



Genetic Variation in Maize Germplasm Revealed by Morphological and Yield-Related Traits

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Abstract

Genetic variation for plant architecture and yield components is essential for maize (*Zea mays* L.) improvement. This study assessed variation among 20 maize genotypes at the University of Agriculture, Faisalabad, during spring 2023, using a randomized complete block design with three replications. Ten traits were recorded: plant height, ear height, stem diameter, internodal length, cob length, rows per cob, seeds per row, 100-grain weight, cob diameter, and pith diameter. Data were analyzed by ANOVA, means were separated with Tukey's HSD test, and Pearson correlations were calculated among traits. Genotypes differed significantly ($P < 0.01$) for all traits. Stem diameter was strongly and positively correlated with plant height ($r = 0.7664$) and ear height ($r = 0.6969$), while 100-grain weight showed only weak positive correlations with cob length ($r = 0.1559$) and seeds per row ($r = 0.0848$). Genotype 2014 Sib had the highest plant height, ear height, and stem diameter. Genotype 113 had the highest 100-grain weight, cob diameter, and pith diameter. PBG3 (X) had the longest internodes, 6160 (X) the longest cobs, 110 the most rows per cob, and 129 the most seeds per row. Genotype 113 is a good option where high grain weight and large cobs are wanted, and 2014 Sib is a good option where tall plants with thick stems are needed. These results come from a single season, so they should be confirmed across more environments.

Keywords: maize, germplasm, genetic variation, morphological traits, yield-related traits, correlation, 100-grain weight.

Introduction

Maize is a major cereal crop used for food, feed, and industrial processing. In Pakistan, maize was grown on an estimated 1.44 million hectares in FY2025, and production was put at 8.24 million tonnes, down 15.4 percent from 9.74 million tonnes the year before, mainly because less area was sown (Government of Pakistan, 2025). When area shrinks, the yield potential of the material that is planted matters even more. That potential comes from more than released hybrids. It also depends on the variation held in breeding populations and germplasm. Recent studies keep reporting wide differences among maize inbred lines and landraces for plant height, ear traits, kernel traits, and yield components, so phenotypic characterization is still a practical way to find contrasting materials for selection and crossing (Ezin et al., 2022; Rivas et al., 2022; Guo et al., 2025).

Morphological evaluation is a sensible first step in germplasm work because plant height, ear height, cob length, kernel number, and grain weight can all be measured directly in the field. Ezin et al. (2022) found clear differences among maize accessions for plant architecture, ear position, and yield components across several environments. Rivas et al. (2022) reported marked morphological variation among

landraces, but their morphological groups did not always match their molecular groups. Guo et al. (2025) combined both kinds of data and again found substantial diversity among inbred lines.

Stem traits are measured less often than ear and kernel traits. Stem diameter, internodal length, and pith diameter influence how well a plant stands and carries its ear [add citation], yet most of the studies above focus on ear and kernel characters. How useful a trait is for selection also depends on how it relates to other traits. Correlation analysis shows whether selecting for one character is likely to change another. Fadhli et al. (2023) reported useful relationships among cob weight, grain yield, and related traits in hybrid maize. Javaid et al. (2024) found positive relationships involving plant height and 100-grain weight under contrasting moisture conditions. Similar links among plant height, ear height, kernel traits, and grain yield appear in recent variability studies (Bohara et al., 2025; Lamsal et al., 2026).

The size and pattern of variation change with genetic background and environment. Kamal et al. (2024) found substantial variation for agronomic and grain-yield traits among maize inbred lines tested in Pakistan. Vaishnavi et al.

(2024) named plant height, kernel number per row, and rows per cob as useful selection traits in tropical inbred lines. Work from 2026 also reports significant genotype effects for plant height, ear height, kernel number, and grain weight, and advises testing material across environments before choosing it for wide adaptation (Yogitha et al., 2026). Results from one germplasm set or location cannot simply be carried over to another, and information on stem traits in locally grown maize is limited. This study therefore characterized 20 maize genotypes for plant architecture and yield-related traits under field conditions at Faisalabad. The objectives were to assess variation among the genotypes and to examine relationships among the measured traits using Pearson correlation analysis.

Materials and Methods

Experimental site and plant material

The field experiment was conducted during spring 2023 in the field area of the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan. The maize germplasm was obtained from the maize research group of the same department. Twenty genotypes were evaluated: PBG1 (X), PBG2 (X), PBG3 (X), PBG4 (X), 2070, CRT3-6196 (X), 6176 (X), 2072 (X), 110, 6276 (X), 113, 6160 (X), 289 (X), 2033, 2014 Sib, 6269 (X), 235, 129, CH13949-6071 (X), and CH131266-6084 (X).

