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GENETIC VARIABILITY IN PARENTAL LINES OF MAIZE (*ZEA MAYS* L.)

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ABSTRACT

Seven maize parental lines were evaluated for sixteen (16) morphological characters. The experiment was laid out in a randomized block design with three replications. Analysis of variance for the genotypes for all the characters was highly significant ($p < 0.01$) except days to 50% tasselling, days to 50% silking, 100-grain weight, shelling %, and harvest index. However, a significant difference ($p < 0.05$) was observed in the Anthesis- silking interval (ASI) and days to 50% maturity. High (>60%) to moderate (30-60%) broad sense heritability was observed in most of the characters while Days to 50% tasseling and Days to 50% silking exhibited low (< 30%), heritability of 3.61% and 1.33% respectively. The highest values for the Phenotypic coefficient of variation (PCV) and Genotypic coefficient of variation, (GCV) of 188.89% and 124.44% respectively were recorded in ASI. Yield and yield components recorded high values. The cluster divided parental lines into four clusters at the dissimilarity coefficient of 0.68. In the Principal Component Analysis (PCA), the first two principals accounted for 59.80. However, PCA1 and PCA2 accounted for 37.04% and 22.76%, respectively. The correlation coefficient shows a highly significant positive phenotypic correlation between yield/ha and all growth and yield parameters.

Key words : Genetic gain, Genotypic coefficient of variation, Phenotypic coefficient of variation, Heritability, Open-pollinated varieties.

Introduction

Maize (*Zea mays* L.) as an out-crosser, is a species with complex genome and a very high degree of variability which breeders often exploit in achieving heterosis. The fundamental step towards developing maize and other crop hybrid varieties in breeding programs is identifying and selecting broad genetic base resource (parental lines) with useful and desirable agronomic characters in different heterotic groups (Li *et al*., 2018; Kim *et al*., 2021). Information on genetic variability of a germplasm in plant breeding programmes is of utmost importance to plant breeders because it facilitates adequate and judicious use of genetic resources to achieves their objectives. Utilization of a broad genetic based parental lines which can be inbred lines, land race or open pollinated varieties in hybridization program has been reported to yield better hybrids (Subramanian and Subbaraman, 2014). Many studies have revealed tremendous variabilities among maize germplasms. The need to improve or develop high yielding hybrids is imperative. The use of cluster analysis is most frequently

used in the identification and classification of maize germplasm by breeders and geneticist into subsets or homogenous groups with potential for a specific breeding program. The grouping is such that the germplasms in within a group response in a similar pattern across different environments. The magnitudes and pattern of the genetic variations among the germplasm is measured using the multivariate analysis based on Principal Component Analysis (PCA), Cluster analysis and discriminate analysis as applied in several crops such as rice (Oladosu *et al.*, 2014), oil palm (Myint *et al.*, 2019) and wheat (Aslani *et al.*, 2012). In this study, principal component analysis was used to determine the relationship between variables and genotype classification as well as pattern analysis, which used ordination and classification to explore the structures of inherent pattern among the germplasm while cluster analysis was used to classify unclassified materials. The objectives of this study are to study inter and intra-population variation based on quantitative characters and to determine genetic components and heritability values of all the characters under study in the seven maize parental lines.

Materials and Methods

Description of the experimental site

This study was carried out at Research and demonstration Field 15 of Universiti Putra Malaysia between January - April 2019. The experimental site is located at 3º 10'N, 113º 2'E and 175m above sea level with an average annual rainfall of 2429mm. Monthly average minimum and maximum temperature of 21-23ºC and 31-33ºC at night and day, respectively.

Planting materials

The sevenmaize accessions namely; TZSTR 190, TZSTR 193, TZEI 114, SAMMAZ 14, SAMMAZ 16 and SAMMAZ 17 were collected from IITA and IAR in Nigeria and SUWAN from Thailand for this research (Table 1).

Field experimental design

The seven accessions were evaluated for their performances in a field trial laid in a randomized complete block design (RCBD) with plot size of 11.25m² (5m × 2.25m) made up of four rows each, giving a total of 78.75m² and replicated 3 times. Planting was done at a spacing of 0.75m x 0.5m and two-three seeds were placed per hole and later thinned to 2 plants per hole to achieve plant population density of 53,333 plants per hectare. Weeds were controlled by application of Atrazine, a pre-emergence herbicide at the rate of 6 L/ha and hand weeding was employed subsequently, when necessary.

NPK fertilizer was applied at the rate of 140N, 80P and 60K at 2 weeks, 4 weeks and 6 weeks after planting. Rainfall was complimented by irrigating the field when necessary. Harvesting was done at maturity when the ears turn brown.

Table 1 : Descriptions of seven parental lines of maize used as for the experiment.

Ent no.	Name	Maturity	Grain colour	Reaction to *Striga*	Source
1	TZSTR 190	Late	White	Resistant	IITA
2	TZSTR 193	Late	White	Resistant	IITA
3	TZEI 114	Late	White	Susceptible	IITA
4	SAMMAZ 14	Medium	White	Resistant	IAR
5	SAMMAZ 16	Medium	White	Tolerant	IAR
6	SAMMAZ 17	Late	White	Susceptible	IAR
7	SUWAN	Late	Yellow	Susceptible	Thailand

Data collection

Data were collected on maturity parameters, yield and yield components parameters and growth parameters of the maize plant.

