Correlation and Path Coefficient Analysis of Drought Tolerant Open Pollinated Maize (*Zea mays* L.) Genotypes in Ethiopia

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Authors' contributions

This work was carried out in collaboration between both authors. Both authors read and approved the final manuscript.

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ABSTRACT

The development of high yielding genotypes of maize is greatly influenced by the features that are associated with yield and yield components. The Jigjiga Pastoral and Agricultural Research Center's main experimental station was the study site for twenty-four open pollinated maize genotypes planted in a randomized complete block design. The study's objectives were to determine the relationship between and the direct and indirect effects of different character components on yield. The yield-related components (harvest index, thousand kernel weights, number of ears per plant, number of kernels per row, number of ears per plot, biological yield, plant height, leaf area index, anthesis-silking interval, and ear height) of grain yield exhibited significantly positive phenotypic and genotypic correlations. However, a phenotypic association that was

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considerably unfavorable was found between grain yield and flowering features. Days to silking and number of ears per plot had strong genotypic negative direct impacts, whereas harvest index and biological yield similarly had the greatest genotypic positive direct effects on the main trait. Therefore, the combination of these features along with yield could be used in indirect selection indices for the breeding by selection of potentially high yielding maize genotypes.

Keywords: Agronomic attributes; correlation coefficient; open pollinated maize genotypes; path coefficient.

1. INTRODUCTION

"Correlation is of great value in the evaluation of the most effective procedures for selection of superior genotypes. When there is positive association between grain yield and its components breeding would be very effective but difficult to exercise simultaneous selection when associated negatively" [1]. Correlation evaluation between different traits in maize can supply vital information in breeding programs [2].

"In selecting high yielding genotypes correlation studies provide reliable information on the nature, extent and direction of selection. The knowledge of correlation coefficients between different yield attributes helps the breeder to find out nature and magnitude of association between the traits which are mostly used to obtain better yield" [3]

"Understanding the relationship of component traits supports in determining which trait to select when enhancement of the related complex trait is desired. Correlation of specific trait with other traits contributing to grain yield is crucial for indirect selection of genotypes for higher grain yield" [4] and "path coefficient analysis helps partitioning the correlation coefficient into its direct and indirect effects" [5] "Path coefficient analysis has been used successfully to illustrate interrelation between yield and other traits of maize" [6]."However, association between these traits and grain yield is vital, but estimation of correlation coefficient alone does not specify the essence of relationship between traits"[7]. Blum et al. [8] stated that "drought stress causes reduction of genetic variance and yield heritability which restricts efficiency of selection for yield under stress situation".

"Knowledge of the associations among lines would help to identify a set of inbreds that have maximal diversity for the analysis of the effects of genetic background. Use of maize inbreds in association analysis requires that population structure among lines be factored into the analysis" [9]. "Selection is the oldest method and its success in plant breeding largely depends upon many factors such as the association of various traits" [10]. Therefore, the aim of this study was to calculate the genetic and phenotypic associations between yield and yield-related variables in open-pollinated, drought-tolerant maize genotypes.

2. MATERIALS AND METHODS

2.1 Experimental Design and Methods

The association of different yield components on sixteen traits of twenty-four drought tolerance open pollinated maize (ZM309, ZM401, VP051, VP05118, VP05147, VP05163, VP05179, VP05194, VP0610, VP065, VP0712, VP0713, VP0716, VP0720, VP0721, VP0730, VP0731, VP079, VP086, ZM421, ZM423,ZM521, ZM523 and ZM525) genotypes were included. The genotype seeds used in this investigation were sourced from the Melkasa Agricultural Research Center. During the rainy season, the seeds were sown at the Jigjiga Pastoral and Agricultural Research Centre's main station in the Somali Regional State of Ethiopia. Three replications and a randomized complete block design were used for the experiment. The plot measured 15 m2 and consisted of four rows with a row length of 5 m and an intra-row and inter-row spacing of 0.75 m and 0.25 m, respectively.

Version 8.0 (1999-2000) of the SAS statistical program was used to do the analysis of variance. For each trait, the mean significant differences between the genotypes were divided using Duncan's Multiple Range Test. The Dabholkar [11] approach was utilized to investigate the estimation of correlation coefficients between genotype and phenotype.

