

# Genetic Parameters, Trait Associations and Path Coefficient Analysis of Yield and its Component Traits for Hybrid Maize (*Zea mays* L.) Genotypes in Benishangul Gumuz Region at Pawe District, Western Ethiopia

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**Abstract:** Maize (*Zea mays* L.,  $2n=20$ ) is the first productive and sources of food in Benishangul Gumuz Regional State, mainly at Metekel zone. However striga weed, improved varieties and certified seed access are the major challenges. Therefore the objectives of this study were: to evaluate the agronomic performance of maize hybrids depend on different genetic parameters, genotypic and phenotypic coefficient of variation, heritability and genetic advance and estimate the genotypic and phenotypic association with direct and indirect effects through path analysis to identify the relative associations and contributions of traits. The experiment comprised 13 genotypes in RCBD with 3 replications in 2016. The ANOVA showed significant ( $P < 0.05$ ) to highly significant ( $P < 0.01$ ) differences. The highest grain yield ( $9.07 \text{ t ha}^{-1}$ ) was recorded for BH546 followed by BH 547 ( $9.05 \text{ t ha}^{-1}$ ). The PCV values for GLS, TLB, no.of cobs harvested and grain yield were moderate. The highest PCV and GCV values were recorded for ear height, plant and ear aspects while low PCV and GCV values recorded for days to 50% silking, days to 50 % anthesis and plant height exhibited the environmental effects on the expression of the traits are also lower. High heritability and GA recorded for plant and ear heights show the influence of environment on those traits is insignificant. Stand count at harvest exhibited significantly and positively associated at the genotypic and phenotypic levels with grain yield and positive direct effect. Breeders bounce attention for the enhancement of long and short duration variety development. Plant and ear heights negatively and non-significantly associated and directly influenced the grain yield at the genotypic and phenotypic levels indicate as extreme long, lodging will influence or extreme dwarf exposed to animals damage for yield loss. Generally BH546 and BH 547 varieties are recommended to the maize production.

**Keywords:** Correlation, GA, GCV, Genotypes, heritability, maize, path analysis and yield

## 1. INTRODUCTION

Maize (*Zea mays* L.,  $2n=20$ ) belongs to the family Poaceae and the tribe Maydae, it is one of the very important sources of food energy and income for small holder farmers in Sub-Saharan Africa (Mason and Smale, 2013). It is also the queen leading cultivated crop in terms of production volume per unit area and second in its area coverage next to tef among cereals in Ethiopia. Maize is obviously known that an exotic crop and introduced and spread in Africa around 1502 through Portuguese traders from Latin America (Miracle, 1965) and it was also introduced and domesticated in Ethiopia around the late 17<sup>th</sup> century (Huffnagel, 1961). It is the only amazing crop adaptable to wide agro ecologies since of its wide range of diversity. According to the CSA (2020) report, the national average maize productivity in Ethiopia was  $4.24 \text{ t ha}^{-1}$ . Similarly maize is also the first productive and stable food crop in Benishangul Gumuz Regional State with annual average productivity of  $4.23 \text{ t ha}^{-1}$ , mainly in Metekel zone it is the most productive among cereals with its productivity of  $4.32 \text{ t ha}^{-1}$ . Starting from the Tana Belles project till now maize is highly produced and served as stable food and a source of income for small holder farmers in different areas across Metekel zone (CSA, 2020; Damtie *et al.*, 2021).

However, sufficient production of maize is hindered in its low yields. Due to various biotic and abiotic factors mainly striga weed poor soil fertility, lack of well adapted improved varieties and absence of seed enterprise in the region and lack certified seed access are the major yield determinant factors for maize. Hence there is a need to increase the production and productivity of maize through various

techniques mostly breeding integrated with an agronomic practice has an indispensable role improving the production per unit area.

