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GENETIC VARIABILITY, CORRELATION AND PATH COEFFICIENT ANALYSIS OF EXOTIC WHITE MAIZE (*Zea mays* L.) GENOYTPES

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Abstract

Seventeen exotic white maize (*Zea mays* L.) inbred lines collected from CIMMYT, Mexico were evaluated at the experimental farm of Sher-e-Bangla Agricultural University, Dhaka in a Randomized Complete Block Design (RCBD) with three replications, during October 2016 to April 2017. The mean performance, variability, correlation matrix and path analysis on different yield parameters and yield were estimated. Maximum grain yield plant^{-1} (170.01 g) was recorded in the genotype, CLTHW15008, whereas the minimum grain yield plant^{-1} (44.52 g) was recorded in CLTHW15007.The phenotypic co-efficient of variation was higher than the genotypic co-efficient of variation for all the yield contributing traits. In the correlation study, a significant positive association was recorded for grain yield plant^{-1} with the base diameter of the plant (1.00), leaf breadth (1.00), cob length (0.979), cob diameter (0.930), number of rows cob^{-1} (0.979), number of grains row^{-1} (0.999), 100-grain weight (0.992). Path analysis revealed that plant height (0.412), leaf breadth (0.073), days to 50% flowering (0.280), number of rows cob^{-1} (0.462), number of grains row^{-1} (0.209) had a positive direct effect on yieldplant^{-1}. The results indicated that for improving white maize grain yield, selection based on plant height, cob length, cob diameter, number of rows cob^{-1}, number of grains row^{-1}, 100-grain weight would be useful for future breeding program.

Keywords: Correlation coefficients, Path analysis, Variability, White maize.

Introduction

Maize is the supreme food and feed crop in the world and in terms of global production, maize ranks third after rice and wheat (Muhammad *et al.*, 2023). It is known as the queen of cereals, because of its highest genetic yield potential (Shree *et al.*, 2018). It is also referred to as a “contingency crop” since it may be used at any every stage of development like tender green fodder in the early stages, baby corn in the very early stages of cob development, green cob in the slightly later stages, and maize grain in the fully developed stages (Yadav *et al.*, 2014). Substantial genetic variability was found among various maize cultivars. Generally, yellow and white maize based on endosperm

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color are predominantly grown around the world. Yellow-colored maize is largely grown in the Southeast Asian region and is predominantly used for poultry and animal feed. However, white maize is widely cultivated in Africa and America where it is used as a staple food due to its nutritional properties (Arora *et al.,* 2024). The demand for white maize flour is notably increasing in the Indo-Bangladesh regions due to the higher consumer preference in recent years.

In Bangladesh, maize cultivation is also increasing rapidly because of its versatile uses as food, feed, raw materials for industry, and edible oil with low cholesterol levels for human and livestock consumption. It is a short-duration crop cultivated in the spring and summer seasons to meet the desirable yield and boost the economy (Dogar *et al.,* 2023). The area and production of maize in both seasons in 2022-23 were1227 thousand acres and 45.63 lac million tons, respectively (BBS, 2023) while the demand is almost 2.0 million tons (Islam *et al.,* 2022). The acreage and production of maize in the country are increasing but not encouraging enough compared to the world perspective and the demand for crops in the country is increasing at a higher rate. Additionally, the coverage of white maize production is very low, resulting in Bangladesh paying a sheer amount of foreign exchange to export maize products. To meet the ever-increasing demand of the increasing population of Bangladesh, maize breeders need to pay special attention to investigating the genetic variability of white maize that could help to isolate promising inbred lines.