Genotypic correlation coefficient

$$(r_{g_{xy}}) = \frac{\sigma_{g_{xy}}}{\left[\sqrt{\sigma^2 g_x * \sigma^2 g_y}\right]}$$

Phenotypic correlation coefficient

$$(r_{p_{xy}}) = \frac{\sigma_{P_{XY}}}{\left[\sqrt{\sigma^2_{P_X} * \sigma^2_{P_Y}}\right]}$$

Where, $r_{g_{xy}}$ = Genotypic correlation coefficients between characters x and y

$r_{p_{xy}}$ = phenotypic correlation coefficients between characters x and y

σgxy =Genotypic covariance between characters x and y

$\sigma 2gx$ = Genotypic variance of character x
$\sigma 2gy$ = Genotypic variance of character y
σpxy = Phenotypic covariance of characters x and y

$\sigma 2px$ = Phenotypic variance of character x
$\sigma 2py$ = Phenotypic variance of character y

Using n-2 degree of freedom and 5% and 1% levels of significance, phenotypic correlation coefficients were examined for significance using the t-test, where n is the number of observations and r is the correlation coefficient:

t = rp/SE (rp)

Where, rp = Phenotypic correlation; $SE (rp)$ = Standard error of phenotypic correlation obtained using the following formula [12]:

$SE (rp) = \sqrt{(1 - r2 p)/(n-2)}$

Where, n is the number of genotypes tested.

The following formula, which Robertson [13] described, was used to determine the significance of the coefficients of correlations at genotypic levels:

t = rgxy/SErgxy

Where, $rgxy$ = Genotypic correlation coefficient of variables x and y.

The calculated "t" value was compared with the tabulated "t" value at (n-2) degree of freedom at 5% level of significance.

SErgxy = √(1- rgxy)2/2h2x.h2y

Where, $h2x$ = Heritability of trait x
$h2y$ = Heritability of trait y

Using the formula of Dewey and Lu [14] and the statistical program created by Doshi [15], the path coefficient analysis (direct and indirect impacts of the independent factors on grain yield) was carried out:

rij = Pij + ΣrikPkj

Where rij = The correlation coefficient indicates the degree of association between the independent variable (i) and dependent variable (j), Pij is the path coefficient-measured component of the direct influence of the independent variable (i) on the dependent variable (j). The indirect effects of a given independent variable (i) on a given dependent variable (j) through all other independent variables are added up to form Σrik Pkj.

The method outlined in Dewey and Lu [14] was used to estimate the residual factor (P2R):

P2R = 1 - ΣPijrij

In separate path coefficient analysis, grain yield served as the dependent character, while the other characters were used as independent variables as needed.

3. RESULTS AND DISCUSSION

3.1 Association of Characters

Knowledge about the nature and magnitude of association among characters were mostly used to improve yield of the genotypes indirectly through utilization of other closely related traits with high heritability. Table 1 displays the estimated genotypic and phenotypic correlation coefficients between every pair of characteristics that were examined. The majority of the time, there were inherent genetic correlations between different traits and less environmental effect when the phenotypic correlation coefficients were smaller than the genotypic correlation coefficients.

3.2 Correlation of Grain Yield with Other Characters

The grain yield and harvest index had the highest genotypic and phenotypic association coefficients (0.84**), followed by the grain yield and thousand kernel weight (0.76**).

Table 1. Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients of the 16 quantitative traits of open pollinated maize genotypes

