



RESEARCH ARTICLE

Genetic variability, heritability, trait associations and path coefficient analysis of maize (*Zea mays* L.) inbred lines

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ABSTRACT

In Ethiopia, maize (*Zea mays* L.) ranks second in productivity, but first for production area. However, biotic and abiotic elements influence its growth and output. Lack of adaptable maize varieties or inbred lines is another major issue. As a result, this study sought to analyse genetic variability, heritability, as well as their link to grain yield and direct and indirect effects using route coefficient analysis. The experiment used 23 inbred lines with RCB design and 3 replications at Pawe Agricultural Research Center. The results showed substantial (P0.01) differences in yield and yield-related parameters between inbred lines. Plant height, ear height, and grain yield all showed moderate to high genotypic coefficients of variation, heritability, and genetic progress. Plant height, ear height, and number of ears all showed favourable phenotypic and genotypic correlations with grain yield. Conversely, days to 50% anthesis and silk emergence, plant and ear features exhibited negative genotypic and phenotypic correlations with grain yield. A7033 (8.3 t ha⁻¹), CML197 (6 t ha⁻¹) and CML202 (5.5 t ha⁻¹) had the highest grain yields and could be used in foreign crop maize enhancement initiatives.

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INTRODUCTION

Maize is the first most vital cereal share in productivity and the second in its production area coverage next to *tef*, in Ethiopia (Abate et al., 2015). It is mainly used as a staple food crop, but it's also an essential industrial raw material in different parts of the country. It is also a versatile and stable food crop in Benishangul Gumuz Regional State next to sorghum and first in its production per unit area (Yaregal and Firew, 2018). In the region, maize is highly produced at Metekel, Kamashi and Assosa zones, including Maokomo special district with 4t⁻¹ha productivity (CSA, 2018). It has a substantial role in the food security and used to prepare injera; "kita", porridge (genfo) and to make local alcoholic drink likes "tella" and "Borde". The crop has distinctive value in the producers and its stalk and its straw after harvesting has several meanings in the local community comparable for animal fodder. However, the potential of maize grain yield significantly affected by biotic and abiotic factors. *Striga hermontica* is the major problem among biotic constraints in the region mainly at Metekel zone while stalk and root lodging are the second main problem among abiotic factors mostly at Pawe District.

Genetic information is mainly found as genetic variation involving individuals and populations. A cram of various characters primarily related to yield is very considerable for breeders to desire prospect crossing materials through selection traits to commence in a breeding program. Various studies showed that different primary and secondary yield-related traits such as expected means, phenotypic and genotypic variances, and heritability are incredibly critical to identify the best-inbred lines to improve the grain yield efficiency breeding. For example, PVC and GCV are required to detect the presence and quantity of variability in a trait. The efficiency of selection to reduce inbred line variability depends on heritability and genetic advance (GA) of each feature (Sesay et al., 2018).

Heritability provides data on how much a specific morphogenetic trait can be passed down to offspring (Bello et al., 2012). Heritability and high GA could

potentially be more helpful in selecting prospective inbred lines. When more than one feature is sought, studying the correlation coefficients between characters is critical to the initial selection of plants, or instantaneous assortment. That's why indirect selection uses fewer multipart variables with good heritability and natural assessment. This could lead to advanced genetic improvement balancing direct selection. Generally, the study sought to achieve the following goals: Identify genotypic and phenotypic connections between significant qualities of maize inbred lines.

MATERIALS AND METHODS

The experiment used 23 inbred lines from the Ethiopian national maize development programme at Bako. It was laid out in an RCBD with three replications. Planting was done with 0.75m between rows and 0.25m between plants. Each plot has two 5m rows. Each row included 21 stations, with two seeds planted at each, and trimmed two weeks later. This assumes 53,333 plants per hectare. The blanket advised 100 kg NPS and 150 kg urea per hectare. It was applied during plating, and urea was applied after thinning but before flowering. Similarly, all agronomic practises were followed.

