Genetic Variability, Heritability, Trait Associations and Path Coefficient Analysis of Maize (*Zea mays* L.) Inbreed Lines at Pawe Northwestern Ethiopia

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ABSTRACT

Maize (Zea mays L.) is the first most vital cereal share for the productivity, but the second in its production area coverage next to tef, in Ethiopia. However, its invention and productivity is influenced by biotic and abiotic factors i.e. striga and root lodging is the major ones in Benishangul Gumuz Region mainly at Pawe District. The absence of resistant/tolerant maize verities and or inbreed lines also another significant problem. Therefore, the present study was targeted to assess the magnitude of genetic variability, heritability and genetic advance of traits, to verify the genotypic and phenotypic associations between important traits and to determine the relationship of traits with grain yield and direct and indirect effects using path coefficient analysis. The experiment was conducted at Pawe Agricultural Research Center using 23 inbreed lines with RCB design 3 in replications. Results revealed that strong significant (P<0.01) variations were sensible between inbreed lines in yield and yield related-traits. Moderate to high genotypic coefficient of variation, heritability and genetic advance as the percentage of mean values were recorded for plant height, ear height and grain yield. Plant height, ear height and number of ears harvested in a plot were observed significant to highly significant positive phenotypic and genotypic associations with grain yield while days to 50% anthesis and silk emergence, plant and ear aspects were showed negative highly significant associations with grain yield at both genotypic and phenotypic levels. Tolerating the above constraints the highest grain yield were recorded from A7033 (8.3 t/ha), CML197 (6 t/ha) and CML202 (5.5 t/ha). Hence the authors recommended these lines as best parents for variety advancement and seed producers as female parent.

Key words: *Heritability; Maize; Path analysis; Variability*

Introduction

Maize (*Zea mays* L.) is the first most vital cereal share in terms of productivity and the second in its production area coverage next to *tef*, in Ethiopia [1,2]. It is mainly used as a staple food crop but it's also an important industrial row material in different parts of the country. Itis also a versatile and the second stable food crop in Benishangul Gumuz Regional State next to sorghum and first in its production per unit area [3]. In the region maize is highly produced at Metekel, Kamashi and Assosa zones including Maokomo special district with the mean of $4t^{-1}ha$ productivity [4]. 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 also distinctive value in the producers and its stalk together with its straw after harvesting have several meaning in the local community comparable for animal fodder. However the potential of maize grain yield extremely affected by biotic and biotic factors. Striga hermontica is the major problem among biotic constraints in the region mainly at Metekel zone while stalk and root lodging is the second main problem among abiotic factors in the area mainly at Pawe District.

The breeder desires to recognize the causes of variability in yield wherever precise environment before yield improvements can be achieved [5]. Genetic information is mainly found as genetic variation involving individuals and populations. A cram of various characters mainly those related with yield is very considerable for breeders to desire prospect crossing materials through selection traits to commence in 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 inbreed lines to decide the efficiency for improving the grain yield

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through breeding. For instance Phenotypic Coefficient of Variation (PVC) and Genotypic Coefficient of Variation (GCV) are imperative to detect the existence and mount of variability in a given trait. Maize is both phenotypically and heritably miscellaneous crop. The effectiveness through which inbreed lines variability can be subjugated via selection depends upon heritability and the Genetic Advance (GA) of every character [6]. Heritability generates information on the amount to which exacting morphogenetic trait can be transferred to consecutive progeny [7]. Heritability together with high GA could be also more constructive in expecting the ensuing cause in the choice of promising inbreed lines for yield and yield related characters [8]. Investigate of the association between characters, in the course of correlation coefficients, are imperative to the initial selection of plants or inbred lines or to the instantaneous assortment when more than individual character is desired. That is why the indirect selection based on associated retort, via the mechanism of fewer multipart traits with high heritability and natural assessment. This might end with advanced genetic improvement in balance to the exercise of direct selection. Generally, the study was conducted to address the following objectives: 1) to assess the magnitude of genetic variability, heritability and genetic advance of traits in different maize inbreed lines, 2) to determine genotypic and phenotypic associations between important traits of maize inbreed lines and 3) to determine the relationship of traits with grain yield and direct and indirect effects.

Materials and Methods

Experimental Site

The experiment was conducted at Pawe Agricultural Research Center on station in 2019 cropping season. Pawe Agricultural Research Center is located 575 km far in the North Western part from Addis Ababa with the geographical position 11º19ˊN latitude and 36º24ˊE longitudes with an altitude of 1120 m.a.s.l. It receives the maximum annual rain fall about 1587 mm for extended period and the minimum and maximum mean annual temperature is 16.3ºC and 32.6ºC respectively with Nitisol type.

