

## Genetic Variability, Heritability, Correlation and Path Coefficient Analysis for Grain Yield and Yield Component in Maize (*Zea mays* L.) Hybrids

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### Abstract

Knowledge of genetic variability, heritability and association existing between different traits determine the progress of selection in crop improvement programs. The objective of this study is to estimate genetic variability, heritability, correlations and path coefficients for grain yield and yield component traits of maize hybrids. 88 maize hybrids were evaluated in alpha-lattice design with two replications at Pawe Agricultural Research Center in North Western Ethiopia. Analysis of variance revealed highly significant differences among the genotypes for grain yield and yield related traits. The genotypic coefficient of variation ranged from 2.51% for days to maturity to 17.20% for gain yield while the phenotypic coefficient of variation ranged from 2.94% for days to maturity to 19.70% for gain yield. Very high heritability estimates were observed for days to 50% anthesis and silking. Moderately high heritability estimate value was recorded for grain yield. High heritability combined with high genetic advance was observed for grain yield indicates the dominance of additive gene action in governing the trait. Grain yield had a positive and significant phenotypic and genotypic correlation with days to maturity ( $r_g=0.78$ ,  $r_p=0.61$ ), ear length ( $r_g=0.71$ ,  $r_p=0.45$ ), number of kernels per row ( $r_g=0.67$ ,  $r_p=0.45$ ), plant height ( $r_g=0.65$ ,  $r_p=0.44$ ), 1000-kernel weight ( $r_g=0.63$ ,  $r_p=0.50$ ) and ear height ( $r_g=0.56$ ,  $r_p=0.37$ ). Path analysis model accounted for 87% of variation in grain yield has been explained through the independent variables. Days to 50% anthesis, number of kernel per row, ear diameter, ear height and days to maturity exert favorable direct effects on grain yield. Number of kernels per row, ear height, days to maturity, ear length and plant height could be used as target traits to improve maize grain yield because of their significant genotypic correlations with grain yield and favorable direct and indirect effects via the other yield attributing traits.

**Keywords:** Genetic variability; Heritability; Genetic advance; Correlation; Path coefficient analysis; Maize (*Zea mays* L.)

### Introduction

Maize (*Zea mays* L.) is the most important cereal food crop in Sub-Saharan Africa, particularly in Eastern and Southern Africa. Among the cereal crops, maize ranks second in area coverage and first in total annual production and productivity in Ethiopia [1]. Over the past 10 years, the area allocated, production and the productivity level of maize has been increased. Its production area has expanded from 1.398 million ha in 2004 [2] to 2.135 million ha in 2016 [1].

Similarly, total grain production and productivity of maize has increased from 2.394 million tons to 7.847 million tons and 1.7 to 3.7 t ha<sup>-1</sup>, respectively. However, maize production and productivity is still remains far below the world averages. Low yields of maize are attributed to limited availability and use of high yielding, disease and insect resistant varieties, moisture stress, high incidence of pests and diseases, use of traditional and unimproved cultural practices, poor soil fertility and changing rainfall patterns (climate change). Genetic improvement of maize provides an option to address some of these constraints through exploitation of the genetic variability present in maize germplasm.

The efficiency with which genotypic variability can be exploited by selection depends upon heritability and the genetic advance of individual traits [3]. Heritability estimates are useful for breeding quantitative traits because it permits to determine the most effective

selection strategy, breeding method to use in a breeding program and to predict gain from selection [4]. In addition to genetic variability and heritability estimate, knowledge of association (genotypic and phenotypic correlation) existing between different traits determine the progress of selection in crop improvement programs [5]. Moreover, Grain yield is a complex trait which is influenced by several component traits and direct selection for grain yield is often not effective. Grain yield improvement in maize is a stepwise and indirect process through the selection of yield component and secondary traits. Therefore, breeding gains or improvement in any of the yield component and secondary traits would be expected to contribute to final yield.

Secondary traits are the morpho-physiological traits that do not directly affect the yield but assist in the identification of the genotypes that can easily adapt with the stressed environment and indirectly affect the yield of the crop [6]. Phenotypic correlation ( $r_p$ ) involves both genetic and environmental effects. It can be directly observed from measurements of the two characters in a number of individuals in a population [7]. Genetic correlation ( $r_g$ ) is the association of breeding values (i.e., additive genetic variance) of the two characters [8]. Correlation estimates are useful in determining the components that influence a trait either positively or negatively. However, they do not provide exact information of the relative importance of direct and indirect effects of component traits on complex traits such as yield. Path analysis provides more information among variables than do correlation coefficients. Path coefficient analysis is a standardized partial regression coefficient that permits partitioning of correlation

coefficient into components of direct and indirect effects of various traits towards dependent variable [9]. The path coefficient analysis is used to partition the correlation coefficients of the grain yield attributing traits into direct and indirect effects on grain yield and to determine the degree of relationship between grain yield and its components. In path coefficient analysis, grain yield is considered as dependent variable and the remaining traits are considered as independent variables [10]. Thus, it is essential to study the association of yield components with yield and their direct and indirect effect on grain yield through path coefficient analysis. Therefore, the objective of the present investigation was to estimate of genetic variability, heritability, correlations and path coefficients for grain yield and yield component traits of maize hybrids.