Traits	DT	DA	DS	ASI	LAI	PH	EH	DM	NEP	NEPP	NKRPE	NKPR	BY	TKWT	GY	HI
DT		0.92**	0.96**	-0.59*	-0.01	-0.24	0.03	0.56*	-0.43*	-0.43*	-0.09	-0.31	-0.13	-0.69*	-0.69*	-0.79**
DA	0.92**		0.97**	-0.37	-0.12	-0.37	-0.13	0.54*	-0.47*	-0.44*	-0.05	-0.26	-0.14	-0.61*	-0.62*	-0.68*
DS	0.95**	0.97**		-0.57*	-0.09	-0.34	-0.08	0.52*	-0.43*	-0.40	-0.04	-0.31	-0.16	-0.67*	-0.66*	-0.72**
ASI	-0.41	-0.17	-0.39*		-0.06	0.04	-0.15	-0.17	0.04	0.06	-0.05	0.32	0.17	0.51*	0.48*	0.50*
LAI	-0.32*	-0.40*	-0.38*	-0.004		0.82**	0.79**	-0.17	0.47*	0.43*	0.43*	0.54*	0.75**	0.26	0.42*	0.02
PH	-0.61**	-0.69**	-0.67**	0.08	0.75**		0.89**	-0.35	0.63*	0.58*	0.31	0.51*	0.73**	0.32	0.51*	0.14
EH	-0.39*	-0.48**	-0.45**	-0.01	0.79**	0.85**		-0.34	0.45*	0.39	0.27	0.47*	0.68*	0.14	0.29	-0.10
DM	0.69**	0.67**	0.67**	-0.16	-0.38*	-0.56**	-0.57**		-0.44*	-0.46*	-0.23	-0.19	-0.17	-0.24	-0.44*	-0.42*
NEP	-0.49**	-0.49**	-0.47**	0.04	0.47**	0.59**	0.44*	-0.39*		0.99**	-0.01	0.32	0.58*	0.51*	0.71*	0.54*
NEPP	-0.47**	-0.44*	-0.43*	0.08	0.44*	0.54**	0.40*	-0.38*	0.98**		-0.03	0.34	0.56*	0.50*	0.73**	0.58*
NKRPE	-0.25*	-0.21	-0.23	0.15	0.42*	0.38*	0.33*	-0.30*	0.08	0.09		0.29	0.11	-0.10	0.13	0.09
NKPR	-0.48**	-0.45**	-0.47**	0.19	0.57**	0.60**	0.51**	-0.29*	0.43*	0.44**	0.36*		0.63*	0.53*	0.72**	0.49*
BY	-0.38*	-0.40*	-0.41*	0.15	0.70**	0.72**	0.69**	-0.39*	0.57**	0.55**	0.19	0.62**		0.56*	0.64*	0.14
TKWT	-0.61**	-0.54**	-0.57**	0.27*	0.33*	0.44*	0.26*	-0.28*	0.52**	0.51**	0.09	0.64**	0.52**		0.78**	0.62*
GY	-0.58**	-0.48**	-0.51**	0.26*	0.43*	0.49**	0.35*	-0.34*	0.69**	0.70**	0.19	0.70**	0.59**	0.76**		0.84**
HI	-0.38*	-0.23	-0.27*	0.22	-0.05	0.003	-0.15	-0.09	0.41*	0.45**	0.08	0.35*	-0.06	0.50**	0.76**	

*and ** indicated significant and highly significant at p = 0.05 and p = 0.01 probability level, respectively.DT: days to tasseling, DA: days to anthesis, DS: days to silking, ASI: anthesis-silking interval, LAI: leaf area index (cm), PH: plant height (cm), EH: ear height (cm), DM: days to maturity, NEP: numbers of ears per plot, NEPP: number of ears per plant, NKRPE: number of kernel rows per ear, NKPR: number of kernels per row, BY: biological yield (kg/ha), TKWT: thousand kernel weights (g), GY: grain yield (kg/ha), HI: harvest index (%)

Table 2. Estimate of direct effect (bold face and diagonal) and indirect effects (off diagonal) at genotypic level in 24 open pollinated maize genotypes