Table 1. List of maize genotypes included in the experiment.

Sr. No.	Genotypes	Sr. No.	Genotypes
1	PBG1 (X)	11	113
2	PBG2 (X)	12	6160 (X)
3	PBG3 (X)	13	289 (X)
4	PBG4 (X)	14	2033
5	2070	15	2014 Sib
6	CRT3-6196(X)	16	6269 (X)
7	6176 (X)	17	235
8	2072 (X)	18	129
9	110	19	CH13949-6071 (X)
10	6276 (X)	20	CH131266-6084 (X)

Experimental design and data recording

As indicated in the source document, the investigation followed a randomized complete block design (RCBD). Nonetheless, the field material followed standard agronomic recommendations. Data collection occurred when the plants reached physiological maturity. The height of plants was

taken starting at the ground level up to where the tassel is located. To determine ear height, measurements were taken on the cobs starting from the base of the plants. A Vernier caliper was used to take measurements of the stem diameter, which were then averaged for values obtained at the top and bottom of the stem. Distances between two nodes were measured using a tape measure to determine internodal length.

At the end of the day, the lengths of the cobs were determined using husked and dried ones. Manual counting was used to determine the number of kernel rows per cob and seeds per row. An electronic balance was used to count and weigh one hundred seeds. The diameter of the cob was determined by use of a vernier caliper at two points (middle and edges) on certain cobs, after which an average was taken. After taking out the kernels, the diameter of the pith was measured at the center of the cob.

Statistical analysis

Variations in genotype for each observed trait were analyzed using analysis of variance. If there was a significant effect of genotype, then Tukey's honestly significant difference (HSD) test was applied to compare the means in pairs. To determine how the traits relate to each other in terms of strength and direction, Pearson correlation coefficients were computed at an alpha level of 0.05.

Results

In the ANOVA tables, the various genotypes showed significant variance across every trait measured (10 in total), as evident from the P-value of 0.0000 for genotype across the board. However, this did not mean that the extent of the observed difference was equalized on all traits since some had bigger/lower F-values than others. Mean comparison results also divided the genotypes into sets having similar members within them for every trait.

Plant height

The height of the plants was not the same for every genotype, as shown by the highly significant F value (220.88; $P=0.0000$; Table 2). On average, plants were 71.667 cm tall. The highest mean was recorded for 2014 Sib (95.000 cm), followed by 289 (X) (90.667 cm) and PBG3 (X) (87.000 cm). The lowest mean was recorded in CH13949-6071 (X) (50.333 cm). According to the Tukey groups, there were many different means across genotypes that could be separated statistically.

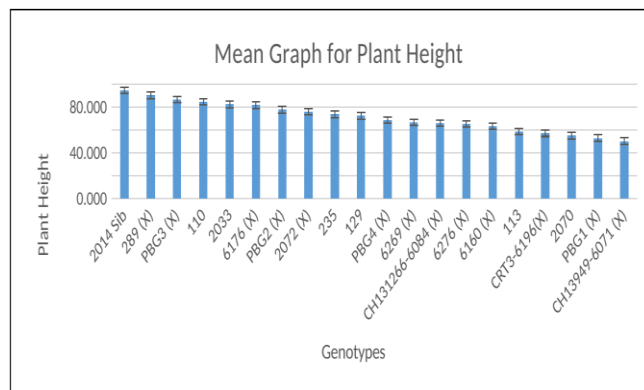
Table 2. Analysis of variance for plant height

Source	DF	Sum of Square	Mean Square	F value	P value
Replications	2	0.63	0.317		
Genotypes	19	9648.93	507.839	220.88	0.0000
Error	38	87.37	2.299		
Total	59	9736.93			

Table 3. Tukey HSD all-pairwise comparison test of plant height

Genotypes	Mean	Homogeneous Group
2014 Sib	95	A
289 (X)	90.667	AB
PBG3 (X)	87	BC
110	85	CD
2033	82.667	CDE
6176 (X)	82	DE
PBG2 (X)	78	EF
2072 (X)	76.333	FG
235	74	FG
129	72.667	GH
PBG4 (X)	69	HI
6269 (X)	67	IJ
CH131266-6084 (X)	66	IJ
6276 (X)	65.667	IJ
6160 (X)	63.333	JK
113	59	KL
CRT3-6196(X)	57.333	LM
2070	55.333	LM
PBG1 (X)	53	MN
CH13949-6071 (X)	50.333	N

Figure 1. Mean plant height for 20 maize genotypes



Ear height

Genotype greatly influenced ear height, as shown by the results in Table 4 ($F = 87.83$, $P = 0.0000$). On average, ear height was at 33.133 cm. The maximum average ear height occurred in 2014 Sib (50.000 cm), while it was minimal for PBG1 (X) and CH13949-6071 (X) at 20.667 cm. Nonetheless, there were different genotypes that belonged to the same Tukey groups, as not all the differences in numbers were significant of that kind.

