

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

ABSTRACT

Association of traits between yield and yield components plays a great importance for the development of high yielding maize genotypes. The study included twenty-four open pollinated maize genotypes planted in a randomized complete block design at the main experimental station of Jigjiga Pastoral and Agricultural Research Center with the aim of establishing the association and direct and indirect effect of various components of characters on yield. Grain yield showed significantly positive phenotypic and genotypic correlations with its 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). However, significantly negative phenotypic relationship was observed between flowering traits and grain yield. Harvest index and biological yield also exerted maximum genotypic positive direct effects on the primary trait, while high genotypic negative direct effects were exerted by days to silking and number of ears per plot. Therefore, the combination of these traits along with yield could be used in indirect selection indices for the breeding by selection of potentially high yielding maize genotypes.

Keywords: Agronomic traits, correlation coefficient, open pollinated maize genotypes, path coefficient

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 (Nemati et al., 2009). Correlation evaluation between different traits in maize will supply vital information in breeding programs (Khodarahmpour and Hamidi, 2012).

In selecting high yielding genotypes correlation studies supply 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 attain better yield (Ali et al., 2010).

Understanding on the relationships 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 (Kumar et al., 2010) and path coefficient analysis helps partitioning the correlation coefficient into its direct and indirect effects (Ashofteh et al., 2011). Path coefficient analysis has been used successfully to illustrate interrelation between yield and other traits of maize (Khazaei et al., 2010). However, association between these traits and grain yield is vital, but computing of correlation coefficient alone does not specify the essence of relationship between traits (Vaeziet al., 2000). Blum et al. (1980) 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 (Thornsberry et al., 2001). Selection is the oldest method and its success in plant breeding largely depends upon many factors such as the association of various traits (Ilker, 2011). Hence, the objective of this investigation was to estimate the association of yield and yield-related traits in drought tolerant open pollinated maize genotypes at both genotypic and phenotypic level.

MATERIALS AND METHODS

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. For this study, the seeds of genotype were obtained from Melkasa Agricultural Research Centre. The seeds were planted at the main station of Jigjiga Pastoral and Agricultural Research Centre, Somali Regional State of Ethiopia during rainy season. The experiment was conducted in randomized complete block

design with three replications. The plot size was four rows with inter-row and intra-row spacing of 0.75 m and 0.25 m respectively with row length 5 m and plot size of 15 m².

Analysis of variance was carried out using SAS statistical software version 8.0 (1999-2000). Duncan's Multiple Range Test was used to separate the mean significant differences among the genotypes for all traits. Estimation of genotypic and phenotypic correlation coefficients was analyzed based on the procedure of Dabholkar (1992).

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

$$\text{Phenotypic correlation coefficient } (r_{p_{xy}}) = \frac{\sigma_{p_{xy}}}{\left[\sqrt{\sigma^2_{p_x} * \sigma^2_{p_y}} \right]}$$

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

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

$\sigma_{g_{xy}}$ = Genotypic covariance between characters x and y

$\sigma^2_{g_x}$ = Genotypic variance of character x

$\sigma^2_{g_y}$ = Genotypic variance of character y

$\sigma_{p_{xy}}$ = Phenotypic covariance of characters x and y

$\sigma^2_{p_x}$ = Phenotypic variance of character x

$\sigma^2_{p_y}$ = Phenotypic variance of character y

Phenotypic correlation coefficients were tested for significance using n-2 degree of freedom at 5% and 1% levels of significance, where n is the number of observation and r is the correlation coefficient, using t-test:

$$t = rp / SE(rp)$$

Where, rp = Phenotypic correlation; $SE(rp)$ = Standard error of phenotypic correlation obtained using the following formula (Sharma, 1998):

$$SE(rp) = \sqrt{(1 - r^2_p) / (n - 2)}$$

Where, n is the number of genotypes tested.

