VARIABILITY FOR GROWTH AND YIELD TRAITS IN SINGLE CROSS HYBRIDS OF MAIZE (*Zea mays* L.)

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ABSTRACT. Sixteen single-cross hybrids of maize were evaluated in a randomized complete block design with three replications to investigate genetic variability and correlation among growth and yield traits at Khumaltar, Lalitpur, Nepal from March 13 to September 05, 2021. The hybrids were grouped into four clusters using Euclidean Average Linkage method. The cluster analysis showed the presence of genetic variability in the evaluated hybrids. The maximum distance between cluster centroids (194.28) was found between cluster 2 and cluster 4, indicating genetic dissimilarity. Grain yield had the maximum values of phenotypic coefficient of variation (PCV) (35.02%), followed by ear height (17.82%) and plant height (12.22%). Similarly, grain yield had the maximum values of genotypic coefficient of variation (GCV) (26.24%) followed by the number of kernel rows/cob (8.77%) and days to 50% silking (8.72%). Days to 50% silking and days to 50% tasseling had the highest values of heritability (86%) followed by cob diameter (84%) and no. of kernel rows in cob (68%). The leaf area per plant had the maximum values of genetic advance (GA) (74.87 cm^2), followed by plant height (27.80 cm) and days to 50% silking (9.66 days). Similarly, the maximum values of genetic advance as percent of the mean (GAM) was found for grain yield (40.50%) followed by days to 50% silking (16.70%) and days to 50% tasseling (16.17%). The hybrids namely KWM-91 × KWM-93 produced the maximum values of grain yield (9.99 t ha^{-1}) followed by KWM-93 × KWM-91 (9.63 t ha^{-1}) and KWM-92 × KWM-93 (9.40 t ha^{-1}). Grain yield showed positive and significant phenotypic correlation with days to 50% silking (r = 0.41), days to 50% tasseling (r = 0.39), plant height (r = 0.37), cob diameter (r = 0.49) and the number of kernel rows in cob (r = 0.38). Therefore, utilization of present genetic variability along with indirect selection for traits having significant association with grain yield, high heritability and GAM could aid in the improvement of maize productivity.

Introduction

Maize (*Zea mays* L.) is Nepal's second most important cereal crop, with an area of 9 40 886 ha and a yield of 26 53 243 t (MoALD, 2020). It contributes 3.15% to the national gross domestic product (GDP) and 9.5% to agricultural GDP. It covers 27.39% area of total food crops and contributes 24.97% of total cereal production (MoALD, 2020). There is a considerable gap between the yield potential of the improved varieties and the national average yield. So far, seven hybrid maize varieties have been released in the country. Maize breeding efforts are focusing on developing high-yielding hybrid maize varieties to boost the yield potential furthermore.

The understanding of germplasm diversity among elite breeding materials has a major impact on crop improvement (Hallauer *et al.*, 1988). Crop improvement relies on variability (Welsh, 1981). Maize germplasm has been found to have a large genetic diversity in terms of growth, development, and grain yield, and this variability has fueled the search for the development of new genotypes with desirable characteristics (Betran *et al.*, 2003; Liu *et al.*, 2003). Khan *et al.* (2018) and Khalil *et al.* (2011) found variation among the traits in maize hybrids. Similarly, Hallauer and Schos (1973) and Grzesiak (2001) found significant genotype diversity among maize genotypes for various traits. The genetic makeup of maize genotypes influences maize

growth, development, and productivity. Furthermore, critical environmental factors like soil fertility and climatic change-related parameters can have a major impact on maize growth and productivity (Oseni, Masarirambi, 2011). Grain yield is determined by a combination of genetic and environmental factors. Genetic variability across maize genotypes is a major determinant of grain yield (Tahir *et al*., 2008). Heritability and the genetic advance of the individual trait determine the efficiency with which genotypic variability can be utilized by selection. Understanding the association between yield and its component traits can help breeders to improve the effectiveness of selection (Kalla *et al*., 2001; Zeeshan *et al*., 2013).

The present study was conducted to quantify the variability, heritability, genetic advance, and the correlation between yield and its contributing traits among single-cross maize hybrids.