Determination of genetic variation is a prerequisite for crop improvement programs. The production capabilities of a plant are largely contributed by the interaction effects of genetic factors and environmental conditions. The variability components are effective tools for plant breeding that estimate the transmission capabilities of a trait over the environment and set a sound basis for plant breeders to formulate effective breeding strategies (Ahmed *et al.,* 2020). Furthermore, the yield performance of a variety, which is the ultimate goal of breeding programs, is reflected by the joint effects of multiple traits. Hence, pair wise association among the yield-attributing traits is an urgent need in varietal improvement programs. Proper knowledge of such interrelationships between yield and its attributing traits thus helps to efficiently improve the yield performance and the selection indices (Amin *et al.,* 2022). Correlation analyses are used to determine such interrelationships, such that the values of two characters are analyzed on a paired basis, the results of which may be either positive or negative (Prasad and Shivani, 2017). As the number of variables increases, the measurement of the contribution of each variable towards the observed correlations is imperative. Therefore, partitioning the observed correlation coefficients into components of direct and indirect influences provides perceptions in the characterization of more complex traits like yield (Shikha *et al.,* 2020). The technique of path coefficient analysis developed by Wright (1921) and demonstrated by Dewey and Lu (1959) facilitates the partitioning of correlation coefficients into direct and indirect contributions of various characters to yield. Keeping these in mind, seventeen white maize genotypes were evaluated addressing the following objectives: The genetic variability among the collected germplasms of white maize and analyze the correlation and path coefficient analysis among the yield contributing traits that can be employed in future varietal improvement programs.

Materials and Methods

The experiment was conducted using seventeen (17) exotic white maize inbred lines collected from CIMMYT, Mexico and local open-pollination white maize variety, Suvra (Table 1.) to investigate the genetic variability, heritability, correlation and path co-efficient analysis for yield and its contributing factors and genetic diversity at Sher-e-Bangla Agricultural University (SAU), Sher-e-Bangla Nagar, Dhaka, Bangladesh. The field experiment was carried out from October to April 2016-2017.

Table 1. Name and origin of the white maize (*Zea mays*) inbred lines and variety used in the present study

Sl.	Genotypes	Source of collection
1.	CLTHW15004	CIMMYT, Mexico
2.	CLTHW15005	CIMMYT, Mexico
3.	CLTHW15006	CIMMYT, Mexico
4.	CLTHW15007	CIMMYT, Mexico
5.	CLTHW15008	CIMMYT, Mexico
6.	CLTHW15009	CIMMYT, Mexico
7	CLTHW15003	CIMMYT, Mexico
8	CLTHW15010	CIMMYT, Mexico
9	CLTHW15011	CIMMYT, Mexico
10	CLTHW15012	CIMMYT, Mexico
11	CLTHW15001	CIMMYT, Mexico
12	CLTHW15014	CIMMYT, Mexico
13	CLTHW15015	CIMMYT, Mexico
14	CLTHW14001	CIMMYT, Mexico
15	CLTHW14003	CIMMYT, Mexico
16	CLTHW13001	CIMMYT, Mexico
17	Suvra	BARI, Gazipur

Location of the experimental site

The investigation was carried out at the experimental field of Sher-e-Bangla Agricultural University, Dhaka. The location of the site is $23^0 74^/$N latitude and $90^0 35^/$E longitude with an elevation of 8.2 meters from sea level with a sub-tropical climate.

Soil

The soil of the experimental site belongs to “The Madhupur Tract”, AEZ-28 (FAO, 1988). Topsoil was silty clay in texture, olive-gray with common fine to medium distinct dark yellowish-brown mottles, the pH was 5.6 and had an organic matter of 0.45%. The soil analyses were done by the Soil Resource and Development Institute (SRDI), Dhaka. The experimental area was flat having an available irrigation and drainage system and above flood level. The selected plot was medium-high land.

Experimental design and layout

The experiment was laid out in randomized complete block design (RCBD) with three replications. The field was partitioned into three blocks. The individual block size was 33.15 m × 2.5 m. Each plot was 2.5 m in length and 2 m in breadth containing three rows. The plant spacing provided was 65 cm between rows and 25 cm between plants of the same row. All the recommended intercultural operations (weeding, thinning, gap filling, fertilizer application, irrigation, and plant protection) were followed.