Plot and plant base data were obtained. Insect pest damage, disease and pest days to anthesis and silking were measured plot-based. Plant height, ear height, and other data were obtained from plants. The grain yield was determined for each inbred line using the harvest field weight per plot in kg ha⁻¹ using the CIMMYT technique (1988).

The data were analysed using Genstat 18th edition (Goedhart and Thissen, 2010). To compare means, we used a fisher protected least significant difference (LSD) of 5%. The heritability and genetic progress were also computed using the methods of Burton and De Vane (1953), Singh and Chaudhary (1985), and Johnson et al. (1955). The phenotypic and genotypic

association between two variables was calculated using Singh and Chaudhary's formula (1985). The route coefficient analysis was conducted using Dewey and Lu's (1959) approach and Doshi's (1991) statistical package to identify the most influential attribute on grain yield.

RESULT AND DISCUSSION

These differences were found in the number of plants per plot, number of ears and grain yield (Table 1). The results revealed significant diversity among the evaluated inbred lines. Muchie and Fentie's prior investigations showed similar outcomes (2016). CML334 and CML204 had the lowest at 2.71 and 2.72 t ha⁻¹.

Number of ears per plot by itself may not significantly contribute to increasing the grain yield, but the number of ears with its ear size. The present study confirmed this inspiration, for instance, the inbred line KUBA/GUDAC1½ has 62 ears and provided a grain yield of 4.3 t ha⁻¹, whereas an inbred line A7033 has 50 ears but offered 8.3 t ha⁻¹ (Table 1). This result also agreed with the investigation of Mehdi *et al.* (2001) and Taimur *et al.* (2011) attained a smaller amount of coefficient of variation for several traits in maize and conferring to Singh and Chaudhry (1997), 10% or less CV are acceptable for selection of traits in improving the program for the population. Days to 50% pollen shedding for maize hybrids ranged from 62 to 76 (Table 1).

The maximum days to pollen shedding (76 days) were obtained from 142-1-e, and CML334 inbred lines while the minimum 50% pollen shading day (62 days) was recorded from 124b (113) inbred line. Similarly, the maximum days to 50% silk emerging (80 days) was obtained from CML204, and BKL001 inbred lines, whereas the minimum (65 days) was from inbreeding line 124b (113).

The maximum anthesis silking interval (ASI) (7 days) were recorded from inbreeding lines 124-b (109) and F-7215 while the minimum (1 day) was from A7033 and KUBA/GUDAC1½ inbred lines. This study suggested that ASI between 1-7 days is very successful and compatible with male to female in

crossing. Hence A7033 and CML197 were found the promising inbred lines which can be used as better female parents for seed production. Therefore, the variance result analysis exhibited the existence of a substantial extent of variation among the evaluated inbred lines. The association of disease mainly TLB and CLR with the grain yield revealed significantly and negatively affects each inbred lines, primarily BKL001, CML165 and KUBA/GUDAC1½.

The PCV, GCV, and GA levels were previously reported by Sesay *et al.* (2016). For all characters studied, phenotypic variance outperformed genotypic variance (Table 3). The PCV values for days to 50% anthesis and silk appearing were low (10%), while plant height, plant aspect, and number of plants harvested in a plot were medium (10-20%), and grain yield was high (>20%).

The highest PCV was for ear height (37.5%), followed by grain yield (34.9 percent). The upper features indicate moderate to high phenotypic diversity in the examined inbred lines. A similar outcome was pragmatic (Bello *et al.*, 2012; Muchie and Fentie, 2016; Ferdoush *et al.*, 2017). It shows the studied inbred lines had considerable phenotypic diversity on these traits.