Material and Methods

Plant materials

Sixteen single-cross hybrids of maize were selected and used for this study (Table 1). National Plant Breeding and Genetics Research Centre (NPBGRC), Khumaltar, Lalitpur, Nepal, was the source of genotypes.

Table 1. List of single-cross hybrids of maize used in the experiment

S. No.	Maize hybrids
1	KML-1A × RML-4
2	KWM-91 × KWM-93
3	Rampur Hybrid-2
4	KWM-93 × KWM-91
5	Khumal Hybrid-2
6	KML-2A × KYM-86
7	KML-4A × KYM-86
8	KML-5A × RML-4
9	KML-8A × RML-4
10	KML-4A × RML-4
11	Super-951
12	KML-3B × RML-4
13	KML-5A × KYM-33
14	KML-8A × KYM-33
15	KML-4B × KYM33
16	KWM-92 × KWM-93

Experimental site

The study was conducted at the research field of the National Plant Breeding and Genetics Research Centre in Khumaltar, Lalitpur, Nepal from March 13 to September 05, 2021. It is located at 27°40'0" north latitude, 85°20'0" east longitude, and 1350 m above sea

level. The soil of the research plot was clay loam type. The climatic data of the site during the experiment period (2021) is given in Table 2.

Table 2. Climate data of the experimental location in 2021

Month	Maximum temperature, °C	Minimum temperature, °C	Precipitation, (mm)	Sun Hours, h
March	24	10	75.4	364.8
April	27	13	222.9	351.5
May	27	14	447.9	347.5
June	27	16	705	324.7
July	25	17	1097.5	314.8
August	26	16	995.6	320.3
September	25	15	599.6	330.2

(Source: Meteorology station, National Agronomy Research Centre, Khumaltar, Lalitpur)

Experimental design and cultural practices

The experiment was laid out in a randomized complete block design (RCBD) with three replications. Individual plots comprised four rows of five meters each, with a 60 cm × 25 cm spacing (row to row × plant to plant). One week before sowing, well-decomposed farmyard manure was incorporated @ 6 t ha^{-1} into the soil and the chemical fertilizer @ 180:60:40 kg N:P$_2$O$_5$: K$_2$O [(nitrogen (N), phosphorus (P), and potassium (K)] ha^{-1} was applied *via* Urea, Diammonium Phosphate (DAP), and Muriate of Potash (MOP). During final land preparation, as a basal dose, a half dose of N, full dose of P$_2$O$_5$ and K$_2$O was applied. The remaining half dose of N was divided into two parts and administered 45 and 90 days after sowing. Two manual weeding and hoeing operations were completed during the maize growing season. The first weeding was performed 18 days after sowing, and the second weeding 36 days later. The irrigation was applied at three important growth stages: knee-high stage, tasseling stage, and milking stage.

Data collection and observations

Data were collected for all traits from ten plants chosen at random from each experimental plot. The phenological traits (days to 50% silking, days to 50% tasseling) of these selected plants, as well as biometrical variables (plant and ear height, leaf area per plant, cob length, and cob diameter), yield, and yield attributing traits (Number of kernel rows in cob), were observed. The following formula (Eq. 1) was used to compute grain yield (kg ha^{-1}) at 12% moisture content using fresh ear weight:

$$\text{Grain yield}, \text{t ha}^{-1} = \frac{\text{F.W.}, \text{kg plot}^{-1} \times (100 - \text{HMP}) \times \text{S} \times 10\,000}{(100 - \text{DMP}) \times \text{NPA} \times 1000}, \tag{1}$$

where
F.W. – the fresh weight of ear per plot (kg) at harvest;
HMP – moisture percentage of grain at harvest;
DMP – desired moisture percentage, *i.e.* 12%;
NPA – the area of net harvest plot, m^2;
S – shelling coefficient, *i.e.* 0.8.