Data recording

Five individual plants from each genotype from every replication were randomly selected to measure various yield-contributing traits. Thirteen parameters were measured viz., plant height (cm), base to cob distance (cm), base diameter of plant (cm), leaf length (cm), leaf Breadth (cm), days of 50% flowering, days to maturity, cob length (cm), cob diameter (cm), number of rows cob^{-1}, number of grains cob^{-1}, 100-grain weight yield plant^{-1}(g).

Statistical analysis

The mean values of all the thirteen characters were evaluated and analysis of variance was performed by the 'F' test. Genotypic and phenotypic variances were estimated with the help of the formula suggested by Johnson *et al*. (1955). The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated by the formula suggested by Burton (1952). Heritability in broad sense was estimated by the formula as suggested by Johnson *et al*. (1955). The formula suggested by Allard (1960) was used to estimate the expected genetic advance for different characters under selection. Genetic advance in percentage of mean was calculated by the formula given by Comstock and Robinson (1952). Simple correlation was estimated for different traits with the formula (Singh and Chaudhary, 1985). Path co-efficient analysis was carried out according to the procedure employed by Dewey and Lu (1959) also quoted in Singh and Chaudhary (1985), using simple correlation values. The data collected were subjected to statistical analysis using Statistix10 and Genstat v. 2017 to determine the genetic variability of test genotypes.

Results and Discussion

Performance analysis of 17 white maize varieties

The analysis of variance indicated a significant amount of genetic variation among all the characters studied, levering ample opportunity of improving white maize high-yield varieties (Table 2). Moreover, the white maize varieties assessed in the current study revealed that the test genotype varied substantially in yield and yield-attributing traits (Table 3). Among the growth-related characters, plant height ranged from 172.67 cm (CLTHW14001) to 223.93 cm (CLTHW15010). The maturity indicating traits viz., the days to 50% flowering extended from 78.13 (CLTHW15008) to 84.87 DAS(CLTHW15011). Furthermore, inbred line CLTHW15012 showed the earliest maturity duration whereas the longest maturity duration was noted in CLTHW15014 (151.67). Collectively, inbred CLTHW15004, CLTHW15008, CLTHW15011, CLTHW15001 and CLTHW14001 can be selected as potential resources to develop early maturing and short-stature white maize varieties.

In maize production, cob length and diameter are two important traits, those provide an indication of yield performance. In the present study, the highest cob length was recorded in CLTHW15008 (16.47 cm) while the lowest was in CLTHW15007 (13.17 cm). Moreover, the maximum cob diameter was recorded in CLTHW15008 (4.85 cm) whereas inbred CLTHW15007 exhibited the minimum diameter of the cobs. Again, the highest number of seed row cob^{-1} was 16.57, produced by the CLTHW15008 and the lowest number of seed row cob^{-1} was 12.11, found in CLTHW15007.The maximum number of grains row^{-1}was found in the genotype CLTHW15008 (30.14) with an average of number 23.54. In case of grain yield performance, the yield plant^{-1} varied from 44.52g (CLTHW15006) to 170.01 g (CLTHW15008) whereas inbred lines CLTHW15004 (137.30 g), CLTHW15011 (127.08 g) and CLTHW15015 (117.23 g) out performed in yielding. Additionally, the maximum 100-seed weight was found in CLTHW15008 (34.10 g) and minimum in CLTHW15007 (20.54g). Ahmed *et al.,* (2020) and Muhammad et al., (2023) also evaluated different maize genotypes on their morphological and yield contributing characteristics and suggested the best varieties for further maize improving scheme. Ahmed *et al.*, (2020) found maximum value 21.60 for cob length, 5.50 for cob diameter,18 for number of rows cob^{-1} ,748 for number of seeds cob^{-1} , 9.25 for yield. Considering the agronomic performances of the maize genotypes it could be suggested that CLTHW15004, CLTHW15005, CLTHW15006, CLTHW15008, CLTHW15001 and CLTHW15015 are the promising lines for their higher yield, number of seed row cob^{-1}, cob length and number of grains row^{-1}. Therefore, these selected lines can be utilized in breeding programs for developing high-yielding maize-inbred lines in the future.

