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

ABSTRACT

Association of traits between yield and yield components plays a great ~~importance~~ significance for the developmentof high yielding maize genotypes. The study included twenty-four open pollinated maize genotypesplanted in a randomized complete block design at the main experimental station of Jigjiga Pastoral andAgricultural Research Center with the aim of establishing the association and direct and indirect effectof various components of characters on yield. Grain yield showed significantly positive phenotypic andgenotypic 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, plantheight, leaf area index, anthesis-silking interval and ear height). However, significantly negativephenotypic relationship was observed between flowering traits and grain yield. Harvest index andbiological yield also exerted maximum genotypic positive direct effects on the primary trait, while highgenotypic 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 indicesfor the breeding by selection of potentially high yielding maize genotypes.

Comment [A1]: Study conducted at single or two locations??

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

INTRODUCTION

Comment [A2]: Add some points in introduction like, what is the actual benefit of correlation to bred new varieties

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~~ cansupply vital information in breeding programs (Khodarahmpour and Hamidi, 2012).

In selecting high yielding genotypes, correlation studies~~supply~~ providereliable 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~~ obtainbetter yield (Ali et al., 2010).

Understanding ~~on~~ the relationship~~s~~ of component traitssupports in determining which trait to select whenenhancement of the related complex trait is desired.Correlation of specific trait with other traits contributing tograin yield is crucial for indirect selection of genotypes forhigher grain yield (Kumar et al., 2010) and path coefficientanalysis helps partitioning the correlation coefficient intoits direct and indirect effects (Ashofteh et al., 2011). Pathcoefficient analysis has been used successfully toillustrate interrelation between yield and other traits of maize (Khazaei et al., 2010). However, associationbetween these traits and grain yield is vital, but~~computing~~ estimationof correlation coefficient alone does notspecify the essence of relationship between traits (Vaeziet al., 2000). Blum et al. (1980) stated that drought stresscauses reduction of genetic variance

and yield heritabilitywhich restrictsefficiency of selection for yield understress situation.

Comment [A3]: This sentence is irrelevant to ongoing discussion

Knowledge of the associations among lines would helpto identify a set of inbreds that have maximal diversity forthe analysis of the effects of genetic background. Use ofmaize inbreds in association analysis requires thatpopulation structure among lines be factored into theanalysis (Thornsberry et al., 2001). Selection is the oldestmethod and its success in plant breeding largely dependsupon many factors such as the association of varioustraits (Ilker, 2011). Hence, the objective of thisinvestigation was to estimate the association of yield andyield-related traits in drought tolerant open pollinatedmaize genotypes at both genotypic and phenotypic level.

Comment [A4]: How can different lines associate with each other?

MATERIALS AND METHODS

Experimental design and methods

The association of different yield components on sixteen traits oftwenty-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 thisstudy, the seeds of genotype were obtained from MelkasaAgricultural Research Centre. The seeds were planted at the mainstation of Jigjiga Pastoral and Agricultural Research Centre, SomaliRegional State of Ethiopia during rainy season. Theexperiment was conducted in randomized complete block

Comment [A5]: Rewrite this sentence, and give material in tabular form, with pedigree and source of this material

Comment [A6]: Mention year

designwith three replications. The plot size was four rows with inter-rowand intra-row spacing of 0.75 m and 0.25 m respectively with therow length 5 m and plot size of 15 m^2.