The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) provide information on the level of variability in a population, whereas heritability depicts the component of a character that is passed down to future generations (Girma *et al.*, 2018; Pal *et al.*, 2016). The phenotypic coefficients of variation (Eq. 3) and genotypic coefficients of variation (Eq. 2) were estimated using the formula given by Singh and Chaudhary (1985). The estimation of heritability (in the broad sense) (Eq. 4) was carried out using the formula given by Johnson *et al.* (1955). Similarly, genetic advance (Eq. 5) was calculated using the formula given by Burton (1952), and genetic advance as a percentage of the mean (GAM) (Eq. 6) was calculated using the formula given by Johnson *et al.* (1955).

$$GCV, \% = \frac{\sqrt{\delta^2 g}}{x} \times 100, \qquad (2)$$

$$PCV, \% = \frac{\sqrt{\delta^2 p}}{x} \times 100, \qquad (3)$$

where
$\delta^2 g$ – genotypic variance;
$\delta^2 p$ – phenotypic variance;
x – Sample mean.

$$\text{Heritability in board sense } (h^2 bs) = \frac{\delta^2 g}{\delta^2 p}, \qquad (4)$$

$$\text{Genetic advance (GA)} = (K)(\delta^2 p)(h^2), \qquad (5)$$

where
GA – expected genetic advance;
K – selection differential that varies depending upon the selection intensity and stands at 2.056 for selecting 5% of the genotypes;
δp – phenotypic standard deviation;
h^2 – heritability (in the broad sense).

According to Shukla *et al.* (2006), the expected genetic advance as a percentage of the mean (GAM) was estimated as below (Eq. 6);

$$GAM = \frac{GA}{x} \times 100, \qquad (6)$$

where x – grand mean.

The correlation coefficient aids in determining the degree of relationship as well as the degree to which traits are interdependent (Bocanski *et al.*, 2009; Nagabhushan *et al.*, 2011). By examining genotypic and phenotypic differences in yield and yield components of many crop genotypes, a breeder will be able to determine how much the environment influences yield (Ullah *et al.*, 2012). The correlation between traits in this study was assessed using Pearson's correlation coefficient approach.

Multivariate analysis is the most used method for assessing genetic variability. Crop plant genetic diversity is required to maintain high levels of productivity (Tripathi *et al.*, 2013). Multivariate analysis of various

agro-morphological traits has successfully been employed by numerous researchers to delineate the inherent diversity in the germplasm (Nachimuthu *et al.*, 2014; Ravikumar *et al.*, 2015). Cluster analysis with Euclidean distance is an effective statistical technique for evaluating genetic diversity. The Euclidean average linkage Method was used in this study.

Statistical analysis

The experimental data were processed using MS Excel 2010, and the data was analyzed using R-studio 3.5.0 and SPSS 20. The data were analyzed using a randomized complete block design (RCBD) with one-way ANOVA. The least significant difference (LSD) was used to compare the treatment means at a 5% level of significance (Gomez, Gomez, 1984). The Pearson correlation coefficient of growth, yield and its attributing traits was worked out using SPSS 20.

Results and Discussion

Agro-morphological variability

The presence of significant variation in genotypes for most of the traits was given in Table 3. The non-significant difference was found for ear height, cob length and the number of kernel rows in cob, whereas a significant difference ($P < 0.05$) was found for plant height and grain yield. Days to 50% silking, days to 50% tasseling, leaf area per plant and cob diameter had highly significant differences ($P < 0.01$) (Table 3). The maximum coefficient of variation (17.5%) was found in ear height followed by grain yield (13.1%). The minimum coefficient of variation (2.3%) was found in cob diameter (Table 3).

The hybrids namely KWM-91 × KWM-93 produced the maximum grain yield (9.99 t ha⁻¹) followed by KWM-93 × KWM-91 (9.63 t ha⁻¹) and KWM-92 × KWM-93 (9.40 t ha⁻¹) (Figure 1).
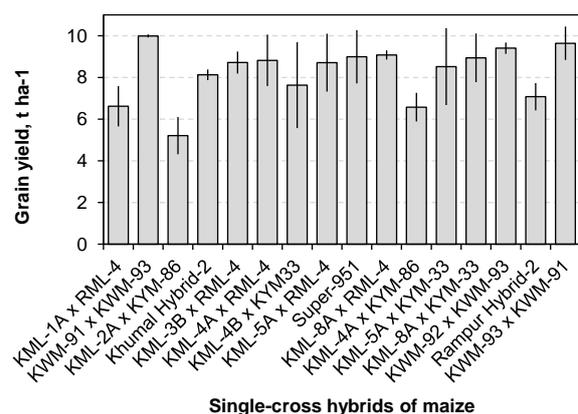
Figure 1. Bar diagram showing mean and standard deviation of grain yield of sixteen single-cross hybrids of maize