Variability components among the yield-attributing traits

In crop improvement programs, determining the genetic variability among the desired traits is the foremost objective of plant breeders, and it allows them to get an insight into the inheritance patterns that aid in fabricating an effective breeding program to improve the crop further. Additionally, the estimation of variance components provides an understanding of the genetics or interaction of the genetics with surrounding environmental factors that regulate the expression of the phenotypic variance (Shompa *et al.*, 2020).In the present investigation, there were significant genotypic and phenotypic differences among maize genotypes for yield and other morphological attributes (Table 4). Among the traits study, phenotypic coefficient variation (PCV) is higher or slightly higher than genotypic coefficient variation (GCV) in almost all parameters except plant height (PCV-10.48, GCV- 4.18) and leaf length (PCV-11.63, GCV-1.82). Conversely, a minimal fluctuation between PCV and GCV was noted in base diameter of plant (PCV-8.75, GCV-8.55), leaf breadth (PCV-8.87, GCV-8.72), days to 50% flowering (PCV-3.35, GCV-3.33), cob length (PCV-6.87, GCV-6.54), cob diameter (PCV-4.63, GCV-4.50), no of grains row^{-1} (PCV-13.50, GCV-13.20), 100-grain weight (PCV-12.51, GCV-12.50) and yield plant^{-1} (PCV-32.89, GCV-32.77) indicated that genes controlling the inheritance of these traits were largely influenced by the genetic factors rather than the environmental interactions on the phenotypic expressions of these traits (Bartaula *et al.*, 2019). Therefore, the direct selection of these selected traits could be beneficial in formulating efficient breeding programs. Moreover, utilizing heritability estimates alongside genetic advance enhances the reliability and utility of selection procedures (Reddy *et al.*, 2024). In this present study, the joint effects of high heritability and genetic advance (%) were recorded in yield plant^{-1} (99.24, 64.24), leaf breadth (96.56, 17,65), cob length (90.67,12,83), number of grains row^{-1}(95.54, 26.58). Reddy *et al*., (2024) documented similar results for yield. On the other hand, plant height and leaf length showed low heritability coupled with low GA mean percentage (15.90, 3.43) and (2.45, 0.59) respectively. Direct selection would not be effective in this case and these characteristics were controlled by non-additive genes. Previously, Magar *et al.*, (2021) and Kumar *et al.*, (2024) suggested that traits possessing broad sense higher heritability (>60%) and genetic advance in percentage of mean (>20%) are highly advantageous during selection as these traits are regulated by the fixable additive genes and can be transmitted over the generations. Hence, the aforesaid traits can be considered in future breeding programs in developing high-yielding white maize cultivars.

Table 2. Analysis of variance (ANOVA) of different characters in white maize

Sources of variation	df	Mean sum of squares												
		Plant Height (cm)	Distance between base to cob (cm)	Base diameter of plant (cm)	Leaf length (cm)	Leaf breadth (cm)	Days to 50% flowering	Days to maturity	Cob length (cm)	Cob diameter (cm)	No. of row cob^{-1}	No of grains row^{-1}	100-grain weight	Yield plant^{-1}
Genotypes	16	604.78**	369.84**	0.82	63.47**	1.44	24.03**	96.45**	2.97**	0.13	3.93**	29.41**	34.57**	15505.68**
Replications	2	1079.99	181.017	1.311	177.361	0.739	12.505	55.902	0.090	0.013	0.032	2.013	115.006	300.233
Error	32	385.926	6.123	0.013	59.024	0.017	0.088	17.860	0.099	0.003	0.085	0.451	0.010	77.477

Table 3. Mean performance of 13 yield and yield components of 17 white maize Genotypes