The GCV value detects the genetic variability within a trait. Therefore, the GCV values of ear aspect, DA, DS and number of plants in a harvest plot were low. Plant and, plant and ear aspect, and number of ears harvested in a plot were medium. In contrast, higher GCV value was obtained for grain yield (Table 3). The present investigation was revealed similar outcomes like El-Nagouli *et al.* (1983) and Taimur *et al.* (2011) who confirmed that yield was openly influenced by ear height. Ferdoush *et al.* (2017) also reported that lower GCV values were recorded for DA and medium for EH. This pronouncement is also agreed to some extent with the exploration of Muchie and Fentie (2016).

The breeder understood heritability because it describes the precision with which an inbred line can be conventional via phenotypic expression. Moderate heritability was found in traits including grain yield

and plant height, along with significant GCV and PCV, and genetic progress as a percentage of mean values. That these features have the highest potential heritability due to additive gene effects suggests trait selection in the initial generations (Table 2).

The moderate heritability indicated how environmental pressure influenced certain features. Thus, selection can be made between these features' phenotypic expression in distinct plants using simple selection approaches. Bello et al. (2012) and Ferdoush et al (2017). The percentage of mean heritability will be proficiently shared with genetic progress via recognising the key pressure for identifying better parent of inbred lines, according to Muchie and Fentie (2016).

The association study indicates the nature and level of the relationship presented among couples of traits. Correlation is also determined that point to characters to be considered to enhance the yield. However, the genotypic and phenotypic association of days to 50% pollen shedding and silking, plant and ear aspect with grain yield is negative and significant. Plant height is positive and significantly associated with ear height both at the genotypic and phenotypic level ($r_g = 0.86$ and $r_p = 0.8$). In contrast, plant and are negatively and significantly associated with CLR and TLB at the genotypic and phenotypic level, whereas the remaining traits are not significant.

In general, in this investigation grain yield ($t\ ha^{-1}$) showed some involvement explained positive and highly significant correlation with PH, EH, NE and NP. In contrast, DA and DS, TLB and CLR indicated negative and strong significant association at the genotypic and phenotypic level (Table 3). This result is similar to the previous investigation of Taimur et al. (2011), Mhoswa et al. (2016) and Ferdoush et al. (2017). Therefore, this association can be applied as a benchmark for trait selection if a comparative study is accomplished in the prospect through extra morphological characters.

As indicated in Table 4, the path analysis model's strength of mind (R^2) coefficient was 0.77, indicating that the causal table's factors explained 77% of the variation in the dependent variable grain yield. Days to 50% silk emergence ($p_c = -0.5382$) had the most significant negative direct effect on grain yield, although plant height ($p_c = 0.18$), ear height ($p_c = 0.296$), and number of ears harvested ($p_c = 0.22$) exhibited positive significant effects. Days to 50% silk emergence, plant and ear height also influenced grain yield and number of harvested ears (Table 4).

The continuation of these traits displays the connection coefficient with grain yield. Plant height also had the strongest indirect beneficial influence on grain yield via ear weight ($p_c = 0.25$). Other elements could have influenced grain yield, however. Days until blooming, plant and ear height, and the number of ears harvested each plot are crucial traits to consider when selecting for high production.

Days to 50% silk emerging ($p_c = -0.36$) had also the highest significant negative direct effect followed by turicum leaf blight ($p_c = -0.25$) on the grain yield while ear height ($p_c = 0.26$), number of ears harvested in a plot ($p_c = 0.21$), number of plots at harvest ($p_c = 0.13$) and plant height ($p_c = 0.05$) had moderate to the medium significant positive effect on the grain yield (Table 5).

Consequently, the character NE, PH, EH and NP, which have high association with most, morphological characters, are preferable for selection since of the point of the reserve in time and employment in the measurements and its precision.

Table 1. Mean performance of 23 maize inbred lines for different agronomic traits Evaluated at Pawe Agricultural Research Center in 2019 main season.