Data was collected on Striga parameters, growth parameters, yield and yield components of the maize plant. The number of Striga emergences was counted on each plot at 7 and 10 weeks after planting (WAP). The damage rate was visually rated at each trial on the two middle rows at 7 and 10 WAP using a scale of 1-9 (Kim, 1991). Days to tasseling, days to silking, anthesis-silking interval (ASI), days to maturity, number of ears, plant height (m), ear height (m), number of ears, ear length (cm), ear weight per plant (g), ear diameter (cm), number rows per ear, number of seeds per row per ear, grain yield per hectare (g), 100-grain weight (g), shelling percentage and harvest index were recorded.

Statistical analysis

Data on all characters collected were subjected to Analysis of variance (ANOVA) and mean comparison procedure using SAS version 9.4 to reveal the main and single factor using Fisher's Least Significant Difference (LSD) at 5% significance difference.

Genetic components

The formulae for computing genetic components are as follows:

Genotypic components

$$\delta_g = (MS_2 - MS_3)/r$$
$$\delta_e = MS_3$$

Phenotypic components

$$\delta_p = \delta_g + \delta_e$$

Coefficients of variability were also computed using the following formulae:

$$PVC = \sqrt{\delta^2_p}/\mu \times 100$$

$$GVC = \sqrt{\delta^2_g}/\mu \times 100$$

Here, δ_g = Genotypic variance; δ_p = Phenotypic variance; δ_e = Error variance; PVC = Phenotypic coefficient of variation; GCV = Genotypic coefficient of variation; MS_2 = Mean square of populations; MS_3 = Mean square of error; r = Number of replications; μ = Mean of the character.

Heritability

Broad sense heritability is the ratio of genetic variance (σ^2_g) to phenotypic variance (σ^2_p).

Genetic advance (GA) and Genetic gain (GG) as a percent of the mean, assuming selection of the super 5% of the accessions were computed using the following formulae:

$$GA = k \times \sqrt{\sigma^2_p} \times h^2_B$$

$$GG = k \times \sqrt{\sigma^2_p} \times \mu \times h^2_B \times 100$$

Where,

K = constant (which varies depending upon the selection intensity and, if the latter is 5%, stands at 2.06); $\sqrt{\sigma^2_p}$ = phenotypic standard deviation; h^2_B = broad sense heritability and μ = mean of the character being evaluated.

Correlation coefficient

Correlation coefficient was used to evaluate the association or relationship among various character in this study.

Person correlation was used using the formula:

$$r(X,Y) = \frac{\sum \left[(Xi - \bar{X})(Yi - \bar{Y}) \right]}{\sqrt{\sum \left[(Xi - \bar{X})^2 (Yi - \bar{Y})^2 \right]}}$$

Where, $r_{(X, Y)}$ = correlation between characters X and Y; Xi and Yi = character X and Y in the ith; $\bar{X}$ and $\bar{Y}$ = mean value of character X and Y.

Cluster analysis

The cluster analysis was carried out using NTSYS-PC version 2.1 to determine morphological diversity of the maize genotypes for all characters under study (Rohlf, 2002). Jaccard's similarity coefficient was used to produce a dendrogram for which the UPGMA algorithm and SAHN clustering (unweighted pair group method using arithmetic average) was used for depicting the genetic relationships.

Results and Discussion

Analysis of variance, genetic variance, heritability and genetic parameters

The mean squares from that analysis of variance for all the characters are presented in Table 2. The mean squares for the genotypes for all the characters were highly significant ($p < 0.01$) except days to 50% tasseling, days to 50% silking, 100 grain weight, shelling % and harvest index. However, significant difference ($p < 0.05$) was observed in Anthesis-silking interval and days to 50% maturity. This indicates that there is large amount of genetic variation among the parental line population under study, therefore suggest that they are amenable to selection procedure and can be exploited for hybridization breeding program. This is in agreement with the findings of Akaogu *et al.* (2020); Badu-Apraku *et al.* (2016) and Islam *et al.* (2020) in their separate works. The result also implies that there was no significant effect of environmental variation in the replications in most characters except for days to 50% maturity, cob length, cob diameter, number of grains/row and grain yield/ha which shows significant difference at $p < 0.05$.

The result of the component variance showed greater genetic variability was observed in the population for all the characters than the error variance except in DTT, DTS, ASI, HGW, SHP and HIDX. This could be attributed to the greater environmental effects on these six characters. A similar finding was reported by Bisen (2018).

Broad sense heritability, genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for all characters as presented in Table 2 shows high (>60%) to moderate (30-60%) broad sense heritability for PH, EH, CW, CL, CD, NRPC, NSPR, GYPP, GYP and ASI, DTM, HGW, SHP and HIDX, respectively. However, DTT and DTS exhibited low (< 30%), heritability of 3.61% and 1.33%, respectively. This indicates that selection of the parental lines used in this study for those characters with high to moderated broad sense heritability as listed above would be highly effective as genetic base for improvement of yield. This finding is in consonance with the findings of Belay (2018), Ahmad (2018), Ogunniyan and Olakojo (2014), Murtadha *et al.* (2018), where they reported in their separate works high heritability in most of the characters especially in Anthesis-silking interval and grain yield. The values of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) are veritable tools in breeding programs for the selection of potential superior characters. They are used to identify characters with

Table 2 : Analysis of Variance of seven parental lines, genetic variances and variance components for 16 characters in maize.

