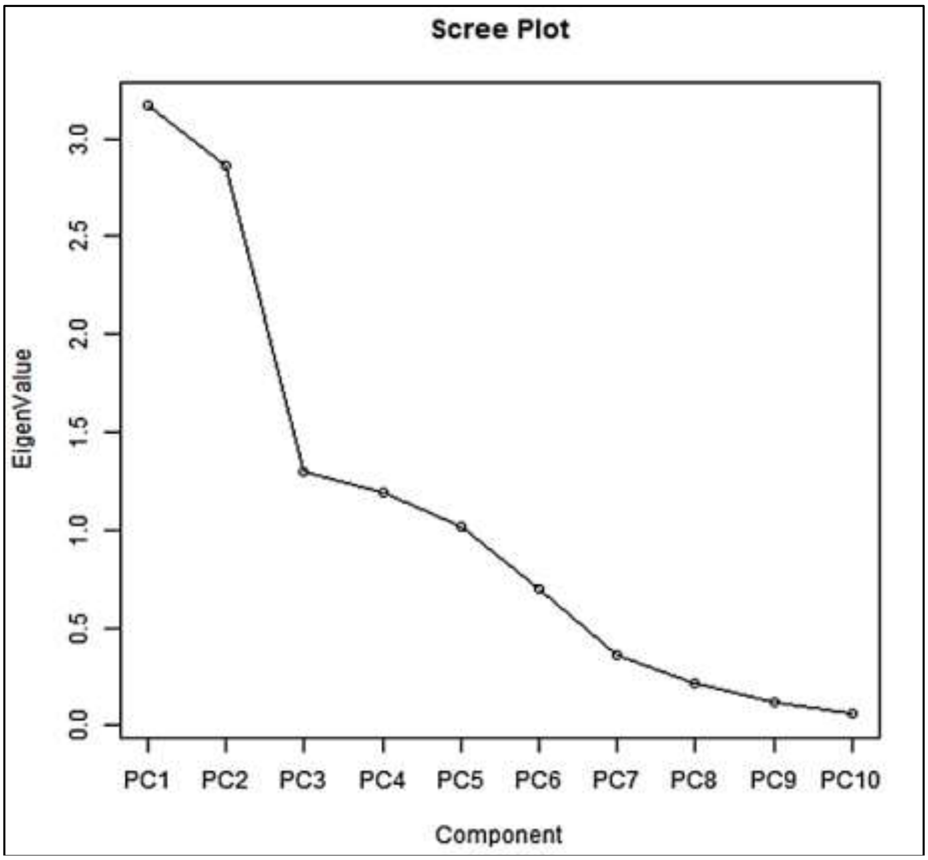

Fig 1: Scree plot for Principal Component Analysis (PCA)

The first principal component vector (PC I) observed 28.78% of the total variability. It could be seen from the first vector that the characters like cob length (0.116), number of kernel rows per cob (0.088), number of kernels per row (0.246) and grain yield (0.212) displayed maximum positive contribution towards genetic divergence, while, the remaining characters like plant height (-0.008), ear height (-0.063), days to 75% tasseling (-0.532), days to 75% silking (-0.541), days to 75% brown husk (-0.513), tassel length (-0.162), cob girth (-0.067) displayed negative contribution. However, the second vector (PC II) accounted for 26.04% of total variation present in the population. All the characters that contributed to the second component showed positive contribution.

PC III accounted 11.76% of the total variability. The traits like plant height (-0.513), ear height (-0.571), tassel length (-0.027) and number of kernels per row (-0.042) had maximum negative contribution towards genetic diversity. However, characters *viz.* days to 75% tasseling (0.098), days to 75% silking (0.114), days to 75% brown husk (0.093), cob length (0.398), cob girth (0.207), number of kernel rows per cob (0.120) and grain yield (0.401) displayed positive contribution towards genetic diversity. The fourth vector, PC IV accounted for 10.81% total variability. The major characters that contributed to the fourth component include traits like plant height (0.079), ear height (0.113), tassel length (0.431), cob length (0.177) and number of kernel rows per cob (0.750) displayed positive contribution towards genetic diversity.

Fifth vector (PC V) accounted for 9.24% total variability. The traits like plant height (0.010), ear height (0.083), days to 75% tasseling (0.194), days to 75% silking (0.085), days to 75% brown husk (0.167), number of kernel rows per cob (0.483), number of kernels per row (0.168) and grain yield (0.213) showed positive contribution towards genetic diversity. These findings are also confirmation with Nachimuthu *et al.* (2014) [10], Mahendran *et al.* (2015) [8], Gour *et al.* (2017) [5], Ojha *et al.* (2017) [11], Amrita *et al.* (2014) [2], Iqbal *et al.* (2008) [6] and Miladinovic *et al.* (2006).

