P-ISSN: 2305-6622; E-ISSN: 2306-3599
International Journal of Agriculture and Biosciences
www.ijagbio.com; editor@ijagbio.com
Review Article https://doi.org/10.47278/journal.ijab/2022.029

Morphological Standard Based Genetic Diversity Among Maize (*Zea mays* L.) Accessions Indigenous to Pakistan

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Article History: 22-295 Received: 02-Aug-2022 Revised: 23-Sep-2022 Accepted: 19-Oct-2022

ABSTRACT

The present study was conducted to assess the genetic diversity among maize accessions indigenous to Pakistan. The research was directed in the field area of plant breeding and genetics, University of Agriculture Faisalabad. The experiment was laid down in a randomized complete block design with three replications. The characters that are studied were Days to 50% tasseling, Days to 50% silking, Anthesis silking interval, Plant height (cm), Ear height (cm), Cob length (cm), Cob diameter (mm), No of grains per cob, 100-grain weight (g), Cob yield per plant (g), Grain yield per plant (g). At the maturity, stage data were collected for all the traits. Analysis of variance revealed that all the genotypes under study were highly significant for all the traits. The principal component analysis (PCA) showed that the first four principal component analysis displayed eigenvalues with >1 and imparted 83.44% share to total variability. According to scatter plot genotypes UAF-PB-805, UAF-PB-378, UAF-PB-794, UAF-PB-364, and UAF-PB-871 were genetically diverse and should be considered for selection program. Dendrogram classified twenty genotypes into nine clusters based on their similarity. Cluster 9 had maximum intra-cluster distance depicting more variability as compared to other clusters. The genotypes in these clusters had high variability for study attributes. These results showed that the inbred lines having widely divergent clusters can be utilized in the hybrid breeding program.

Key words: Maize, Genetic diversity, PCA, Cluster, Variability

INTRODUCTION

Globally used staple food (maize) is ranked 3rd among important cereals after wheat and rice as it contributes 38% in annual global food production which exceeds than the production of rice and wheat that is 20% and 30% respectively. It has high nutritional profile including 72% starch, 10% protein, 8.5% fiber and 3% sugar (Singh et al., 2017a). Some corn varieties contain vitamin (B & C), Pro vitamin A, and folic acid in addition combined with rice and wheat (Kumar et al., 2015). In the struggling state for sustainability of food security it supplies at least 30 percent of the daily caloric intake for over 4.5 billion individuals in 94 developing economies. (Bekele & Rao, 2014).

Maize production grows best when the temperature is between 22 and 32°C during the day and night, and between 16.7 and 23.30°C. If the temperature is within this range, the growth of the plant will increase, but if the temperature drops above 5 ° C or rises above 32 °C, the plant will be greatly affected. If the humidity is insufficient and the temperature is above the optimal range, the pollen will dry out after it is released from the silk. The intensity of plant damage is determined by its intensity and persistence. of exposure to high temperatures. Pollen grains have a very thin outer shell, so they change with temperature. Therefore, at the time of pollination as well as at the time of seed production, temperature really matters. The yield suffers significantly when the corn plant is exposed to high temperatures, up to 35 ° C. In Pakistan, due to high and low temperatures, salinity, drought, and other factors, corn production was less than 1.59 times the rest of the world average (Sinsawat et al., 2004).

Maize is used as a model organism for research activities in modern breeding programs. Among cereals such as rice, wheat, barley and sorghum, maize is the leading crop which has been studied in more detail. Attractions that can be used in genomic and cytogenetic research activities are due to multiple mutations,

Cite This Article as: Mahmood T, Ghafoor S, Shahid M, Ahmad B, Tahir N, Abdullah M, Aslam M, xxxx. Morphological standard based genetic diversity among maize (*Zea mays* L.) accessions indigenous to Pakistan. Int J Agri Biosci, 11(4): 212-221. https://doi.org/10.47278/journal.ijab/2022.029

accumulation of heterochromatic chromosomes, accumulation of huge variations in nucleotides, a sample organism for studying plant domestication, genome evolution, quantitative inheritance, comparison of genomics, etc (Strable & Scanlon, 2009).

Crops can be genetically improved depending on the amount of genetic variability in breeding materials (Hemavathy, 2015; Zafar et al., 2020). The amount of genetic variation in crop germplasm is determined by the degree of recombination, mutation, selection, and random genetic drift. Certain alleles are removed by selection and genetic drift, whereas mutation and recombination contribute new variations into a population (Pervaiz et al., 2010; Zafar et al., 2022). The ability to widen genetic base of a crop germplasm to develop desirable varieties depends on efficient discovery of diverse sources of beneficial alleles and their successful introgression into existing genetic backgrounds (Meseka et al., 2015).

Genotypic and phenotypic coefficients of variation are important statistics used in detecting the extent of variability present in a germplasm. Heritability estimates provide information on the genotypic component that is contributing to variation (Govindaraj et al., 2015; Zafar et al., 2021b). Demand for maize grain is increasing year after year. To enhance maize production genetic diversity in maize germplasm must be continuously explored. The term "genetic diversity" refers to the variation in heritable traits found in populations of the same species. It exploits maximum heterosis for hybrid production (Ferdoush et al., 2017; Zafar et al., 2021a) and to improve genetic diversity it is essential to find the amount of already existing genetic variability through advance breeding methods (Singh et al., 2017b; Farooq et al., 2022).

Using biometrical procedure for genetic diversity such as using cluster analysis and principal component analysis, the level of biological population divergence can be determined. It also determines how much each variable contributes to intra- and inter-cluster total divergence (Singh et al., 2020; Kumari et al., 2017; Sahar et al., 2021). Determining the genetic diversity, heritability, and genetic variability of plant attributes that contribute to grain yield across maize genotypes was the objective of the current study.

MATERIALS AND METHODS

A study was conducted in the field area of department of Plant Breeding and Genetics, University of Agriculture Faisalabad, during season of February 2019 and August 2019. Twenty genotypes of maize were collected from the department of Plant Breeding and Genetics. The list genotypes are listed in Table 1.

Twenty inbred lines were sown in field during season February 19 with three replications in randomized block design. Row to row and plant to plant distances were maintained as 75 cm and 25 cm respectively. Standard agronomic and cultural practices were also given to the experimental area throughout the crop season followed by (Dutta et al., 2018). At the flowering stage cob silks were covered with butter paper bag before anthesis and selfing was done. The cobs were harvested and shelled manually by hands. The seeds were stored for next season. Data were noted to check diversity among various inbred lines for following characters.