SOC	DF	DTT	DTS	ASI	DTM	PH (cm)	EH (cm)	CW (g)	CL (cm)	CD (cm)	NRPC	NSPR	GYPP (g)	GYH (tonnes)	HGW (g)	SHP	HIDX
REP	2	1.76ns	5.14ns	4.76ns	21.76*	327.8ns	24.16ns	4550.91ns	14.85*	37.87*	1.58ns	101.34*	3211.00ns	10.13*	14.48ns	35.57ns	0.003ns
GEN	6	1.76ns	1.52ns	5.41*	39.60*	3164.33**	1636.18**	12203.10**	47.31**	48.30**	11.97**	198.96**	7348.76**	21.79**	63.05ns	56.23ns	0.005ns
ERR	12	1.60	1.48	1.65	8.48	170.53	00.002	1328.20	2.53	6.06	1.43	19.14	1087.67	2.35	28.97	19.59	0.002
σ^2_g		0.06	0.02	1.25	10.37	997.93	506.49	3625.00	14.92	14.08	3.51	59.94	2087.00	6.48	12.05	12.21	0.001
σ^2_p		1.66	1.50	2.90	18.85	1168.45	623.21	5413.58	17.45	20.14	4.94	79.08	3477.33	9.94	38.96	31.81	0.003
σ^2_e		1.60	1.48	1.65	8.48	170.53	00.002	1328.20	2.53	6.06	1.43	19.14	1087.67	2.35	28.97	19.59	0.002
PCV		2.52	2.26	188.89	4.84	17.13	23.52	42.98	26.21	10.10	15.26	33.83	46.85	47.51	19.27	7.91	27.27
GCV		0.49	0.26	124.44	3.59	15.83	21.21	35.17	24.20	8.44	12.85	29.45	36.29	38.46	10.72	4.89	13.64
h^2_B		3.61	1.33	43.10	55.01	85.41	81.27	80.00	69.91	85.50	71.05	75.80	60.01	65.17	30.93	38.38	33.33
GA		0.10	0.03	1.51	4.92	60.14	41.79	121.26	6.02	7.91	3.25	13.88	72.90	4.23	3.98	4.46	0.04
GG		0.19	0.06	167.71	5.49	30.14	39.38	70.83	37.74	17.79	22.33	52.82	57.92	63.78	12.28	6.25	18.73
CV		2.47	2.23	142.0	3.25	6.54	10.83	21.31	9.97	5.54	8.15	16.64	44.79	45.16	16.62	6.21	17.85

DTT=Days to 50% tasseling, DTS=Days to 50% Silking, ANI=Anthesis-silking interval, DTM=Days to 50% maturity, PH=Plant height, EH=Ear height, CW= Cob weight, CL=Cob length, CD=Cob diameter, NRPC=No. of rows/cob, NSPR=No. of seeds/row, GYPP=Grain yield/plant, GYH=Grain yield/ha, HGW=100 grain weight, SHP=Shelling%, HIDX=Harvest index.

high selection response. The values range of PCV and GCV are categorized as low from 0-10, moderate from 10-20% and high from >20% (Oladosu *et al.*, 2014; Suryanarayana *et al.*, 2017).

The highest values for PCV and GCV of 188.89% and 124.44% respectively were recorded in ASI. Yield and yield components recorded high values ranging from 24.20% in CL to 47.51% (GYH) while growth parameter, EH recorded high PCV and GCV; 23.52% and 21.21%, respectively, PH had moderate PCV and GCV range 17.13% and 15.83%, respectively. Characters with low heritability and low GCV indicates greater influence of the environment on such a character as observed in DTT and DTS while high heritability and high genetic gains as recorded in ASI, CW, NSPR, GYPP and GYH indicates that the high heritability of these characters is due to additive gene effect while those with high heritability and low genetic gain like in DTM, CL, CD and NRPC are due to non-additive gene effect. This is in line with the findings of Islam *et al.* (2020), Kamal *et al.* (2020), Myint *et al.* (2019) and Oladosu *et al.* (2014) in their separate works.

High heritability estimates of a character projects an effective measure of selection based on the phenotype of the character. The high genetic gain and high broad sense heritability for PH (60.14%, 85.41%), EH (41.79, 81.27), CW (121,26%, 80.00%) and GYP (72.90%, 60.01%) in this study indicate the dominance of additive gene action in governing these characters hence these characters present an important and more reliable for selection in maize breeding program. This is in agreement with the findings of the findings of Hamid (2018), Belay (2018) and Islam *et al.* (2020).

Mean performance of seven parental lines of maize in 16 characters

The mean performance of the seven parental lines (per se performance) is presented in Table 3. The characters that do not show significant difference are not discussed. From the result of the Table 3, TZSTR 192 and TZEI 114 shows the highest positive Anthesis-silking interval (ASI) of 2.33 days, while SAMMAZ 17 shows the highest negative value of -1.33 days followed by SAMMAZ 16 with -0.33 days showing a significant difference between the highest positive value and the least negative value. With respect to days to 50% maturity, Suwan took the longest days of 93.67days to attain 50% maturity, which was followed by SAMMAZ 17 and SAMMAZ 14 with

91.67 days each while TZSTR 192 shows the least days of 83.00 days, which shows earliness.