Table 4. Analysis of variance for ear height

Source	D F	Sum of square	Mean square	F value	P value
Replications	2	0.93	0.467		
Genotypes	19	4174.93	219.733	87.83	0.0000
Error	38	95.07	2.502		
Total	59	4270.93			

Table 5. Tukey HSD all-pairwise comparison test of ear height

Genotypes	Mean	Homogeneous Group
2014 Sib	50	A
PBG2 (X)	42.333	B
289 (X)	42.333	B
2033	42	B
6176 (X)	41.333	B
PBG4 (X)	40.667	B
110	39	BC
PBG3 (X)	35.333	CD
CH131266-6084 (X)	34.333	CDE
235	33	DEF
129	33	DEF
6276 (X)	31	DEF
6160 (X)	30.333	EF
6269 (X)	30.333	EF
2072 (X)	29	F
113	23.667	G
CRT3-6196(X)	22.667	G
2070	21	G
PBG1 (X)	20.667	G
CH13949-6071 (X)	20.667	G

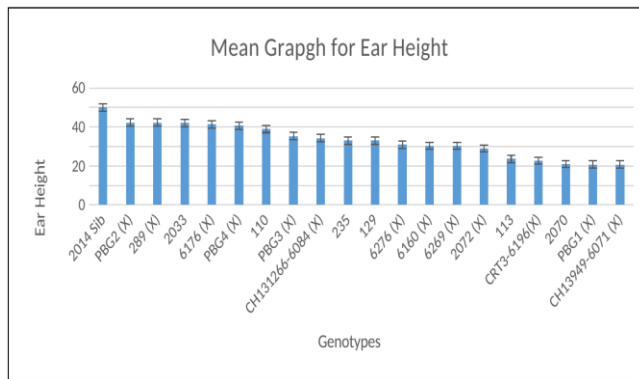


Figure 2. Mean ear height for 20 maize genotypes

Stem diameter

Different genotypes had significant variations in stem diameter, as indicated by $F = 14.72$ and $P = 0.0000$ (Table 6), with an overall average of 2.833 cm. In terms of the mean stem diameter, 2014 Sib took the lead with 4.000 cm. On the other hand, the lowest mean of 2.000 cm was recorded in PBG1 (X), 2070, CRT3-6196 (X), and CH13949-6071 (X).

Table 6. Analysis of variance for stem diameter

Source	D F	Sum of square	Mean square	F value	P value
Replications	2	6.9083	3.45417		
Genotypes	19	25.2125	1.32697	14.72	0.0000
Error	38	3.42503	0.09013		
Total	59	35.5458			

Table 7. Tukey HSD all-pairwise comparison test of stem diameter

Genotypes	Mean	Homogeneous Groups
2014 Sib	4.0000	A
289 (X)	3.6667	AB
PBG3 (X)	3.5	AB
6176 (X)	3.5	AB
110	3.5	AB
2033	3.5	AB
235	3.5	AB
6269 (X)	3.1667	ABC
PBG2 (X)	2.8333	BCD
2072 (X)	2.5	CD
6276 (X)	2.5	CD
6160 (X)	2.5	CD
129	2.5	CD

CH131266-6084 (X)	2.5	CD
PBG4 (X)	2.3333	CD
113	2.1667	D
PBG1 (X)	2	D
2070	2	D
CRT3-6196(X)	2	D
CH13949-6071 (X)	2	D

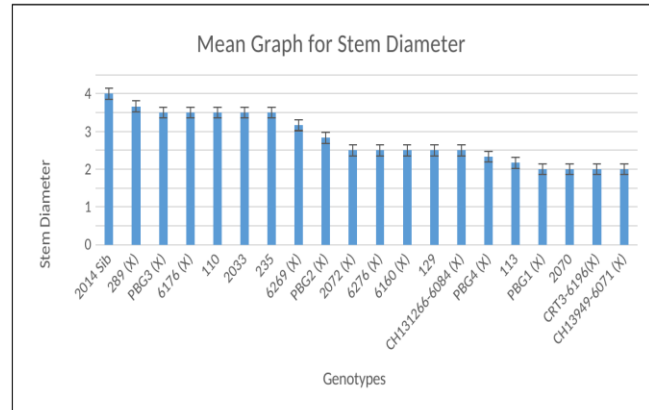


Figure 3. Means of stem diameter for 20 maize genotypes

Internodal length

The length between nodes was not the same for all genotypes, as shown by the analysis ($F = 17.47$, $P = 0.0000$; Table 8), where the overall average was 2.467 cm. The highest mean was recorded in PBG3 (X) at 3.833 cm, while 110 and 2014 Sib came second with means of 3.667 cm each. On the other hand, CH13949-6071 (X) recorded the lowest mean of 1.333 cm. **Table 8. Analysis of variance for internodal length**