The coefficients of correlations at genotypic levels were tested for their significance by the formula described by Robertson (1959) as indicated below:

$$t = rg_{xy} / SErg_{xy}$$

Where, rg_{xy} = 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.

$$SE_{rgxy} = \sqrt{(1 - r_{gxy})^2 / 2h^2_x \cdot h^2_y}$$

Where, h^2_x = Heritability of trait x
 h^2_y = Heritability of trait y

The path coefficient analysis (direct and indirect effects of the independent variables on grain yield) was done using the formula of Dewey and Lu (1959) and with statistical package developed by Doshi (1991):

$$r_{ij} = P_{ij} + \sum r_{ik} P_{kj}$$

Where, r_{ij} = Association between the independent variable (i) and dependent variable (j) as measured by correlation coefficient, P_{ij} = Component of direct effect of the independent variable (i) on the dependent variable (j) as measured by path coefficient, $\sum r_{ik} P_{kj}$ = Summation of components of indirect effects of a given independent variable (i) on a given dependent variable (j) via all other independent variables.

The residual factor (P^2_R) was estimated as described in Dewey and Lu (1959):

$$P^2_R = 1 - \sum P_{ij} r_{ij}$$

Grain yield was used as the dependent character in separate path coefficient analysis and the remaining characters were used as independent variables as required.

RESULTS AND DISCUSSION

Association of characters

Knowledge about the nature and magnitude of associations among characters were mostly used to improve yield of the genotypes indirectly through utilization of other closely related traits with high heritability. Estimates of genotypic and phenotypic correlation coefficients between each couple of characters were studied and presented in Table 1. In most cases, the phenotypic correlation coefficients were less in magnitude than the genotypic correlation coefficients that revealed the presence of inherent genetic associations among various characters and less dependent on environment.

Correlation of grain yield with other characters

The highest genotypic and phenotypic correlation coefficients were recorded among grain yield and harvest index (0.84**) followed by grain yield with harvest index and thousand kernel weight (0.76**), respectively.

In genotypic association, grain yield showed highly significant and positive association with harvest index, thousand kernel weight, number of ears per plant and number of kernels per row that indicated possibility of indirect selection for grain yield by using these characters if their heritability is better than the primary trait in target environment. It was similarly reported for thousand kernel weight by Kumar et al. (2006), Nastasic et al. (2010) and Pavan et al. (2011), number of kernels per row by Sadek et al. (2006) and both thousand kernel weight and number of kernels per row by Ram Reddy et al. (2012).

Grain yield showed significant and positive correlation with number of ears per plot, biological yield, plant height, anthesis-silking interval and leaf area index. The results were in conformity with Alvi et al. (2003) for the correlation among grain yield and plant height, Aminu and Izge (2012) for the association of grain yield with number of ears per plot and anthesis-silking interval.

However, non-significant positive relationships were observed with ear height and number of kernel rows per ear. In contrast to Bocanski et al. (2009) for ear height and Mostafavi et al. (2011) for number of kernel rows per ear, these traits showed significant positive correlations with grain yield. Yousuf and Saleem (2003) also reported low negative correlations between grain yield and number of kernel rows per ear.

Grain yield had significant and negative correlation with days to tasselling, days to silking, days to anthesis and days to maturity at genotypic and phenotypic levels, indicating that selection for early tasselling, silking and maturities are desirable to increase grain yield in areas with short rainfall period. The results were in accordance with the findings of Netaji et al.

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 tasselling, 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: grainyield (kg/ha), HI: harvest index (%).

(2000), Pavan et al. (2011), Atnafua and Nageshwar (2014) and Lingaiah et al. (2014). However, it contradicted to Aminu and Izge (2012) who reported negative, non-significant association of grain yield with days to tasselling and days to silking at genotypic and phenotypic levels. At phenotypic level, grain yield showed highly significant and positive correlation with harvest index, thousand kernel weights, number

of kernels per row, number of ears per plant, number of ears per plot, biological yield and plant height. This indicated that selection based on these characters could be more efficient to maximize grain yield of maize. The results are in accordance with the findings of Shelake et al. (2005) for harvest index and biological yield; Gautam et al. (1999), Bello et al. (2010) and Lingaiah et al. (2014) for

plant height. However, it contradicted to the findings of Yousef (2012) who reported that grain yield association with plant height was not significant and positive; and Bocanski et al. (2009) for thousand kernel weight, number of kernels per row and plant height; Khayatnezhad et al. (2010) for thousand kernel weights and Yousef (2012) reported highly positive correlations with thousand kernel weight and number of kernels per row.