The selfed seed of 20 genotypes was sowed during the season August 2019 under field conditions. The experiment was laid out according to RCBD design by replicating each genotype three times. All the standard cultural and agronomic practices followed for raising good crop. Row to Row and plant to plant distance was 75 cm and 25 cm maintained respectively. At the maturity stage data was collected for 11 characters.

Statistical Analysis

Data from field will be analyzed by using biometrical techniques. The significance of recorded data was checked by Analysis of Variance (ANOVA) by using Statistix 8.1 given by Steel and Torrie (1997). The character association was assessed by using Pearson Correlation following Johnson et al., (1955). A path analysis is used for measuring direct and indirect effects of all the characters on grain yield by Dewey & Lu, (1959).

Table 1: List of 20 Maize Genotypes indigenous to Pakistan

Sr No.	Genotypes	Sr. NO	Genotypes
1	UAF-PB-805	11	UAF-PB-364
2	UAF-PB-788	12	UAF-PB-871
3	UAF-PB-884	13	UAF-PB-890
4	UAF-PB-471	14	UAF-PB-806
5	UAF-PB-378	15	UAF-PB-776
6	UAF-PB-593	16	UAF-PB-889
7	UAF-PB-347	17	UAF-PB-794
8	UAF-PB-370	18	UAF-PB-813
9	UAF-PB-829	19	UAF-PB-342
10	UAF-PB-562	20	UAF-PB-803

RESULTS AND DISCUSSION

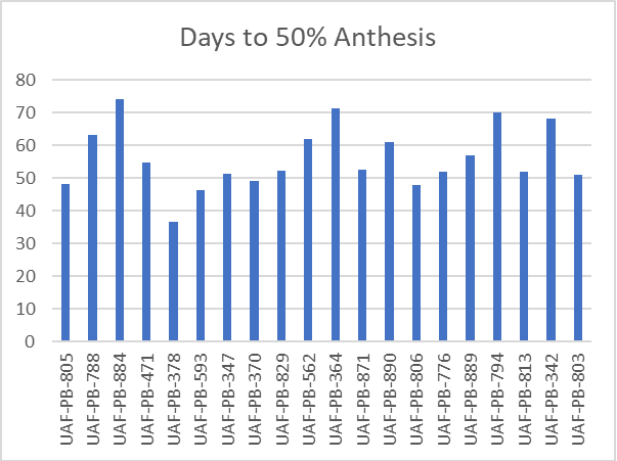
Analysis of Variance

The genetic variability amongst genotypes was assessed by analysis of variance. The outcomes revealed significant differences for the studied attributes among the genotypes (Table 2). The mean performance of all the genotypes for yield related attributes is presented in form of graphs (Fig. 1 to Fig. 11). Saritha & Patil (2020) reported that to get desired genotypes in the end of breeding experiment, maximal genetic variability should be present in amongst studied genotypes. The genotypes exhibiting high variability for yield and its contributing traits should be selected.

Principle Component Analysis (PCA)

Principal component analysis (PCA) is commonly used in plant sciences to classify genotypes and reduce the number of variables (Dutta et al., 2018). Understanding the genetic diversity and population structure of inbred lines is useful for allocating lines for heterotic groups, establishing crosses for inbred lines and hybrids, and protecting plant genomes, hence facilitating the generation and transmission of novel variations (Zhang et al., 2018). PCA is the simplest and most fundamental method for evaluating genetic diversity and variation in plant breeding activities (Vathana et al., 2019).

XLSTAT was utilized to evaluate genetic divergence across 20 maize genotypes by analysing the mean values of all variables using PCA. It provided information on factor loading and total factor variability. The total variance consists of eleven components. On the first two computers,


Days to 50% Anthesis
80
70
60
50
40
30
20
10
0
UAF-PB-805
UAF-PB-788
UAF-PB-884
UAF-PB-471
UAF-PB-378
UAF-PB-593
UAF-PB-347
UAF-PB-370
UAF-PB-829
UAF-PB-562
UAF-PB-364
UAF-PB-871
UAF-PB-890
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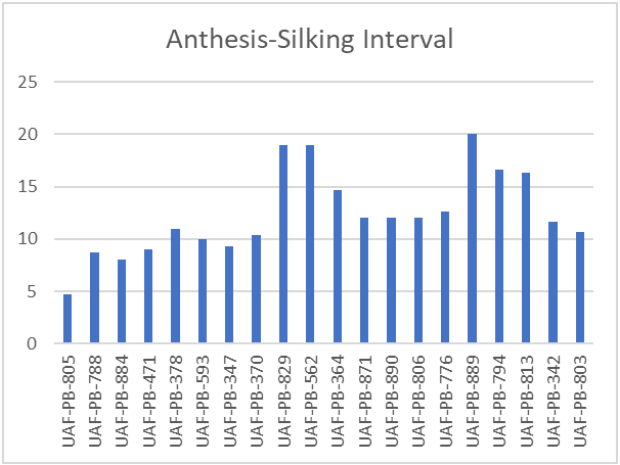
UAF-PB-794
UAF-PB-813
UAF-PB-342
UAF-PB-803


Anthesis-Silking Interval
25
20
15
10
5
0
UAF-PB-805
UAF-PB-788
UAF-PB-884
UAF-PB-471
UAF-PB-378
UAF-PB-593
UAF-PB-347
UAF-PB-370
UAF-PB-829
UAF-PB-562
UAF-PB-364
UAF-PB-871
UAF-PB-890
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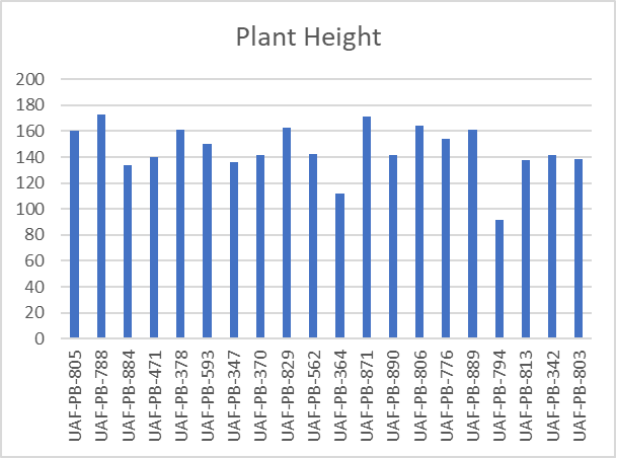
UAF-PB-794
UAF-PB-813
UAF-PB-342
UAF-PB-803