No.	Pedigree	DA	DS	EA	PA	EH	PH	NP	NE	Yield (t ha ⁻¹)
1.	124b (113)	61.67 ^k	65.00 ^g	1.83 ^{gh}	2.67 ^{b-d}	81.67 ^{e-i}	185.00 ^{d-h}	41.00 ^f	34.67 ^{d-f}	4.85 ^{b-d}
2.	142-1-e	75.67 ^{ab}	79.33 ^a	3.17 ^{ab}	3.00 ^{ac}	146.67 ^a	256.70 ^a	40.33 ^f	36.67 ^{d-f}	4.25 ^{b-f}
3.	A7033	64.67 ^{ij}	66.00 ^g	2.00 ^{f-h}	2.33 ^{de}	128.33 ^{ab}	228.30 ^{a-c}	39.67 ^{ef}	49.67 ^{bc}	8.26 ^a
4.	BKL002	70.67 ^{ef}	73.00 ^{de}	2.50 ^{c-f}	2.83 ^{a-d}	75.00 ^{f-j}	158.30 ^{g-i}	39.00 ^{d-f}	35.33 ^{d-f}	4.04 ^{c-f}
5.	BKL001	74.67 ^{a-c}	80.33 ^a	2.67 ^{b-e}	3.00 ^{a-c}	90.00 ^{d-h}	188.30 ^{d-h}	38.67 ^{c-f}	40.00 ^{c-f}	3.72 ^{c-f}
6.	BKL003	68.67 ^{f-h}	73.67 ^{de}	2.33 ^{d-g}	2.50 ^{c-e}	90.00 ^{d-h}	161.70 ^{f-i}	36.67 ^{b-f}	36.00 ^{d-f}	3.85 ^{c-f}
7.	BKL004	73.33 ^{b-d}	76.00 ^c	2.67 ^{b-e}	2.667 ^{b-d}	71.67 ^{g-i}	171.70 ^{e-i}	37.00 ^{b-f}	37.67 ^{d-f}	3.76 ^{c-f}
8.	CML161	71.00 ^{d-f}	73.67 ^{de}	2.83 ^{a-d}	2.50 ^{c-e}	63.33 ^{ij}	153.30 ^{hi}	33.67 ^{bc}	45.67 ^{b-d}	4.54 ^{b-f}
9.	CML165	73.00 ^{c-e}	76.33 ^{bc}	3.33 ^a	2.50 ^{c-e}	75.00 ^{f-j}	158.30 ^{g-i}	33.33 ^b	43.33 ^{b-e}	2.92 ^{ef}
10.	CML312BK	74.67 ^{a-c}	78.33 ^{ab}	2.67 ^{b-e}	2.83 ^{a-d}	95.00 ^{d-g}	183.30 ^{d-h}	39.00 ^{d-f}	33.67 ^{ef}	3.89 ^{c-f}
11.	CML144	70.67 ^{ef}	73.67 ^{de}	2.33 ^{d-g}	2.83 ^{a-d}	83.33 ^{e-i}	171.70 ^{e-i}	35.00 ^{b-e}	38.33 ^{d-f}	3.84 ^{c-f}
12.	CML202	70.33 ^f	72.67 ^{de}	2.17 ^{e-h}	2.83 ^{a-d}	73.33 ^{g-j}	176.70 ^{e-i}	36.67 ^{b-f}	40.00 ^{c-f}	5.54 ^{bc}
13.	CML159	70.00 ^f	72.33 ^e	3.00 ^{a-c}	2.83 ^{a-d}	68.33 ^{h-j}	191.70 ^{d-g}	39.67 ^{ef}	40.33 ^{c-f}	4.73 ^{b-e}
14.	SC22	67.00 ^{g-i}	73.00 ^{de}	3.17 ^{ab}	2.50 ^{c-e}	91.67 ^{d-h}	195.00 ^{c-f}	38.33 ^{b-f}	35.33 ^{d-f}	4.80 ^{b-d}
15.	CML395	69.33 ^{fg}	72.00 ^{ef}	2.33 ^{d-g}	2.50 ^{c-e}	80.00 ^{e-i}	156.7 ^{g-i}	38.33 ^{b-f}	38.00 ^{d-f}	4.61 ^{b-e}
16.	CML204	75.33 ^{a-c}	80.00 ^a	2.83 ^{a-d}	3.33 ^a	80.00 ^{e-i}	176.70 ^{e-i}	34.33 ^{b-d}	35.00 ^{d-f}	2.72 ^f
17.	KUBA/GUDAC1i ₂ ½	65.33 ⁱ	66.67 ^g	3.00 ^{a-c}	3.17 ^{ab}	53.33 ^j	161.70 ^{f-i}	40.67 ^f	61.67 ^a	4.317 ^{b-f}
18.	124-b (109)	62.67 ^{ik}	70.00 ^f	2.00 ^{f-h}	2.67 ^{b-d}	101.67 ^{c-e}	198.30 ^{c-e}	38.67 ^{c-f}	40.00 ^{c-f}	5.38 ^{bc}
19.	CML197	69.00 ^{fg}	74.67 ^{cd}	1.67 ^h	2.00 ^e	125.00 ^{a-c}	236.70 ^{ab}	40.67 ^f	53.67 ^{ab}	6.00 ^b
20.	CML334	76.33 ^a	78.33 ^{ab}	3.00 ^{a-c}	2.67 ^{b-d}	98.33 ^{d-f}	215.00 ^{b-d}	40.00 ^{ef}	30.33 ^f	2.71 ^f
21.	MBRC5BCF10-8-2-3-1	66.33 ^{hi}	71.67 ^{ef}	3.17 ^{ab}	3.00 ^{a-c}	68.33 ^{h-j}	143.30 ⁱ	39.00 ^{d-f}	39.67 ^{c-f}	3.13 ^{d-f}
22.	CML536	74.67 ^{a-c}	76.67 ^{bc}	2.17 ^{e-h}	2.50 ^{c-e}	83.33 ^{e-i}	216.7 ^{b-d}	25.67 ^a	35.67 ^{d-f}	3.78 ^{c-f}
23.	F-7215	69.00 ^{fg}	76.00 ^c	2.33 ^{d-g}	2.50 ^{c-e}	110.0 ^{b-d}	238.3 ^{ab}	41.00 ^f	40.67 ^{c-f}	5.20 ^{bc}
	Grand men	70.17	73.88	2.57	2.70	88.41	188	37.67	40.06	4.38
	LSD (0.05)	2.39	2.29	0.63	0.54	23.63	21.88	5.07	11.02	1.86
	CV (%)	2.10	1.90	14.80	12.20	16.20	11.60	8.20	16.70	25.70