Grain yield showed significant and positive correlation with leaf area index, ear height and anthesis-silking interval. Similar findings were reported by Ali et al. (2010) for leaf area index and Bello et al. (2010) for ear height. It also displayed non-significant positive correlation with number of kernel rows per ear. Contrarily, with the results of Khayatnezhad et al. (2010) and Yousef (2012) suggested that number of kernel rows per ear was significantly correlated with grain yield.

Correlation among other traits

The highest association was revealed between number of ears per plant and number of ears per plot (0.99** and 0.98**) at genotypic and phenotypic levels as shown in Table 1. This showed the importance of these yield-related traits for increasing grain yield.

Genotypic correlation among traits

At genetic level, highly significant and positive correlations of days to tasselling with days to anthesis and days to silking were recorded. A positive and significant association was also observed between days to tasselling and days to maturity. The results were in line with the reports by Ram Reddy et al. (2012). However, it had highly significant and negative association with harvest index. It was also observed significant and negative association with anthesis-silking interval, number of ears per plot, number of ears per plant and thousand kernel weights.

Highly significant and positive correlations were found among days to anthesis and days to silking as much related as significantly between days to anthesis and days to maturity. Although, significant and negative association of days to anthesis with harvest index, thousand kernel weights, number of ears per plant and number of ears per plot were observed. Days to silking showed significant and positive association with days to maturity, in agreement with the

findings of Ram Reddy et al. (2012). However, it had negative and highly significant correlation with harvest index. It was also exhibited negative and significant relationship with thousand kernel weights, number of ears per plot and anthesis-silking interval. Anthesis-silking interval had significant positive association with harvest index and thousand kernel weight.

Leaf area index showed highly significant and positive correlation with plant height, ear height and biological yield. It had also significant association with number of ears per plot, number of ears per plant, number of kernel rows per ear and number of kernels per row. Contrarily, plant height exhibited positive and highly significant association with ear height and biological yield as related as significant with number of ears per plot, number of ears per plant and number of kernels per row. Similar findings were reported by Shabbir et al. (2007) and Yusuf (2010) for ear height and Ram Reddy et al. (2012) for ear height and number of kernels per row, reported significantly positive associations with plant height. Ear height had positive and significant relationship with number of ears per plot, number of kernels per row and biological yield, in line with the finding of Ram Reddy et al. (2012) for its correlation with number of kernels per row. Days to maturity also registered negative and significant association with number of ears per plot, number of ears per plant and harvest index.

Number of ears per plot also showed significant positive correlation with number of ears per plant, harvest index, thousand kernel weights and biological yield. Number of ears per plant had positive and significant association with biological yield, thousand kernel weights and harvest index. Similarly, number of kernels per row showed positive and significant correlation with biological yield, thousand kernel weights and harvest index in conformity with Ram Reddy et al. (2012) for its relationship with thousand kernel weights. Biological yield showed significant positive relationship with thousand kernel weights. A significant and positive association between thousand kernel weight and harvest index was also recorded.

Phenotypic correlation among traits

At phenotypic level (Table 1), plant height had positive and significant association with ear height, number of ears per plot, number of ears per plant, number of kernels per row, biological yield, thousand kernel weights and number of kernel rows per ear, but it showed significant and negative correlation with days to maturity. The results were in line with Alvi et al. (2003) for number of kernel rows per ear, Zeeshan et al. (2010) for biological yield and number of kernels per row, Tengan et al. (2012) for ear height and Sandeep kumar et al. (2011) for number of kernels per row and thousand kernel weights.

Correlation of days to tasselling with days to anthesis, days to silking and days to maturity were significantly positive, but it registered significant and negative relationships with the remaining characters. Similarly, Sandeep kumar et al. (2011) 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 result for number of kernel rows per ear was in line with Alvi et al. (2003) and Dana and Sherwan (2014).

Associations of days to anthesis with days to silking and days to maturity were significantly positive. Similar findings were reported by Ram Reddy et al. (2012). However, significant and negative correlations were observed with most of the characters excluding anthesis-silking interval, number of kernel rows per ear and harvest index. Significantly negative association of thousand kernel weights with days to anthesis was recorded by Zeeshan et al. (2010). Contrarily, Bello et al. (2010) and Zeeshan et al. (2010) reported significantly positive correlations of days to anthesis with plant height, ear height, number of kernel rows per ear and biological yield.