Materials and Design

The experimental materials used consisted of 23 inbreed lines obtained from the national maize improvement program at Bako, Ethiopia. It was laid out using a randomized complete block design (RCBD) with three replications. Plating was done using the space 0.75 m and 0.25 m between rows and plants respectively. Each plot has two rows with 5m length. Twenty one stations were established at each row and two seeds were planted at each station, then two weeks later germination it was thinned. This considers having 53,333 plant populations per hectare. The blanket recommended 100 kg NPS and 150 kg urea per hectare was applied. The NPS fertilizer was applied at plating while urea was applied after thinning and before flowering. All agronomic practices were carried out per the recommendation similarly.

Data Collected

Data were collected at both plot and plant base. Days to anthesis and silking, plant aspect, ear aspect, stalk lodging, disease and insect pest damage were taken at plot based. Whereas plant height, ear height and others were the plant based data. The grain yield (Yld) was calculated for each inbreed lines from the data of field weight per plot in kg ha^{-1} at harvest, then converted into ton ha^{-1} by the method of CIMMYT [9]:

$$Grain\ yeild\left(\frac{ton}{ha}\right)=\frac{\text{Field }weight\left(\frac{kig}{plot}\right)\times(100-MC)\times 0.8\times 10000}{1000(100-15)\times 7.65}$$

Where, MC = moisture content in grains at harvest (%), 0.8 = shelling co-efficient, 7.6 = harvested plot area in m^2), 1 hectare = 10,000 m^2, 1 ton= 1000kg and 85% = Standard Value of Grain Moisture at 15%.

Statistical Analysis

Data were subjected to analysis of variance using Gen stat 18th edition. Means were compared using fisher protected least significant difference at 5% level of significance. Genotypic and phenotypic variance components, heritability and genetic advance were also calculated using the method given by Burton and De Vane, Singh and Chaudhary, and Johnson et al. respectively [10-12] (Table 1).

Both phenotypic and genotypic relationship among yield and yield attributed traits of two variables was prepared via the formula developed by Singh and Chaudhary [11].

The phenotypic and genotypic analysis among.

Table 1: The formula used for estimating the variance components, heritability and genetic variance components.

No.	Variances	Formula	References
1.	Genotypic Variance	$\sigma^2 g = \dfrac{MSg - MSe}{r}$	Burton and De.Vane (1953)
2.	Phenotypic Variance	$\sigma^2 p = \sigma^2 g + \sigma^2 e$	Burton and De Vane (1953)
3.	Phenotypic Coefficient of Variation	$PCV = \dfrac{\sqrt{\sigma^2 p}}{X} *100$	Burton and De Vane (1953)
4	Genotypic Coefficient of Variation	$GCV = \dfrac{\sqrt{\sigma^2 g}}{X} *100$	Burton and De Vane (1953)
5.	Heritability	$h^2 = \dfrac{\sigma^2 g}{\sigma^2 p} *100$	Singh and Chaudhary (1985)
6.	Genetic Advance	$GA = \sigma_p *h^2 *K$	Johnson *et al.* (1955)

Where, σ^2_p = phenotypic variance, $\sigma^2 g$ = Genotypic variance; $\sigma^2 e$ = Environmental variance (Variance of error mean square); σp = phenotypic standard deviation, MSg = mean square of genotypes; MSe = mean square of error (Mean square of environment), GCV = Genotypic coefficient of variation, PCV= Phenotypic coefficient of variation, X = population mean, h^2 = heritability, GA = Genetic Advance, K = 2.063 (selection differential at 5%) and r = number of replications.

$$r_{ph} = \frac{\sigma^2 p12}{\sqrt{(\sigma^2 p1)(\sigma^2 p2)}}, \quad r_{gh} = \frac{\sigma^2 g12}{\sqrt{(\sigma^2 g1)(\sigma^2 g2)}}$$

Where, r_{p12}= phenotypic association coefficient between two characters, r_{g12}= genotypic association coefficient between two characters, σ^2_{P12}=the phenotypic covariance between the two traits, σ^2_{P1}= the phenotypic covariance of the first character and σ^2_{P2}=the phenotypic covariance of the second character, $\sigma^2 g_{12}$=the genotypic covariance between the two characters, $\sigma^2 g_1$= the genotypic covariance of the first character and $\sigma^2 g_2$= the genotypic covariance of the second character.