Table 2. PCV, GCV, GA and h² of mean grain yield and other related traits in 2019 main season at Pawe Agricultural Research Center

Traits	Means ± SE	Range	σ ² P	σ ² g	σ ² e	PCV (%)	GCV (%)	h ²		
								(%)	GA	GAPM (%)
DA	70.17 ± 1.45	62-76	19.02	16.91	2.11	6.22	2.07	11.09	1.00	1.42
DS	73.88 ± 1.4	65-80	19.20	17.26	1.95	5.93	1.89	10.14	0.92	1.24
EA	2.57 ± 0.38	1.7-3.3	0.32	0.18	0.144	22.00	14.78	45.16	0.53	20.49
PA	2.70 ± 0.33	2-3.3	0.16	0.05	0.109	14.78	12.23	68.41	0.56	20.86
EH	88.41 ± 14.4	53-147	1097.0	890.90	206.1	37.46	16.24	18.79	12.84	14.52
PH	188 ± 36.0	143-257	814.67	335.67	479.0	15.18	11.64	58.80	34.62	18.42
NP	37.67 ± 3.1	26-41	18.54	9.03	9.511	11.43	8.19	51.30	4.56	12.10
NE	40.06 ± 6.7	30-62	79.11	34.23	44.88	22.20	16.72	56.73	10.41	25.99
Yield	4.38 ± 1.127	2.7 - 8.2	2.33	1.06	1.27	34.86	25.74	54.53	1.72	39.21