Plant Height
200
180
160
140
120
100
80
60
40
20
0
UAF-PB-805
UAF-PB-788
UAF-PB-884
UAF-PB-471
UAF-PB-378
UAF-PB-593
UAF-PB-347
UAF-PB-370
UAF-PB-829
UAF-PB-562
UAF-PB-364
UAF-PB-871
UAF-PB-890
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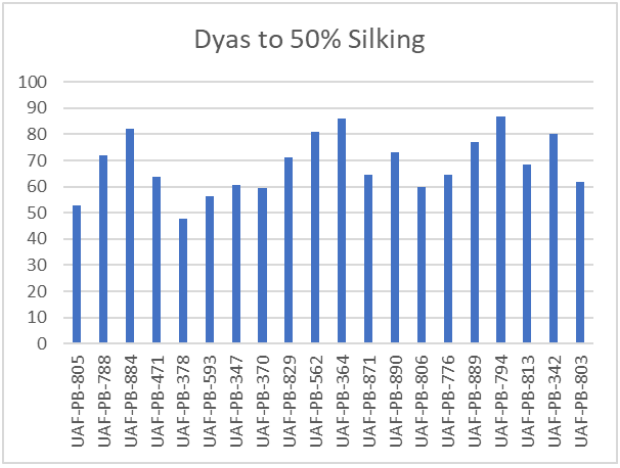
UAF-PB-794
UAF-PB-813
UAF-PB-342
UAF-PB-803


Dyas to 50% Silking
100
90
80
70
60
50
40
30
20
10
0
UAF-PB-805
UAF-PB-788
UAF-PB-884
UAF-PB-471
UAF-PB-378
UAF-PB-593
UAF-PB-347
UAF-PB-370
UAF-PB-829
UAF-PB-562
UAF-PB-364
UAF-PB-871
UAF-PB-890
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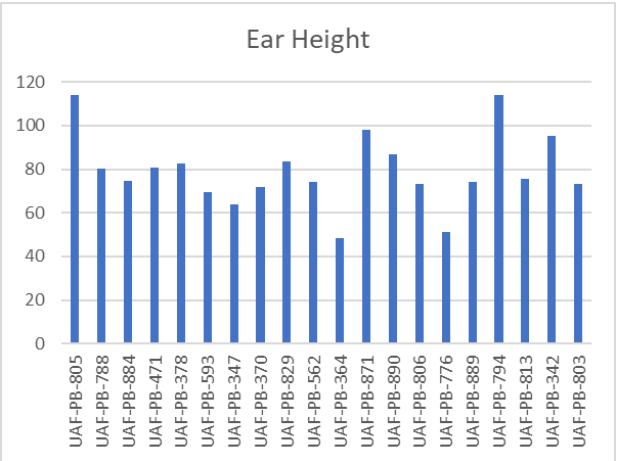
UAF-PB-889
UAF-PB-794
UAF-PB-813
UAF-PB-342
UAF-PB-803


Ear Height
120
100
80
60
40
20
0
UAF-PB-805
UAF-PB-788
UAF-PB-884
UAF-PB-471
UAF-PB-378
UAF-PB-593
UAF-PB-347
UAF-PB-370
UAF-PB-829
UAF-PB-562
UAF-PB-364
UAF-PB-871
UAF-PB-890
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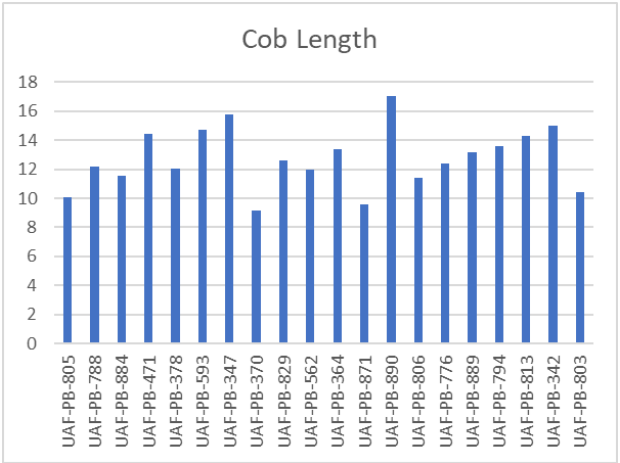
UAF-PB-813
UAF-PB-342
UAF-PB-803


Cob Length
18
16
14
12
10
8
6
4
2
0
UAF-PB-805
UAF-PB-788
UAF-PB-884
UAF-PB-471
UAF-PB-378
UAF-PB-593
UAF-PB-347
UAF-PB-370
UAF-PB-829
UAF-PB-562
UAF-PB-364
UAF-PB-871
UAF-PB-890
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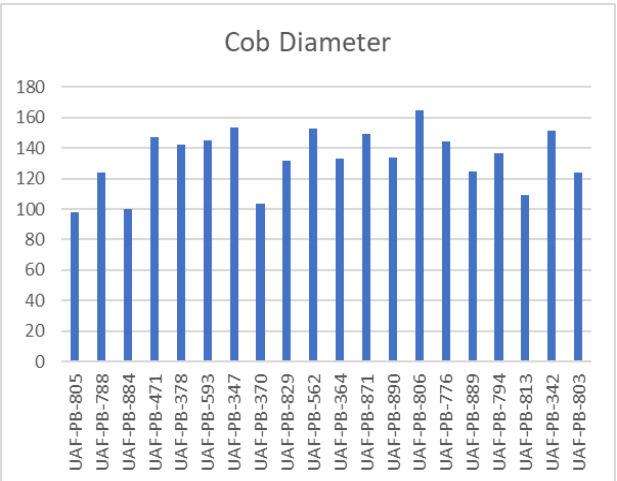
UAF-PB-813
UAF-PB-342
UAF-PB-803


Cob Diameter
180
160
140
120
100
80
60
40
20
0
UAF-PB-805
UAF-PB-788
UAF-PB-884
UAF-PB-471
UAF-PB-378
UAF-PB-593
UAF-PB-347
UAF-PB-370
UAF-PB-829
UAF-PB-562
UAF-PB-364
UAF-PB-871
UAF-PB-890
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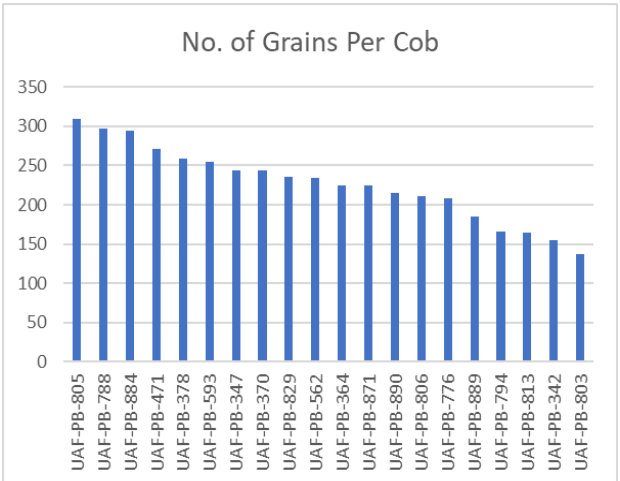
UAF-PB-813
UAF-PB-342
UAF-PB-803