Traits	DT	DA	DS	ASI	LAI	PH	EH	DM	NEP	NEPP	NKRPE	NKPR	BY	TKWT	HI	rg
DT	0.27	0.15	-0.40	0.05	0.0001	-0.04	-0.005	-0.05	0.12	-0.09	7.91	-0.002	-0.07	-0.034	-0.60	-0.69*
DA	0.25	0.16	-0.40	0.03	0.002	-0.06	0.02	-0.05	0.13	-0.09	4.4	-0.002	-0.08	-0.03	-0.52	-0.62*
DS	0.26	0.15	-0.41	0.05	0.001	-0.05	0.012	-0.04	0.12	-0.08	3.52	-0.002	-0.09	-0.03	-0.55	-0.66*
ASI	-0.16	-0.06	0.24	-0.08	0.001	0.006	0.023	0.014	-0.01	0.012	4.39	0.003	0.093	0.025	0.38	0.48*
LAI	-0.003	-0.019	0.037	0.005	-0.015	0.13	-0.12	0.014	-0.13	0.086	-0.0004	0.004	0.41	0.013	0.015	0.42*
PH	-0.064	-0.06	0.14	-0.003	-0.012	0.16	-0.14	0.03	-0.18	0.12	-0.0003	0.004	0.40	0.016	0.11	0.51*
EH	0.008	-0.02	0.03	0.013	-0.012	0.14	-0.155	0.029	-0.13	0.078	-0.0002	0.004	0.37	0.007	-0.08	0.29
DM	0.15	0.086	-0.20	0.014	0.0025	-0.05	0.053	-0.09	0.125	-0.09	0.0002	-0.002	-0.09	-0.012	-0.32	-0.44*
NEP	-0.12	-0.075	0.18	-0.003	-0.007	0.099	-0.07	0.037	-0.28	0.198	8.79	0.0026	0.32	0.025	0.41	0.71*
NEPP	-0.12	-0.07	0.165	-0.005	-0.006	0.091	-0.06	0.039	-0.28	0.20	2.64	0.003	0.31	0.024	0.44	0.73**
NKRPE	-0.02	-0.008	0.017	0.004	-0.006	0.049	-0.042	0.019	0.003	-0.006	-0.0009	0.002	0.06	-0.005	0.07	0.13
NKPR	-0.084	-0.04	0.13	-0.027	-0.008	0.08	-0.073	0.016	-0.09	0.068	-0.0003	0.008	0.345	0.026	0.37	0.72**
BY	-0.035	-0.02	0.07	-0.014	-0.01	0.115	-0.11	0.014	-0.16	0.11	-9.67	0.005	0.548	0.027	0.11	0.64*
TKWT	-0.186	-0.097	0.28	-0.043	-0.0038	0.05	-0.02	0.02	-0.14	0.10	8.79	0.004	0.31	0.049	0.47	0.78**
HI	-0.20	-0.10	0.297	-0.04	-0.0003	0.02	0.015	0.036	-0.15	0.12	-7.90	0.004	0.077	0.03	0.757	0.84**

Residual factor = 0.099, rg: genotypic direct effect, DT: days to tasseling, DA: days to anthesis, DS: days to silking, ASI: anthesis-silking interval, LAI: leaf area index (cm), PH: plant height (cm), EH: ear height (cm), DM: days to maturity, NEP: numbers of ears per plot, NEPP: number of ears per plant, NKRPE: number of kernel rows per ear, NKPR: number of kernels per row, BY: biological yield (kg/ha), TKWT: thousand kernel weights (g), HI: harvest index (%)

Table 3. Estimate of direct effect (bold face and diagonal) and indirect effects (off diagonal) at phenotypic level in 24 open pollinated maize genotypes

Traits	DT	DA	DS	ASI	LAI	PH	EH	DM	NEP	NEPP	NKRPE	NKPR	BY	TKWT	HI	rp
DT	0.42	-2.03	2.06	-0.24	-0.04	-0.13	0.08	-0.17	-1.35	1.29	0.014	0.0025	-0.21	-0.056	-0.31	-0.58**
DA	0.38	-2.20	2.10	-0.099	-0.046	-0.15	0.10	-0.17	-1.35	1.21	0.011	0.0024	-0.22	-0.049	-0.19	-0.48**
DS	0.39	-2.14	2.17	-0.23	-0.043	-0.15	0.097	-0.17	-1.29	1.18	0.013	0.0025	-0.22	-0.05	-0.22	-0.51**
ASI	-0.17	0.375	-0.85	0.585	-0.0005	0.017	0.002	0.04	0.11	-0.22	-0.008	-0.001	0.082	0.025	0.18	0.26*
LAI	-0.13	0.88	-0.83	-0.002	0.114	0.164	-0.17	0.097	1.30	-1.20	-0.023	-0.003	0.38	0.03	-0.04	0.43*
PH	-0.25	1.52	-1.45	0.047	0.086	0.219	-0.18	0.14	1.63	-1.48	-0.02	-0.003	0.39	0.04	0.002	0.49**
EH	-0.16	1.06	-0.98	-0.006	0.09	0.186	-0.216	0.15	1.22	-1.10	-0.018	-0.0027	0.38	0.024	-0.12	0.35*
DM	0.29	-1.48	1.45	-0.094	-0.043	-0.12	0.123	-0.26	-1.08	1.04	0.016	0.0015	-0.21	-0.026	-0.07	-0.34*
NEP	-0.20	1.08	-1.02	0.023	0.054	0.129	-0.095	0.099	2.762	-2.69	-0.004	-0.0023	0.31	0.048	0.34	0.69**
NEPP	-0.19	0.97	-0.93	0.047	0.05	0.129	-0.086	0.097	2.70	-2.74	-0.0049	-0.002	0.30	0.047	0.37	0.71**
NKRPE	-0.10	0.46	-0.50	0.088	0.048	0.08	-0.07	0.077	0.22	-0.247	-0.055	-0.0019	0.104	0.008	0.066	0.19
NKPR	-0.19	0.99	-1.02	0.11	0.065	0.13	-0.11	0.074	1.19	-1.20	-0.02	-0.005	0.34	0.059	0.287	0.70**
BY	-0.16	0.88	-0.89	0.088	0.079	0.158	-0.15	0.099	1.57	-1.50	-0.01	-0.003	0.55	0.048	-0.05	0.59**
TKWT	-0.25	1.19	-1.24	0.158	0.038	0.096	-0.056	0.07	1.44	-1.40	-0.005	-0.003	0.28	0.09	0.40	0.76**
HI	-0.16	0.50	-0.59	0.13	-0.006	0.001	0.03	0.023	1.13	-1.23	-0.004	-0.0019	-0.03	0.046	0.819	0.76**