## Materials and Methods

### Experimental site

The study was conducted during the main cropping season of 2010 at Pawe Agricultural Research Center in North Western Ethiopia. Pawe is located at 11°15'N and 36°05'E, with an elevation of 1050 meters above sea level. The mean annual rainfall is 1148.40 mm, and the mean minimum and maximum temperatures of the area are 17.06 and 31.47°C, respectively. The soil is nitosol with a pH ranging from 5.3-6.0.

### Experimental materials

The experiment comprised 88 maize hybrids including 86 testcrosses formed by crossing 43 elite inbred lines to two testers in line × tester mating design and two standard hybrid checks (BH-543 and Melkassa-2) (Table 1). The inbred lines were introduced from CIMMYT-Zimbabwe and were bred for resistance to various biotic and abiotic stresses of Africa. The most important stresses against which the inbred lines were selected include diseases (maize streak virus, grey leaf spot, leaf rust and turicum leaf blight, low nitrogen, high density and drought). The two testers used are single crosses of commercial CIMMYT inbred lines of known heterotic groups; viz. CML312/CML442 (tester A) and CML202/CML395 (tester B), which are commonly used by CIMMYT and many other national maize research programs in Africa. The lines × tester crosses were made during the main season of 2009.

### Experimental design and management

The experimental design for the field evaluation of the materials was 8 × 11 alpha-lattice design [11] with eight plots per an incomplete

block and 11 incomplete blocks in each replication. The experiment was planted in two replications. Each plot consisted of one row of 5 m long with 75 cm and 25 cm spacing between rows and plants, respectively. Two seeds were planted per hill to ensure uniform and enough stand and then thinned to one plant per hill. 100 kg/ha DAP and 50 kg/ha urea was applied at planting while 50 kg/ha urea was side dressed at knee height. Other crop management practices were applied following the recommendation of the location.

### Data collection and statistical analysis

Data were recorded to plant height (cm), ear height (cm), ear length (cm), ear diameter (mm), 1000-kernel weight (g), number of kernel per row and number of kernel rows per cob on 5 randomly selected plants, while the number of days to 50% anthesis (days), days to 50% silking (days), anthesis-silking interval (number of days between anthesis and silking dates) days to maturity (days) and grain yield (t/ha) were determined on whole plot basis.

Data was subjected to analysis of variance using agricolae package of R statistical software in RStudio [12,13], considering genotypes as fixed effects and replications and incomplete blocks within replications as random. Phenotypic, genotypic and environmental variances were computed from the respective mean squares following the procedures suggested by Allard [14]. The genotypic and phenotypic coefficients of variation were estimated according to the procedure outlined by Johnson et al. [15]. GCV and PCV values were categorized as low when less than 10%, moderate, 10-20% and high, greater than 20% as indicated by Deshmukh et al. [16]. Broad-sense heritability was estimated according to the procedure suggested by Singh and Chaudhary [17]. Heritability percentage was categorized as low when less than 40%, medium, 40-59%, moderately high, 60-79% and very high, 80% and above as indicated by Singh [18]. Genetic advance (GA) and genetic advance as percent of the mean (GAM), assuming selection of the superior 5% of the genotypes, were determined by the formula illustrated by Johnson et al. [15]. Multivariate restricted maximum likelihood (REML) estimation method was used to estimate phenotypic ( $r_p$ ) and genotypic correlations ( $r_g$ ) among pair of traits and their corresponding standard errors using PROC MIXED procedure of SAS 9.3 software [19,20]. Correlation estimates were considered significant when their 95% confidence intervals did not include zero [19]. The genetic correlation coefficients of all the traits were partitioned into direct and indirect effects by path coefficient analysis, using the Genes program [21] following the procedure Dewey and Lu [9].