Bearing in mind the genetic variability exist in a given crop species for the traits in advancement is imperious for the achievement of every plant breeding program. The factors like genotypic and phenotypic coefficient of variations (PCV and GCV) are essential for identifying the amount of variability present in a given individual (Sesay *et al.*, 2016). The proficiency with which genotypic variability can be exploited via selection is contingent on heritability ( $h^2$ ) and the genetic advance (GA) of individual trait (Bilgin *et al.*, 2010). Genetic enhancement of crops for measurable traits needs reliable estimates of heritability to plan proficient breeding program (Akinwale *et al.*, 2011). Heritability delivers information on the level to which a specific morphogenetic trait can be transferred to consecutive generations (Bello *et al.*, 2012). Heritability together with large GA value is more valuable in expecting the result and has the impact in the choice of best genotypes for yield and its contributing traits (Singh *et al.*, 2011). The association estimated by the explicit coefficient is significant in plant breeding since it measures the degree of genotypic and phenotypic correlation between two or more traits, allowing the indirect selection. The association between traits, through correlation coefficients, is critical to the initial selection of inbred lines or variety or else the concurrent selection when more than one trait is preferred. The phenotypic and genotypic associations of the traits were intended as per the method stated by Al-Jibouri *et al.* (1958) while partitioning the association coefficients into direct and indirect effects at genotypic and phenotypic level were also ended through determining path coefficients via the system recommended by Wright (1921). Therefore the objectives of this study were: (i) to evaluate the agronomic performance of maize hybrids and identify, depend on different genetic parameters, genotypic and phenotypic coefficient of variation, heritability and genetic advance, and (ii) estimates the genotypic and phenotypic association with direct and indirect effects through path analysis, to identify the relative associations and contributions of different metric traits as selection criteria in high grain yield at each genotype.

## **2. MATERIALS AND METHODS**

The experiment was established in a randomized complete block design (RCBD) with three replications comprised of 13 maize hybrids (Table 3) maintained under rain fed conditions in the 2016 main season at Pawe Agricultural Research Center.

Each plot comprised two harvestable rows and one row at the initial and another one row at the end of each rep border rows. Each plot also contained 5.1m long rows, with spacing 0.75m between rows and 0.3m between plants. Two seeds per hill were sown and later thinned at knee height or four-leaves stage to make one healthy plant per hill. During the experiment, DAP and Urea fertilizers were used with recommended rate of 100kg ha<sup>-1</sup> DAP and 100kg ha<sup>-1</sup> of urea, but now the DAP is replaced by NPS. The DAP fertilizer was applied at planting, while Urea was used as a split application, half at planting and the remaining half after thinning at the knee height stage of the crop. All other agronomic practices were applied uniformly throughout the experimental plots as prescribed by the manufacturers. Data were recorded on the plot and plant bases for the following features: Days to 50% anthesis, Days to 50% silking, Plant and Ear height (cm), Gray leaf spot and Turicum leaf blight (1-5 scales), Stand count at harvest, Plant and Ear aspect (1-5 scales), Number of cobs, harvested per plot, Grain yield kg plot<sup>-1</sup> then converted to ton ha<sup>-1</sup> using the following yield conversion formula stated by CIMMYT (1988)

Grain yield  $\frac{\text{ton}}{\text{ha}} = \frac{\text{FW} \frac{\text{kg}}{\text{plot}} * (100 - \text{MC}) * (0.8 * 10000)}{1000 * \text{HPA} * (1000 - \text{DMP})}$ , where MC = moisture content at harvest in %, HPA = harvestable plot area, FW = field weight at harvest in kg per plot and DMP = Desired Moisture Percentage (15%).

Analysis of variance (ANOVA) was done using SAS software (9.4 versions) at 5% of significance probability level. The phenotypic (PCV) and genotypic (GCV) coefficients of variations were employed conforming to the recommended published method as per entries in Table 1. Broad sense heritability (H) was calculated as the percentage of the ratio of the genotypic variance to the phenotypic variance as defined by Allard (1960). Genotypic and phenotypic associations and their direct and indirect effect through path coefficient analysis were also detected.

**Table1.** Formulas used for estimating the phenotypic and genetic variance components

SN	Variance Components	Formula Used	References
1	Genotypic Variance ( $\sigma_g^2$ )	$\sigma_g^2 = \frac{MSg - MSe}{r}$	Allard (1960).
2	Phenotypic Variance ( $\sigma_p^2$ )	$\sigma_p^2 = \sigma_g^2 + \sigma_e^2$	Allard (1960).
3	Phenotypic Coefficient of Variation (PCV)	$PCV = \frac{\sqrt{\sigma_p^2}}{\mu} * 100$	Burton and De Vane (1953).
4	Genotypic Coefficient of Variation (GCV)	$GCV = \frac{\sqrt{\sigma_g^2}}{\mu} * 100$	Burton and De Vane (1953).
5	Broad Sense Heritability (H)	$H = \frac{\sigma_g^2}{\sigma_p^2} * 100$	Singh and Dash (2000).
6	Genetic Advance (GA)	$GA = \sigma_p * H * K$	Johnson <i>et al.</i> (1955).
7	Genetic Advances as % Mean (GAM)	$GAM = \frac{GA}{\mu} * 100$	Falconer (1996).