Residual factor = 0.142, rp: phenotypic direct effect, DT: days to tasseling, DA: days to anthesis, DS: days to silking, ASI: anthesis-silking interval, LAI: leaf area index (cm), PH: plant height (cm), EH: ear height (cm), DM: days to maturity, NEP: numbers of ears per plot, NEPP: number of ears per plant, NKRPE: number of kernel rows per ear, NKPR: number of kernels per row, BY: biological yield (kg/ha), TKWT: thousand kernel weights (g), HI: harvest index (%).

Grain yield displayed a highly significant and positive genotypic association with the harvest index, thousand kernel weight, number of ears per plant, and number of kernels per row. This suggested that, in the event that these characters' heritability is superior to the primary trait in the target environment, there may be an indirect selection process for grain yield using these characters. Similar reports were made for the thousand kernel weight by Kumar et al. [16], the number of kernels per row by Sadek et al. [17], the thousand kernel weight and the number of kernels per row by Nastasic et al. [18] and Pavan et al. [19], and both by Ram Reddy et al. (2012).

The number of ears per plot, biological yield, plant height, anthesis-silking interval, and leaf area index all significantly and positively correlated with grain production. The findings were consistent with those of Alvi et al. [20] about the relationship between grain yield and plant height and Aminu and Izge [21] regarding the relationship between grain yield and the number of ears per plot and the gap between anthesis and silking.

However, ear height and the number of kernel rows in each ear showed non-significant positive associations. These characteristics demonstrated statistically significant positive relationships with grain yield, in contrast to Bocanski et al. [22] for ear height and Mostafavi et al. [23] for the number of kernel rows per ear. Low negative associations between the number of kernel rows per ear and grain yield were also noted by Yousuf and Saleem [24].

At the genotypic and phenotypic levels, grain yield showed a significant and negative correlation with the durations of tasseling, silking, anthesis, and maturity. This suggests that early tasseling, silking, and maturities are desirable to increase grain yield in regions with short rainfall periods. The outcomes supported the conclusions of Lingaiah et al. [25], Atnafua and Nageshwar [26], Pavan et al. [19], and Netaji et al. [27]. It was in contrast to Aminu and Izge's [21] findings, which showed a negative, non-significant correlation between grain production and the number of days till silking and tasselling at both the genotypic and phenotypic levels. Grain yield at the phenotypic level had a highly substantial and positive association with the biological yield, plant height, thousand kernel weights, number of kernels per row, number of ears per plant, and number of ears per plot. This

suggested that selecting for these traits would be a more effective way to increase maize grain production. The results support the conclusions of Shelake et al. [28] regarding biological yield and harvest index; Gautam et al. [29], Bello et al. [30], and Lingaiah et al. [25] regarding plant height. Nevertheless, it was in opposition to the results of Yousef [31], who stated that the relationship between grain yield and plant height was not significant or positive; Bocanski et al. [22] for the thousand kernel weight, number of kernels per row, and plant height; Khayatnezhad et al. [32] for the thousand kernel weights; and Yousef [31] for the highly positive correlations with the thousand kernel weight and number of kernels per row.

Grain yield exhibited considerable and positive association with leaf area index, ear height and anthesis-silking interval. Bello et al. [30] and Ali et al. [3] reported similar results for ear height and leaf area index, respectively. Additionally, a non-significant positive connection was seen with the quantity of kernel rows in each ear. On the other hand, the findings of Yousef [31] and Khayatnezhad et al. [32] indicated a substantial correlation between grain yield and the number of kernel rows per ear.