S No	Pedigree
<b>Inbred lines</b>	
1	[[Ent320:92SEW2-77/[DMRESR-W]EarlySel-#I-2-4-B/CML386]-B-11-3-B-2-#B*4]
2	[INTA-F2-192-2-1-1-1-B*7-6-B]
3	[ZEWBc1F2-216-2-2-B-1-B]
4	[[SC/CML204//FR812]-X-30-2-3-2-1-BBB]
5	[ZEWAc1F2-219-4-3-B-1-B*5]

6	[[CML141/[CML141/CML395]F2-1sx]-4-2-1-B*6]
7	[[[Ent52:92SEW1-2/[DMRESR-W]EarlySel-#L-2-1-B/CML386]-B-22-1-B-4-#[[TIWD-EarlySelSynS1#-2-XX-2-B/[SW1SR/COMPE1-W]-126-2-1-B]-B-11-4-B-2-#]-B-2-B-1-B*5]
8	[Syn01E2-64-2-B-2-B]
9	[[INTA-2-1-3/INTA-60-1-2]-X-11-6-3-BBB]
10	[[[P501c2/[EV7992#/EV8449-SR]C1F2-334-1(OSU8i)-1-1-X-X-BB]-4-1-1-4-2-1-B/[K64R/G16SR]-39-1/[K64R/G16SR]-20-2]-5-1-2-B*4/CML390]-B-38-1-B-3-#]-B-7-B-1-B*6]
11	[PL15QPMc7-SR(BC0FS#)-balbreedbulk-31-1-4-4-2-B-3-B]
12	[DTPWC9-F104-5-6-1-1-B*4]
13	[[CLQRCWQ50/CLQRCWQ26]-B-47-BB]
14	[[NC348-BB/[Ent67:92SEW1-17/[DMRESR-W]EarlySel-#I-3-3-B/CML391]-B-31-B-3-#-2-B/[NAW5867/P30-SR//NAW5867]-84-1/[NAW/P30//NAW]-3-1]-6-2-2-1-3-B-3-B]-2-1-1-BBB]
15	[[INBRED-A/INBRED-B]-BBB-1-BBB]
16	[[CML395/CML444]-B-4-1-3-1-B/CML444/[TUXPSEQ]C1F2/P49-SR]F2-45-7-1-2-BBB]-2-1-2-2-B*5]
17	[[CML198/90323(B)-1-X-5-SN]-B-31-2-1-B*6]
18	[[CML199/[EV7992#/EV8449-SR]C1F2-334-1(OSU8i)-6-3-Sn]-B-23-2-2-B*8]
19	[[CML312/[TUXPSEQ]C1F2/P49-SR]F2-45-3-2-1-BB//INTA-F2-192-2-1-1-1-B*4]-1-5-1-1-1-B*7]
20	[[CML312/[TUXPSEQ]C1F2/P49-SR]F2-45-3-2-1-BB//INTA-F2-192-2-1-1-1-B*4]-1-5-1-1-2-B*6]
21	[[CML312/CML445/[TUXPSEQ]C1F2/P49-SR]F2-45-3-2-1-BBB]-1-2-1-1-1-B*5]
22	[[CML312/CML445/[TUXPSEQ]C1F2/P49-SR]F2-45-3-2-1-BBB]-1-2-1-1-2-B*5]
23	[[CML442/CML197/[TUXPSEQ]C1F2/P49-SR]F2-45-7-3-2-BBB]-2-1-1-1-1-B*4]
24	[[CML442/CML197/[TUXPSEQ]C1F2/P49-SR]F2-45-7-3-2-BBB]-2-1-1-2-1-B*4]
25	[[CML442/CML197/[TUXPSEQ]C1F2/P49-SR]F2-45-7-3-2-BBB]-2-1-1-2-3-B*5]
26	[[CML444/CML395//DTPWC8F31-1-1-2-2-BB]-4-2-2-2-1-B*4]
27	[[CML444/CML395//SC/ZM605#b-19-2-X]-1-2-X-1-1-B*6]-2-2-2-1-B*5]
28	[[LZ955355/LZ956441]-B-2-3-3-B-3-B*7]
29	[[SYN-USAB2/SYN-ELIB2]-12-1-1-1-B*4]
30	[[SYN-USB2/SYN-ELIB2]-81-1-1-1-B*6]
31	[[TS6C1F238-1-3-3-1-2-#-BB/[EV7992#/EV8449-SR]C1F2-334-1(OSU8i)-10-7(I)-X-X-X-2-BB-1]-1-1-2-1-1-B*6]
32	[CML312-B]
33	[CML442-B]
34	[CML443-B]
35	[CML489-B]
36	[MAS[206/312]-23-2-1-1-B*5]
37	[MAS[MSR/312]-117-2-2-1-B*4]
38	[P501SRc0-F2-4-2-1-1-BBB]
39	[P501SRc0-F2-47-3-1-1-BBB]
40	[Z97SYNGLS(B)-F2-188-2-1-2-B*6]

41	[ZM523A-16-2-1-1-B*4]
42	[ZM523B-29-2-1-1-B*4]
43	[ZM621A-10-1-1-1-2-B*6]
<b>Testers</b>	
1	CML312/CML442 (tester A)
2	CML202/CML395 (tester B)
<b>Standard Checks</b>	
1	BH543
2	Melkassa-2