Days to silking had significant and positive correlation with days to maturity. It also showed significant and negative associations with most of the traits, but not significantly correlated with number of kernel rows per ear. The results were in conformity with Sandeep Kumar et al. (2011), who has reported that number of kernels per row, thousand kernel weights and days to maturity were significantly negative and positive associations with days to silking, respectively. Significantly positive correlation among anthesis-silking interval and thousand kernel weights was exhibited.

Table 2: Estimate of direct effect (bold face and diagonal) and indirect effects (off diagonal) at genotypic level in 24 openpollinated 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 tasselling, 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 (%)

Number of ears per plot showed significant and positive association with biological yield, number of ears per plant, number of kernels per row, thousand kernel weights and harvest index.

Leaf area index showed significant positive association with most of the traits. In harmony with the results of Ahsan (1999) and Sadek et al. (2006), who reported for plant and ear height while Sandeep kumar et al. (2011) has recorded for number of kernels per row, thousand kernel weights and number of kernel rows per ear. It also exhibited significant and negative relationship with days to maturity, but not significantly with harvest index. Days to maturity had significantly negative correlation with number of ears per plot, number of ears per plant, number of kernel rows per ear, number of kernels per row, biological yield and thousand kernel weights. Similarly, Ram Reddy *et al.* (2012), reported for number of kernel rows per ear, number of kernels per row and thousand kernel weights.

A significant positive association of number of ears per plant with number of kernels per row, biological yield, harvest index and thousand kernel weights was observed. Positive and significant correlation of number of kernel rows per ear was found with number of kernels per row. Number of kernels per row had also significant and

positive association with biological yield, thousand kernel weight and harvest index. The result for thousand kernel weight was not in line with Zeeshan et al. (2010), who reported that significant negative correlation with number of kernels per row. Biological yield had highly significant and positive association with thousand kernel weights. A positive and significant correlation among thousand kernel weights and harvest index was also found. Similar finding was recorded by Zeeshan et al. (2010) for relationships between harvest index and thousand kernel weights. The positive associations imply positive responses in the levels of one character when the other is selected for, while the negative associations indicate the reverse situation (Eleweanya et al., 2005). In the present study, genotypic and phenotypic positive correlation coefficients among the desired characters were important in facilitating the selection process for improvements especially in productivity.

Path coefficient analysis

Path coefficient analysis was performed to identify the important yield attributes by estimating the direct effects of traits contributing to grain yield and separating the direct effect from the indirect effects through other related traits by partitioning the correlation coefficient and finding out the relative importance of different characters as selection criteria. Moreover, it had also been estimated at genotypic and phenotypic levels by taking grain yield as dependent variable while the other traits as causal effects as presented in Tables 2 and 3, respectively. In most cases, the magnitudes of the phenotypic direct and indirect effects were slightly greater than the genotypic effects.

Genotypic direct and indirect effects of various characters on grain yield

High magnitude and maximum positive direct effects on grain yield was applied by harvest index (0.757) followed by biological yield (0.548). Moreover, positive direct effects were found for days to tasselling, number of ears per plant, days to anthesis, plant height, and thousand kernel weights. A minimum positive direct effect by number of kernels per row (0.008) was exerted. Hence, based on the aforementioned characters direct selection would be effective for enhancing the grain yield of the genotypes. Similarly, the high positive direct effect of harvest index and biological yield were reported by Sandeep Kumar et al. (2011). In agreement with the findings of days to tasselling by Venugopal et al. (2003), but contrary with the findings of Mohan et al. (2002) and Kumar and Singh (2004) who reported negative direct effect of days to tasselling on grain yield; plant height and thousand kernel weights (Kumar et al., 2006), plant height (Bello et al., 2010) and number of kernels per row (Raghu et al., 2011).