Source	DF	Sum of square	Mean square	F value	P value
Replications	2	0.2583	0.12917		
Genotypes	19	35.6000	1.87368	17.47	0.0000
Error	38	4.0750	0.10724		
Total	59	39.9333			

Table 9. Tukey HSD all-pairwise comparison test of internodal length

Genotypes	Mean	Homogeneous Groups
PBG3 (X)	3.8333	A
110	3.6667	AB
2014 Sib	3.6667	AB
289 (X)	3.5	AB
6176 (X)	3.1667	ABC
2033	3.1667	ABC
PBG2 (X)	2.8333	ABCD
235	2.6667	BCDE
129	2.3333	CDEF
6276 (X)	2.1667	CDEF

6160 (X)	2.1667	CDEF
6269 (X)	2.1667	CDEF
129	2.1667	CDEF
113	2	DEF
PBG4 (X)	1.8333	DEF
CH131266-6084 (X)	1.8333	DEF
2070	1.6667	EF
CRT3-6196(X)	1.6667	EF
PBG1 (X)	1.5	F
CH13949-6071 (X)	1.3333	F

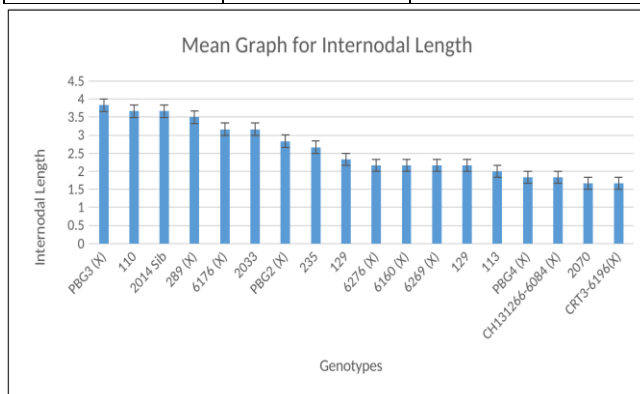


Figure 4. Means of internodal length for 20 maize genotypes

Cob length

Genotype had a significant influence on cob length as indicated by the F statistics (42. 13) and its probability value (0. 0000) as shown in Table 10. The overall average was 14. 333 cm. 6160 (X) had the longest cob length on average at 19. 000 cm, then came 2014 Sib with 18. 833 cm, and lastly 113 with 18. 167 cm. On the other hand, 289 (X) gave the lowest value of 8. 167 cm.

Table 10. Analysis of variance for cob length

Source	DF	Sum of square	Mean square	F value	P value
Replications	2	0.133	0.0667		
Genotypes	19	313.146	16.4814	42.13	0.0000
Error	38	14.867	0.3912		
Total	59	328.146			

Table 11. Tukey HSD all-pairwise comparison test of cob length

Genotypes	Mean	Homogeneous groups
6160 (X)	19	A
2014 Sib	18.833	A
113	18.167	AB
PBG4 (X)	17.5	AB
2033	17.5	AB
110	17.167	ABC
PBG3 (X)	16.833	BCD

129	16.833	BCD
2070	16.5	BCDE
CRT3-6196(X)	16.5	BCDE
6176 (X)	16.5	BCDE
2072 (X)	16.5	BCDE
6269 (X)	16.5	BCDE
CH131266-6084 (X)	15.5	CDEF
PBG2 (X)	15.333	CDEF
235	15	DEFG
PBG1 (X)	14.667	EFG
CH13949-6071 (X)	14.5	FG
6276 (X)	13.333	G
289 (X)	8.167	H

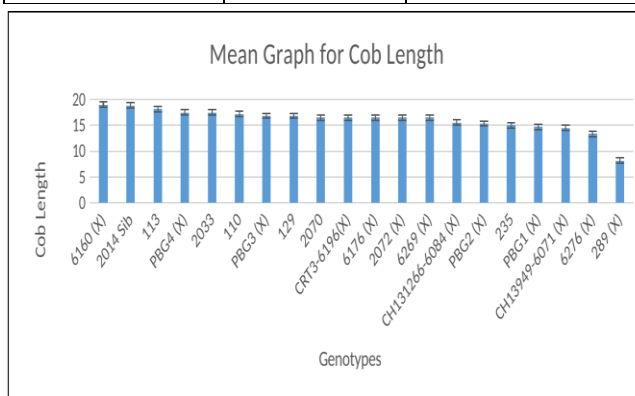


Figure 5. Means of cob length for 20 maize genotypes

Number of rows per cob

Genotypes showed significant variations in number of rows per cob ($F = 7.08$, $P = 0.0000$) as indicated in Table 12 and supported by a grand mean of 14. 667. The order of genotypes from the highest to the lowest mean of number of rows per cobs is as follows: 110 (17. 000), CH13949-6071 (X) (16. 167), 2072 (X) (16. 000) were followed by 6276 (X) which had the lowest mean value of 11. 167

Table 12. Analysis of variance for number of rows per cob.