**Table 1:** Pedigree of inbred lines, testers and checks used for the study.

## Results

### Analysis of variance

Means, ranges, coefficient of variation (CV) and mean squares of the 12 characters are presented in Table 2. The analysis of variance revealed highly significant ( $P < 0.01$ ) genotypic mean squares observed among the genotypes for all quantitative characters studied except anthesis-silking interval. Further genetic analysis was not done for anthesis-silking interval with non-significant genotypic mean square. The variation observed for grain yield ranged from 4.20 to 10.88 t/ha with a mean of 7.26 t/ha.

Traits	Range of Variation	Genotypic Mean Square (DF=67)	Mean	CV (%)	Error Mean Square (DF=87)	SE
AD	59.15-69.98	10.56**	65.47	1.6	1.1	0.79
SD	61.48-71.94	10.52**	67.65	1.7	1.29	0.83
ASI	1.43-3.53	0.22ns	2.18	25.4	0.31	0.4
DM	122-142	30.65**	132.96	2.2	8.3	2.11
PH	171.23-231.17	292.86**	204.54	4.2	72.9	7.18
EH	68.12-113.67	165.31**	89.71	8.6	59.36	6.32
EL	14.89-22.38	3.52**	17.77	6.1	1.17	0.86
ED	4.28-5.31	0.08**	4.83	2.9	0.02	0.11
KRE	11.60-15.20	1.15**	14	4.8	0.43	0.47
NKR	33.30-47.04	12.38**	40.16	5.1	4.1	1.52
TKWT	246.02-417.79	2874.70**	323.73	12.3	1583.3	32.74
GY	4.20-10.88	4.09**	7.26	13.6	0.97	0.83

**Table 2:** Analysis of variances for grain yield and yield components in maize. \*\*=Significant at  $P < 0.01$  level of probability, ns=Non significant,

DF=Degree of freedom, SE=Standard error of the mean, AD=days to 50% anthesis, SD=days to 50% silking, ASI=anthesis-silking interval, DM=days to maturity, PH=plant height, EH=ear height, EL=ear length, ED=ear diameter, KRE=number of kernel rows per ear, NKR=number of kernels per row, TKWT=1000- kernels weight, GY=grain yield.

### Genetic variability

Estimates of phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) and components of variances for the 11 traits are presented in Table 3. Genotypic variance was higher than the environmental variance at mean level for all traits studied except thousand kernel weight. GCV value ranged from 2.51% for days to maturity to 17.20% for gain yield, whereas PCV ranged from 2.94% for days to maturity to 19.70% for gain yield. Moderate PCV and GCV values were recorded for grain yield. While ear height and thousand kernel weight showed moderate PCV value only. On the other hand, low PCV and GCV values were recorded for days to 50% anthesis, days to 50% silking, days to maturity, plant height, ear diameter, ear length, number of kernel rows per cob and number of kernel per row.

### Heritability and genetic advance

Estimates of heritability in broad sense and genetic advance as percentage of means among hybrids are presented in Table 3. Days to 50% anthesis and days to 50% silking showed very high heritability estimate ( $>80\%$ ). Similarly, moderately high heritability values (60-79%) were recorded for days to maturity, grain yield, plant height, ear height, ear diameter, ear length, number of kernel rows per cob and number of kernel per row. On the other hand, medium broad sense heritability estimate (40-59%) was observed for thousand kernel weight. The estimated of genetic advance as percent of mean (GAM) in the present study was very high ( $>20\%$ ) only for grain yield. Moderate GAM values (10-20%) were recorded for ear height, ear length and thousand kernel weights. Traits such as days to 50% anthesis, days to 50% silking days to maturity, plant height, ear diameter, number of kernel rows per cob and number of kernel per row showed low GAM values ( $<10\%$ ).

Traits	Genotypic variance	Environmental variance	Phenotypic variance	GCV(%)	PCV (%)	H2(%)	GA	GAM (%)
AD	4.73	0.55	5.28	3.32	3.51	90	4.23	6.46
SD	4.615	0.645	5.26	3.18	3.39	88	4.14	6.12
DM	11.175	4.15	15.325	2.51	2.94	73	5.87	4.41
PH	109.98	36.45	146.43	5.13	5.92	75	18.69	9.14
EH	52.975	29.68	82.655	8.11	10.13	64	11.98	13.35
EL	1.175	0.585	1.76	6.1	7.47	67	1.82	10.25
ED	0.03	0.01	0.04	3.59	4.14	75	0.31	6.39
KRE	0.36	0.215	0.575	4.29	5.42	63	0.98	6.97
NKR	4.14	2.05	6.19	5.07	6.2	67	3.42	8.52
TKWT	645.7	791.65	1437.35	7.85	11.71	45	35.02	10.82
GY	1.56	0.485	2.045	17.2	19.7	76	2.24	30.89

**Table 3:** Estimates of genetic parameters for grain yield and yield components in maize. PCV: Phenotypic coefficient of variation, GCV: genotypic coefficient of variation, H<sup>2</sup>: broad sense heritability, GA: genetic advance, GAM: genetic advance as percent of mean.