Days to silking (-0.41) exhibited high negative direct effect on grain yield followed by number of ears per plot (-0.28). For days to silking and number of ears per plot, their negative direct influences were counter balanced by the positive indirect effects through number of kernel rows per ear leading to significant positive correlations. Additionally, ear height, days to maturity, anthesis-silking interval, leaf area index and number of kernel rows per ear were having negatively direct effects on grain yield. This revealed that indirect selection *via* yield related traits would be effective for high grain yield. The negative direct influence of days to maturity, anthesis-silking interval, number of kernel rows per ear and the other traits were counter

balanced by the positive indirect effects *via* days to tasselling, number of kernel rows per ear, harvest index and biological yield, respectively. Similar result was reported by Bello et al. (2010) and Ram

Reddy et al. (2012), who suggested that days to silking exerted high negative direct effect on grain yield, but contradicted to Pavan et al. (2011) who reported high positive direct effect on grain yield. Maximum positive indirect effect on grain yield was shown by thousand kernel weights and number of ears per plot through number of kernel rows per ear (8.79) followed by the indirect effect of days to tasselling through number of kernel rows per ear (7.91). Its genotypic correlation with thousand kernel weights and number of ears per plot was found positive and significant, but its correlation with days to tasselling was significant and negative. A non-significantly positive correlation also observed with number of kernel rows per ear. The results were in accordance with Pavan et al. (2011) for number of kernel rows per ear and thousand kernel weights.

Maximum negative indirect effect was exhibited by biological yield (-9.67) followed by harvest index (-7.9) through number of kernel rows per ear. The residual factor determines the intense association of cause and effect among variables and their correlations with grain yield. The magnitude 9.9% indicated that the existed traits in the direct and indirect effects were expressed as 90.1% of variation on grain yield due to their genetic makeup.

Phenotypic direct and indirect effects of various characters on grain yield

High positive direct effects were exerted on grain yield by 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 tasselling (0.42) and plant height (0.219). This indicated that the contributions of these traits had great role for improvement of grain yield in maize. In addition, low positive direct effect was exhibited by thousand kernel weights and leaf area index.

However, maximum positive indirect effects on grain yield were exerted by number of ears per plant with number of ears per plot (2.70) followed by days to anthesis with days to silking (2.10). Moreover, its phenotypic correlation with these traits was highly significantly positive and negative, respectively. In conformity with the findings by Sandeep kumar et al. (2011) for days to tasselling, plant height and thousand kernel weights, but contradict with the results for days to silking, anthesis-silking interval and leaf area index that recorded a negative direct effects on grain yield.

Maximum negative direct effect on grain yield was exerted by number of ears per plant (-2.74) followed by days to anthesis (-2.20), but number of ears per plant had highly significant and positive association with grain yield at phenotypic level.

In addition, for days to maturity, ear height, number of kernel rows per ear and number of kernels per row were also apply minimum negative direct effect on grain yield. The result of days to maturity was in line with Sandeep kumar et al. (2011). The negative direct influences of these traits were counter balanced by the positive indirect effects *via* days to anthesis, days to silking and number of ears per plot. High negative indirect influence on grain yield was exerted 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 residual effects permit precise explanation about the pattern of interference of other possible components on grain yield.

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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 tasselling, 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 (%).

Its magnitude showed 14.2% revealed that the existed traits in the path analysis were considered as 85.8% of variation on grain yield due to their physical expression. In the present study, the maximum positive and negative direct effect of harvest index and days to silking, and number of ears per plot and number of ears per plant at genotypic and phenotypic level, respectively had the greatest impact for their significant associations with grain

yield. Hence, direct selection for these components of grain yield could be useful in improving yields in maize (Tables 2 and 3).

Conclusion

Grain yield association was highly significant and positive with harvest index, thousand kernel weights, number of ears per plant and number of kernels per row at both genotypic and

phenotypic levels. Similarly, highly significant and positive phenotypic associations of grain yield with biological yield, plant height and number of ears per plot were also observed. However, grain yield had significantly negative associations with flowering traits at genotypic and phenotypic level reflecting possibility of increasing productivity through selection for earliness in areas with short rainfall period.

Harvest index and biological yield had the highest positive direct effects on grain yield at both phenotypic and genotypic level. Number of ears per plot was applied by the maximum positive phenotypic direct effects followed by days to silking, anthesis-silking interval, days to tasselling and plant height on grain yield. On the other hand, high negative phenotypic direct effects on grain yield was observed by number of ears per plant followed by days to anthesis. The maximum positive indirect effects on grain yield were exerted by ears per plot followed by days to anthesis with days to silking. However, high negative phenotypic indirect effects on grain yield were exerted by number of ears per plot through number of ears per plant followed by days to silking via days to anthesis. Hence, these relationships suggested the important role of both yield components and flowering traits in development of improved genotypes through selection in target environment.

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