No. of Grains Per Cob
350
300
250
200
150
100
50
0
UAF-PB-805
UAF-PB-788
UAF-PB-884
UAF-PB-471
UAF-PB-378
UAF-PB-593
UAF-PB-347
UAF-PB-370
UAF-PB-829
UAF-PB-562
UAF-PB-364
UAF-PB-871
UAF-PB-890
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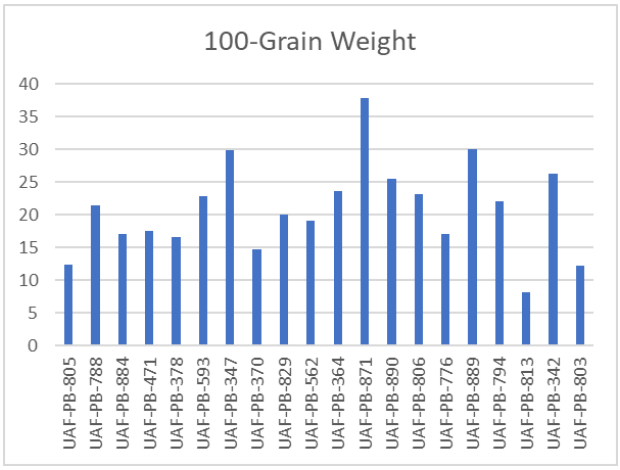
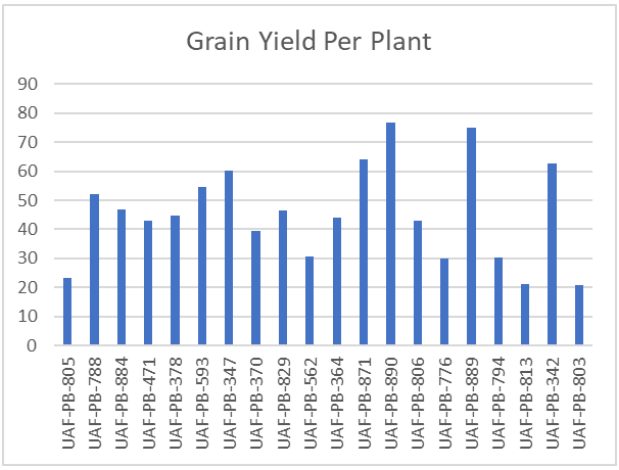
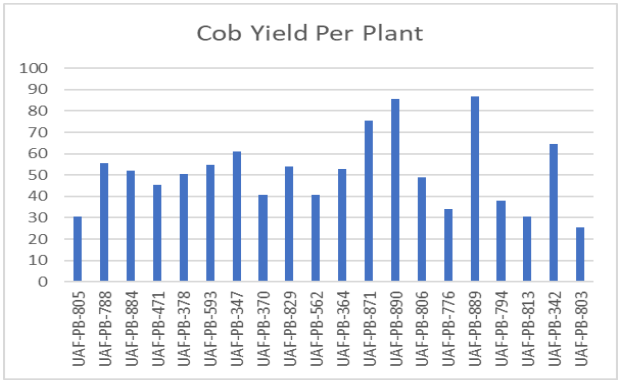
UAF-PB-794
UAF-PB-813
UAF-PB-342
UAF-PB-803







two-dimensional representation was examined. The first four of the eleven principal components had multiple eigenvalues and accounted for the great majority of the total variability. The PCA analysis produced Eigenvalues for thirteen maize genotypes across ten variables (plant traits), as well as cumulative (%) variances explained and variability percentages. Eigenvalues measure the contribution and importance of each component to total variance based on its Eigenvalue (Nuruzzaman et al., 2019).

PC-I, II, III and IV had share of 31.73%, 27.07%, 12.89% and 11.73% to total variability respectively (Table 3). These 4 PCs imparted 83.44% to total variability among studied genotypes. Rest of the PCs had <1 eigen value therefore should not be discussed further.

Stansluos et al. (2019) reported similar results. The genotypic variation was portioned into 22 PCs out of which four components had Eigenvalues greater than or equal to one. The first four principal components explained 86.76 per cent of the total variation. Mushtaq et al. (2016) also show similar results. In their study on maize, reported that PCA abridged the total variation into four principal components. Similar findings of PCs contribution to the total variability were also observed in maize genotypes (Kumari et al., 2017). The percentage variability was explained by Eigenvalues while Eigenvectors demonstrated the relation among all the variables. The Eigenvalues are displayed in Table 3.

PC-I and PC-II contributed 31.73% and 27.07% to total variation. It was mainly related to C.L, C.D, GW, GYP and GYP while PC-II revealed higher and positive values for 50% A, 50% S, P.H, E.H, G.C and GYP. The genotypes having higher values for PC-I included UAF-PB-889, UAF-PB-890 and UAF-PB-342 while genotypes related to PC-II were UAF-PB-378, UAF-PB-871 and UAF-PB-593. PC-III and PC-IV had 12.89% and 11.73% share to total variability. PC-III had high and positive values for attributes including C.D, G.C, P.H and GW (Table 5). The selection of attributes with positive values should be done. PC-IV displayed positive and higher values for 50% A E.H, C.L, C.D and G.C. UAF-PB-890 and UAF-PB-813 displayed higher values of percentage variability for PC-III while for PC-IV related genotypes were UAF-PB-871, UAF-PB-884 and UAF-PB- 805 (Table 6).

PC1 had main contribution from C.L, GW, GYP and GYP while the least contribution was recorded P.H, E.H and G.C. PC-II had contribution to total variation due to 50% A, 50% S P.H and E.H. Similarly, PC-III got main contribution from C.D and G.C. 50% A, E.H, C.L and C.D were the main contributors for PC-IV (Table 5).