### Estimates of genotypic and phenotypic correlations

Estimates of phenotypic and genotypic correlations grain yield and other yield-related traits are indicated in Table 4. Grain yield showed positive and significant phenotypic and genotypic correlations with days to maturity ( $r_g=0.78$ ,  $r_p=0.61$ ), ear length ( $r_g=0.71$ ,  $r_p=0.45$ ), number of kernels per row ( $r_g=0.67$ ,  $r_p=0.45$ ), plant height ( $r_g=0.65$ ,  $r_p=0.44$ ), 1000-kernel weight ( $r_g=0.63$ ,  $r_p=0.50$ ) and ear height ( $r_g=0.56$ ,  $r_p=0.37$ ). Number of kernels per row exhibited significant

and positive phenotypic and genotypic association with ear length ( $r_g=0.64$ ,  $r_p=0.67$ ) and with 1000-kernel weight ( $r_g=0.20$ ,  $r_p=0.23$ ). All agronomic traits, except number of kernel rows per cob, were significantly and positively correlated with plant height at genotypic level. Days to 50% anthesis and days to 50% silking exhibited positive significant genotypic correlation with days to maturity, plant height, ear height, ear length and number of kernels per row.

Traits	AD	SD	DM	PH	EH	EL	ED	KRE	NKR	TKWT	GY
AD	1.00	1.00 <sup>‡</sup> (0.004)	0.83 <sup>‡</sup> (0.09)	0.50 <sup>‡</sup> (0.04)	0.53 <sup>‡</sup> (0.13)	0.45 <sup>‡</sup> (0.13)	0.27 <sup>‡</sup> (0.13)	-0.16 (0.15)	0.34 <sup>‡</sup> (0.13)	0.51 <sup>‡</sup> (0.04)	0.25 (0.13)
SD	0.98 <sup>‡</sup> (0.004)	1.00	0.79 <sup>‡</sup> (0.07)	0.48 <sup>‡</sup> (0.11)	0.50 <sup>‡</sup> (0.13)	0.43 <sup>‡</sup> (0.13)	0.25 (0.13)	-0.13 (0.15)	0.32 <sup>‡</sup> (0.14)	0.32 (0.18)	0.22 (0.13)
DM	0.53 <sup>‡</sup> (0.06)	0.51 <sup>‡</sup> (0.07)	1.00	0.67 <sup>‡</sup> (0.11)	0.62 <sup>‡</sup> (0.13)	0.62 <sup>‡</sup> (0.12)	0.66 <sup>‡</sup> (0.12)	0.08 (0.18)	0.57 <sup>‡</sup> (0.13)	0.44 <sup>‡</sup> (0.14)	0.78 <sup>‡</sup> (0.08)
PH	0.36 <sup>‡</sup> (0.03)	0.35 <sup>‡</sup> (0.08)	0.43 <sup>‡</sup> (0.07)	1.00	0.85 <sup>‡</sup> (0.07)	0.56 <sup>‡</sup> (0.05)	0.77 <sup>‡</sup> (0.1)	0.27 (0.18)	0.38 <sup>‡</sup> (0.14)	0.65 <sup>‡</sup> (0.2)	0.65 <sup>‡</sup> (0.06)
EH	0.35 <sup>‡</sup> (0.08)	0.34 <sup>‡</sup> (0.08)	0.39 <sup>‡</sup> (0.07)	0.70 <sup>‡</sup> (0.05)	1.00	0.59 <sup>‡</sup> (0.14)	0.48 <sup>‡</sup> (0.14)	0.02 (0.2)	0.27 (0.17)	0.47 <sup>‡</sup> (0.22)	0.56 <sup>‡</sup> (0.13)
EL	0.24 <sup>‡</sup> (0.09)	0.22 <sup>‡</sup> (0.09)	0.43 <sup>‡</sup> (0.07)	0.47 <sup>‡</sup> (0.02)	0.38 <sup>‡</sup> (0.08)	1.00	0.39 (16.44)	0.11 (0.19)	0.64 <sup>‡</sup> (0.1)	0.61 (0.61)	0.71 <sup>‡</sup> (0.1)
ED	0.14 (0.09)	0.14 (0.09)	0.41 <sup>‡</sup> (0.08)	0.47 <sup>‡</sup> (0.03)	0.34 <sup>‡</sup> (0.08)	0.35 (8.25)	1.00	0.17 <sup>‡</sup> (0.08)	0.07 (0.16)	0.59 <sup>‡</sup> (0.17)	0.57 (2.37)
KRE	-0.06 (0.09)	-0.02 (0.09)	-0.05 (0.09)	0.06 (0.09)	0.09 (0.09)	-0.04 (0.09)	0.26 <sup>‡</sup> (0.08)	1.00	-0.15 (0.18)	-0.59 <sup>‡</sup> (0.21)	0.03 (0.17)
NKR	0.16 (0.09)	0.13 (0.09)	0.39 <sup>‡</sup> (0.08)	0.27 <sup>‡</sup> (0.08)	0.23 <sup>‡</sup> (0.08)	0.67 <sup>‡</sup> (0.05)	0.16 (0.09)	-0.13 (0.09)	1.00	0.20 <sup>‡</sup> (0.05)	0.67 <sup>‡</sup> (0.11)