3.3 Correlation among Other Traits

Table 1 displays the strongest correlation found at the genotypic and phenotypic levels between the number of ears per plant and the number of ears per plot (0.99** and 0.98**). This demonstrated how crucial these yield-related characteristics are for raising grain yield.

3.4 Genotypic Correlation among Traits

At genetic level, significantly substantial and positive associations of days to tasseling with days to anthesis and days to silking were found. Days to tasseling and days to maturity also showed a positive and substantial correlation. The outcomes matched the reports written by Ram Reddy and colleagues (2012). Nonetheless, there was a strong negative correlation with the harvest index. The anthesis-silking interval, the number of ears per plot, the number of ears per plant, and the thousand kernel weights were also found to be significantly and negatively correlated.

Days to anthesis and days to silking showed highly substantial and positive relationships,

which were just as strongly correlated as days to anthesis and days to maturity. Nonetheless, it was found that the harvest index, thousand kernel weights, number of ears per plant, and number of ears per plot all significantly and negatively correlated with the days to anthesis. The results of Ram Reddy et al. (2012) were supported by the significant and positive correlation that was found between days to silking and days to maturity. It did, however, have a highly substantial negative connection with the harvest index. Additionally, a negative and significant connection was observed with the anthesis-silking interval, thousand kernel weights, and the number of ears per plot. Harvest index and thousand kernel weight were significantly positively correlated with anthesis-silking interval.

Plant height, ear height, and biological yield were all positively correlated with the leaf area index in a highly significant way. Along with the number of ears per plant, number of rows of kernels per ear, number of ears per plot, and number of ears per row, it also showed a strong correlation. On the other hand, ear height and biological yield were positively and significantly correlated with plant height. Additionally, there was a strong correlation between plant height and the number of ears per plot, plant, and row. For ear height, Shabbir et al. [33] and Yusuf [34] showed similar results; Ram Reddy et al. (2012) found substantial positive relationships with plant height for both ear height and quantity of kernels per row. Ear height showed a strong and favorable correlation.

The number of ears per plant, harvest index, thousand kernel weights, and biological yield all significantly positively correlated with the number of ears per plot. The number of ears on a plant was positively and significantly correlated with harvest index, thousand kernel weights, and biological yield. In line with Ram Reddy et al. (2012) about its link with thousand kernel weights, the number of kernels per row also shown a positive and substantial correlation with harvest index, biological yield, and thousand kernel weights. Biological yield exhibited substantial positive association with thousand kernel weights. Additionally, a noteworthy and favorable correlation was found between harvest index and thousand kernel weight.

3.5 Phenotypic Correlation among Traits

Plant height, at the phenotypic level (Table 1), showed a significant and negative correlation with days to maturity, but a positive and significant association with ear height, number of ears per plot, number of ears per plant, number of kernels per row, biological yield, and thousand kernel weights. The findings were consistent with the findings of Alvi et al. [20], Zeeshan et al. [35], Tengan et al. [36], Sandeep Kumar et al. [37], and Zeeshan et al. [35] regarding biological yield and number of kernels per row, as well as ear height.

Days to tasseling had a considerably positive correlation with days to anthesis, days to silking, and days to maturity; nevertheless, it showed significant and negative correlations with the other features. Similarly, Sandeep kumar et al. [37] reported that days to silking and maturity were significantly positive, while significantly negative associations of days to silking were observed with anthesis-silking interval, number of kernel rows per ear, number of kernels per row and thousand kernel weights.

Characters comprising number of kernels per row, biological yield, number of ears per plot, number of ears per plant, number of kernel rows per ear and thousand kernel weights were significantly and positively correlated with ear height, but it had negative and significant association with days to maturity. The number of kernel rows per ear result was consistent with the findings of Dana and Sherwan [38] and Alvi et al. [20].

Days to anthesis showed a strong positive correlation with days to silking and days to maturity. Ram Reddy et al. (2012) reported similar results. With the exception of the anthesis-silking interval, the number of kernel rows per ear, and the harvest index, significant and negative relationships were found with most of the features. Zeeshan et al. [35] found a significantly negative correlation between thousand kernel weights and days to anthesis. On the other hand, days until anthesis were found to be significantly positively correlated with plant height, ear height, number of kernel rows per ear, and biological yield by Bello et al. [30] and Zeeshan et al. [35].