Scree Plot

On a graph between Eigenvalues and the principal components, the Scree plot, which represents the variance percentage according to all of the principal components, is displayed (Shakeel et al., 2018). A scree plot is generated by plotting principal components on the x-axis and Eigenvalues on the y-axis in a graph to represent the proportion of variability present in each PC. PC1 had the highest degree of variability, 31.7%, and the highest eigenvalue, 3.4911. PC9, PC10, and PC11 displayed the lowest variability with eigenvalues of 0.0369, 0.0085, and 0.0000 respectively. PC1 has the greatest genetic variety; hence, its genotypes must be chosen for selection.

Scatter Plot

The genotypes closer to the origin were considered to be similar to each other for the studied traits in scatter plot whereas the genotypes that were at greater distance from the origin and presented at the edge were considered more genetically diverse (Shah et al., 2018).

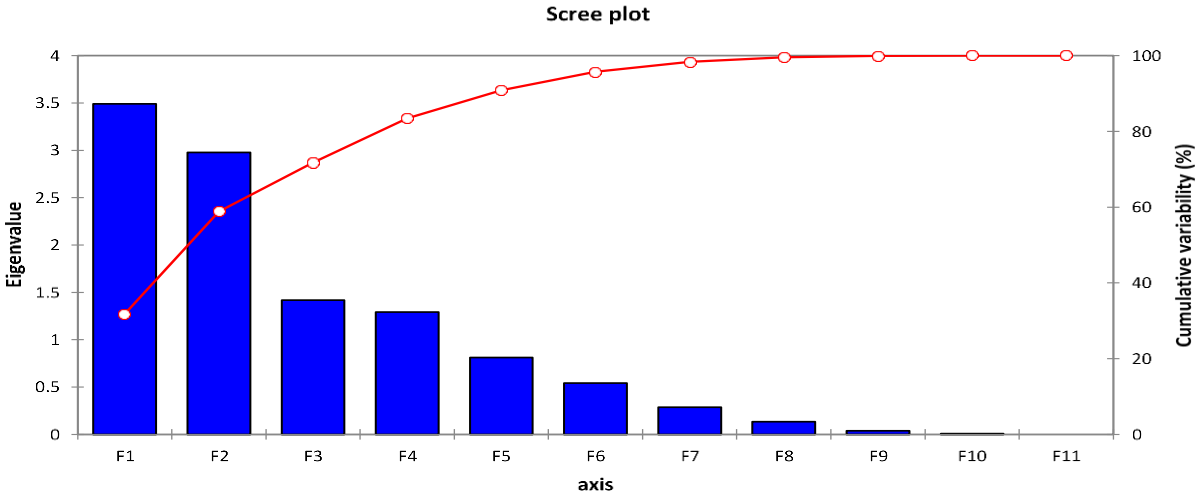


Fig. 12: Scree plot of principal component analysis.

Table 2: Randomized Complete Block ANOVA Table for Yield and Yield Related Traits of Maize

Source	DF	50%A	50%S	ASI	P.H	E.H	C.L	C.D	GC	100GW	CYP	GYP
Replication	2	14.46	8.55	2.31	68.96	75.33	0.43	46.56	130.45	41.67	51.38	41.14
Genotype	19	279**	372.50**	49.55**	1166.21**	781.17**	13.12*	1112**	7016.28**	146.98**	885.37**	830.22**
Error	38	1.94	2	1.94	9.62	9.76	6.73	8.88	40.54	10.88	11.37	8.37

Table 3: Eigenvalues

	PC1F1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11
Eigenvalue	3.4911	2.9786	1.4181	1.2910	0.8130	0.5406	0.2880	0.1343	0.0369	0.0085	0.0000
Variability (%)	31.7370	27.0781	12.8915	11.7360	7.3905	4.9149	2.6184	1.2212	0.3354	0.0771	0.0000
Cumulative %	31.7370	58.8151	71.7066	83.4425	90.8330	95.7479	98.3663	99.5875	99.9229	100.0000	100.0000

Table 4: Eigenvectors

	F1	F2	F3	F4	F5	F6	F7	F8	F9	F10	F11
A	0.2660	-0.3781	0.1880	0.3932	-0.1985	0.0191	0.3968	-0.0209	0.0202	-0.0195	-0.6308
S	0.3089	-0.4118	0.0623	0.2996	0.1190	0.0980	0.2832	-0.0620	0.0433	0.0171	0.7289
ASI	0.2157	-0.2321	-0.2754	-0.1114	0.7971	0.2235	-0.1650	-0.1204	0.0707	0.0931	-0.2659
PH	-0.0732	0.4818	-0.1854	0.1564	0.2924	0.0623	0.6053	0.4899	0.0889	-0.0050	0.0000
EH	-0.0928	0.3758	0.0286	0.4655	-0.0807	0.6598	-0.1514	-0.3907	0.1172	0.0380	0.0000
CL	0.3269	-0.0497	0.3094	-0.4387	-0.1781	0.5747	-0.0795	0.4580	0.1555	-0.0124	0.0000
CD	0.2497	0.0771	-0.5125	-0.4303	-0.2852	0.1612	0.4093	-0.4199	-0.1747	-0.0479	0.0000
GC	0.0798	0.2629	0.6197	-0.2863	0.2509	-0.1808	0.2807	-0.4467	0.2861	-0.0505	0.0000
GW	0.4373	0.1704	-0.2960	0.1185	-0.1784	-0.2880	-0.2181	0.0303	0.7175	0.0035	0.0000
CYP	0.4558	0.2626	0.0700	0.1479	0.1061	-0.0903	-0.1891	0.0368	-0.4012	-0.6920	0.0000
GYP	0.4458	0.2911	0.1215	0.0808	-0.0066	-0.1445	-0.0990	0.0247	-0.3983	0.7108	0.0000

Table 5: Contribution of the variables (%)

	PC-IF1	PC-II	PC-III	PC-IV
A	7.0741	14.2922	3.5346	15.4585
S	9.5398	16.9597	0.3875	8.9785
ASI	4.6536	5.3855	7.5861	1.2405
PH	0.5363	23.2087	3.4384	2.4446
EH	0.8610	14.1252	0.0819	21.6722
CL	10.6896	0.2471	9.5738	19.2469
CD	6.2334	0.5942	26.2632	18.5153
GC	0.6361	6.9135	38.4065	8.1988
GW	19.1238	2.9034	8.7625	1.4035
CYP	20.7754	6.8976	0.4905	2.1888
GYP	19.8770	8.4731	1.4751	0.6525

In scatter plot genotypes UAF-PB-805, UAF-PB-378, UAF-PB-794, UAF-PB-364 and UAF-PB-871 were present at maximum distance from the origin therefore, these were genetically diverse and should be considered for selection program. While the other genotypes were present closer to each other in same are because these were not genetically diverse and should not be considered for selection.