TKWT	0.16 <sup>‡</sup> (0.01)	0.13 (0.08)	0.40 <sup>‡</sup> (0.05)	0.27 <sup>‡</sup> (0.08)	0.24 <sup>‡</sup> (0.08)	0.37 (0.19)	0.40 <sup>‡</sup> (0.07)	-0.31 <sup>‡</sup> (0.08)	0.23 <sup>‡</sup> (0.03)	1.00	0.63 <sup>‡</sup> (0.06)
GY	0.12 (0.09)	0.09 (0.09)	0.61 <sup>‡</sup> (0.06)	0.44 <sup>‡</sup> (0.02)	0.37 <sup>‡</sup> (0.08)	0.55 <sup>‡</sup> (0.06)	0.53 (1.16)	-0.01 (0.09)	0.45 <sup>‡</sup> (0.07)	0.50 <sup>‡</sup> (0.03)	1.00

**Table 4:** Estimates of genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients, and their standard errors (in parentheses) of 11 traits in maize genotypes. <sup>‡</sup>Correlation coefficient significantly different from zero, when |correlation| > 1.96 × SE.

### Genotypic path coefficient analysis

The genotypic direct and indirect effects of yield-related traits on grain yield are presented in Table 5. The coefficient of determination in the path analysis ( $R^2$ ) has presented magnitude 0.87. The highest positive direct effect on grain yield was recorded for days to 50% anthesis (1.92) followed by and number of kernel per row (0.59), ear diameter (0.52), ear height (0.51), days to maturity (0.28), number of kernel rows per cob (0.14) and ear length (0.05). On the other hand, negative direct effects on grain yield were found for days to 50% silking (-2.24), plant height (-0.53) and thousand kernel weight (-0.03). Days to 50% silking, plant height and 1000-kernel weight showed high positive indirect effect on grain yield via days to 50% anthesis.

### Discussion

Significant differences observed among the hybrids for grain yield and yield components observed from analysis of variance suggests the presence of substantial variation among the genotypes studied, which allows the selection of high yielding hybrids. Large ranges of values for grain yield and yield related traits also confirm the variability exists among the genotypes. Similar to the present finding, Matin et al. [22] reported significant genotypic differences for these traits in maize hybrids. Non-significant differences among genotypes for anthesis-silking interval disagree with the findings of Parajuli et al. [6]. The contrasts in this finding could be explained by the differences in genotype and test locations used.

Knowledge on the relative magnitude of genetic parameters is useful since it provides an opportunity to the plant breeder to utilize his skill and art in making useful selections from genetic variability present in germplasm. The estimated variance components observed in this study indicated that genotypic variance was higher than the environmental variance at mean level suggested the existence of genetic variability for all traits studied except thousand kernel weight. The presence of this variation among the genotypes provides an opportunity in the genetic improvement of the crop through selection and hybridization. The higher difference observed between phenotypic variance and genotypic variance for thousand kernel weight suggests that the phenotypic expression of this character was highly influenced by the environmental factors. In contrary to this result, Sessay et al. [23] reported a slight difference between phenotypic variance and genotypic variance for thousand kernel weight.