Table 3. The phenotypic correlation is indicated on the above diagonal while genotypic correlation has shown below diagonal studied in 2019 main season at Pawe Agricultural Research Center

Variable	DA	DS	PH	EH	TLB	CLR	NP	RL	PA	EA	NE	Yield
DA		0.88***	0.07	0.01	-0.20	-0.03	-0.35**	0.08	0.24*	0.39**	-0.33***	-0.49**
DS	0.91***		0.14	0.13	-0.23	-0.09	-0.25*	0.11	0.20	0.36	-0.37	-0.48**
PH	0.13	0.20		0.80***	-0.35**	-0.47***	0.20	0.33	-0.25*	-0.22	0.11	0.38**
EH	0.07	0.20	0.86***		-0.37***	-0.43***	0.27*	0.28*	-0.32**	-0.22	0.07	0.44**
TLB	-0.28	-0.29	-0.55***	-0.48*		0.36***	0.21	0.17	0.35***	0.21	-0.10	-0.31**
CLR	-0.07	-0.13	-0.63***	-0.59**	0.37		-0.19	-0.12	0.20***	0.11	-0.19	-0.27**
NP	-0.39	-0.30	0.21	0.31	0.33	-0.33		0.41**	-0.08	-0.11	0.21	0.32**
RL	0.08	0.14	0.54***	0.51*	0.06	-0.40	0.52		0.07	0.07	-0.08	-0.04
PA	0.24	0.19	-0.31	-0.36	0.40	0.13	0.05	0.12		0.48	-0.26*	-0.51
EA	0.41*	0.37	-0.27	-0.29	0.21	0.16	-0.03	0.13	0.49*		-0.21	-0.54**
NE	-0.39	-0.44*	0.01	-0.05	-0.15	-0.20	0.19	-0.06	-0.16	-0.11		0.47**
Yield	-0.58**	-0.58**	0.43*	0.44*	-0.32	-0.37	0.33	-0.02	-0.51*	-	0.46*	

Table 4. Effect of genotypic path coefficient analysis in 2019 main season at Pawe Agricultural Research Center

Traits	Days to 50% anthesis pollen shading	Days to 50% silk emerging	Plant height (cm)	Ear height (cm)	Plant aspect (1-5 scale)	Ear aspect (1-5 scaling)	Number of ears harvested (counting)	Grain yield (t ha ⁻¹)
Days to 50% anthesis pollen shading	<u>0.0676</u>	-0.4898	0.0229	0.0207	-0.0299	-0.0860	-0.0856	-0.58**
Days to 50% silk emerging	0.0615	<u>-0.5382</u>	0.0352	0.0592	-0.0236	-0.0776	-0.0966	-0.58**
Plant height (cm)	0.0087	-0.1076	<u>0.1764</u>	0.2549	0.0386	0.0566	0.0021	0.43*
Ear height (cm)	0.0047	-0.1076	0.1517	<u>0.2964</u>	0.0448	0.0608	-0.0109	0.44**
Plant aspect (1-5 scale)	0.0162	-0.1022	-0.0546	-0.1067	<u>-0.1246</u>	-0.1027	-0.0351	-0.51*
Ear aspect (1-5 scaling)	0.0277	-0.1991	-0.0476	-0.0859	-0.0610	<u>-0.2098</u>	-0.0241	-0.6**
Number of ears harvested (counting)	-0.026	0.2368	0.0017	-0.0148	0.0199	0.0230	<u>0.2196</u>	-0.58**

Table 5. Effect of phenotypic path coefficient analysis in 2019 main season at Pawe Agricultural Research Center