SAMMAZ 17 exhibited the highest plant height (232.47m) and ear height (129.65m), while TZSTR 190 was the least in both plant height (148.61m) and ear height (67.91). Suwan had the highest cob weight/plant (236.67g) and cob length (21.52cm) followed SAMMAZ 16 with 227.00 and 18.50cm, respectively. However, there was no significant difference between them while TZSTR 190 had the lowest cob weight and cob length 69.91g and 11.14cm, respectively. TZSTR 192 had the highest cob diameter of 51.74cm and number of rows/cob of 19.05, while TZSTR 190 had the least cob diameter of 38.98cm. SUWAN had the least number of rows/cob but with the highest number of seeds per row of 35.08, while TZSTR 190 had the least. With respect to yield, SAMMAZ 16 had the highest yield/plant of 174.00g as well as yield/ha (9.30 tonnes) followed by SUWAN with 167.67g yield/plant and 8.98 tonnes/ha, however, there was no significant difference between them in yield while TZSTR 190 was the lowest yielder of 42.67g/plant and 2.29 tonnes/ha. SAMMAZ 17 had the highest 100 grain weight, while TZSTR 190 had the least. For shelling percentage, the highest value of 75.88% was observed in SAMMAZ 16 followed by SAMMAZ 17 with 74.81%, while TZSTR 190 had the least (63.04%). For harvest index, the highest value of 0.257 was recorded by SAMMAZ 17 followed by SAMMAZ 16 which recorded 0.252, while TZSTR 190 recorded the least harvest index of 0.159.

Cluster analysis

Cluster analysis was used to group the seven parental lines with greater genetic similarities together based on their morphological characters. The cluster analysis in this study was done based on morphological data using UPGMA dendrogram. The seven parental lines were divided into four clusters at the dissimilarity coefficient of 0.68 (Fig. 1). This showed the presence of high level of morphological diversity among the seven parental lines under study. Cluster IV is the largest cluster with 4 parental lines which are all open pollination varieties (OPVs), however, this cluster is further divided into three sub-clusters, P4 (SAMMAZ 14) originally known as ACR 97 developed by IITA, Nigeria, P5 and P6 (SAMMAZ 16 and SAMMAZ 17) developed at IAR, Nigeria and SUWAN from Thailand. Cluster I, II and III had one genotype each and are all inbred line from IITA, Nigeria. Cluster I and II (P1 and P2) are of 8th generation inbred while Cluster III is a 6th generation Inbred line (Table 4). The cluster means in Table 5 was observed that cluster

Table 3 : Mean performance of seven parental lines in 16 characters.

GEN	DTT	DTS	ASI	DTM	PH (cm)	EH (cm)	CW (g)	CL (cm)	CD (cm)	NRPC	NSPR	GYPP (g)	GYH (tonnes)	HGW (g)	SHP	HIDX
P1	50.67	55.67	1.00	89.67	148.61	69.91	69.00	11.14	38.98	14.67	13.01	42.67	2.29	26.33	63.04	0.159
P2	50.33	54.00	2.33	83.00	165.83	86.17	134.67	12.42	51.74	19.05	20.67	110.33	5.18	28.00	71.52	0.240
P3	50.33	54.67	2.33	86.67	190.34	90.86	121.67	12.25	43.09	13.95	20.76	83.33	4.45	29.00	69.13	0.228
P4	51.67	54.57	1.33	91.67	226.40	121.02	188.33	17.51	44.05	13.73	30.88	138.33	7.39	34.00	73.76	0.219
P5	51.67	53.67	-0.33	91.00	224.55	120.42	227.00	18.50	46.68	14.67	31.15	174.00	9.30	34.33	75.88	0.252
P6	51.33	54.67	-1.33	91.67	232.47	129.65	221.00	18.28	44.69	13.58	32.42	164.67	8.80	37.67	74.81	0.257
P7	52.33	53.67	1.00	93.67	208.61	124.83	236.67	21.52	41.90	12.20	35.08	167.67	8.98	37.33	70.94	0.194
Mean	51.19	54.42	0.90	89.62	199.54	106.12	171.19	15.95	44.45	14.55	26.28	125.86	6.63	32.38	71.30	0.22
LSD	2.25	2.16	2.89	5.18	23.23	20.45	64.84	2.83	4.38	2.13	7.78	58.67	2.73	9.58	7.88	0.22