Grain yield showed moderate PCV and GCV values suggesting a good amount of variability among the hybrids for this trait. Hence selection to improve this character can be applied effectively. These results were in agreement with previous studies in maize [23-26]. While lower values of GCV for ear length, ear diameter, number of kernel rows per cob, number of kernel per row and thousand kernel weight indicate that the genotypes do not show much variation among themselves with respect to these characters and selection would not be

effective for these traits due to narrower genetic variability. The results of low GCV values recorded in this study were previously reported by different investigators on ear length, ear diameter, number of kernel rows per cob and number of kernel per row [27,28] and thousand kernel weight [26]. Similarly, low PCV and GCV values were observed for days to 50% anthesis, days to 50% silking, days to maturity and plant height. In line with the present study, low GCV and PCV values for days to 50% anthesis, days to 50% silking, days to maturity and plant height reported by Sesay et al. [23]. Phenotypic plasticity could be the possible reason for low GCV and PCV values for days to 50% anthesis, days to 50% silking and days to maturity. The magnitude of PCV in the present study was slightly higher than GCV for the traits studied indicating that there was little influence of environmental factors on phenotypic expression of these traits. This indicates that selection can be effective for these traits even at phenotypic level. The same results were found previously [29,30].

Heritability estimates are useful for breeding quantitative traits as it provides information on the extent to which a particular trait can be inherited to subsequent generations [31]. In the present study, the broad sense heritability estimates were very high for days to 50% anthesis and days to 50% silking. These results were in accordance with previous reports by Hefny [32] and Nzube et al. [25]. Similarly, days to maturity, grain yield, plant height, ear height, ear diameter, ear length, number of kernel rows per cob and number of kernel per row showed moderately high broad sense heritability estimates. Begum et al. [25] reported moderately high heritability for ear diameter, ear length, number of kernel per row and grain yield. Moderately high heritability estimate also found for ear height, plant height and number of kernel rows per cob [27]. High heritability value show high proportion of variation in a trait that is genetic and low influence of environment in expression of these traits, indicating improvement of the traits can be made based on phenotypic performance. On the other hand, medium broad sense heritability estimate (40-59%) was observed for thousand kernel weight. This result agrees with those obtained by Kharel et al. [33] and Nzube et al. [24].

Johnson et al. [15] suggested that heritability estimates combined with genetic advance would be more useful in predicting selection for superior genotypes than heritability estimates alone. In the present study, moderately high estimate of heritability and high GAM value was observed for grain yield. According to Panse [34], traits combining high heritability and genetic advance are predominantly controlled by additive gene action while high heritability coupled with low genetic advance indicates the non-additive gene effects in the inheritance of a particular trait. Hence, high estimates of heritability and GAM for grain yield in this study suggest the preponderance of additive gene effect in controlling the expression of the trait and improvement of this trait can be made through direct selection. Sesay et al. [23] reported moderately high heritability estimate combined with high values of GAM for grain yield in top-cross hybrids. High heritability estimate with low GAM observed for days to 50% anthesis, days to 50% silking,

days to maturity, plant height, ear diameter, number of kernel rows per cob and number of kernel per row suggested the presence of non-additive gene action in the expression of the traits that will make selection difficult for the improvement of these traits.

Grain yield showed positive and significant phenotypic and genotypic correlations with days to maturity, ear length, and number of kernels per row, plant height, 1000-kernel weight and ear height. This suggested that hybrids with taller plants, longer maturity periods and ear length and higher 1000-kernel weight and number of kernels per row were high yielders. Hence, these traits could be considered for indirect selection criteria to improve grain yield. These results are in consistent with earlier report of Reddy and Jabeen [29]. Similarly, Parajuli et al. [6] reported positive and significant association of grain yield with plant height and 1000-kernel weight. The correlation coefficients of the pairs of yield component traits showed the presence of significant and positive genotypic and phenotypic association of number of kernels per row with ear length and 1000-kernel weight indicating that increase in ear length and 1000-kernel weight will lead to simultaneous increase in number of kernels per row. These results agree with those obtained by Selvaraj and Nagarajan [35] and Bekele and Rao [36]. Number of kernel rows per ear revealed positive and significant genotypic and phenotypic association with ear diameter indicating the possibility of simultaneous improvement of number of kernel rows per ear and ear diameter. However, negative and significant genotypic and phenotypic association was observed between number of kernel rows per ear and 1000-kernel weight. Similar results were reported by Wannows et al. [37] and Kinfel et al. [38]. All agronomic traits, except number of kernel rows per cob, were significantly and positively correlated with plant height at genotypic

level, indicating that the selection of tall plants simultaneously promotes selection of other traits. These results corroborate those obtained by Varalakshmi et al. [39]. Days to 50% anthesis and days to 50% silking exhibited positive significant genotypic correlation with days to maturity, plant height, ear height, ear length and number of kernels per row. Selvaraj and Nagarajan [35] found that days to 50% anthesis and days to 50% silking were positive and significantly correlated with plant height, ear height, ear length and number of kernels per row. Similarly, significant and positive association of days to 50% anthesis and days to 50% silking with days to maturity is also reported by Patil et al. [40]. Significant positive association could be observed either due to the strong coupling linkage between the genes or as a result of pleiotropic effects of genes that controlled these characters in the same direction [41]. Generally, higher genotypic correlation coefficients than phenotypic correlation coefficients were observed for most of the traits. This suggests that the apparent associations might be largely due to inherent relationship among the traits.