Genotypes	Plant height (cm)	Distance between base to cob	Base diameter of plant (cm)	Leaf length (cm)	Leaf breadth (cm)	Days to 50% flowering (DAS)	Days to maturity (DAS)	Cob length (cm)	Cob diameter (cm)	No of rows cob^{-1}	No of grains row^{-1}	100-grain weight	Yield plant^{-1} (g)
CLTHW15004	203.73	89.80	6.90	63.53	8.90	86.17	130.33	16.23	4.82	15.73	27.40	31.85	137.30
CLTHW15005	201.53	99.00	6.19	67.00	8.09	87.17	136.00	15.40	4.67	15.00	24.53	27.85	102.57
CLTHW15006	208.27	97.40	6.33	60.60	8.31	81.17	131.33	15.73	4.72	15.20	25.43	29.25	113.23
CLTHW15007	210.53	121.80	5.10	60.00	6.63	82.17	134.67	13.17	4.06	12.11	17.89	20.54	44.52
CLTHW15008	195.81	75.20	7.20	72.21	9.39	78.17	131.67	16.47	4.85	16.57	30.14	34.10	170.01
CLTHW15009	215.03	100.60	6.13	68.21	7.94	86.17	130.33	15.23	4.65	15.00	24.22	27.45	99.80
CLTHW15003	221.60	106.67	5.81	66.26	7.59	86.17	129.33	14.22	4.53	14.07	22.27	26.14	82.00
CLTHW15010	223.93	104.67	5.95	76.19	7.66	84.17	129.67	14.96	4.58	14.62	23.05	26.94	90.77
CLTHW15011	202.68	90.73	6.53	69.83	8.51	87.83	133.67	16.15	4.81	15.70	26.77	30.25	127.08
CLTHW15012	216.60	102.93	6.08	66.13	7.78	85.83	129.00	15.08	4.62	14.85	23.47	27.25	95.00
CLTHW15001	200.27	97.93	6.23	66.00	8.20	85.83	130.33	15.55	4.70	15.07	24.97	28.85	108.54
CLTHW15014	181.93	109.67	5.61	73.78	7.44	86.83	151.67	13.98	4.48	13.43	21.20	24.74	70.39
CLTHW15015	208.53	95.40	6.39	59.47	8.43	85.83	139.33	15.98	4.77	15.53	25.70	29.35	117.23
CLTHW14001	172.67	109.33	5.75	66.87	7.53	85.83	129.33	14.21	4.51	14.00	21.47	24.94	74.86
CLTHW14003	195.40	117.20	5.47	64.47	6.98	79.83	133.33	13.75	4.28	12.84	19.10	22.94	56.46
CLTHW13001	192.47	105.80	5.90	67.68	7.65	87.83	135.00	14.45	4.58	14.30	22.55	26.14	84.40
Suvra	223.87	112.33	5.57	68.94	7.23	85.83	139.33	13.83	4.35	13.40	20.07	22.99	61.85
Minimum	172.67	75.20	5.10	59.47	6.63	78.17	129.00	13.17	4.06	12.11	17.89	20.54	44.52
Maximum	223.93	121.80	7.20	76.19	9.39	87.83	151.67	16.47	4.85	16.57	30.14	34.10	170.01
Mean	204.40	102.15	6.07	66.89	7.90	84.87	133.78	14.96	4.59	14.55	23.54	27.15	96.24
SE (±)	2.96	1.86	0.10	3.16	0.13	0.77	0.98	0.53	0.09	0.08	0.89	0.76	3.78

Table 4. Estimation of genetic parameters for 13 characters of 17 white maize (*Zea mays*) genotypes