**NB:** k = selection differential value (k = 2.063 at 5% selection intensity),  $\sigma_p$  = phenotypic standard deviation, H = broad sense heritability and  $\mu$  = population mean in which selection will be employed.

## Results and Discussion

### Analysis of variance

The analysis of variance (ANOVA) results of measurable traits of evaluated genotypes are indicated in Table 2. The genotypes showed highly significant differences ( $P < 0.01$ ) in days to 50% anthesis, days to 50% silking, plant and ear heights and grain yield. Plant and ear aspects also indicated significant difference ( $P < 0.05$ ) while gray leaf spot, turcicum leaf blight, number of cobs harvested and stand count at harvest showed non-significant differences. Muchie and Fentie (2016); Ferdoush *et al.* (2017) also reported the presence of highly significant variation for days to 50% anthesis, days to 50% silking, plant and ear heights and grain yield.

As shown in Table 3, the mean grain yield ranged from 5.55 to 9.07 t ha<sup>-1</sup>. The highest grain yield (9.07 t ha<sup>-1</sup>) was recorded for BH546 maize hybrid followed by BH 547 (9.05 t ha<sup>-1</sup>); while the lowest (5.55 t ha<sup>-1</sup>) was recorded for CANDIDATE2. The highest mean days to 50% anthesis and days to 50% silking date (79.33 and 81.67 days), respectively, were recorded for CANDIDATE2. Similarly the highest mean plant and ear heights (264 cm and 147 cm), respectively, were measured for BH660 variety (Table 3). In general the ANOVA results revealed that there was substantial variation among evaluated maize genotypes.

**Table2.** Analysis of Variance (ANOVA) result for 11 traits of hybrid maize genotypes in the 2016 Main Production Season

**NB:** ns = non-significant, \*Significant at 5 percent level, \*\* significant at 1 percent level and \*\*\* significant at 0.1 percent level.

SN.	Traits	Mean squares		
		Replications (Df = 2)	Treatments (Df = 12)	Error (Df = 24)
1.	Days to 50% anthesis	10.79	15.60***	1.88
2.	Days to 50 % silk emergence	6.64	17.12***	1.61
3.	Plant height (cm)	390.49	651.06***	103.40
4.	Ear height (cm)	115.87	487.94***	72.87
5.	Gray leaf spot (1-5)	0.79	0.188ns	0.15
6.	Turcicum leaf blight (1-5)	0.54	0.19ns	0.15
7.	Stand count at harvest	2.64	4.53ns	3.92
8.	Plant aspect (1-5)	0.10	0.78*	0.29
9.	Ear aspect (1-5)	0.54	0.59*	0.23
10.	Number of cobs harvested	116.85	41.36ns	24.59
11.	Grain Yield (t/ha)	5.33	4.81***	0.89

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**Table 3.** Mean Performance Values and Comparisons among 13 Maize hybrids with their yield and yield attributed traits Evaluated in 2016 Main Season.