DTT=Days to 50% tasseling, DTS=Days to 50% Silking, ANI=Anthesis-silking interval, DTM=Days to 50% maturity, PH=Plant height (cm), EH=Ear height (cm), CW= Cobweight (g), CL=Cob length (cm), CD=Cob diameter (cm), NRPC=No. of rows/cob, NSPR=No. of seeds/row, GYPP=Grain yield/plant (g), GYH=Grain yield/ha (tonnes/ha), HGW=100 grain weight (g), SHP=Shelling percentage (%), HIDX=Harvest index
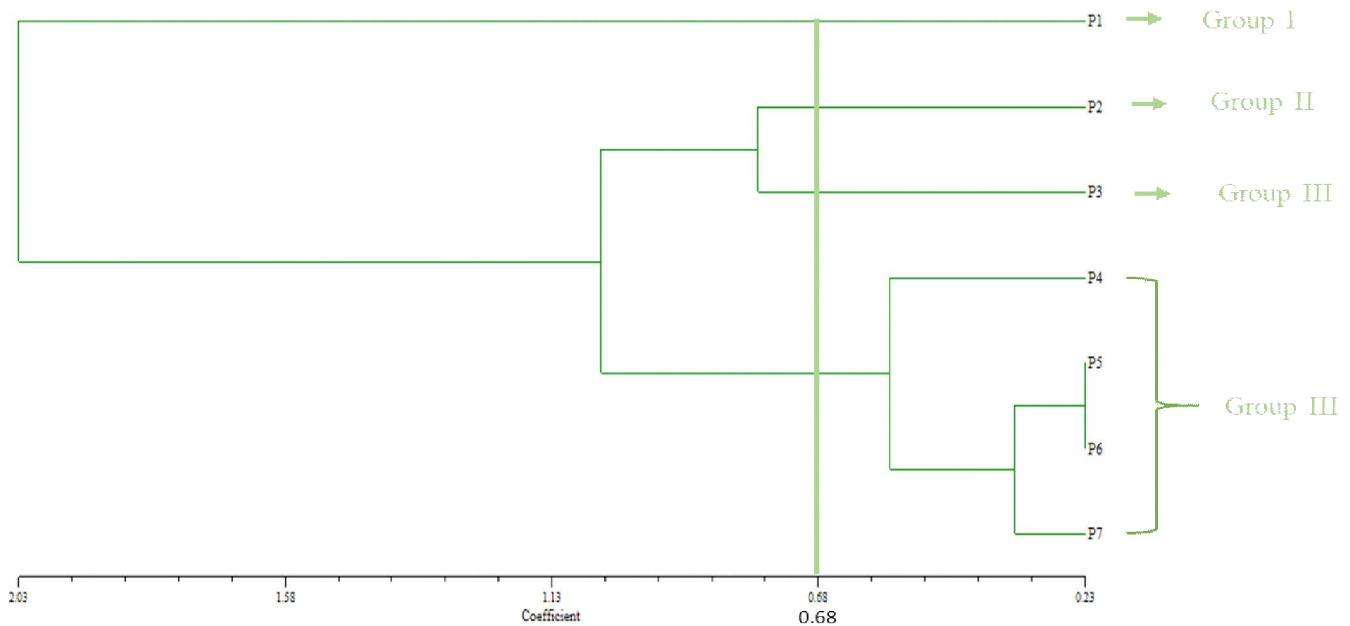
Fig. 1 : Dendrogram of morphological characters derived from 7 parental lines maize genotypes constructed using UPGMA method. The scale is based on Jaccard's similarity coefficient. **Note:** P1 = TZSTR 190; P2 = TZSTR 193; P3 = TZI 114; P4 = SAMMAZ 14; P5 = SAMMAZ 16; P6 = SAMMAZ 17; P7 = SUWAN
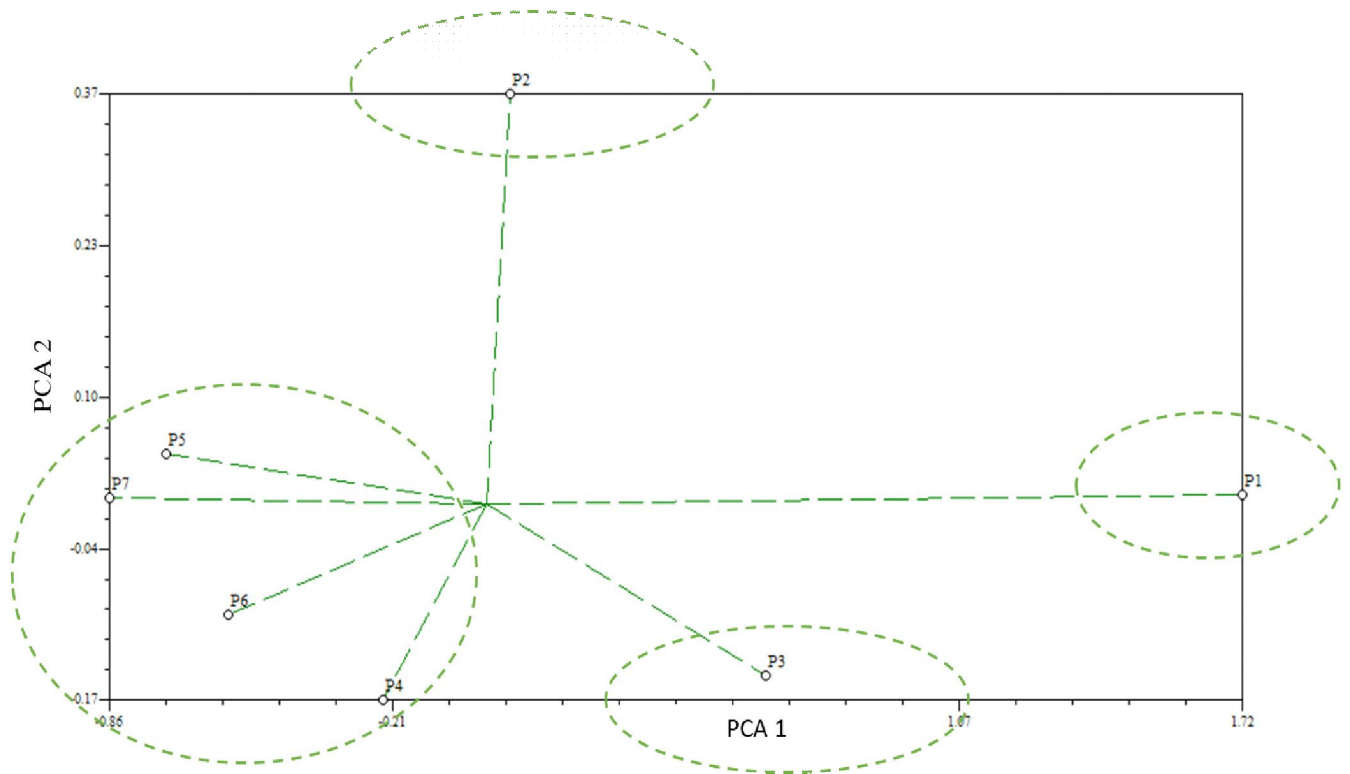
Fig. 2 : Principal component analysis based on 16 characters in seven parental maize genotypes.