Source	DF	Sum of square	Mean square	F value	P value
Replications	2	0.633	0.31667		
Genotypes	19	121.683	6.40439	7.08	0.0000
Error	38	34.367	0.90439		
Total	59	156.683			

Table 13. Tukey HSD all-pairwise comparison test of number of rows per cob.

Genotypes	Mean	Homogeneous Groups
110	17	A
CH13949-6071 (X)	16.167	AB

2072 (X)	16	AB
2070	15.667	ABC
129	15.667	ABC
PBG1 (X)	15	ABC
6176 (X)	15	ABC
CH131266-6084 (X)	15	ABC
PBG3 (X)	14.333	ABC
235	14.333	ABC
CRT3-6196(X)	14	BCD
2014 Sib	14	BCD
PBG2 (X)	13	CD
PBG4 (X)	13	CD
113	13	CD
6160 (X)	13	CD
289 (X)	13	CD
2033	13	CD
6269 (X)	13	CD
6276 (X)	11.167	D

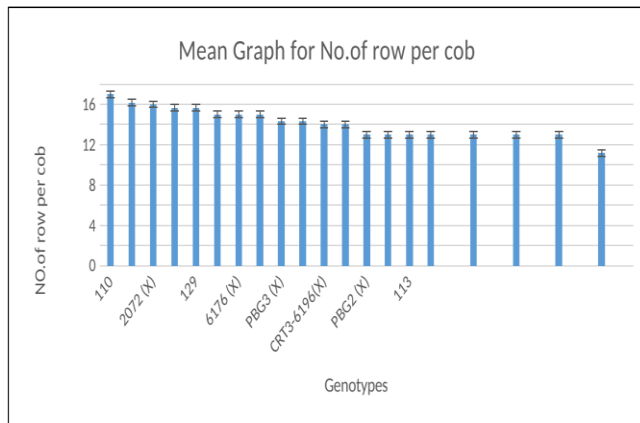


Figure 6. Mean number of rows per cob for 20 maize genotypes

Number of seeds per row

The number of seeds per row greatly depended on the genotype ($F = 249.86$, $P = 0.0000$; Table 14). On average, there were 27.400 seeds in one row. It was seen that genotype 129 had the greatest mean with 48.000 followed closely behind, with 113 with 44.667 and CRT3-6196 (X) came third with 42.000. On the other hand, 289 (X) gave the least mean at 12.667.

Table 14. Analysis of variance for number of seeds per row.

Source	DF	Sum of square	Mean square	F value	P value
Replications	2	0.83	0.417		
Genotypes	19	4101.82	215.885	249.86	0.0000
Error	38	32.83	0.864		
Total	59	4135.48			

Table 15. Tukey HSD all-pairwise comparison test of number of seeds per row

Genotypes	Mean	Homogeneous Groups
129	48	A
113	44.667	B
CRT3-6196(X)	42	B
6269 (X)	35	C
2033	32	D
2014 Sib	31	D
235	30.333	D
2070	30	D
CH131266-6084 (X)	27	E
2072 (X)	26	EF
110	26	EF
PBG3 (X)	25.833	EF
6160 (X)	25.667	EF
6176 (X)	25.333	EF
PBG2 (X)	24	FG
PBG1 (X)	22.167	G
PBG4 (X)	22	G
6276 (X)	22	G
CH13949-6071 (X)	22	G
289 (X)	12.667	H

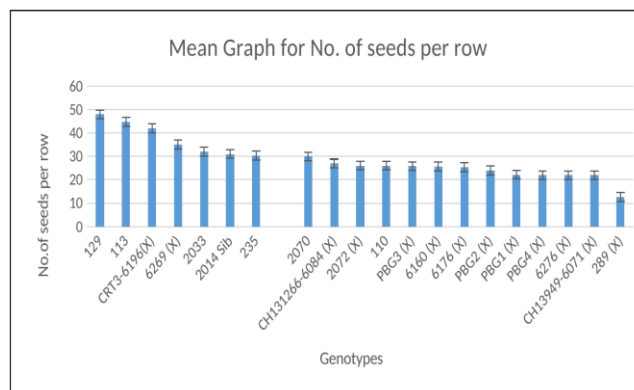


Figure 7. Mean number of seeds per row for 20 maize genotypes

100-grain weight

According to Table 16, there were significant differences in the 100-grain weight across genotypes, as evidenced by an F-value of 206.70 and P-value of 0.0000, and the overall mean was 36.933 g. The greatest average weight was registered by genotype 113 with 47.000 g, then came 235 with 44.500 g, and 129 with 42.500 g. On the other hand, CRT3-6196 (X) recorded the smallest mean at 26.167 g, while 2070 followed it closely with 28.833 g.