Table 6: Contribution of the observations (%)

	PC-I	PC-II	PC-II	PC-IV
805	-4.0586	1.3644	0.3510	1.9247
788	0.1038	0.8045	0.4916	1.2361
884	-0.0666	-1.3122	2.1983	1.8710
471	-0.3499	0.2016	0.1921	-0.7861
378	-1.5853	2.2780	-0.3502	-1.3147
593	0.3366	1.6095	0.7461	-1.8435
347	1.5978	0.8302	-0.0959	-1.6095
370	-2.2339	0.4679	1.3222	0.1669
829	0.2230	0.2333	-0.7280	0.2443
562	0.1321	-1.9570	-1.7857	0.2166
364	1.5873	-2.9656	0.2937	-0.0113
871	1.4065	2.4106	-2.4882	1.9044
890	3.1284	1.3817	2.1096	-0.2665
806	-0.3008	1.2988	-1.3175	-1.0304
776	-1.1842	-0.7859	-0.8527	-1.2995
889	2.9823	0.8966	-0.1017	0.7613
794	0.8369	-4.5022	-0.7994	-0.1985
813	-1.9134	-1.2380	1.5044	-0.9353
342	2.2996	0.1187	0.2167	0.8040
803	-2.9417	-1.1348	-0.9063	0.1659

Table 7: Distribution of 11 characters into 9 clusters

Variable	Cluster1	Cluster2	Cluster3	Cluster4	Cluster5	Cluster6	Cluster7	Cluster8	Cluster9
A	48.333	53.524	58.333	53.666	56.500	61.666	52.667	57.000	70.000
S	53.000	65.048	69.889	64.666	71.334	75.334	64.667	77.000	86.667
ASI	4.667	11.524	11.555	11.000	14.834	13.667	12.000	20.000	16.667
PH	160.030	154.166	137.650	145.805	140.390	132.950	171.430	161.120	91.220
EH	114.080	80.056	74.013	78.225	73.745	49.905	97.950	74.040	48.050
CL	10.040	13.349	11.681	15.865	11.215	12.885	9.577	13.170	13.613
CD	97.750	144.963	104.157	139.655	138.380	138.565	149.530	124.290	136.760
GC	184.240	233.136	275.037	303.275	159.380	209.380	165.710	243.770	136.610
GW	12.347	22.159	13.324	24.231	15.687	20.340	37.880	30.083	22.003
CYP	30.587	54.310	41.072	70.288	33.106	43.400	75.470	86.897	38.027
GYP	23.363	50.288	35.867	65.632	25.738	36.923	64.017	75.030	30.157

Table 8: Cluster wise distribution of maize genotypes in 9 clusters

Class	Frequency	Genotypes
1	1	UAF-PB-805
2	1	UAF-PB-871
3	7	UAF-PB-788, UAF-PB-829, UAF-PB-378, UAF-PB-806, UAF-PB-471, UAF-PB-347, UAF-PB-342
4	1	UAF-PB-889
5	2	UAF-PB-364, UAF-PB-776
6	2	UAF-PB-562, UAF-PB-803
7	1	UAF-PB-794
8	3	UAF-PB-884, UAF-PB-370, UAF-PB-813
9	2	UAF-PB- 593, UAF-PB-890

Table 9: Distance between central objects

	Cluster1	Cluster2	Cluster3	Cluster4	Cluster5	Cluster6	Cluster7	Cluster8	Cluster9
Cluster1	0.000	86.174	105.328	145.451	69.370	91.254	89.122	113.593	121.818
Cluster2	86.174	0.000	65.121	74.315	82.891	49.420	78.000	50.879	125.725
Cluster3	105.328	65.121	0.000	63.774	121.422	78.743	135.528	77.293	153.686
Cluster4	145.451	74.315	63.774	0.000	154.572	107.428	142.565	68.402	186.462
Cluster5	69.370	82.891	121.422	154.572	0.000	58.509	74.405	115.513	64.103
Cluster6	91.254	49.420	78.743	107.428	58.509	0.000	89.972	79.160	85.606
Cluster7	89.122	78.000	135.528	142.565	74.405	89.972	0.000	89.268	116.433
Cluster8	113.593	50.879	77.293	68.402	115.513	79.160	89.268	0.000	148.125
Cluster9	121.818	125.725	153.686	186.462	64.103	85.606	116.433	148.125	0.000

Scatter plots of the first three principal components were made to determine the graphical display of the pattern of genetic diversity among the maize genotypes (Iqbal, Shinwari, & Rabbani, 2015). Distribution of 39 exotic maize genotypes in a two-dimensional scatter diagram based on PCA scores (Zaman & Islam, 2013).

Biplot

In a principal component analysis, variables superimposed on a biplot plot are represented as vectors, with the relative length of the vectors indicating the variability of each variable. These variables were represented on the plot as vectors using a biplot. The contribution of each variable to the overall variance of the PC-1 and PC-2 germplasm was highlighted by the variables' relative distances from the origin (Shakeel et al., 2018). An important subject in plant breeding is how to utilize the data for morphological characterization to its fullest potential. Standardized data were shown on a Genotype Trait (GT) biplot to show the genetic variety of maize genotypes. By plotting the PC1 scores versus the PC2 scores for each genotype and trait, a genotype by trait biplot is created. Every calculation made use of the XLSTAT GT biplot tool (Al-Naggar et al., 2020).

A positive correlation exists between two parameters if the angle between their vectors is less than 90 degrees, and vice versa. A biplot depicts the relationship between many traits in this way (also a measure of 90o angle between two parameters will be treated as no correlation). The principal component Biplot expressed that variables are imposed as vectors on the graph.

The line joining the character to the origin is called traits vector while the angle that represent the association amongst all the characters is cosine angle. Characters with less than 90^{o}cosine angle had positive correlation while characters with more than 90^{o}angle were negatively correlated (Latif et al., 2015). G.C, C.D, C.L and anthesis silking interval showed minimum differences as they were close to the origin whereas P.H, E.H, GYP, GYP, GW, 50% A and 50% S displayed maximum differences as they were at greater distance from origin.

The PCA analysis revealed the many ways in which distinct qualities contributed to total variation. In addition, it highlighted how traits and genotypes influence plant yield and illustrated the diversity of the examined genotypes. Due to this diversity and variability, the relevant trait in the germplasm can be enhanced, resulting in enhanced yield performance.