These findings support those of Akbar *et al.* (2009), Prasai *et al.* (2015), Shrestha (2016), Adhikari *et al.* (2018), Dhakal *et al.* (2018), Shrestha *et al.* (2019), Kafle *et al.* (2020), Shrestha *et al.* (2018) and Bastola *et al.* (2021) who found significant changes in grain

production between maize genotypes. The genetic makeup of maize genotypes varied, which resulted in variances in grain yield.

Table 3. Mean sum of squares for different traits of sixteen single-cross hybrids of maize

Traits	Mean	SE	CV, %	LSD (0.05)	Signifi-cance
Plant height, cm	267.10	17.67	9.4	53.27	*
Ear height, cm	143.20	17.77	17.5	53.57	NS
Days to 50% silking	57.81	1.41	3.5	4.26	***
Days to 50% tasseling	55.91	1.31	3.3	3.97	***
Leaf area per plant, cm^2	676.6	24.25	5.1	73.11	***
Cob length, cm	21.95	0.91	5.9	2.74	NS
Cob diameter, cm	4.92	0.08	2.3	0.24	***
Number of kernel rows in cob	14.50	0.61	6.0	1.86	NS
Grain yield, t ha^{-1}	8.25	0.76	13.1	2.29	*

NS – not significant, *-significant at P <0.05, ***-significant at P <0.001, SE – standard error of the mean, CV – coefficient of variation, LSD – least significance difference

Phenotypic and genotypic coefficients of variation

The GCV values were smaller than PCV values for all traits studied, showing that the characters were more influenced by their surrounding environments. Deshmukh *et al.* (1986) grouped the PCV and GCV values as low (0–10%), moderate (10–20%), and high (>20%). The maximum values of GCV were observed in grain yield (26.24%), followed by the number of kernel rows in cob (8.77%). The minimum values of GCV were observed in ear height (3.07%) followed by cob length (3.40%) (Table 4). Similarly, the maximum values of PCV were observed in grain yield (35.02%), followed by ear height (17.82%). The minimum PCV values were observed in cob diameter (5.86%) followed by cob length (6.79%) (Table 4). Similar findings were found by Kandel *et al.* (2017) and Sharma *et al.* (2018). The difference between phenotypic and genotypic variance was larger in the leaf area showing that these

features were substantially impacted by the environment. The results were the same as those of Ojo *et al.* (2006) and Kashiani *et al.* (2010).

Heritability and genetic advance

Heritability estimates are classified as low (5–10%), medium (10–30%) and high (30–60%) (Dabholkar, 1992). The maximum values of broad-sense heritability values were observed in days to 50% silking (86%), days to 50% tasseling (86%) and cob diameter (84%). The minimum value of heritability value was found in ear height (3%) (Table 4)**.** Alemu *et al.* (2017) found similar results. Cob diameter produced the maximum values of heritability, according to Swamy *et al.* (1971) and Lias *et al.* (1987). Most of the factors had high estimates of heritability, showing that variations were handed down to progeny, implying that a high-yielding variety may be generated by choosing suitable genotypes. Because of the high values of heritability, there were more alternatives for picking plant material that had the desired characteristics.

Estimation of genetic advance (at 5% selection intensity), and the corresponding genetic advance as a per cent of the mean (GAM) were estimated for each measured character. The leaf area per plant had the maximum values of genetic advance (GA) (74.87 cm^2), followed by plant height (27.80 cm) and days to 50% silking (9.66 days) (Table 4). Similarly, the maximum values of genetic advance as per cent of the mean (GAM) was found for grain yield (40.50%) followed by days to 50% silking (16.70%) and days to 50% tasseling (16.17%) (Table 4). In our study, high values of heritability did not associate with genetic advances. Najeeb *et al.* (2009) found that high values of heritability are not always associated with high genetic advances. Since high values of heritability do not always indicate high genetic advance, it is recommended to consider heritability in conjunction with genetic advance to predict the effect of selecting superior plant varieties.