Table 16. Analysis of variance for 100-grain weight

Source	DF	Sum of square	Mean square	F value	P value
Replications	2	0.68	0.3375		
Genotypes	19	1721.67	90.6140	206.70	0.0000
Error	38	16.66	0.4384		
Total	59	1739.00			

Table 17. Tukey HSD all-pairwise comparison test of 100-grain weight

Genotypes	Mean	Homogeneous Groups
113	47	A
235	44.5	B
129	42.5	BC
CH131266-6084 (X)	42.167	C
2033	41.833	C
CH13949-6071 (X)	39.167	D
2072 (X)	38.167	DE
6160 (X)	38.167	DE
6269 (X)	38.167	DE
6176 (X)	37.333	DEF
PBG1 (X)	36.167	EFG
PBG2 (X)	35.5	FGH
110	34.5	GH
PBG3 (X)	33.5	HI
PBG4 (X)	33.5	HI
6276 (X)	32	I
289 (X)	31.833	I
2014 Sib	29	J
2070	28.833	J
CRT3-6196(X)	26.167	K

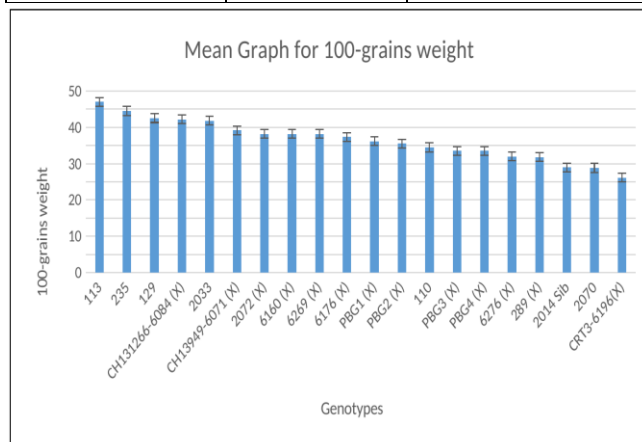


Figure 8. Means of 100-grain weight for 20 maize genotypes.

Cob diameter

There was a significant influence of genotype on cob diameter ($F = 336.49$, $P = 0.0000$; Table 18), which averaged 40.367 mm overall. The highest average cob diameter was

observed in genotype 113 at 49.500 mm, while genotypes 2072 (X) and 6176 (X) came second with 48.000 mm and 47.000 mm, respectively. On the other hand, PBG1 (X) recorded the lowest average at 28.167 mm.

Table 18. Analysis of variance for cob diameter

Source	DF	Sum of square	Mean square	F value	P value
Replications	2	1.61	0.804		
Genotypes	19	2168.93	114.154	336.49	0.0000
Error	38	12.89	0.339		
Total	59	2183.43			

Table 19. Tukey HSD all-pairwise comparison test of cob diameter

Genotypes	Mean	Homogeneous Groups
113	49.5	A
2072 (X)	48	AB
6176 (X)	47	BC
6269 (X)	46.833	BC
CH131266-6084 (X)	46.167	CD
CRT3-6196(X)	44.5	DE
PBG4 (X)	44.167	E
129	44.167	E
PBG3 (X)	43.5	EF
CH13949-6071 (X)	42	FG
2033	41.5	G
110	37.833	H
2014 Sib	37.5	HI
PBG2 (X)	36.833	HIJ
6276 (X)	36	IJK
289 (X)	35.5	JK
6160 (X)	34.833	K
2070	32.5	L
235	30.833	L
PBG1 (X)	28.167	M