SN	Genotypes	Days to 50% anthesis	Days to 50% silking date	Plant height (cm)	Ear height (cm)	Gray leaf spot (1-5)	Turcicum leaf blight (1-5)	Stand count at harvest	Plant aspect (1-5)	Ear aspect (1-5)	Number of cobs harvested	Grain yield (t/ha)
1.	BH-140	73.00	75.67	229.00	121.67	2.00	2.00	30.67	1.67	1.33	31.67	6.31
2.	BH-540	71.67	74.33	230.67	112.67	1.67	2.00	32.00	1.67	1.33	32.00	6.25
3.	BH-543	72.00	74.67	225.67	117.33	1.67	2.00	28.67	1.33	1.67	39.67	7.12
4.	BHQPY-545	73.67	76.00	234.67	114.00	1.67	1.67	31.67	2.00	2.00	42.00	8.29
5.	BH-546	71.67	75.00	242.33	117.67	1.33	1.33	32.00	1.00	1.00	34.33	9.07
6.	BH-547	72.33	74.67	224.33	122.67	1.67	1.67	31.33	1.00	1.00	33.67	9.05
7.	BHQP-548	75.67	79.00	210.33	98.00	2.00	2.00	31.33	1.67	1.33	36.00	6.36
8.	BH-661	76.33	79.67	258.00	140.33	1.67	1.67	28.67	2.00	1.67	30.33	5.91
9.	BH-660	75.67	79.00	264.00	147.00	1.67	2.00	30.67	3.00	2.33	28.33	5.71
10.	SPHR2	73.67	76.33	241.33	122.00	1.67	1.67	30.67	1.33	1.33	33.33	6.65
11.	SBHR1	74.33	77.33	235.33	115.33	2.00	1.67	31.33	1.67	1.00	33.00	6.95
12.	CANDIDAT E1	72.00	74.33	218.33	107.00	2.00	1.33	32.33	1.67	1.00	32.33	8.61
13.	CANDIDAT E2	79.33	81.67	235.67	115.00	1.33	2.00	29.33	1.67	2.00	31.33	5.55
	<b>Mean</b>	<b>73.95</b>	<b>76.74</b>	<b>234.59</b>	<b>119.28</b>	<b>1.72</b>	<b>1.77</b>	<b>30.82</b>	<b>1.67</b>	<b>1.46</b>	<b>33.69</b>	<b>7.07</b>
	<b>R- value</b>	<b>0.82</b>	<b>0.85</b>	<b>0.78</b>	<b>0.78</b>	<b>0.44</b>	<b>0.48</b>	<b>0.39</b>	<b>0.57</b>	<b>0.59</b>	<b>0.55</b>	<b>0.76</b>
	<b>CV (%)</b>	<b>1.85</b>	<b>1.66</b>	<b>4.33</b>	<b>7.16</b>	<b>24.95</b>	<b>21.86</b>	<b>6.42</b>	<b>32.70</b>	<b>33.02</b>	<b>14.72</b>	<b>13.41</b>
	<b>LSD (at 5%)</b>	<b>2.30***</b>	<b>2.14**</b>	<b>17.14**</b>	<b>14.39***</b>	<b>0.72</b>	<b>0.65</b>	<b>3.34</b>	<b>0.92*</b>	<b>0.81*</b>	<b>8.36</b>	<b>1.59**</b>

**Phenotypic and Genotypic Variation**

The PCV was parted into GCV and environmental variance to estimate the involvement of the individual variance to the entire variation. However, the PCV values were larger than the GCV values for the whole traits, indicating that the effects of environmental factors is significant on these traits as shown in Table 4. Comparable results were reported by Bello *et al.* (2012), Begum *et al.* (2016), and Ferdoush *et al.* (2017). The PCV value for ear height (75.37) was higher than all the rest, whereas PCV values for ear aspect (40.48) and plant aspect (40.40) followed second. This indicated that for these traits, the phenotypic variation among the genotypes is high (Muchie and Fentie, 2016). Different previous studies had also recorded similar PCV results for ear aspect, number of cobs harvested and grain yield in maize (Ghimire and Timsina, 2014; Neupane. *et al.*, 2020). The PCV values of GLS (23.04), TLB (22.84), number of cobs harvested (16.31) and grain yield (t ha<sup>-1</sup>) (20.98) were medium. This shows that the phenotypic variance between maize hybrids with these traits is moderate. This outcome is partially consistent with the result of Ferdoush *et al.* (2017). Days to 50% anthesis, days to 50% silking and plant height (cm) had low PCV values, which indicates the environmental effect on the expression of those traits is lower; and selection based on those traits will be effective for considerable genetic enhancement. This result is also in line with the finding stated by Muchie and Fentie (2016) and Ferdoush *et al.* (2017). The GCV detects the genetic variability within a trait. The GCV values for days to 50% anthesis, days to 50% silking, plant height (cm), GLS, TLB, stand count at harvest and number of cobs harvested were low. Medium GCV values were also receded for grain yield (t ha<sup>-1</sup>), and plant and ear aspects (1-5 scale). While the highest GCV value was recorded for ear height (61 cm). Similar evaluations have been stated for days to 50% anthesis and days to 50% silking by Muchie and Fentie, (2016) and Ferdoush *et al.* (2017).