Parameters	Gen MS	σ^2_g	σ^2_e	σ^2_P	GCV	PCV	h^2_b	GA	GA (% mean)	CV (%)
Plant height (cm)	604.78	72.95	385.92	458.87	4.18	10.48	15.90	7.02	3.43	9.61
Distance between base to cob	369.84	121.23	6.12	127.36	10.78	11.05	95.19	22.13	21.66	2.42
Base diameter of plant (cm)	0.82	0.26	0.01	0.28	8.55	8.75	95.36	1.04	17.19	1.89
Leaf length (cm)	63.47	1.48	59.02	60.50	1.82	11.63	2.45	0.39	0.59	11.49
Leaf breadth (cm)	1.43	0.47	0.01	0.49	8.72	8.87	96.56	1.39	17.65	1.64
Days to 50% flowering (DAS)	24.03	7.98	0.08	8.07	3.33	3.35	98.91	5.79	6.82	0.35
Days to maturity (DAS)	96.45	26.19	17.86	44.05	3.83	4.96	59.46	8.13	6.08	3.16
Cob length (cm)	2.97	0.95	0.09	1.05	6.54	6.87	90.67	1.92	12.83	2.10
Cob diameter (cm)	0.13	0.04	0.002	0.04	4.50	4.63	94.47	0.41	9.02	1.10
No. of rows cob^{-1}	3.93	1.28	0.08	1.36	7.78	8.04	93.80	2.26	15.53	2.00
No. of grains row^{-1}	29.41	9.65	0.45	10.10	13.20	13.50	95.54	6.26	26.58	2.85
100-grain weight (g)	34.57	11.52	0.01	11.53	12.50	12.51	99.91	6.99	25.74	0.37
Yield plant^{-1}	2991.01	994.45	7.64	1002.10	32.77	32.89	99.24	64.71	67.24	2.87

Table 5. Genotypic and phenotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotypes of white maize

Traits	Correlations	Distance Between base to cob	Base diameter of plant	Leaf length (cm)	Leaf breadth (cm)	Days to 50% flowering	Days to maturity	Cob length (cm)	Cob diameter (cm)	No of rows cob^{-1}	No of grains row^{-1}	100-grain weight	Yield plant^{-1}
Plant height (cm)	r_g	0.013	-0.022	-1.000**	-0.129	0.010	-0.391	0.031	-0.048	-0.028	0.013	-0.044	-0.025
	r_p	0.041	-0.030	-0.066	-0.069	0.004	-0.285	0.040	-0.046	0.031	-0.020	-0.032	-0.026
Distance between base to cob	r_g		-0.999**	-0.570*	-1.000**	0.093	0.273	-0.990**	-0.931**	-0.989**	-1.000**	-0.992**	-1.000**
	r_p		-0.986**	-0.160	-0.990**	0.093	0.226	-0.948**	-0.924**	-0.966**	-0.993**	-0.985**	-0.995**
Base diameter of plant (cm)	r_g			0.241	1.000**	-0.087	-0.332	0.994**	0.945**	0.986**	1.000**	0.999**	1.000**
	r_p			0.088	0.993**	-0.087	-0.284	0.962**	0.932**	0.967**	0.989**	0.991**	0.993**
Leaf length (cm)	r_g				0.259	0.500*	0.779**	0.211	0.502*	0.234	0.608**	0.546*	0.410
	r_p				0.079	0.127	0.172	0.013	0.140	0.123	0.111	0.113	0.100**
Leaf breadth (cm)	r_g					-0.067	-0.239	0.979**	0.962**	0.976**	1.000**	0.998**	1.000**
	r_p					-0.065	-0.220	0.961**	0.941**	0.967**	0.993**	0.991**	0.993**
Days to 50% flowering (DAS)	r_g						0.232	-0.002	0.181	0.042	-0.048	-0.060	-0.125
	r_p						0.207	0.000	0.178	0.044	-0.047	-0.060	-0.124
Days to maturity (DAS)	r_g							-0.299	-0.264	-0.346	-0.300	-0.310	-0.308
	r_p							-0.280	-0.225	-0.309	-0.258	-0.280	-0.271
Cob length (cm)	r_g								0.989**	1.000**	0.993**	0.986**	0.979**
	r_p								0.953**	0.976**	0.973**	0.968**	0.961**
Cob diameter (cm)	r_g									1.000**	0.969**	0.965**	0.930**
	r_p									0.977**	0.952**	0.956**	0.921**
Noof rows cob^{-1}	r_g										1.000**	0.989**	0.979**
	r_p										0.982**	0.977**	0.966**
No of grains row^{-1}	r_g											1.000**	0.999**
	r_p											0.995**	0.995**
100-grain weight	r_g												0.992**
	r_p												0.991**