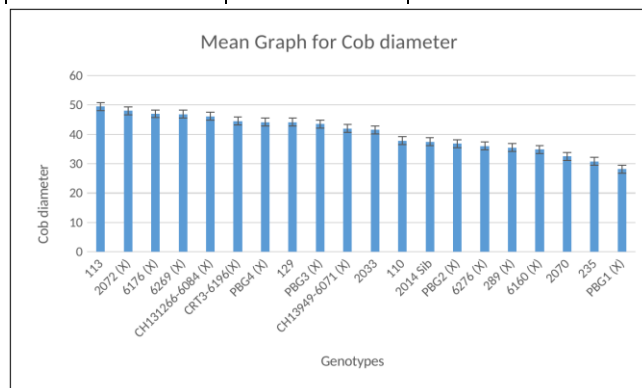


Figure 9. Means of cob diameter for 20 maize genotypes

Pith diameter

The pith diameters showed significant variation between genotypes, as indicated by the ANOVA results, $F(12, 185) = 486.72$, $P < 0.0001$, Table 20. On average, the overall mean was 26.310 mm. Genotype 113 had the greatest average value of 34.500 mm, trailed by 2072 (X) at 33.000 mm and PBG4 (X) at 32.500 mm. On the other hand, PBG1 (X) had the lowest mean of 15.500 mm.

Table 20. Analysis of variance for pith diameter

Source	DF	Sum of square	Mean square	F value	P value
Replications	2	3.41	1.7060		
Genotypes	19	1823.89	95.9941	486.72	0.0000
Error	38	7.49	0.1972		
Total	59	1834.79			

Table 21. Tukey HSD all-pairwise comparison test of pith diameter

Genotypes	Mean	Homogeneous Groups
113	34.5	A
2072 (X)	33	B
PBG4 (X)	32.5	B
CH131266-6084 (X)	32.167	BC
6269 (X)	31.833	BC
PBG3 (X)	31	CD
2014 Sib	30	DE
129	28.833	E
2033	26.833	F
CRT3-6196(X)	26.5	F
6176 (X)	26.5	F
6276 (X)	26.5	F
CH13949-6071 (X)	26	FG
PBG2 (X)	24.833	G
110	22.5	H
6160 (X)	22.5	H
235	19.7	J
289 (X)	18.833	J
2070	16.167	J
PBG1 (X)	15.5	J

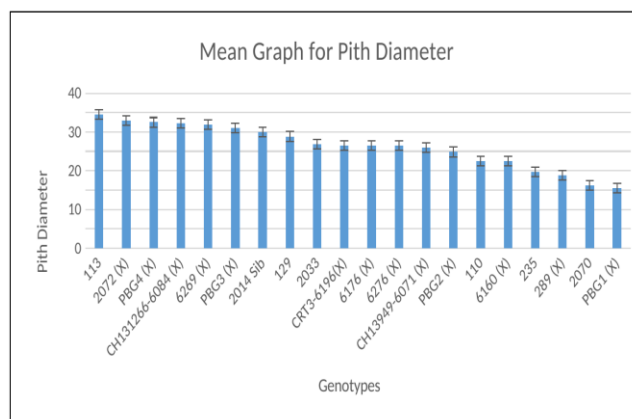


Figure 10. Means of pith diameter for 20 maize genotypes

Correlation among traits

The analysis of Pearson correlation coefficients revealed some distinct correlations between the variables under study (Table 22). For instance, as indicated by a coefficient of 0.8768, there exists a very strong positive correlation between plant height and ear height; 0.7664 also shows that there is a positive relationship although weaker between plant height and stem diameter while internodal length has the highest positive correlation coefficient with plant height at 0.8891. In addition, ear height increased with bigger stem diameter ($r = 0.6969$) as well as longer internodal length ($r = 0.7416$). There was also a correlation between stem diameter and internodal length ($r = 0.7197$).

The analysis also looked at some characters related to yield. Cob length had a positive relationship with number of seeds per row ($r = 0.5430$) and pith diameter ($r = 0.4159$). The more seeds in a given number on a row, the higher the 100-grain weight ($r = 0.3017$). It also showed positive correlations with cob diameter ($r = 0.4175$) and pith diameter ($r = 0.3704$). Cob diameter and pith diameter had the highest correlation in the matrix ($r = 0.8701$). On the other hand, 100-grain Weight had very low negative relationships with plant height (-0.1271), Ear height (-0.1004), Stem diameter (-0.0201), and Internodal length (-0.1290). Nevertheless, it was positively related to cob length with a correlation of 0.1559.