Analysis of variance was carried out using SAS statisticalsoftware version 8.0 (1999-2000). Duncan's Multiple Range Testwas used to separate the mean significant differences among thegenotypes for all traits. Estimation of genotypic and phenotypiccorrelation coefficients was analyzed based on the procedure ofDabholkar (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 correlationcoefficients between characters x and y

$r_{p_{xy}}$ =phenotypic correlation coefficients between ~~characters~~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

Phenotypic correlation coefficients were tested for significanceusing n-2 degree of freedom at 5% and 1% levels of significance,where n is the number of observation and r is the correlationcoefficient, 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):

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

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:

$$t = rgxy/SErgxy$$

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.

$$SErgxy = \sqrt{(1 - rgxy)2/2h2x.h2y}$$

Where, $h2x$ = Heritability of trait x
$h2y$ = 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):

$$rij = Pij + \Sigma rik\ Pkj$$

Where, rij = Association between the independent variable (i) and dependent variable (j) as measured by correlation coefficient, Pij = Component of direct effect of the independent variable (i) on the dependent variable (j) as measured by path coefficient, $\Sigma rik\ Pkj$ = 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):

$$P2R = 1 - \Sigma Pij\ rij$$

Grain yield was used as the dependent character inseparate path coefficient analysis and the remainingcharacters were used as independent variables asrequired.

RESULTS AND DISCUSSION

Comment [A7]: Where is ANOVA?

Association of characters

Knowledge about the nature and magnitude ofassociation~~s~~ among characters were mostly usedto improve yield of the genotypes indirectlythrough utilization of other closely related traitswith high heritability. Estimates of genotypic andphenotypic 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~~ influence of ~~on~~ environment.

Correlation ofgrain 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 showedhighly significant and positive association withharvest index, thousand kernel weight, number ofears per plant and number of kernels per row thatindicated possibility of indirect selection for grainyield by using these characters if their heritabilityis better than the primary trait in targetenvironment. It was similarly reported for thousandkernel weight by Kumar et al. (2006), Nastasic etal. (2010) and Pavan et al. (2011), number ofkernels per row by Sadek et al. (2006) andboththousand kernel weight and number of kernels perrow 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~~tasseling, days to silking, days to anthesis and days to maturity at genotypic and phenotypic levels, indicating that selection for early ~~tasselling~~tasseling, silking and maturities are desirable to increase grain yield in areas with short rainfall period. The results were in accordance with the findings ofNetaji 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 etal. (2014). However, it contradicted to Aminu and Izge(2012) who reported negative, non-significant associationof grain yield with days to ~~tasselling~~tasseling and days to silking atgenotypic and phenotypic levels. At phenotypic level,grain yield showed highly significant and positivecorrelation 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 characterscould be more efficient to maximize grain yield of maize.The results are in accordance with the findings ofShelake et al. (2005) for harvest index and biologicalyield; Gautam et al. (1999), Bello et al. (2010) andLingaiah et al. (2014) for plant height. However, itcontradicted to the findings of Yousef (2012) whoreported that grain yield association with plant height wasnot significant and positive; and Bocanski et al. (2009) forthousand kernel weight, number of kernels per row andplant height; Khayatnezhad et al. (2010) for thousandkernel weights and Yousef (2012) reported highly positivecorrelations with thousand kernel weight and number ofkernels per row.

Grain yield showed significant and positive correlationwith leaf area index, ear height and anthesis-silkinginterval. Similar findings were reported by Ali et al. (2010)for leaf area index and Bello et al. (2010) for ear height. Italso displayed non-significant positive correlation withnumber of kernel rows per ear. Contrarily, with the resultsof Khayatnezhad et al. (2010) and Yousef (2012)suggested that number of kernel rows per ear wassignificantly 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** and0.98**) at genotypic and phenotypic levels as shown inTable 1. This showed the importance of these yieldrelated traits for increasing grain yield.

Genotypic correlation among traits

At genetic level, highly significant andpositive correlationsof days to tasselling with days to anthesis and days tosilking were recorded. A positive and significantassociation was also observed between days totasselling and days to maturity. The results were in linewith the reports by Ram Reddy et al. (2012). However, ithad highly significant and negative association withharvest index. It was also observed significant andnegative association with anthesis-silking interval,number of ears per plot, number of ears per plant andthousand kernel weights.