Table 4: Principal component scores of different maize inbreds

Maize inbreds	PC1	PC2	PC3	PC4	PC5
1	3.14	1.44	-0.68	-0.59	-0.59
2	-0.60	2.22	0.11	-1.31	-0.84
3	-0.64	-4.23	0.49	-0.83	-0.86
4	0.28	0.27	-1.55	-0.19	-1.24
5	-2.51	-0.76	0.04	-0.06	0.11
6	-1.29	-1.79	0.64	0.47	-1.93
7	3.95	1.05	0.17	0.46	-0.79
8	-0.99	-0.41	-0.32	0.43	-0.03
9	2.14	-0.21	0.62	0.12	0.63
10	-0.54	2.64	2.69	-0.57	-0.75
11	0.58	-0.61	-0.12	0.94	-1.28
12	1.72	-0.24	1.18	-2.62	1.01
13	1.68	-2.37	-1.64	-0.95	1.02
14	-1.61	-1.26	1.44	1.44	1.07
15	0.06	-2.59	0.21	0.04	-0.32
16	-0.04	-0.38	0.88	1.77	2.20
17	-2.54	1.22	-1.37	0.96	-0.81
18	-0.98	-0.44	-0.30	0.51	0.48
19	1.06	-1.18	0.22	0.45	-0.59
20	-2.36	1.90	-1.29	-0.60	-0.19
21	1.13	-0.24	-0.07	-0.79	0.44
22	2.29	1.80	-1.24	2.56	0.41
23	-0.75	2.20	2.21	0.27	0.26
24	-2.25	1.50	-1.16	-1.13	0.66
25	-0.93	0.46	-1.16	-0.79	1.95

High principal factor score for a particular genotype in a particular factor denotes high values for the variables in that particular genotype. Table 4 revealed that genotypes 1, 7, 9, 12, 13, 19, 21 and 22 had high principal component scores in factor 1 indicating that they had high cob length, number of kernel rows per cob, number of kernels per row and grain yield which, this principal factor is representing. Similarly, principal component scores of 1, 2, 7, 10, 17, 20, 22, 23 and 24 genotypes were high in factor 2 indicating high plant height, ear height, days to 75% silking, cob length, cob girth, number of kernels per row and grain yield. Likewise, principal component scores of 10, 12, 14 and 23 genotypes were high in factor 3 indicating high days to 75% tasseling, days to 75% silking, days to 75% brown husk, cob length, cob girth, number of kernel rows per cob and grain yield. Principal component scores of 14, 16 and 22 genotypes were high in factor 4 indicating high plant height, ear height, tassel length, cob length and number of kernel rows per cob. Similarly, genotypes 12, 13, 14, 16 and 25 exhibited high plant height, ear height, days to 75% tasseling, days to 75% silking, days to 75% brown husk, number of kernel rows per cob, number of kernels per row and grain yield.

Figure 2 displays the distribution of maize genotypes for the first two principal components. Genotypes that were distant from the other genotypes indicates their usefulness in breeding programmes. However, the biplot diagram (Figure-3) between PC 1 and PC2 explained the distribution and the nature of diversity for both variables and the genotypes. The biplot shows that the traits PT, PS, BH and TL together whereas PH, EH, EL, EG, KE, KR and GY are further and they form a different grouping Pahadi *et al*., 2017 [12]. We can thus observe the traits in such group behave similarly. The loading plot depicted that almost all the genotypes and variables showed high degree of variation.