Note: *= significant at 5% and **= significant at 1% whereas r_g = Genotypic correlation coefficient and r_p = Phenotypic correlation coefficient

Table 6. Path coefficient analysis showing direct and indirect effects of different characters on yield of white maize.

Characters	Direct effect	Indirect effect												Genotypic correlation with yield
		PH	DBC	BD	LL	LB	DF	DM	CL	CD	RPC	GPR	SGW	
PH	0.412		-0.030	-0.204	0.031	-0.005	-0.052	-0.005	-0.023	-0.067	-0.120	-0.078	0.116	-0.025
DBC	-0.214	-0.023		-0.153	-0.122	-0.068	-0.210	-0.037	-0.113	-0.067	-0.066	-0.099	0.174	-1.000**
BD	-0.614	0.234	0.108		0.079	0.122	0.085	0.235	0.221	0.073	0.120	0.125	0.212	1.000**
LL	-0.467	0.007	0.030	-0.021		0.042	0.094	0.073	0.427	0.081	0.057	0.050	0.037	0.410
LB	0.073	-0.120	0.111	-0.002	0.049		0.110	0.067	0.181	0.294	0.073	0.106	0.059	1.000**
DF	0.280	-0.072	0.051	0.081	-0.103	-0.018		-0.029	-0.095	0.021	-0.163	-0.028	-0.050	-0.125
DM	-0.262	-0.054	-0.014	0.325	0.031	-0.038	-0.020		-0.088	-0.087	-0.060	-0.086	0.045	-0.308
CL	-0.725	0.107	0.095	0.189	0.339	0.105	0.131	0.088		0.046	0.181	0.091	0.330	0.979**
CD	-0.355	0.165	0.119	0.038	0.158	0.126	0.094	0.093	0.019		0.155	0.135	0.183	0.930**
RPC	0.462	-0.027	0.093	0.103	0.077	0.096	-0.023	0.110	-0.083	0.048		0.109	0.015	0.979**
GPR	0.209	-0.132	0.116	0.080	0.061	0.082	0.058	0.176	0.157	0.019	0.123		0.052	0.999**
HSW	-0.472	-0.020	0.144	0.197	0.074	0.079	0.098	0.113	0.421	0.136	0.134	0.088		0.992**

Note: *= significant at 5% and **= significant at 1% whereas PH- Plant height (cm), DBC- Distance between base to cob (cm), BD- Base diameter, LL- Leaf length (cm), LB- Leaf breadth (cm), DF- Days to 50% flowering (DAS), DM- Days to maturity (DAS), CL- Cob length (cm), CD- Cob diameter (cm), RPC- Number of row cob^{-1}, GPR- Number of grains row^{-1}, HSW- 100 seeds weight (g).