Highly significant and positive correlations were foundamong days to anthesis and days to silking as muchrelated as significantly between days to anthesis anddays to maturity. Although, significant and negativeassociation of days to anthesis with harvest index,thousand kernel weights, number of ears per plant andnumber of ears per plot were observed. Days to silkingshowed significant and positive association with days tomaturity, in agreement with the

Comment [A8]: This reference is mentioned in many places in results and discussion but missing from reference section findings of Ram Reddy etal. (2012).However, it had negative and highly significantcorrelation with harvest index. It was also exhibitednegative and significant relationship with thousand kernelweights, number of ears per plot and anthesis-silkinginterval. Anthesis-silking interval had significant positiveassociation with harvestindex and thousand kernelweight.

Comment [A9]: This reference is mentioned in many places in results and discussion but missing from reference section

Leaf area index showed highly significant and positivecorrelation with plant height, ear height and biologicalyield. It had also significant association with number ofears per plot, number of ears per plant, number of kernelrows per ear and number of kernels per row. Contrarily,plant height exhibited positive and highly significantassociation with ear height and biological yield as relatedas significant with number of ears per plot, number ofears per plant and number of kernels per row. Similarfindings were reported by Shabbir et al. (2007) and Yusuf(2010) for ear height and Ram Reddy et al. (2012) for earheight and number of kernels per row, reportedsignificantly positive associations with plant height. Earheight had positive and significant relationship withnumber of ears per plot, number of kernels per row andbiological yield, in line with the finding of Ram Reddyetal. (2012) for its correlation with number of kernels perrow. Days to maturity also registered negative andsignificant 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, harvestindex, thousand kernel weights and biological yield. Number of ears per plant had positive and significantassociation with biological yield, thousand kernel weightsand harvest index. Similarly, number of kernels per rowshowed positive and significant correlation with biologicalyield, thousand kernel weights and harvest index inconformity with Ram Reddy et al. (2012) for itsrelationship with thousand kernel weights. Biological yieldshowed significant positive relationship with thousandkernel weights. A significant and positive associationbetween thousand kernel weight and harvest index wasalso recorded.

Comment [A10]: This is reference is used to support many traits but not mentioned in reference section, then how it is considered as valid referance

Phenotypic correlation among traits

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

Correlation of days to tasselling with days to anthesis,days to silking and days to maturity were significantlypositive, but it registered significant and negativerelationships with the remaining characters. Similarly,Sandeep kumar et al. (2011) reported that days to silkingand maturity were significantly positive, while significantlynegative associations of days to silking were observedwith anthesis-silking interval, number of kernel rows perear, number of kernels per row and thousand kernelweights.

Characters comprising number of kernels per row,biological yield, number of ears per plot, number of earsper plant, number of kernel rows per ear and thousandkernel weights were significantly and positively correlatedwith ear height, but it had negative and significantassociation with days to maturity. The result for numberof 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 anddays to maturity were significantly positive. Similarfindings were reported by Ram Reddy et al. (2012).However, significant and negative correlations wereobserved with most of the characters excluding anthesis-silkinginterval, number of kernel rows per ear andharvest index. Significantly negative association ofthousand kernel weights with days to anthesis wasrecorded by Zeeshan et al. (2010). Contrarily, Bello et al.(2010) and Zeeshan et al. (2010) reported significantlypositive correlations of days to anthesis with plant height,ear height, number of kernel rows per ear and biologicalyield.

Days to silking had significant and positive correlationwith days to maturity. It also showed significant andnegative associations with most of the traits, but notsignificantly correlated with number of kernel rows perear. The results were in conformity with Sandeep kumaret al. (2011), who has reported that number of kernelsper row, thousand kernel weights and days to maturitywere significantly negative and positive associations with days to silking, respectively. Significantly positivecorrelation among anthesis-silking interval and thousandkernel 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 biologicalyield, number of ears per plant, number of kernels perrow, thousand kernel weights and harvest index.