IV performed highest in most of the characters except in cob diameter, number of rows, harvest index; days to 50% tasseling, days to 50% silking (flowering) and days to 50% maturity which cluster II performed better. Days to flowering and days to 50% maturity in this cluster (II) was observed to be lower than other cluster which depicts that they are early maturity which is an ideal and potential character for selection of maize genotype for breeding program. The poor performance of cluster I, II and III in most growth and yield parameters may not be

Table 4 : Morphological character clusters of 7 parental lines revealed by cluster analysis.

Cluster	No. of genotypes	Population	Origin
I	1	TZSTR 190	8th generation Inbred line
II	1	TZSTR 192	8th generation Inbred line
III	1	TZEI 114	6th generation Inbred line
IV	4	SAMMAZ 14,16, 17 and SUWAN	Open pollinated varieties

unconnected with inbreeding depression as a result of continuous selfing over generations. This sentiment was also sheared by Badu-Apraku *et al.* (2016), Olaoye and Bello (2009), Kutka (2011) in their separate works on combination of pure lines and synthetic varieties as parental lines. The clustering pattern observed in this cluster analysis does not recognize geographical diversity where the genotypes were collected rather typified genetic diversity in the characters studied. This is in agreement with the assertions of Myint *et al.* (2019), who studied essential oil content and other yield characters in oil palm germplasms collected from different geographical regions identified three families SEN02.05, SEN05.02 and SEN06.01 among oil palm germplasm as prospective families for high kernel content.

Table 5 : Cluster mean values for 16 characters in seven parental lines of maize.

Character	Cluster			
	I	II	III	IV
Days to 50% Tasseling	50.67	50.33	50.33	51.75
Days to 50% silking	55.67	54.00	54.67	54.15
Anthesis-silking interval	1.00	2.33	2.33	0.17
Days to 50% maturity	89.67	83.00	86.67	92.00
Plant height at maturity	148.61	165.83	190.34	223.01
Ear height at maturity	69.91	86.17	90.86	123.98
Cob weight (g)	69.00	134.67	121.67	218.25
Cob length (cm)	11.14	12.42	12.25	18.95
Cob diameter (cm)	38.98	51.74	43.09	44.33
Number of rows/cob	14.67	19.05	13.95	13.55
Number of grains/row	13.01	20.67	20.76	32.38
Grain yield/plant	42.67	110.33	83.33	161.17
Grain yield/hectare	2.29	5.18	4.45	8.62
Hundred grain weight	26.33	28.00	29.00	35.83
Shelling percentage (%)	63.04	71.52	69.13	73.85
Harvest index	0.16	0.24	0.23	0.23

Principal Component Analysis (PCA)

The use of multivariate statistics technique as a tool like principal component analysis (PCA), clustering and discriminate analysis for analyzing large amount of plant characters in many crops is very effective in evaluation of genetic variations of germplasm. The principal component analysis based on earliness, growth, yield and yield component characters of seven maize genotypes as shown in Fig. 2, showing the two-dimensional principal component analysis revealed that four clusters were formed which corresponds with cluster analysis result. Cluster I, II and III consists of one member each while cluster IV consists of 4 members. From the PCA analysis, the first two principal accounted for 59.80%, which indicate that they presented good percentage of the total variations of characters studied in the seven genotypes. However, PCA1 and PCA2 accounted for 37.04% and 22.76%, respectively.