Traits	DA	DS	PH	EH	TLB	CLR	NP	EA	NE	Yield
DA	<u>-0.0367</u>	-0.3162	0.0036	0.0017	0.0494	-0.0001	-0.0455	-0.0852	-0.0688	0.4978**
DS	-0.0325	<u>-0.3578</u>	0.0071	0.0353	0.0560	-0.0004	-0.0322	-0.0794	-0.0767	0.4804**
PH	-0.0027	-0.0518	<u>0.0494</u>	0.2108	0.0860	-0.0023	0.0259	0.0475	0.02196	0.3849**
EH	-0.0002	-0.0480	0.0395	<u>0.2634</u>	0.0926	-0.0021	0.0343	0.0497	0.01425	0.4436**
TLB	0.0073	0.0805	-0.0171	-0.0981	<u>-0.2490</u>	0.0017	0.0275	-0.0456	-0.0215	0.3141**
CLR	0.0009	0.0313	-0.0233	-0.1143	-0.0894	<u>0.0049</u>	-0.0245	-0.0237	-0.0400	0.2780**
NP	0.0130	0.0899	0.0100	0.0705	-0.0535	-0.0009	<u>0.1282</u>	0.0241	0.0425	0.3241**
EA	-0.0142	-0.1284	-0.0106	-0.0592	-0.0514	0.0005	-0.0140	<u>-0.2211</u>	-0.0433	0.5418**
NE	0.0122	0.1330	0.0052	0.0182	0.0259	-0.001	0.0264	0.0464	<u>0.2061</u>	0.4729**

CONCLUSION

In conclusion, high genetic variability among extensively grown maize inbred lines at Pawe agricultural research centre is a prerequisite for more varietal improvement. The result recommended that there is sufficient prospect for better exploiting the intended maize inbreeds for carefully preferred characters in maize improvement programs as variability subsisted evaluated twenty-three maize inbred lines. Bearing in mind, all the character A7033, CML197 and CML202 are promising lines among the studied inbreeds. Positive significant direct effects of plant and ear height and the number of ears harvested in each plot on grain yield can be attributed to better soil nutrient and carbon assimilation for photosynthesis which could have built up in each ear size and numbers hence providing higher grain yield. Accordingly, this might be the element of an excellent selection index of identifying best male and female parents for yielding advancement maize. Indirect effects also contribute an important role in influencing the yield perspective of inbreeds.