	PH	AH	SD	IL	CL	NR	NS	GW	CD
AH	0.8768								
SD	0.7664	0.6969							
IL	0.8891	0.7416	0.7197						
CL	-0.0594	0.0111	-0.0743	-0.0277					
NR	-0.0559	-0.1763	-0.0571	-0.0483	0.1420				
NS	-0.2077	-0.2485	-0.1562	-0.1966	0.5430	0.0883			
GW	-0.1271	-0.1004	-0.0201	-0.1290	0.1559	0.0848	0.3017		
CD	0.0475	0.0423	-0.0378	-0.0382	0.3093	0.0624	0.4175	0.2774	
PD	0.1453	0.1921	0.0081	0.0272	0.4159	-0.1423	0.3704	0.2679	0.8701

Table 22. Pearson correlation coefficients among the measured traits

Discussion

All ten characteristics recorded significant genotype effects, which shows that the studied materials had different phenotypes in all experimental conditions. This has also been noted for maize genotypes in some contemporary literature. For instance, Ezin et al. (2022) observed significant variations among maize accessions in terms of plant height, ear height, and yield components, while Reddy et al. (2023) reported that there were significant differences in numerous quantitative traits within twenty-one maize genotypes. Therefore, these findings add to the already known fact that there is exploitable variability within maize germplasm.

The variability in plant height and ear height is associated with plant structure. In this case, 1014 Sib had the highest averages for the two traits as well as recording the largest stem diameter. It was noted that plant height had a strong positive association with ear height, stem diameter, and internode length. Such associations imply that vegetative structures among the assessed genotypes were interdependent. Recent studies on maize have also indicated positive correlations between plant height, ear height, and yield-related traits; however, these correlations may become stronger or weaker depending on the genetic makeup and environment of growth (Javaid et al., 2024; Lamsal et al., 2026).

There was significant variation in the different characteristics of cobs. The difference in cob length was very high, measuring 8. 167 cm in 289 (X) up to 19. 000 cm in 6160 (X). Similarly, the number of seeds per row differed drastically; it was lowest at 12. 667 in 289 (X) and highest at 48. 000 in 129. The data showed a positive correlation between cob length & number of seeds per row, which supports other studies linking ear size with certain kernel traits. For instance, Fadhli et al. (2023) saw how

attributes related to cobs could explain variations in maize output, while Vaishnavi et al. (2024) discovered that number of kernels per row & rows per ear were important criteria when choosing tropical maize hybrids.

It was also possible to distinguish between genotypes by looking at their 100-grain weights! The heaviest grains belonged to genotype 113, which also had some of the widest cobs and thickest rinds. Although the correlations were mostly weak or moderate, with 100-grain weight showing positive associations with cob length, seeds per row, cob width & rind thickness, other studies have pointed out that these factors may be important selection criteria in maize.

Different yield traits showed wide variation among them, with grain yield exhibiting a positive association with most traits, as noted by Bohara et al. (2025) and Yogitha et al. (2026), who found that there was a wide variation for 100 kernel weight/kernels counts among the maize lines. It and Pd ($r = 0. 8701$) gave rise to the highest positive coefficient in the current matrix. This makes sense from a biological point of view, as both measurements refer to the size of the cob on cross-section; however, one must not conclude that it causes anything directly. Correlation indicates association rather than cause. Again, the positive correlations of plant height with both stem diameter and internodal length should be taken with similar caution. Testing in multiple environments combined with molecular characterization when feasible would reveal if these associations hold in different settings and among different genotypes. Guo et al. (2025) emphasized that although phenotypic clustering can show differences in grouping, it might group materials in a manner dissimilar from molecular

markers; thus, field data should still be integrated with molecular analyses for thorough genetic typing. The outcomes also affirm the effectiveness of using easily observable features for preliminary selection. Phenotypic evaluation has been found in recent studies on maize landraces and inbred lines to identify differences in plant architecture, ear traits, and grain characteristics (Wei et al., 2026; Dharmendra et al., 2026). These evaluations may be followed with or without some of the evaluations depending on available resources, such as multivariate analyses, molecular markers, and MET, giving more insight into the data obtained. Nevertheless, this can also be achieved through other simple methods available at the moment or in the future. It is evident from the data that certain characteristics like cob length, number of seeds per row, 100-grain weight, and cob diameter varied widely among the studied genotypes and hence may play a role during the subsequent selection process as long as they are consistent over different seasons or environments.

Conclusion

Under Faisalabad field conditions, there was considerable difference among the 20 maize genotypes for the traits of plant, cob and grain. The effect of genotype on each character measured was highly significant. For instance, in 2014, Sib recorded the highest average values in terms of plant height, ear height as well as stem diameter whereas PBG3 (X) had the maximum internodal length observed; about cob length it was found out that 6160 (X) had longer ones; number of rows per cob was greatest in 110; more seeds per row were recorded in 129; as for 113, it had the largest 100-grain weights, including also bigger cobs and pith diameters. Some traits were correlated in a positive manner; for example, plant height was positively correlated with ear height, stem thickness, and internodal length, whereas kernel number and grain weight had a strong association with cob related traits. The study lays down a good phenotypic foundation from which diverse maize can be chosen for breeding. Nonetheless, since this is just one site for one season, the correlations observed here need to be confirmed across other locations before any wide selection is undertaken.

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