Correlation between characters

Phenotypic correlation coefficients between important characters are presented in Table 6. The result of the correlation coefficient was there was positive highly significant phenotypic correlation between yield/ha and all growth and yield parameter namely, PH (0.89), EH (0.96), CW (0.99), CL (0.94), (NSPR (0.96), HGW (0.94) and SHP (0.87). Yield/ha also recorded highly and moderate positive correlation with DTT (0.81), DTM (0.60) and HIDX (0.57) except DTS, ASI and NRPC with significant negative correlation of -0,74, -0.61 and -0.39, respectively. This indicates that growth and yield components characters that show high correlation with yield especially CW, CL, NSPR and HGW majorly contributed to the yields of these genotypes hence can be explored for grain yield improvement. DM though shows positive correlation with yield did not contribute significantly to yield can also be considered in maize improvement breeding programmed. This is in agreement with the findings of Kamal *et al.* (2020), Ogunniyan and Olakojo (2014). However, Kamal *et al.* (2020), reported a highly significant positive correlation between yield; and NRPC and ASI contrary to the findings in this present study which shows a significantly negative correlation with yield and other yield attributes.

These characters can also be explored for maize improvement in breeding program. The findings of this present study also showed that there was significant negative correlation between yield with DTS (-0.74). This indicates that earliness in flowering could play a significant role in yield improvement of the genotypes used in this study. This finding was also supported by the findings of

Table 6 : Correlation coefficient among earliness, growth, yield and yield component characters in maize (*Zea mays*).

	DTT	DTS	ASI	DTM	PH	EH	CW	CL	CD	NRPC	NSPR	GYPP	GYH	HGW	SHP	HIDX
DTT	1.00															
DTS	-0.49	1.00														
ASI	-0.50	0.04	1.00													
DTM	0.88***	-0.07	-0.64	1.00												
PH	0.69	-0.47	-0.61	0.62	1.00											
EH	0.82	-0.58	-0.62	0.69	0.96	1.00										
CW	0.83	-0.74	-0.58	0.62	0.88	0.97	1.00									
CL	0.95**	-0.64	-0.56	0.79	0.82	0.93	0.96	1.00								
CD	-0.23	-0.59	0.13	-0.60	0.10	0.10	0.21	-0.03	1.00							
NRPC	-0.66	-0.06	0.41	-0.87	-0.54	-0.54	-0.43	-0.60	0.76	1.00						
NSPR	0.85	-0.68	-0.52	0.66	0.91	0.98	0.98	0.96	0.39	-0.51	1.00					
GYPP	0.77	-0.78	-0.57	0.52	0.87	0.94	0.99	0.91	0.34	-0.30	0.96	1.00				
GYH	0.81	-0.74	-0.61	0.60	0.89	0.96	0.99	0.94	0.25	-0.39	0.97	0.99	1.00			
HGW	0.85	-0.52	-0.67	0.76	0.89	0.98	0.95	0.96	-0.02	-0.61	0.97	0.91	0.94	1.00		
SHP	0.47	-0.70	-0.46	0.23	0.86	0.83	0.84	0.67	0.58	-0.05	0.81	0.89	0.87	0.72	1.00	
HIDX	-0.01	-0.53	-0.33	-0.19	0.61	0.52	0.53	0.26	0.74	0.24	0.47	0.61	0.57	0.40	0.86	1.00

DTT = Days to 50% tasseling, DTS=Days to 50% Silking, ANI=Anthesis-silking interval, DTM=Days to 50% maturity, PH=Plant height, EH=Ear height, CW= Cob weight, CL= Cob length, CD=Cob diameter, NRPC=No. of rows/cob, NSPR=No. of seeds/row, GYPP=Grain yield/plant, GYH=Grain yield/ha, HGW=100 grain weight, SHP=Shelling%, HIDX = Harvest index.

Kamal *et al*. (2020). The result of this study also showed that there was significant negative correlation between ASI, a character of enormous interest to the maize breeder, yield and most yield components. This implies that the shorter the day difference between silking and pollen shade, the higher the yield of genotype and vise versa. This character should also be considered alongside other characters in a maize improvement breeding program according to Akaogu *et al*. (2013), Murtadha *et al*. (2018) and Ngugi *et al*. (2013), who reported negative correlation between ASI and yield in their separate works.

Conclusion

The result of this present studies revealed large variations in almost all the characters studied among the seven parental line maize genotypes under study. Hence, the seven parental line maize genotypes could be appropriately used in an intensive breeding program. The result of this study showed that the greater genetic variability observed in the population for all the characters was as a result of greater genetic variance than the error variance except in DTT, DTS, ASI, HGW, SHP and HIDX. Hence, a greater influence of environmental effects on these six characters. The significant difference of mean squares for the genotypes at $p < 0.01$ and $p < 0.05$ in all the characters except days to 50% tasseling, days to 50% silking, 100 grain weight, shelling % and harvest index. This indicates that there is large amount of genetic variation among the parental line population under study, therefore suggest that they are amenable to selection procedure and can be exploited for hybridization breeding program. The highly significant positive phenotypic correlation between yield/ha, and DTT, DTM, PH, EH, CW, CL, NSPR, HGW, SHP and HIDX at $p < 0.01$ and $p < 0.05$ and the negative significant correlation between DTS and ASI obtained in this study, indicates the important contributions of these characters to yield in maize crop. Hence, the above characters should of special interest to maize breeders for improved selection for optimizing yield.

Acknowledgements

References

Akaogu, I.C., Badu-Apraku B., Adetimirin V.O., VROH-BI I., Oyekunle M. and Akinwale R.O. (2013). Genetic diversity assessment of extra-early maturing yellow maize inbreds and hybrid performance in Striga-infested and Striga-free environments. *The J. Agricult. Sci.*, **151**, 519-537.