Days to silking and days to maturity showed a strong, favorable relationship. Additionally, it exhibited both positive and negative correlations with the majority of the features, but not with the quantity of kernel rows in each ear. The findings were consistent with the findings of Sandeep Kumar et al. [37], who found that the days to

silking, the number of kernels per row, and the thousand kernel weights had significant negative and positive relationships, respectively, with these variables. The anthesis-silking interval and thousand kernel weights showed a statistically significant positive association.

The harvest index, biological yield, number of ears per plant, number of kernels per row, thousand kernel weights, and number of ears per plot all shown a strong and positive correlation with each other.

The majority of the features had a strong positive correlation with the leaf area index. While Sandeep Kumar et al. [37] documented the number of kernels per row, thousand kernel weights, and number of kernel rows per ear, Ahsan [39] and Sadek et al. [17] reported the plant and ear height. Along with days to maturity, it showed a substantial negative association, but not a significant link with harvest index. The number of ears per plant, the number of rows per ear, the number of kernels per row, the biological yield, and the thousand kernel weights all showed a strongly negative connection with the number of days to maturity. Likewise, Ram Reddy et al. (2012) reported on the quantity of kernels and the number of kernel rows per ear.

The number of ears per plant, number of kernels per row, harvest index, biological yield, and thousand kernel weights were found to be significantly positively correlated. The number of kernels per row and the number of kernel rows per ear were found to positively and significantly correlate. Additionally, there was a substantial and positive correlation between the harvest index, thousand kernel weight, and biological yield and the number of kernels per row. Zeeshan et al. [35] found a substantial negative association between the number of kernels per row and the thousand kernel weight, which was not supported by the results for thousand kernel weight. There was a strong and positive correlation between thousand kernel weights and biological yield. Additionally, a strong and positive association between the harvest index and thousand kernel weights was discovered. Similar conclusion was documented by Zeeshan et al. [35] for connections between harvest index and thousand kernel weights. When one character is chosen for, the positive associations suggest positive responses in that character's levels, whilst the negative associations show the opposite [40]. Positive correlation coefficients between the desired features' genotype and phenotype in the current study were crucial in streamlining the selection process for gains, particularly in productivity.

3.6 Path Coefficient Analysis

By estimating the direct effects of traits that contribute to grain yield, separating the direct effect from the indirect effects through other related traits by partitioning the correlation coefficient, and determining the relative importance of various characters as selection criteria, path coefficient analysis was used to identify the important yield attributes. Furthermore, as shown in Tables 2 and 3, it was also estimated at the genotypic and phenotypic levels using grain yield as the dependent variable and the other attributes as the causative effects. The direct and indirect phenotypic impacts were, for the most part, somewhat larger in magnitude than the genotypic effects.

3.7 Genotypic Direct and Indirect Effects of Various Characters on Grain Yield

Harvest index (0.757) had the largest and most significant positive direct effects on grain yield, followed by biological yield (0.548). Additionally, days to tasseling, number of ears per plant, days to anthesis, plant height, and thousand kernel weights all showed beneficial direct benefits. A minimum positive direct influence by number of kernels per row (0.008) was exerted. Therefore, direct selection would be useful for increasing the genotypes' grain yield based on the previously described features. Sandeep Kumar et al. [37] also observed a high positive direct effect between harvest index and biological yield. In line with Venugopal et al.'s [41] findings regarding days to tasseling, but at odds with those of Mohan et al. [42] and Kumar and Singh [43], who found that days to tasseling had a negative direct impact on grain yield, plant height, thousand kernel weights [16], plant height [30], and number of kernels per row [44].

The number of ears per plot (-0.28) had the most significant direct negative impact on grain yield, followed by days to silking (-0.41). Significant positive correlations resulted from the positive indirect impacts of the number of kernel rows per ear, counterbalancing the negative direct influences of the days to silking and the number of ears per plot. Furthermore, there were adverse direct effects on grain yield from ear height, days to maturity, anthesis-silking interval, leaf area

index, and number of kernel rows per ear. This showed that in order to get high grain production, yield-related traits would be an effective indirect selection strategy. Days to tasseling, number of kernel rows per ear, harvest index, and biological yield were the positive indirect impacts that counterbalanced the negative direct influence of days to maturity, anthesis-silking interval, number of kernel rows per ear, and other features. In contrast to Pavan et al.'s findings [19], which indicated a strong positive direct effect on grain output, similar results were reported by Bello et al. [30] and RamReddy et al. (2012), who revealed that days to silking exhibited a large negative direct effect on grain yield. The thousand kernel weights and the number of ears per plot through the number of kernel rows per ear exhibited the maximum positive indirect influence on grain yield (8.79), which was followed by the days to tasseling through the number of kernel rows per ear (7.91). Its genotypic connection with thousand kernel weights and number of ears per plot was found positive and significant, however its correlation with days to tasseling was significant and negative. The number of kernel rows in each ear was also found to have a non-significantly positive connection. Regarding the number of kernel rows per ear and thousand kernel weights [45], the results were consistent with those reported by Pavan et al. [19].