Cluster Analysis

Cluster analysis makes it simple to identify homogeneous groupings of genotypes from which to start a hybridization program (Dutta et al., 2018). To ascertain whether and to what extent homogenous groupings are generated by common ancestry and whether the obtained

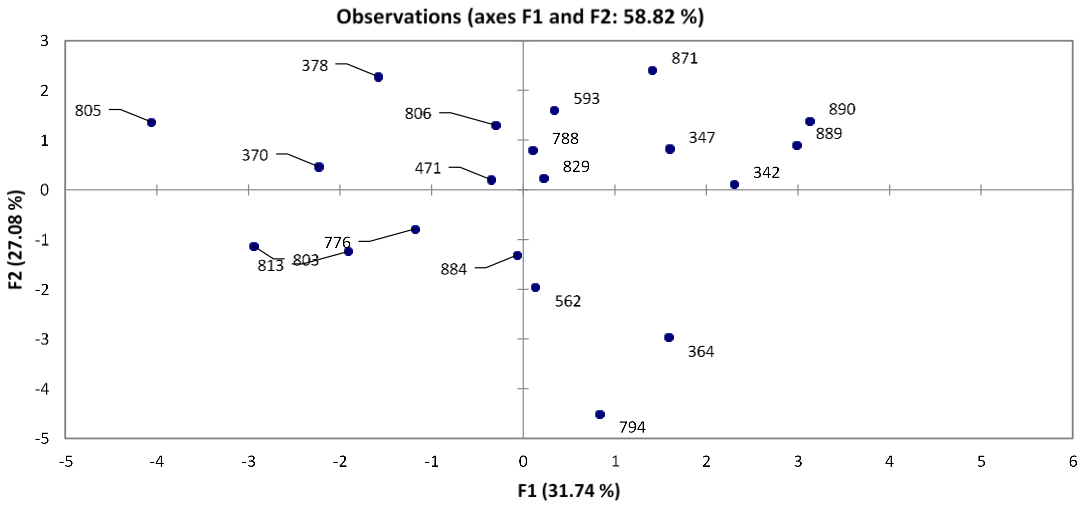


Fig. 13: Two-dimensional orientation of *Zea mays* genotypes on principal component axis I and II

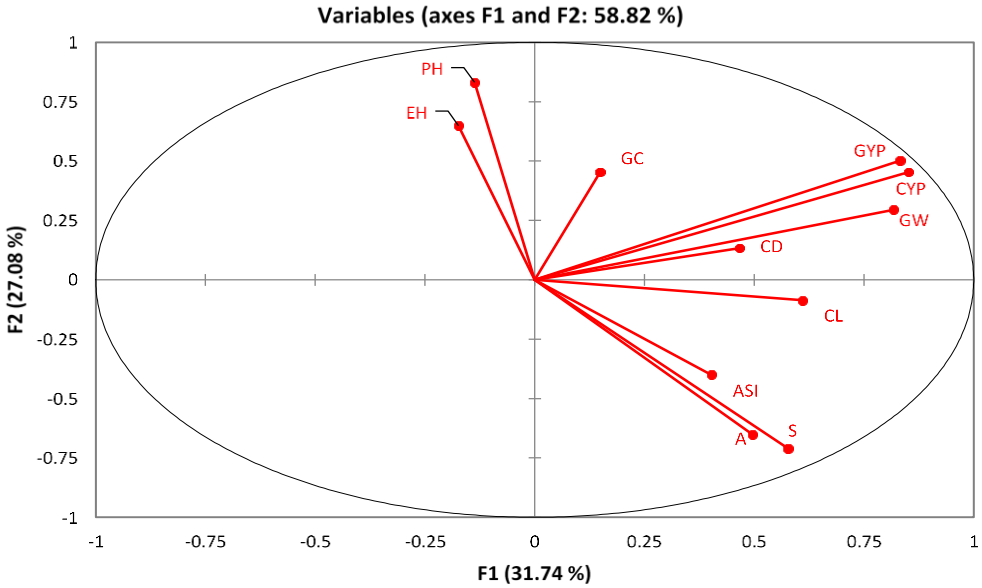


Fig 14: Principle component biplot for contribution of traits

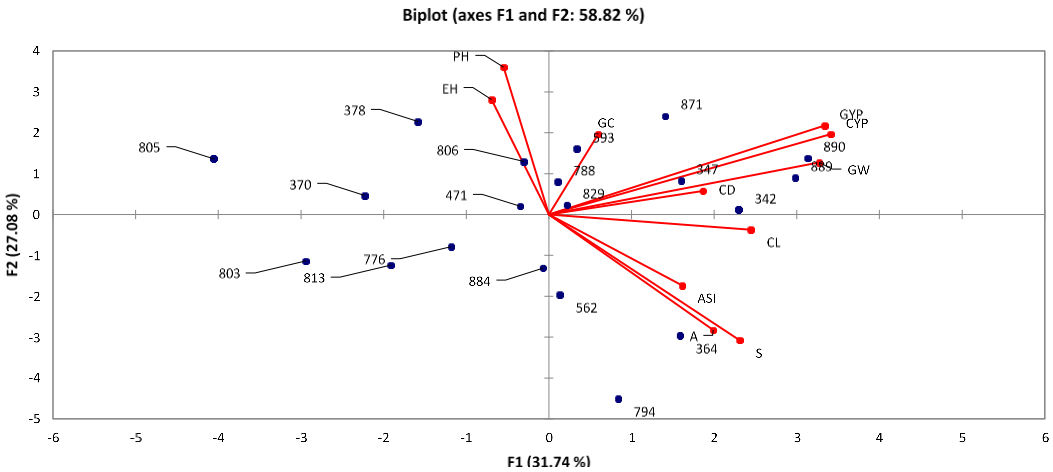


Fig 15: Genotype by trait biplot illustrating the relationship between PC1 and PC2 for 20 genotypes and 11 traits of maize.