The genotypic direct and indirect effects of yield-related traits on grain yield are presented in Table 5. Path coefficient analysis was used to provide further information on the nature of the interrelations among the various characters and their effects on grain yield. The coefficient of determination in the path analysis ( $R^2$ ) has presented magnitude 0.87, and it has indicated that the 87% variation in the dependent variable grain yield in the model has been explained through the independent variables. Days to 50% anthesis, number of kernel per row, ear diameter, ear height, days to maturity, number of kernel rows per cob and ear length had positive direct effects on grain yield.

Effect	AD	SD	DM	PH	EH	EL	ED	KRE	NKR	TKWT
Direct on GY	1.920	-2.240	0.280	-0.530	0.510	0.050	0.520	0.140	0.590	-0.030
Indirect via AD	-	1.923	1.596	0.962	1.019	0.865	0.519	-0.308	0.654	0.981
Indirect via SD	-2.242	-	-1.771	-1.076	-1.121	-0.964	-0.560	0.291	-0.717	-0.717
Indirect via DM	0.236	0.225	-	0.190	0.176	0.176	0.188	0.023	0.162	0.125
Indirect via PH	-0.265	-0.254	-0.355	-	-0.45	-0.297	-0.408	-0.143	-0.201	-0.344
Indirect via EH	0.269	0.254	0.315	0.431	-	0.299	0.244	0.010	0.137	0.239
Indirect via EL	0.021	0.020	0.029	0.027	0.028	-	0.019	0.005	0.030	0.029
Indirect via ED	0.141	0.130	0.344	0.401	0.250	0.203	-	0.089	0.036	0.307
Indirect via KRE	-0.022	-0.018	0.011	0.037	0.003	0.015	0.023	-	-0.020	-0.080
Indirect via NKR	0.202	0.190	0.339	0.226	0.161	0.381	0.042	-0.089	-	0.119
Indirect via TKWT	-0.014	-0.009	-0.012	-0.018	-0.013	-0.017	-0.016	0.016	-0.005	-
Total	0.25	0.22	0.78	0.65	0.56	0.71	0.57	0.03	0.67	0.63

**Table 5:** Path coefficient analysis showing direct and indirect effects of different characters on grain yield of maize. Coefficient of determination: 0.87; Residual variable effect: 0.37.

This indicates that more emphasis should be placed on genetic improvement of these traits to increase grain yield by indirect selection. In line with the present study, Sesay et al. [42] reported a positive direct influence of days to 50% anthesis, ear diameter, ear height, number of kernel rows per cob and ear length on grain yield of

top-cross maize hybrids. Similarly, Varalakshmi et al. [39] observed a direct positive effect of number of kernel per row and days to maturity on grain yield of single cross hybrids in maize. Negative direct effects on grain yield were found for days to 50% silking, plant height and thousand kernel weight, but these traits showed positive correlation

with grain yield. Kumar et al. [43] found similar results. The positive genotypic correlations of these traits with grain yield were due to the positive indirect effects of these traits through other traits. Days to 50% silking, plant height and 1000-kernel weight showed high positive indirect effect on grain yield via days to 50% anthesis. This indicates that selection for these traits would be effective and it could increase yield by influencing the days to 50% anthesis indirectly. Similar results were obtained by Sesay et al. [42].

## Conclusion

The present study revealed presence of genetic variability among the maize genotypes. Thus, there is an opportunity of exploiting the existing variability in maize improvement programs through selection and hybridization. Higher genotypic coefficient variation and broad sense heritability coupled with higher genetic advance observed for grain yield indicated the ease of direct phenotypic selection for the improvement of this trait. Moderately high to medium heritability with moderate estimates of genetic advance were observed for ear length, ear height 1000-kernel weight suggest the existence of intermediate additive and non-additive gene actions, indicating careful selection leads to improvement of these traits. Such traits may be good predictors of grain yield and can be used as index to select for grain yield improvement. Moderately high heritability estimate with low GA observed for most grain yield attributing traits suggest the presence of non-additive gene action in the expression of these traits and thus genetic improvement of these traits could be achieved through heterosis breeding. Number of kernels per row, ear height, days to maturity, ear length and plant height considered as the most important traits because of their highly significant genotypic and phenotypic correlations with grain yield. These traits also exerted favorable direct and indirect effects via the other traits. Therefore, these traits could be considered as important selection criteria for grain yield improvement in maize breeding program. However, further evaluation of these genotypes at more locations and over years is important to get reliable results.

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