Leaf area index showed significant positive associationwith most of the traits. In harmony with the results ofAhsan (1999) and Sadek et al. (2006), who reported forplant and ear height while Sandeep kumar et al. (2011)has recorded for number ofkernels per row, thousandkernel weights andnumber of kernel rows per ear. It alsoexhibited significant and negative relationship with daysto maturity, but not significantly with harvest index. Daysto maturity had significantly negative correlation withnumber of ears per plot, number of ears per plant,number of kernel rows per ear, numberof kernels perrow, biological yield andthousand kernel weights.Similarly,Ram Reddy *et al.*(2012), reported for numberof kernelrows per ear, numberof kernels per row andthousand kernel weights.

A significant positive association of number of ears perplant with number of kernels per row, biological yield,harvest index and thousand kernel weights wasobserved. Positive and significant correlation of numberof kernel rows per ear was found with number of kernelsper row. Number of kernels per row had also significantand positive association with biological yield, thousandkernel weight and harvest index. The result for thousandkernel weight wasnot in line with Zeeshan et al. (2010),who reported that significant negative correlation withnumber of kernels per row. Biological yield had highlysignificant and positive association with thousand kernelweights. Apositive and significant correlation amongthousand kernel weights and harvest index was alsofound. Similar finding was recorded by Zeeshan et al.(2010) for relationships between harvest index andthousand kernel weights. The positive associations implypositive responses in thelevels of one character whenthe other is selected for, while the negative associationsindicate the reverse situation (Eleweanya et al., 2005). Inthe present study, genotypic and phenotypic positivecorrelation coefficients among the desired characterswere important in facilitating the selection process forimprovements especially in productivity.

Path coefficient analysis

Path coefficient analysis was performed toidentifythe important yield attributes by estimating thedirect effects of traits contributing to grain yieldand separating the direct effect from the indirecteffects through other related traits by partitioningthe correlation coefficient and finding out therelative importance of different characters asselection criteria. Moreover, it had also beenestimated at genotypic and phenotypic levels bytaking grain yield as dependent variable while theother traits as causal effects as presented in Tables 2 and 3, respectively. In most cases, themagnitudes of the phenotypic direct and indirecteffects were slightly greater than the genotypiceffects.

Genotypic direct and indirect effects ofvarious characters on grain yield

High magnitude and maximum positive directeffects on grain yield was apply by harvest index(0.757) followed by biological yield (0.548).Moreover, positive direct effects were found fordays to tasselling, number of ears per plant, daysto anthesis, plant height, and thousand kernelweights. A minimum positive direct effect bynumber of kernels per row (0.008) was exerted.Hence, based on the aforementioned charactersdirect selection would be effective for enhancingthe grain yield of the genotypes. Similarly, the high positive direct effect of harvest index andbiological yield were reported by Sandeep kumaret al. (2011). In agreement with the findings ofdays to tasselling by Venugopal et al. (2003), butcontrary with the findings of Mohan et al. (2002)and Kumar and Singh (2004) who reportednegative direct effect of days to tasselling on grainyield; plant height and thousand kernel weights(Kumar et al., 2006), plant height (Bello et al.,2010) and number of kernels per row (Raghu etal.,2011).

Days to silking (-0.41) exhibited high negativedirect effect on grain yield followed by number ofears per plot (-0.28).For days to silking and number of ears per plot, their negative directinfluences were counter balanced by the positiveindirect effects through number of kernel rows perear leading to significant positive correlations.Additionally, ear height, days to maturity,anthesis-silking interval, leaf area index andnumber of kernel rows per ear were havingnegatively direct effects on grain yield. Thisrevealed that indirect selection *via* yield relatedtraits would be effective for high grain yield. Thenegative direct influence of days to maturity,anthesis-silking interval, number of kernel rowsper ear and the other traits were counter balancedby the positive indirect effects *via* days totasselling, number of kernel rows per ear, harvest index and biological yield, respectively. Similarresult was reported by Bello et al. (2010) and Ram Reddy et al. (2012), who suggested that days tosilking exerted high negative direct effect on grainyield, but contradicted to Pavan et al. (2011) whoreported high positive direct effect on grain yield.Maximum positive indirect effect on grain yieldwas showed by thousand kernel weights andnumber of ears per plot through number of kernelrows per ear (8.79) followed by the indirect effectof days to tasselling through number of kernelrows per ear (7.91). Its genotypic correlation withthousand kernel weights and number of ears perplot was found positive and significant, but itscorrelation with days to tasselling was significant and negative. A non-significantly positivecorrelation also observed with number of kernelrows per ear. The results were in accordance withPavan et al. (2011) for number of kernel rows perear and thousand kernel weights.