The biological yield (-9.67) showed the greatest negative indirect effect, followed by the harvest index (-7.9) based on the number of kernel rows per ear. The degree to which variables exhibit a strong cause-and-effect relationship and are correlated with grain yield is determined by the residual factor. Due to their genetic composition, the variables that were present in the direct and indirect impacts were expressed as 90.1% of variation on grain yield, as indicated by the magnitude 9.9% [46].

3.8 Phenotypic Direct and Indirect Effects of Various Characters on Grain Yield

The number of ears per plot (2.762), days to silking (2.17), harvest index (0.819), anthesis-silking interval (0.585), biological yield (0.55), days to tasseling (0.42), and plant height (0.219) all had significant positive direct effects on grain output. This suggested that these features had a significant impact on increasing maize grain production. Additionally, the leaf area index and

thousand kernel weights showed a minimal positive direct influence.

On the other hand, days to anthesis with days to silking (2.10) and number of ears per plant with number of ears per plot (2.70) had the most beneficial indirect influence on grain output. Additionally, it showed a highly substantial positive and negative phenotypic connection with these features, respectively. In line with the findings of Sandeep Kumar et al. [37] for plant height, thousand kernel weights, and days to totasseling; however, in conflict with the findings for days to silking, the anthesis-silking interval, and the leaf area index, which were found to have a negative direct impact on grain output.

The number of ears per plant had the greatest direct negative impact on grain yield (-2.74), followed by the days to anthesis (-2.20). However, at the phenotypic level, there was a strong positive correlation between the number of ears per plant and grain yield.

Furthermore, there was a minimum negative direct effect on grain production for days to maturity, ear height, number of kernel rows per ear, and number of kernels per row. The days to maturity result was consistent with the findings of Sandeep Kumar et al. [37]. Days to anthesis, days to silking, and the number of ears per plot were used as positive indirect effects to offset the unfavorable direct effects of these features. High negative indirect influence on grain output was exhibited by number of ears per plot via number of ears per plant (-2.69) followed by days to silking through days to anthesis (-2.14). The remaining effects provide for a more detailed explanation of the way in which other potential components interact with grain production.

Its size of 14.2% indicated that, as a result of their physical expression, the features that were present in the route analysis were regarded as accounting for 85.8% of the variation in grain production. The study found that the harvest index, days to silking, number of ears per plant, and number of ears per plot at the genotypic and phenotypic levels, respectively, had the strongest positive and negative direct effects on their significant relationships with grain. Therefore, enhancing maize yields through direct selection for these grain yield components may be beneficial (Tables 2 and 3).

4. CONCLUSION

At both the genotypic and phenotypic levels, there was a strong and positive correlation between grain yield and the harvest index, thousand kernel weights, number of ears per plant, and number of kernels per row. Likewise, strong and favorable phenotypic correlations between grain production and biological yield, plant height, and number of ears per plot were noted. Nonetheless, grain output exhibited notably adverse correlations with floral characteristics both at the genotypic and phenotypic levels, suggesting the potential to enhance productivity by means of early selection in regions with brief rainfall cycles.

At the genotypic and phenotypic levels, the greatest beneficial direct effects on grain yield were observed in the harvest index and biological yield. Number of ears per plot was apply by the highest positive phenotypic direct impacts followed by days to silking, anthesis-silking interval, days to tasseling and plant height on grain yield. Conversely, days to anthesis and the number of ears per plant showed strong negative phenotypic direct effects on grain yield. The ears per plot, days to anthesis, and days to silking had the greatest beneficial indirect influence on grain yield. On the other hand, days to silking via days to anthesis, number of ears per plant, and number of ears per plot all had strong negative phenotypic indirect effects on grain yield. Therefore, these associations implied that yield components and flowering features were significant in the generation of better genotypes through selection in the intended environment.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of this manuscript.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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