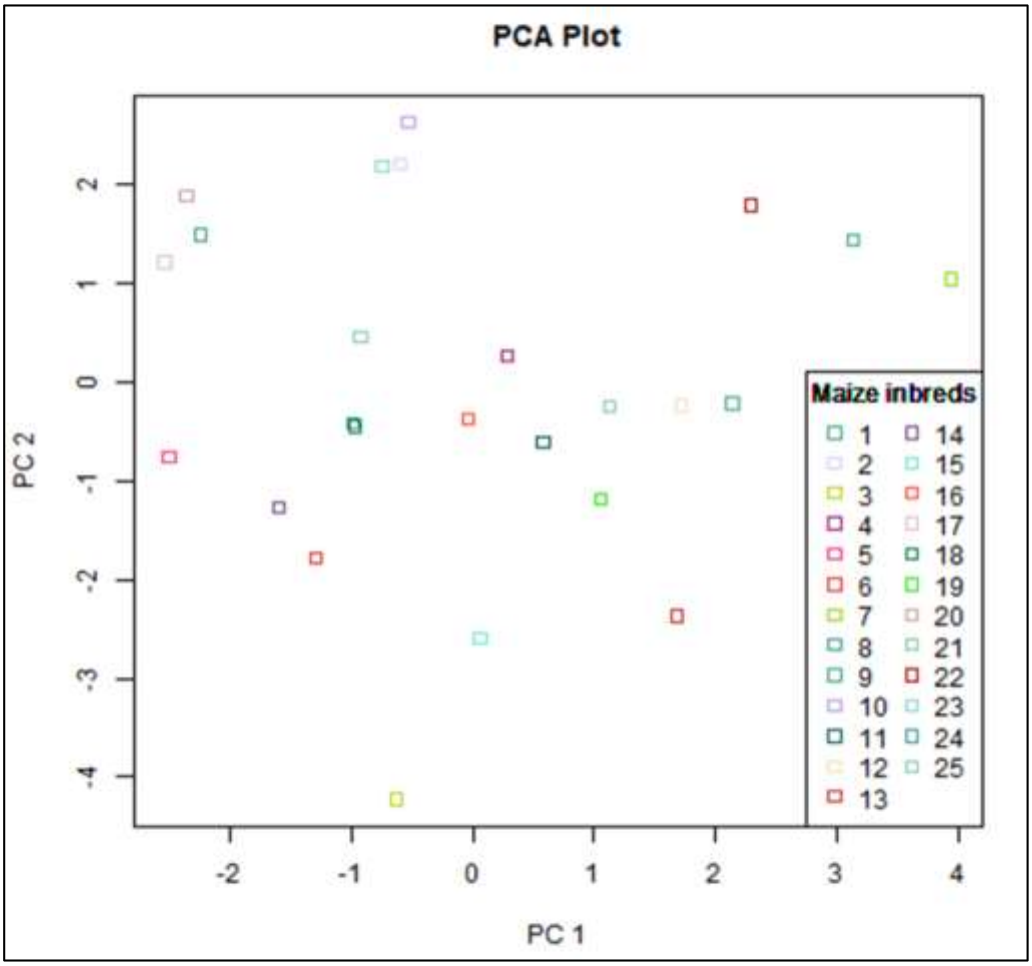

Fig 2: Distribution of maize inbreds for the first two principal components

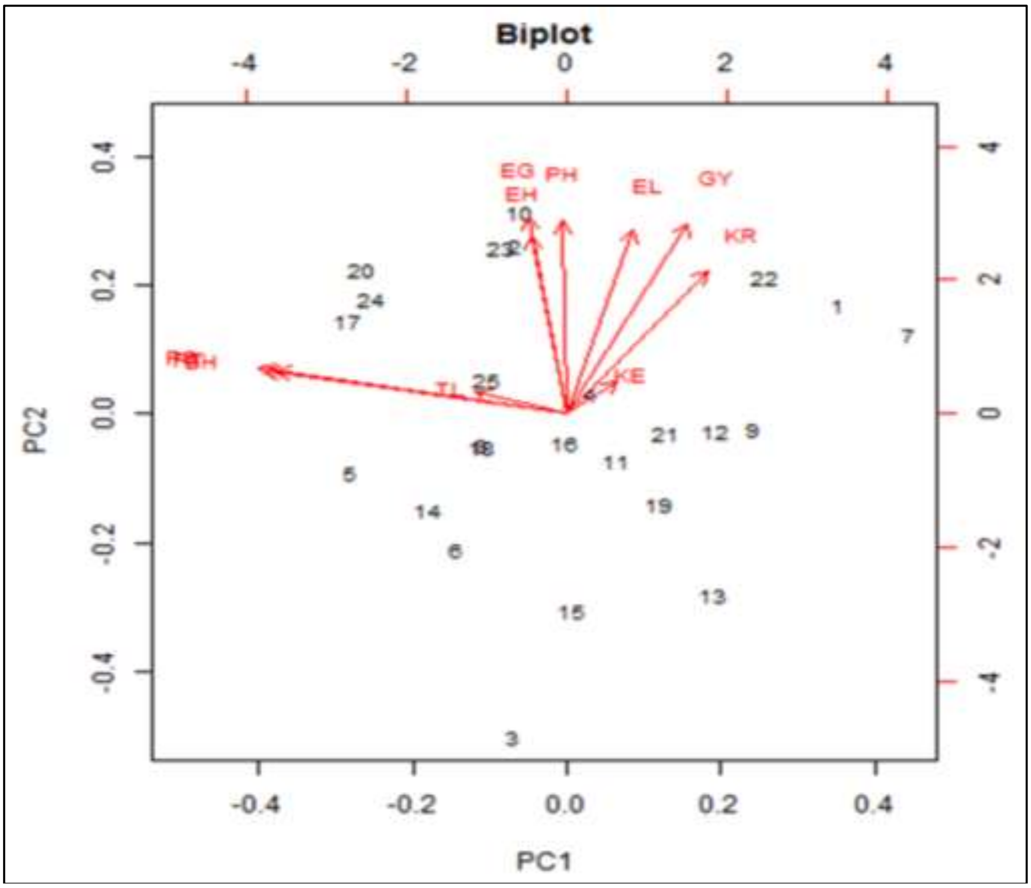

Fig 3: Biplot of the studied 11 variables of 25 maize genotypes

Conclusion

Even though PCA biplot did not reveal any prominent grouping, tested maize inbred lines have a considerable morphological variation that can be used in hybrid breeding programme. The present research revealed that sufficient amounts of variability present in the maize genotypes. The morpho-grain value of the each trait measures the importance and contribution of each component. The results of PCA revealed that the three principal components explained 86.63% of the total variations, thus suggesting that selected traits were the principal discriminatory characteristics. Therefore, the important characters coming collectively in various PCs and contributing towards explaining the variability and have the tendency to remain together this may be kept into consideration during utilization of these traits in breeding programme of maize.

References

1. Ali A, BeshirIssa A, Rahut DB. Adoption and Impact of the Maize Hybrid on the Livelihood of the Maize Growers: Some Policy Insights from Pakistan. Scientifica; c2020.
2. Amrita B, Shrivastava A, Bisen R, Mishra S. Study of Principal Component Analyses for Yield Contributing Traits in Fixed Advanced Generations of Soybean (*Glycine max* (L.) Merrill). Soybean Research, 2014, 44.
3. Bajracharya J, Steele KA, Jarvis DI, Sthapit BR, Witcombe JR. Rice landrace diversity in Nepal: Variability of agro-morphological traits and SSR markers in landraces from a high-altitude site. Field Crops Research. 2006;95:(2-3).
4. Dass SK, JM. Maize holds potential for diversification and livelihood security. Indian Journal of Agronomy. 2012;57(3s):32-37.
5. Gour L, Maurya SB, Koutu GK, Singh SK, Shukla SS, Mishra DK. Characterization of rice (*Oryza sativa* L.) genotypes using principal component analysis including scree plot & rotated component matrix. International Journal of Chemical Studies. 2017;5(4):975-983.