Heritability estimates have remarkable impact for the breeder, and its value shows the precision with which a genotype could be predicted via its phenotypic expression. The heritability value was characterized as low if less than 20%, medium if 20% - 39%, and high if ≥ 40% as recommended by Adhikari *et al.* (2018). Days to 50% silking (76.25%), days to 50% anthesis (70.87%), ear height

(65.5%), plant height (63.84%) and grain yield (59.48%) were high heritable traits. This shows that the traits under study are less influenced in their expression by the environment. Related results were reported by Neupane *et al.* (2020) for days to 50% silking, days to 50% anthesis and grain yield in maize hybrids. Ear height (65.5%) and grain yield (59.48%) were shown to have high heritability, and also with moderately high GCV and PCV values (Table 4). High heritability with high GAM of these traits indicated the influence of environment on those traits is insignificant or very low. Hence, selection could be proficient on the heart of phenotypic appearance of these traits in every plant by applying selection techniques. This result, in line with high heritability value, was verified for ear height and grain yield as stated by Bello *et al.* (2012), and also days to 50% anthesis and days to 50% silking consistent with Neupane *et al.*(2020). However, the heritability value alone cannot indicate the expression of those traits because it is exactly the genetic effect; while heritability together with genetic advance shows a high genetic gain, and is efficiently used for identifying higher genotypes.

**Genetic advance and genetic advance as percent of mean**

High genetic advance (GA) values were recorded for plant height (22.27) and ear height (19.64) while the Genetic advance as the percentage of mean (GAM) value was highest for plant aspect (30.03) followed by ear aspect (28.63) and grain yield (25.74). The GAM was moderate for ear height (16.46) while low GAM vales were recorded for plant height (9.49), number of cobs harvested (6.23), days to 50% silking. (5.34), days to 50% anthesis (5.02), TLB (3.85), GLS (2.02) and stand count at harvest (0.67) as shown in Table 4. The results show control of non-additive gene action on those traits, indicating that heterosis breeding could be valuable for crop advancement. Comparable results were accessible for maize in days to 50% silking and days to 50% anthesis reported by Jilo *et al.* (2018). Hence a GAM expression indicates that most likely the heritability is due to additive gene effects; and for these traits, selection could be real at initial generations.

**Table4.** Variance Components of Mean Grain yield and other related Traits in 2016 Main Season at Pawe Agricultural Research Center

**NB:**  $\sigma_p^2$ = phenotypic variance,  $\sigma_g^2$  = genotypic variance,  $\sigma_e^2$ = environmental variance, PCV = Phenotypic coefficient of variation, GCV = Genotypic Coefficient of variation, H = heritability, GA = genetic advance and GAM = genetic advance as the percentage of mean

SN.	Traits	Means	Range	$\sigma_p^2$	$\sigma_g^2$	$\sigma_e^2$	PCV (%)	GCV (%)	H (%)	GA	GAM (%)
1.	Days to 50% anthesis (DA)	73.95	71.67-79.33	6.45	4.57	1.88	3.44	2.89	70.87	3.71	5.02
2.	Days to 50 % silk emergence (DS)	76.74	74.33-81.67	6.78	5.17	1.61	3.39	2.96	76.25	4.10	5.34
3.	Plant height (cm) (PH)	234.59	210.33-264	285.95	182.55	103.4	7.21	5.76	63.84	22.27	9.49
4.	Ear height (cm) (EH)	19.28	98.00-147.00	211.23	138.36	72.87	75.37	61.00	65.50	19.64	16.46
5.	Gray leaf spot (1-5) (GLS)	1.72	1.33-2.00	0.16	0.01	0.15	23.04	4.75	4.26	0.03	2.02
6.	Turcicum leaf blight (1-5) (TLB)	1.77	1.33-2.00	0.16	0.01	0.15	22.84	6.53	8.16	0.07	3.85
7.	Stand count at harvest (SCH)	30.82	28.67-32.33	4.12	0.20	3.92	6.59	1.46	4.93	0.21	0.67
8.	Plant aspect (1-5) (PA)	1.67	1.00-3.00	0.45	0.16	0.29	40.40	24.25	36.03	0.50	30.03

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9.	Ear aspect (1-5) (EA)	1.46	1.00-2.33	0.35	0.12	0.23	40.48	23.70	34.29	0.42	28.63
10.	Number of cobs harvested (NCH)	33.69	28.33-42.00	30.18	5.59	24.59	16.31	7.02	18.52	2.10	6.23
11.	Grain Yield (t ha <sup>-1</sup> )	7.07	5.55-9.07	2.20	1.31	0.89	20.98	16.18	59.48	1.82	25.74