Table 4. Estimation of PCV, GCV, heritability, genetic advance and GAM for growth, yield and its attributing traits of sixteen single-cross hybrids of maize

Traits	Vg	Vp	PCV, %	GCV, %	h^{2}bs, %	GA	GAM, %
Plant height, cm	440.45	1065.15	12.22	7.86	41	27.80	10.41
Ear height, cm	19.35	651.05	17.82	3.07	3	1.56	1.09
Days to 50% silking	25.43	29.43	9.38	8.72	86	9.66	16.70
Days to 50% tasseling	22.27	25.75	9.08	8.44	86	9.04	16.17
Leaf area per plant, cm^2	2071	3247	8.42	6.73	64	74.87	11.07
Cob length, cm	0.56	2.22	6.79	3.40	25	0.77	3.52
Cob diameter, cm	0.07	0.08	5.86	5.38	84	0.50	10.18
Number of kernel rows in cob	1.62	2.38	10.65	8.77	68	2.16	14.88
Grain yield, t ha^{-1}	9.34	10.7	35.02	26.24	56	3.78	40.50

Vg – genotypic variance, Vp – phenotypic variance, h^{2}bs – heritability in the broad sense, GCV – genotypic coefficient of variation, PCV – phenotypic coefficient of variation, GA – genetic advance at 5% intensity of selection, GAM – genetic advance as per cent of mean

Cluster analysis

The statistical distances between clusters are an indicator of genetic diversity. The inter-cluster distances were larger than the intra-cluster distances which indicated wider genetic diversity among the genotypes of different groups. The 16 single-cross hybrids of maize were grouped on four clusters based on growth and yield traits (Table 5, Figure 2). Among all the

clusters, cluster 2 was the largest containing 6 hybrids followed by clusters 1 (5 hybrids), 3 (4 hybrids) and 4 (1 hybrid) (Table 5). Mounika *et al.* (2018) found similar results after grouping 47 maize inbred lines into seven clusters. In a study by Alom *et al.* (2003), twenty-five maize genotypes were categorized into seven clusters based on morphological traits. Similarly,

Rafique *et al.* (2018) used morphological traits to separate 40 maize inbred lines into ten clusters. Azam (2012) discovered five clusters from 49 maize genotypes. Cluster analysis can be effective for locating high-yielding genotypes, according to Ali *et al.* (2008).

Hybrids of cluster 4 had the maximum values of plant height (318.00 cm), ear height (177.30 cm), leaf area per plant (800.20 cm^2), cob length (23.84 cm), number of kernel rows in cob (16.00) and grain yield (9.40 t ha^{-1}). The hybrids of cluster 2 had the minimum values of plant height (245.03 cm), ear height (126.32 cm), leaf area per plant (627.85 cm^2), cob length (21.63 cm), number of kernel rows in cob (13.83) and grain yield (7.90 t ha^{-1}) (Table 6). Chakma et al. (2012) obtained similar results.

Distance between cluster centroids ranged from 49.83 to 194.28 (Table 7). The minimum distance (49.83) between cluster centroids was found between cluster 3 and cluster 2 indicating genetic similarity and the maximum distance was found in the cluster 4 (KWM-92 × KWM-93) and cluster 2 (KML-2A × KYM-86, KML-4A × KYM-86, KML-5A × RML-4, KML-8A × RML-4, KML-4A × RML-4, Super-951) (194.28) indicating genetic dissimilarity (Table 7).