Correlation analysis of quantitative traits

The study of the interrelationship among the yield components with yield and their direct and indirect contribution to yield is of immense importance in crop improvement programs. Correlation generally helps in identifying the traits that are mutually contributing to enhance each other or impair each other (Shettigar *et al.*, 2024). Direct improvement of yield is difficult as yield is a complicated trait, as a result of the combined effect of several component characters and environment. In the present study, we noted the genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients in most of the cases indicated that the association is largely due to genetic reasons (Table 5). Among the traits under study , yield plant^{-1}showeda highly significant positive correlation with cob length (rg-0.979**, rp-0.961**), base diameter of plant (rg-1.00**, rp-0.993), leaf breadth (rg-1.00**, rp-0.993**), cob diameter (rg-0.930**, rp-0.921**),no of grains row^{-1}(rg-0.999**, rp-0.966**), no. of rows cob^{-1} (rg-0.979**, rp-0.966**) and 100-grain weight (rg-0.992**, rp-0.991**) at the both genotypic and phenotypic levels, respectively, suggesting that simultaneous improvement of these traits could enhance the yield performance of the maize cultivars. Falconer (1981) previously recommended that a positive correlation between two traits is evolving in the same direction and *vice versa*. Khan and Mahmud (2021) also found a strong and positive correlation of yield plant^{-1}with 100-grain weight, cob length and no. of rows cob^{-1}. Therefore, these traits could be effective for the direct selection of white maize improvement program. On the contrary, yield plant^{-1}had a non-significant negative correlation with plant height (rg: -0.025, rp: -0.026), days to maturity (rg: -0.308, rp: -0.271), days to 50% flowering (rg: -0.125, rp: -0.124) at both genotypic and phenotypic levels suggesting that early and short-statured white maize cultivars could be bred in the future.

Path coefficient analysis

The estimation of path coefficient analysis provides a clear indication of the influence of yield-contributing traits on the total yield performance of a plant by separating the correlation coefficient into direct and indirect effects and indicates the relationship in a more meaningful way by providing a cause-effect relationship of the characters (Ara *et al.,* 2015). The results of the path coefficient analysis are presented in Table 6. The present investigation revealed that five out of twelve characters had a positive direct effect on grain yield plant^{-1}. The characters which had a positive direct effect are plant height (0.412), leaf breadth (0.073), days to 50% flowering (0.280), no. of row cob^{-1} (0.461) and no. of grains row^{-1}(0.209) suggesting that these traits had a significant contribution in increasing the grain yields. Therefore, these traits can be considered during selection. Besides, path coefficient analysis revealed that grain yield plant^{-1} was directly influenced by plant height, leaf breadth, days to 50% flowering, no. of rows cob^{-1} and no of grains row^{-1}. Hence, selection for any of these independent traits also leads to improving the genotypes for grain yield plant^{-1}. These findings are consistent with that of Yahaya *et al.,* (2021) and Reddy *et al.,* (2022). However, character *viz.* the distance between base to cob (-0.214), base diameter of the plant (-0.614), leaf length (-0.467), days to maturity (-0.262), cob length (-0.725), cob diameter (-0.355) and

100-seed weight (-0.472) had a negative direct effect on grain yield plant^{-1}. These traits can also exert positive effects on yield and can indirectly contribute to enhancing yield performance. Among the negatively influencing traits, cob length, leaf length, and cob diameter showed a positive indirect effect and strong association with yield plant^{-1}. Therefore, in the next breeding programs, the traits possessing positive direct effects and also traits having positive indirect effects should focused to improve the overall grain yield of the white maize cultivars.

Conclusion

The present study revealed that there are highly significant differences among the accessions for all the traits under study. Characters like plant height (cm), base to cob distance (cm), base diameter of plant (cm), leaf breadth (cm), number of rows cob^{-1}, number of grains row^{-1}, 100-grain weight (gm), yield plant^{-1} exhibited high genotypic and phenotypic coefficient of variation. High heritability, high genetic advance and high genetic percent of mean were noted for the 100-grain weight. In case of correlation and path analysis, high positive and direct effects exerted by plant height, leaf breadth, days to 50% flowering, number of rows cob^{-1}and the number of grains row^{-1}were noted on yield plant^{-1}. Therefore, selection on these traits could bring a key role in the crop improvement program for the continuous yield enhancement.

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Conflicts of interest

The authors declare no conflicts of interest regarding publication of this paper.

Authors' contribution

Roy, G. designed, planned, and executed the experiment and drafted the manuscript; Shompa, B. N., Emu, I. A. and Fatima, K. edited and reviewed the manuscript; Rahman, J. supervised the experiment, analyzed the data, and edited and reviewed the manuscript.

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