6. Iqbal Z, Arshad M, Ashraf M, Mahmood T, Waheed A. Evaluation of soybean [*Glycine max* (L.) Merrill] germplasm for some important morphological traits using multivariate analysis. Pakistan Journal of Botany. 2008;40(6):2323-2328.
7. Jinju H, Xiang ZC, Rouyi C, Fabo C, Fahui C. Analysis on principal components of maize cross combinations in Guizhou. Guizhou Agricultural Sciences. 2009;8:4-6.
8. Mahendran R, Veerabadhiran P, Robin S, Raveendran M. Principal component analysis of rice germplasm accessions under high temperature stress. International Journal of Agricultural Miladinovic Jegor, Hideki Kurosaki, Joe W Burton, Milica Hrustic, Dragana Miladinovic. The adaptability of short season soybean genotypes to varying longitudinal regions. European Journal of Agronomy. 2006;25: 243-249.
9. Muhammad RW, Rukhsana A, Shoib L, Abdul Q, Waqas M, Naveed M, *et al*. Numerical evaluation of local and exotic maize genotypes in arid conditions. Journal of Food Agriculture and Environment. 2012;10(1):624-630.
10. Nachimuthu VV, Robin S, Sudhakar D, Raveendran M, Rajeswari S, Manonmani S. Evaluation of Rice Genetic Diversity and Variability in a Population Panel by Principal Component Analysis. Indian Journal of Science and Technology. 2014;**7**(10):1555-1562.
11. Ojha GC, Sarawgi AK, Bhawana Sharma, Parikh M. Principal component analysis of morpho physiological traits in rice germplasm accessions (*Oryza sativa* L.) under rainfed condition. International Journal of Chemical Studies. 2017;5(5):1875-1878.
12. Pahadi P, Sapkota M, Thapa DB, Pradhan S. Cluster and principal component analysis for the selection of maize (*Zea mays* L.) genotypes. International Journal of Experimental Research and Review. 2017;9:5-10.
13. Ranum P, Peña-Rosas JP, Garcia-Casal MN. Global maize production, utilization and consumption. Annals of the New York Academy of Sciences. 2014;1312(1):105-112.
14. Sandeep S, Bharathi M, Narsimha RV, Eshwari KB. Principal component analysis in inbreds of Maize (*Zea mays* L.). International Journal of Tropical Agriculture. 2015;33(2):213-216.
15. Shrestha J. Cluster Analysis of Maize Inbred Lines. Journal of Nepal Agricultural Research Council. 2016;2:33-36.