**Correlation Co-efficient**

The correlation value represents the nature and extent of association present among pairs of traits. Correlation is also a degree to which traits to be measured are related to increased yield. The genotypic correlation coefficient is heritable and indicates the relationship between two variables while phenotypic association includes both the phenotypic and environmental effects. However significant phenotypic association without significant genotypic correlation has no value. As shown in Table 5, Days to 50% anthesis exhibited significant positive association both at the genotypic (G) and phenotypic (ph) levels with days to 50% silking (Gr = 0.98 and phr = 0.96), plant height with ear height (Gr = 0.89 and phr= 0.77), Plant aspect with ear aspect (Gr = 0.74 and phr = 0.46) and stand count at harvest with grain yield (Gr = 0.56 and phr = 0.47) positively and significantly associated at the genotypic and phenotypic levels respectively. While TLB was negative and significantly associated with the grain yield both at the genotypic and phenotypic levels (Gr = -0.76 and phr = -0.37), days to 50% anthesis with grain yield (Gr = -0.66 and phr = -0.53) and days to 50% silking with grain yield (Gr = -0.69 and phr = -0.56) significantly associated in Table 5. Our results are in line with the conclusions from the findings of Abdelmula and Sabiel (2007) and Khan *et al.* (2011). The findings reported by Mhoswa *et al.* (2016) revealed that days to anthesis, and days to silking exhibited negative association with the grain yield. However, the results were non-significant for the negative correlations of plant and ear heights with the grain yield, both at the genotypic and phenotypic level and this is similar with the finding of Sadaiah *et al.* (2013). This correlation can be used as a basis for trait selection if a similar study is done, and is accompanied in the analysis with extra morphological traits. The negative association among yield and days to 50% silking is very important to the breeder to classify early and late maturing genotypes.

**Path Coefficient Analysis**

The path coefficient analysis has been included at the final point to recognize the imperative yield contributors via estimating the direct effects of contributing traits to yield and identifying the direct from the indirect effects. Over other associated traits through partitioning the correlation coefficient and verdict the virtual prominence of various traits as selection norms. Hence, path coefficient analyses were used to obtain additional evidence on the interrelationships between traits and their influences on grain yield as indicated in Table 6.

**Table5.** Estimates of Genotypic correlations (above diagonal) and phenotypic correlations (below diagonal) among the variables studied of 13 maize hybrids

Traits	DA	DS	PH	EH	GLS	TLB	SC H	PA	EA	NCH	Yield
DA		0.98** *	0.33	0.22	- 0.21	0.38	- 0.52	0.45	0.59*	-0.33	-0.66*
DS	0.96** *		0.39	0.27	- 0.19	0.37	- 0.51	0.49	0.57*	-0.36	- 0.69** *
PH	0.2	0.25		0.89** *	- 0.45	-0.03	- 0.34	0.55	0.53	-0.46	-0.35
EH	0.17	0.22	0.77** *		- 0.28	0.09	- 0.45	0.52	0.48	-0.51	-0.31
GLS	0.01	-0.04	-0.26	-0.19		0.06	0.27	0.16	-0.34	-0.002	-0.05
TLB	0.16	0.16	-0.09	-0.13	0.06		- 0.45	0.36	0.54	-0.07	- 0.76** *

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<b>SCH</b>	-0.24	-0.28	-0.14	-0.19	-	-		-0.13	-0.49	0.07	0.56*
<b>PA</b>	0.29	0.33*	0.27	0.35*	0.03	0	0.17		0.74** *	-0.34	-0.56*
<b>EA</b>	0.34*	0.38*	0.48** *	0.45** *	-	0.12	-	0.46** *		-0.002	-0.55*
<b>NCH</b>	-0.09	-0.19	-0.34*	-0.24	0.00 6	0.04	0.05	-0.14	-0.04		0.46
<b>Yield</b>	-	-	-0.28	-0.19	-0.2	-	0.36 *	-0.24	-0.38*	0.47** *	
	0.53** *	0.56** *				0.37*					

Where: DA = days to 50% of the plot anthesis and pollen shading, DS = days to 50% of the plot silk emergence, PH = plant height (cm), EH = ear height (cm), GLS = gray leaf spot (1-5 scale), TLB = turcicum leaf spot (1-5 scale), SCH = stand count at harvest, PA = plant aspect (1-5 scale), EA = ear aspect (1-5 scale), NCH = number of cobs harvested per plot and Yield = grain yield (t ha<sup>-1</sup>)