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Maximum negative indirect effect was exhibitedby biological yield (-9.67) followed by harvestindex (-7.9) through number of kernel rows perear. The residual factor determines the intenseassociation of cause and effect among variablesand their correlations with grain yield. Themagnitude 9.9% indicated that the existed traits inthe direct and indirect effects were expressed as 90.1% of variation on grain yield due totheirgenetic makeup.

Phenotypic direct and indirect effects of variouscharacters on grain yield

High positive direct effects were exerted on grain yield bynumber 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 plantheight (0.219). This indicated that the contributions ofthese traits had great role for improvement of grain yieldin maize. In addition, low positive direct effect wasexhibited by thousand kernel weights and leaf area index.
However, maximum positive indirect effects on grain yieldwere exerted by number of ears per plant with number ofears per plot (2.70) followed by days to anthesis withdays to silking (2.10). Moreover, its phenotypiccorrelation with these traits was highly significantlypositive and negative, respectively. In conformity with thefindings by Sandeep kumar et al. (2011) for days to tasselling, plant height and thousand kernel weights, butcontradict with the results for days to silking, anthesis-silkinginterval and leaf area index that recorded asnegative direct effects on grain yield.

Maximum negative direct effect on grain yield wasexerted by number of ears per plant (-2.74) followed by days to anthesis (-2.20), but number of ears per plant hadhighly significant and positive association with grain yieldat 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 effectspermit precise explanation about the pattern ofinterference of other possible components on grain yield.

Table 3: Estimate of direct effect (bold face and diagonal) andindirect 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 (%).

Comment [A13]: In all the tables please keep the value with same digit.

Its magnitude showed 14.2% revealed that the existedtraits in the path analysis were considered as 85.8% ofvariation on grain yield due to their physical expression.In the present study, the maximum positive and negativedirect effect of harvest index and days to silking, andnumber of ears per plot and number of ears per plant atgenotypic and phenotypic level, respectively had thegreatest impact for their significant associations withgrain

yield. Hence, direct selection for thesecomponentsof grain yield could beuseful 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 ofears per plant and number of kernels per row at bothgenotypic and

phenotypic levels. Similarly, highlysignificant and positive phenotypic associations of grainyield with biological yield, plant height and number ofears per plot were also observed. However, grain yieldhad significantly negative associations with floweringtraits at genotypic and phenotypic level reflectingpossibility of increasing productivity through selection forearliness in areas with short rainfall period.

Harvest index and biological yield hadthe highestpositive direct effects on grain yield at both phenotypicand genotypic level. Number of ears per plot was applyby the maximum positive phenotypic direct effectsfollowed by days to silking, anthesis-silking interval, daysto tasselling andplant height on grain yield. On the otherhand, high negative phenotypic direct effects on grainyield was observed by number of ears per plant followedby days to anthesis. The maximum positive indirecteffects on grain yield were exerted by ears per plotfollowed by days to anthesis with days to silking.However, high negative phenotypic indirect effects ongrain yield were exerted by number of ears per plotthrough number of ears per plant followed by days tosilking *via*days to anthesis. Hence, these relationshipssuggested the important role of both yield componentsand flowering traits in development of improvedgenotypes through selection in target environment.

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Comment [A14]: References should be from recent years such as above 2020, so add references above 2020.

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