The maximum distance of cluster 1 from centroid was 37.98 and the minimum distance of cluster 4 (0.00) (Table 8). Debnath (1987) found that the inter-cluster distance was greater than the intra-cluster distance in maize genetic variability. Abedin and Hossain (1990) found similar results in maize. To generate a wide spectrum of genotype variation, Yadav *et al.* (2011), Vennila *et al.* (2011), and Latif *et al.* (2011) recommended employing a distantly dispersed cluster genotypes in hybridization procedures.
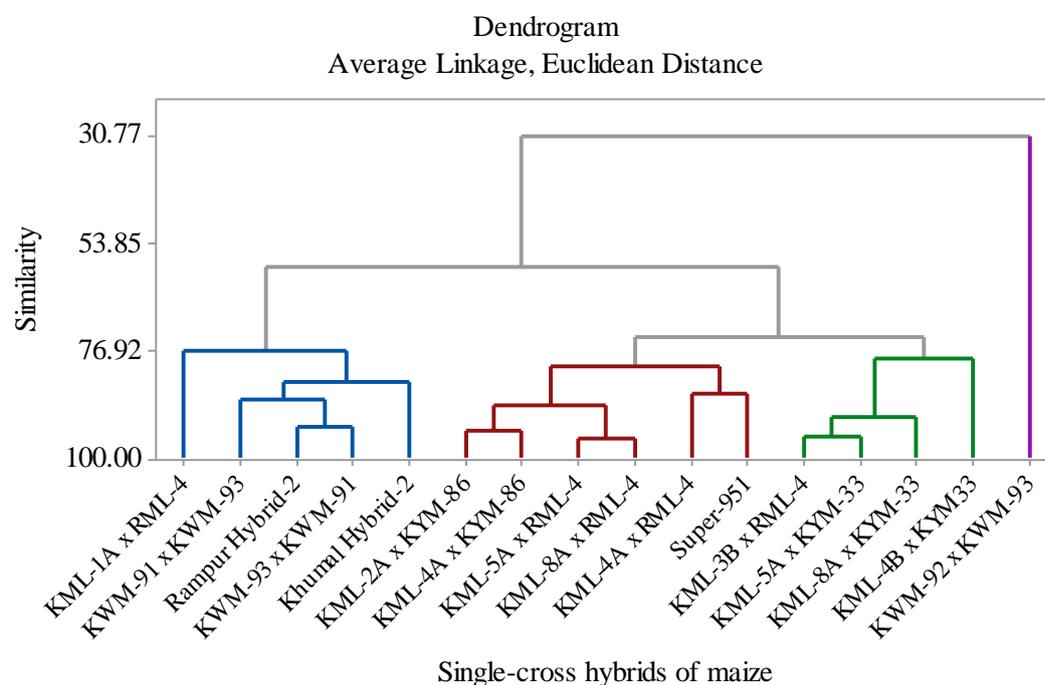
Figure 2. Dendrogram of sixteen single-cross hybrids of maize using Euclidean average linkage method

Table 5. Grouping of sixteen single-cross hybrids of maize by Euclidean average linkage method

Cluster 1	Cluster 2	Cluster 3	Cluster 4
KML-1A × RML-4,	KML-2A × KYM-86,	KML-3B × RML-4,	KWM-92 × KWM-93
KWM-91 × KWM-93,	KML-4A × KYM-86,	KML-5A × KYM-33,	
Rampur Hybrid-2,	KML-5A × RML-4,	KML-8A × KYM-33,	
KWM-93 × KWM-91,	KML-8A × RML-4,	KML-4B × KYM33	
Khumal Hybrid-2	KML-4A × RML-4,		
	Super-951		

Table 6. Cluster means for nine traits of sixteen single-cross hybrids of maize

Variable	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Centroid
Days to 50% tasseling	60.80	51.50	55.88	58.00	55.91
Days to 50% silking	63.00	53.17	57.50	61.00	57.81
Plant height, cm	287.64	245.03	261.73	318.00	267.08
Ear height, cm	159.80	126.32	139.39	177.30	143.23
Leaf area per plant, cm^2	713.69	627.85	672.50	800.20	676.61
Cob Length, cm	21.78	21.63	22.18	23.84	21.95
Cob Diameter, cm	4.90	4.74	5.17	5.17	4.92
Number of kernel rows in cob	14.60	13.83	15.00	16.00	14.50
Grain yield, t ha^{-1}	8.29	7.90	8.45	9.40	8.25