**Genotypic Path Coefficient Analysis**

As shown in Table 6, stand count at harvest showed the highest moderate positive direct effect on the grain yield (pc = 0.2755) and ear aspect (pc = 0.439), days to 50% anthesis (pc = 0.0521) while turcicum leaf blight (TLB) showed high negative direct effect on grain yield (pc = -0.5698), days to 50% silking (pc = -0.4085), plant aspect (pc = -0.465). Bello *et al.* (2010) reported that days to 50% silking has high negative direct effect on grain yield. Plant and ear aspects, number of plants at harvest and turcicum leaf blight also indicate a negative direct effect on the grain yield. This is in agreement with an earlier report by Mhosw *et al.* (2016). It is also shown that plant aspect had the highest moderate indirect positive effect on the grain yield by ear aspect (p = 0.3251); while most other traits showed low to moderate negative indirect effect on the grain yield (Table 6). Generally the direct negative effects that were credited to days to 50% silking, days to 50% anthesis, plant and ear aspect, number of plants at harvest and turcicum leaf blight indicate that those traits highly influence the grain yield and could be considered by the breeders during selection for further breeding strategies and yield improvement.

Table 6. Direct (underlined and bold) and indirect effects of different traits in 13 maize hybrids at Pawe Agricultural Research Center in 2016 Main Season

Traits	DA	DS	TLB	SCH	PA	EA	gr
<b>DA</b>	<u><b>0.0521</b></u>	-0.4023	-0.2182	-0.142	-0.2115	0.25714	<b>-0.6649</b>
<b>Ds</b>	0.05131	<u><b>-0.4085</b></u>	-0.2124	-0.1411	-0.2268	0.24964	<b>-0.6878</b>
<b>TLB</b>	0.01995	-0.1523	<u><b>-0.5698</b></u>	-0.123	-0.169	0.23735	<b>-0.7569</b>
<b>SCH</b>	-0.0269	0.20916	0.25449	<u><b>0.2755</b></u>	0.06195	-0.2192	<b>0.555</b>
<b>PA</b>	0.02368	-0.199	-0.207	-0.0367	<u><b>-0.4654</b></u>	0.3251	<b>-0.5593</b>
<b>EA</b>	0.03053	-0.2324	-0.3083	-0.1377	-0.3449	<u><b>0.43873</b></u>	<u><b>-0.554</b></u>

Where: DA = days to 50% anthesis (pollen shading), DS = days to 50% silking, TLB = turcicum leaf blight (1-5 scale), PA = plant aspect (1-5 scale), EA = ear aspect (1-5 scale).

**3. CONCLUSIONS AND RECOMMENDATION**

The analysis of variance results of most measurable traits of genotypes showed significant to highly significant differences, which revealed the existence of substantial variations among the genotypes. The PCV values for GLS, TLB, number of cobs harvested and grain yield were moderate, and indicated the phenotypic variance between maize hybrids with these traits is low.

The highest PCV and GCV values were recorded for ear height, and plant and ear aspects; while low PCV and GCV values recorded for days to 50% silking, days to 50% anthesis and plant height showed

the environmental effects on the expression of the traits are also lower. High heritability with high genetic advance values were recorded for plant and ear heights, which implies the traits under study shows that the influence of environment on those traits is insignificant or very low. Moreover, it indicates this has a high genetic gain and can be efficiently used for identifying high genotypes while other most traits are highly influenced by the environment. Stand count at harvest was significantly and positively associated both at the genotypic and phenotypic levels with the grain yield, and also had a positive direct effect on the grain yield; which specifies that as the plant population increased, the grain yield also increased if the soil fertility can afford the nutrient for the crop. By contrast, turicum leaf blight, days to 50% anthesis and silking were negatively and significantly associated with the grain yield with high negative direct effects on the yield. So the breeders bounce for the enhancement of long and short duration variety development with disease tolerance. However it is non-significant both plant and ear heights negatively associated and directly influenced with the grain yield both at the genotypic and phenotypic levels indicate as the plant and ear height extreme large, lodging will influence or dwarf exposed to wild animals and dog causing for yield loss. Path coefficient analyses were used to attain additional evidence on the interrelationships between traits and their influences on the grain yield.

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## Genetic Parameters, Trait Associations and Path Coefficient Analysis of Yield and its Component Traits for Hybrid Maize (*Zea mays L.*) Genotypes in Benishangul Gumuz Region at Pawe District, Western Ethiopia

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