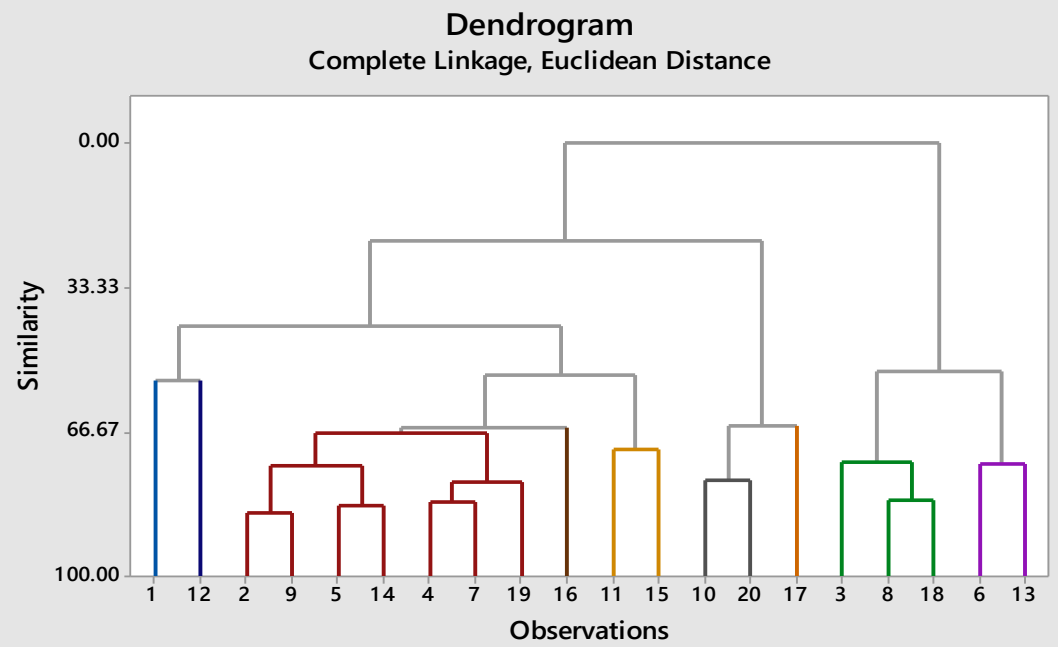


Fig 16: Genetic grouping of maize inbred lines by cluster analysis.

results were consistent with the pedigree of the observed sweet maize inbreds, the phenotypic characterization was used in the cluster analysis. As a result, choosing genotypes for subsequent crossings may benefit from the cluster analysis results (Babić et al., 2010). Two methods hierarchical and non-hierarchical clustering are used in cluster analysis. The choice of method is done based on data size as the results of analysis are highly dependent on variables being studied.

Hierarchical Clustering

In agglomerative hierarchical clustering method, each object first forms its separate cluster. Then the clusters with more similarity combine to form one cluster. This happens with all the clusters and in the end many clusters are obtained. While in non-hierarchical clustering (k means clustering) the objects are first grouped into one large cluster which is then separated into different small clusters with similar objects (Oyekunle et al., 2015).

Agglomerative hierarchical clustering method is used commonly. There are many agglomerative methods used for analysis including single linkage, complete linkage and ward's linkage. Complete linkage method is explained below.

Complete Linkage

Dendrograms, which represent cluster analysis, are very useful for locating homogeneous variables with varied degrees of similarity (Oyekunle et al., 2015). Based on performance for the examined plant attributes, the dendrogram (Complete Linkage and Euclidean Distance) depicts genetic similarity. Using the MINITAB17 software, thirteen maize genotypes were divided into three clusters based on how well they performed for ten plant parameters (Islam et al., 2020).

Data from each criterion was used to create dendrograms of phenotypic variance for each of the 19 genotypes. A major component analysis was calculated using XLSTAT. Using Euclidean distance matrices and the complete linkage approach, agglomerative hierarchical clustering (AHC) analysis and dendrograms were produced (Al-Naggar et al., 2020) Mean values of the agronomic traits for local maize populations were standardized and used for computing Euclidean distances between the agronomic traits using MINITAB software. The cluster analysis reported differentiates between populations based on their similarity. The clustering of local maize populations on the dendrogram in three separate groups resulted from different morphological and qualitative traits. (Aliu et al., 2013). Dendrogram classified 20 genotypes into 9 clusters. The characters being studies are represented by these clusters. The genotypes being displayed by these clusters could be used according to the magnitude of their genetic diversity (Fig 4.5.1).

Table 8 displayed that cluster 3 contained highest number of genotypes followed by clusters 8, 5,6,9,1,2,4 and 7. Cluster1 had genotypes with high values for P.H, E.H and grain per cob. Cluster 2 displayed highest value for C.D, C.L, G.C, GYP and P.H. Cluster 3 had highest mean value for C.D and G.C while cluster 4 had genotypes with highest values for C.L, C.D, G.C, GYP, GW and GYP.

Cluster 5 had highest mean values for C.D, 50% A, 50% S and anthesis silking interval. Cluster 6 showed the highest values for C.D, C.L, GW, 50% A, 50% S and anthesis silking interval. Cluster 7 had highest mean values for P.H, C.D, GW, GYP and GYP. Cluster 8 showed highest values for P.H, C.L, G.C, GW, GYP and GYP. Cluster 9 had highest values for C.L, 50% A, 50% S and anthesis silking interval Table (4.5.2). The genotypes within a cluster are more like each other as compared to genotypes in other clusters.

The average inter-cluster and intra-cluster Euclidean 2 distance was also calculated (Table 9). Cluster 9 had maximum intra cluster distance depicting more variability as compared to other clusters. Clusters 1 and 9 had maximum inter cluster distance (186.462) followed by clusters 3 and 9 (153.686), clusters 8 and 9 (148.125), clusters 7 and 9 (116.433), clusters 2 and 9 (125.725), clusters 1 and 9 (121.818), clusters 6 and 9 (85.606) and,

clusters 5 and 9 (64.103). The genotypes in these cluster had high variability for studies attributes. The lowest inter cluster distance was observed for clusters 2 and 8 (49.420). Similar results are obtained by Al-Naggar et al. (2020) in maize. Their study revealed that the inbred lines showed considerable genetic diversity among themselves by occupying nine different clusters. The information obtained from PCA and cluster analysis will be useful for future fruitful breeding experiments.

Conclusion

Assessment of genetic diversity also provides the breeder an opportunity to identify the gaps in the collection, finding the traits and genotypes for which useful variability is limited and allow maximizing variation in the collection. Therefore, the present findings of identifying potential yield contributing plant traits along with a high level of genetic diversity among the genotypes would be beneficial for maize genotype characterization, conservation, and planning for further maize breeding programs for enhanced yield potential.

Abbreviations

50% A= Days to 50% Anthesis, 50% S = Days to 50% Silking, ASI = Anthesis-Silking Interval, P.H = Plant Height, E.H = Ear Height, C.L = Cob Length, C.D = Cob Diameter, G.C = No. of Grain Per Cob, 100GW = 100-Grain Weight, CYP = Cob Yield Per Plant

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