Akaogu, I.C., Badu-Apraku B., Gracen V., Tongoona P., Gedil M., Unachukwu N., Offei S.K., Dzidzienyo D.K., Hearne S. and Garcia-Oliveira A.L. (2020). Genetic diversity and inter-trait relationships among maize inbreds containing genes from *Zea diploperennis* and hybrid performance under contrasting environments. *Agronomy*, **10(10)**, 1478.

Aslani, F., Mehrvar M.R. and Juraimi A.S. (2012). Evaluation of some morphological traits associated with wheat yield under terminal drought stress. *Afr. J. Agric. Res.*, **7(28)**, 4104-4109.

Badu Apraku, B., Fakorede M.A.B., Gedil M., Annor B., Talabi A.O., Akaogu I.C., Oyekunle M., Akinwale R.O. and Fasanmade T.Y.(2016). Heterotic patterns of IITA and CIMMYT early maturing yellow maize inbreds under contrasting environments. *Agron. J.*, **108(4)**, 1321-1336.

Belay, N. (2018). Genetic variability, heritability, correlation and path coefficient analysis for grain yield and yield component in maize (*Zea mays* L.) hybrids. *Adv. Crop Sci. Tech.,* **6(5)**, 399.

Bisen, N., Rahangdale C.P. and Sahu R.P. (2018). Genetic variability and correlation studies of yield and yield component in maize hybrids (*Zea mays* L.) under Kymore Plateau and Satpura hill region of Madhya Pradesh. *Int. J. Agric. Environ. Biotech.,* **11(1)**, 71-77.

Islam, N.U., Ali G., Dar Z.A., Maqbool S., Baghel S. and Bhat A. (2020). Genetic variability studies involving drought tolerance related traits in maize (*Zea mays* L.) in breds. *Int. J. Chem. Stud.* **8(1)**, 414-419.

Hamid, M. (2018). Heritability and trait association studies in maize F₁ hybrids. *Int. J. Biosci.,* **12(1)**, 18-26.

Kamal, N., Khanum S., Siddique M. and Ahmed M.F. (2020). Phenotypic correlation coefficient studies to determine interrelationships among grain yield and related characters in maize. *Haya Saudi J. Life Sci.,* **5(6)**, 113-116.

Kim, H.R., Sa K.J., Nam-Gung M., Park K.J., Ryu S., Mo C.Y. and Lee J.K. (2021). Genetic characterization and association mapping in near-isogenic lines of waxy maize using seed characteristics and SSR markers. *Genes & Genomics*, **43**, 79-90.

Kutka, F. (2011). Open-pollinated vs. hybrid maize cultivars. *Sustainability*, **3(9)**, 1531-1554.

Li, Z.W., Liu L., Zhang Y.D., Jeffers D.P., Kang M.S. and Fan D.M. (2018). Combining ability analysis of RILs developed from a YML32 × Q11 cross for grain yield and resistance to gray leaf spot. *Crop Sci.,* **58(3)**, 1070-1081.

Murtadha, M.A., Ariyo O.J. and Alghamdi S.S. (2018). Analysis of combining ability over environments in diallel crosses of maize (*Zea mays*). *J. Saudi Soc. Agric. Sci.* **17(1)**, 69-78.

Myint, K.A., Amiruddin M.D., Rafii M.Y., Samad M.Y.A., Ramlee S.I., Yaakub Z. and Oladosu Y. (2019). Genetic diversity and selection criteria of MPOB-Senegal oil palm (*Elaeis guineensis* Jacq.) germplasm by quantitative traits. *Ind. Crops Prod.*, **139**, 111558.

Ngugi, K., Collins J.O. and Muchira S. (2013). Combining, earliness, short anthesis to silking interval and yield based selection indices under intermittent water stress to select for drought tolerant maize. *Aust. J. Crop Sci.,* **7(13)**, 2014-2020.

Ogunniyan, D.J. and Olakojo S.A. (2014). Genetic variation, heritability, genetic advance and agronomic character association of yellow elite inbred lines of maize (*Zea mays* L.). *Niger. J. Genet.,* **28(2)**, 24-28.

Olaoye, G. and Bello O.B. (2009). Combining ability for maize grain yield in Striga endemic and non-endemic environments of the southern guinea savanna of Nigeria. *J. Plant Breed. Crop Sci.,* **1(4)**, 72-79.

Oladosu, Y., Rafii M.Y., Abdullah N., Malek M.A., Rahim H.A., Hussin G., Latif M.A. and Kareem I. (2014). Genetic variability and selection criteria in rice mutant lines as revealed by quantitative traits. *The Scientific World J.*, **2014**.

Subramanian, A. and Subbaraman N. (2010). Hierarchical cluster analysis of genetic diversity in maize germplasm. *Electron. J. Plant Breed.*, **1(4)**, 431-436.

Suryanarayana, L., Sekhar M.R., Babu D.R., Ramana A.V. and Rao V.S. (2017). Cluster and principal component analysis in maize. *Int. J. Curr. Microbiol. Appl. Sci.,* **6(7)**, 354-359.