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REFERENCES

- Abate, T., Shiferaw, B., Menkir, A., Wegary, D., Kebede, Y., Tesfaye, K., & Keno, T. (2015). Factors that transformed maize productivity in Ethiopia. *Food Security*, 7(5), 965-981. <https://doi.org/10.1007/s12571-015-0488-z>
- Akbar, M., Shakoob, M. S., Hussain, A., & Sarwar, M. (2008). Evaluation of maize 3-way crosses through genetic variability, broad sense heritability, characters association and path analysis. *Journal of Agricultural Research*, 46(1), 39-45.
- Bello, O. B., Abdulmalik, S. Y., Afolabi, M. S., & Ige, S. A. (2010). Correlation and path coefficient analysis of yield and agronomic characters among open pollinated maize varieties and their F₁ hybrids in a diallel cross. *African Journal of Biotechnology*, 9(18), 2633-2639.
- Bello, O. B., Ige, S. A., Azeez, M. A., Afolabi, M. S., Abdulmalik, S. Y., & Mahamood, J. (2012). Heritability and genetic advance for grain yield and its component characters in maize (*Zea mays* L.). *International Journal of Plant Research*, 2(5), 138-145.
- Burton, G., & Devane, E. (1953). Estimating heritability in Tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agronomy Journal*, 45, 478-481.
- Central Statistical Agency (CSA). (2018). Area and Production of major Crops, Addis Ababa, April, 2018.
- CIMMYT. (1988). From Agronomic Data to Farmer Recommendations. *An Economic Training Manual. Mexico*. p.79.
- Dewey, D. R., & Lu, K. (1959). A Correlation and Path-Coefficient Analysis of Components of Crested Wheatgrass Seed Production 1. *Agronomy journal*, 51(9), 515-518.
- Doshi, S.P. (1991). Statistical Package for Agricultural Research: *IASRI*, New Delhi.
- El-Nagouly, O. O., Abul-Fadl, M. A., Ismail, A. A., & Khamis, M. N. (1983). Genotypic and phenotypic correlations and path analysis in maize and their implications in selections. *Agronomy Abstracts, Madison, Wisconsin, USA*, p.62-63.
- Ferdoush, A., Haque, M. A., Rashid, M. M., & Bari, M. A. A. (2017). Variability and traits association in maize (*Zea mays* L.) for yield and yield associated characters. *Journal of the Bangladesh Agricultural University*, 15(2), 193-198.
- Goedhart, P. W., & Thissen, J. T. (2010). Biometris GenStat Procedure Library Manual 13th Edition (No. 18.08.10). *Wageningen Universiteit*.
- Johnson, H.W., Robinson, H.F. & Comstock, R.E. (1955). Genotypic and Phenotypic Correlations in Soy Beans and Their Implications in Selection. *Agronomy Journal*, 47, 477-483.
- Mehdi, S. S., Ahmad, N., & Ahsan, M. (2001). Evaluation of S1 maize (*Zea mays* L.) families at seedling stage under drought conditions. *Online Journal of Biological Sciences*, 1(1), 4-6.
- Mhoswa, L., Derera, J., Qwabe, F. N. & Musimwa, T. R. (2016). Diversity and path coefficient analysis of Southern African maize hybrids. *Chilean journal of agricultural research*, 76(2), 143-151.
- Muchie., & Agentive, D. (2016). Performance evaluation of maize hybrids (*Zea mays* L.) in bahir dar zuria district, North Western Ethiopia. *International Invention Journal of Agricultural and Soil Science*, 4(3), 2408-7254.
- Sesay, S., Ojo, D., Ariyo, O., & Meseka, S. (2016). Genetic variability, heritability and genetic advance studies in top cross and three-way cross maize (*Zea mays* L.) hybrids. *Journal of International Institute of Tropical Agriculture*, 61, 1-7.
- Sesay, S., Ojo, D. K., Ariyo, O. J., & Meseka, S. (2018). Genetic variability, heritability and genetic advance studies in top-cross and three-way

- cross maize (*Zea mays* L.) hybrids. *Maydica*, 61(2), 1-7.
- Sharma, S., & Vredenburg, H. (1998). Proactive corporate environmental strategy and the development of competitively valuable organizational capabilities. *Strategic Management Journal*, 19(8), 729-753.
- Silva, T. N., Moro, G. V., Moro, F. V., Santos, D. M. M. D., & Buzinaro, R. 2016. Correlation and path analysis of agronomic and morphological traits in maize. *Revista Ciência Agronômica*, 47(2), 351-357.
- Singh, R. K., & Chaudhary, B.D. (1985). *Biometrical Methods in Quantitative Genetic Analysis*. Kalyani Publishers, New Delhi, India.
- Taimur, M., Khan, M. A. U., Abbas, S. J., Zaheer, A., Mehran, M., & Kamil, M. (2011). Genotypic and phenotypic relationship among maturity and yield traits in maize hybrids (*Zea mays* L.). *International Research Journal of Agricultural Science and Soil Science*, 1(8), 339-343.
- Tyagi, S. D., & Khan, M. H. (2010). Studies on genetic variability and interrelationship among the different traits in *Microsperma* lentil (*Lens culinaris* Medik). *Journal of Agricultural Biotechnology and Sustainable Development*, 2(1), 15-20.
- Yaregal, D., & Firew M. (2018). Genetic variability of improved maize varieties (*Zea mays* L.) for acidic soil tolerance under contrasting environments in Assosa, Ethiopia. *Greener Journal of Agricultural Sciences*, 8(12), 332-350.