Table 7. Distances between cluster centroids in sixteen single-cross hybrids of maize

Clusters	Cluster 1	Cluster 2	Cluster 3	Cluster 4
Cluster 1	0	102.42	53.29	93.44
Cluster 2			49.83	194.28
Cluster 3				144.68
Cluster 4				0

Table 8. Different statistics of Euclidean distance and cluster analysis of sixteen single-cross hybrids of maize

Cluster	No. of observations	Within clusters sum of square	Average distance from centroid	Maximum distance from centroid
Cluster 1	5	3194.15	23.32	37.98
Cluster 2	6	2981.63	21.51	29.82
Cluster 3	4	1820.05	19.15	33.94
Cluster 4	1	0	0	0

Correlation coefficient

The coefficient of variation represents the degree of variability present in a wide range of qualities, but it excludes the heritable component. In maize, traits like plant height, ear height, and the number of kernel rows per ear are reported to have a positive and substantial link with grain yield, according to the study (Sadek *et al*., 2006). The values of the phenotypic correlation of traits are shown in Table 9. Cob length was negatively correlated with days to 50% silking, days to 50% tasseling and the Number of kernel rows in cob. This result was similar to Selvaraj and Pothiraj (2011) who reported a negative correlation between cob length and the number of kernel rows in cob. The positive and significant phenotypic correlation was found between grain yield and days to 50% silking (r = 0.409), days to 50% tasseling (r = 0.386), plant height (r = 0.367), cob diameter (r = 0.490) and the number of kernel rows in cob (r = 0.382) respectively. Alvi et al. (2003), Prakash et al. (2006), Sharma et al. (2021), and Bartaula et al. (2019) reported similar findings. The ear height and plant height were both positively and strongly correlated with grain yield (Nzuve *et al*., 2014). If there is a positive and high correlation between such traits, it would show an indirect selection of genotypes for grain yield.

Table 9. Pearson's correlation coefficient among growth, yield and its attributing traits of sixteen single-cross hybrids of maize

Traits	1.	2.	3.	4.	5.	6.	7.	8.	9.
1. Days to 50% tasseling	1								
2. Days to 50% silking	0.993**	1							
3. Plant height, cm	0.609**	0.635**	1						
4. Ear height, cm	0.569**	0.592**	0.715**	1					
5. Leaf area per plant	0.545	0.559**	0.619**	0.552**	1				
6. Cob length, cm	−0.025	−0.055	0.104	0.04	0.24	1			
7. Cob diameter, cm	0.419*	0.401*	0.215	0.188	0.291	0.424	1		
8. No. of kernel rows in cob	0.445*	0.475**	0.296	0.294	0.199	−0.086	0.294	1	
9. Grain yield, t ha^{-1}	0.386*	0.409*	0.367*	0.218	0.127	−0.082	0.490**	0.382**	1

* – correlation is significant at the 0.05 level, ** – correlation is significant at the 0.01 level

Conclusion

Significantly differed traits were observed except ear height, the number of kernel rows in cob and cob length, implying that maize hybrids have genetic diversity that can be used to increase yield. In all traits, PCV was bigger than GCV, indicating that there was an environmental influence. Days to 50% silking, days to 50% tasseling, plant height, cob diameter and the number of kernel rows in cob were found to have a maximum correlation with grain yield; these traits may boost grain yield. The cluster analysis revealed that the hybrids had genetic variability. The maximum distance between cluster centroids was found between cluster 2 and cluster 4, showing genetic dissimilarity. The hybrids namely KWM-91 × KWM-93 followed by KWM-93 × KWM-91 and KWM-92 × KWM-93 was identified as a superior hybrid for grain yield. The grain yield production can be maximized by growing these maize hybrids.

Conflict of interest

The authors declare that there is no conflict of interest regarding the publication of this paper.

Author contributions

JS – the lead investigator and also responsible for data collection from the field, literature search and write-up.
SS, RA, SS, MS – responsible for the literature review, reviewing the initial draft and providing critical feedback on the manuscript.
All the authors read and approved the final manuscript.

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