The intended phenotypic and genotypic correlation values were verified for their significance using t-test as indicated below: Phenotypic value was verified for its significance via r_{ph}, stands for the phenotypic association coefficient, n= demonstrates the number of genotypes evaluated and also SE_{rph}, stands for = Standard error of the phenotypic association coefficient [13].

$$SE(r_{ph}) = \sqrt{\frac{(1 - r^2 ph)}{(n-2)}}$$

The genotypic coefficients of correlation were also verified concerning their significance via the formulation established in Robertson as stated bellow [14]:

$$t = \frac{r_{gxy}}{SE(r_{gxy})}, \quad SE_{rgxy} = \sqrt{\frac{1 - r^2 gxy}{2h^2 x^{h^2} y}}$$

Where, $h^2 x$= the heritability of character 'x' and $h^2 y$ = the heritability of character 'y'. The analysis of "t" value was associated with tabulated "t" value at (n-2) degree of freedom at 5% significance level. While, 'n' is the number of genotypes verified.

Partitioning yield attributes into direct and indirect causes is of significance to the breeder therefore characters that directly add to yield are preferred. The path coefficient analysis was calculated via the method of Dewey and Lu and with statistical package developed by Doshi to recognize the most important character on the grain yield either directly or indirectly [15,16]. This analysis is very important to understand the inter relation between characters and their effects on the dependent variable (grain yield).

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

Where, r_{ij} is correlation between the independent variable (i) and dependent variable (j) as deliberate by correlation coefficient; P_{ij} is element of direct cause of the independent variable (i) on the dependent variable (j) as calculated by path coefficient and $\Sigma r_{ik} P_{kj}$ is summation of components of indirect causes of a specified independent variable (i) on a specified dependent variable (j) via all other independent variables.

Results and Discussion

Analysis of Variance

The analysis of variance (ANOVA) revealed that highly significant difference (<0.001) for most characters including days to 50% anthesis and silk emerging, ear and plant aspect, ear and plant height, number of plants per plot, number of ears and grain yield (Table 2). The results also showed a considerable quantity of variation among the evaluated inbreed lines. Similar results were observed by the previous findings of Muchie and Fentie [17]. They reported that there is highly significant variation in days to 50% anthesis, plant and ear height and grain yield. The highest grain yield was obtained from inbreed lines A7033 (8.26 t/ha) and CML (6.0 t/ha) while the lowest grain yield was recorded by inbreed lines CML334 and CML204 with the amount of 2.71 and 2.72 t/ha respectively. Number of ears per plot by itself may not have a significant contribution for increasing the grain yield, but the number of ears with its ear size. The present study confirmed this inspiration, for instance the inbreed line KUBA/GUDAC1ï¿½ has 62 ears and provided a grain yield of 4.3 t/ha where as an inbreed line A7033 has 50 ears, but offered 8.3 t/ha (Table 2). This result also agreed with the investigation of Mehdi et al. and Taimur et al. attained a smaller amount of coefficient of variation for several traits in maize and conferring to Singh and Chaudhry, 10% or less CV are acceptable for selection of traits in improving program for the population [11,18,19]. Days to 50% pollen shedding for maize hybrids ranged from 62 to 76 (Table 2).The maximum days to pollen shedding (76 days) were obtained from 142-1-e and CML334 inbreed lines while the minimum 50% pollen shading day (62 days) was recorded from 124b(113) inbreed line. Similarly the maximum days to 50% silk emerging (80 days) was obtained from CML204 and BKL001 inbreed lines whereas the minimum (65 days) was from inbreed line 124b(113). The maximum anthesis silking interval (ASI) (7 days) were recorded from inbreed lines 124b(109) and F-7215 while the minimum (1 day) were from A7033 and KUBA/GUDAC1ï¿½ inbreed lines. From this study we suggested that ASI between 1-7 days is very successful and compatible for male to female in crossing. Hence A7033 and CML197 were found the promising inbreed lines which can be used as better female parents for seed production. Therefore the analysis of variance result exhibited the existence of substantial extent of variation among the evaluated inbreed lines. The association of disease mainly

Table 2: Mean performance of 23 maize inbreed 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	Yld (t/ha)
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[a-c]	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-j]	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]	156.8[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/GUDAC1ï¿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**

TLB and CLR with the grain yield revealed significantly and negatively affects each inbreed lines primarily BKL001, CML165 and KUBA/GUDAC1ï¿½.

Phenotypic and Genotypic Variations

The phenotypic and genotypic discrepancy subsist in plant species is fundamental for developing productive and stable varieties as well as establishing the procreation plan which was earlier reported by Sesay et al. as the PCV, GCV, and GA values grouped and conferred as low (0-10%), moderate (10-20%) and high (>20%) [6]. In the present study phenotypic variance was superior to the genotypic variances for all the studied characters, this showed the pressure of ecological aspect on these characters (Table 3). The PCV values of days to 50% anthesis and silk emerging were showed in the range of low (<10%) while plant height, plant aspect and number of plants in a plot at harvest were medium (10-20%) whereas ear aspect, ear height, number of ears harvested in a plot and grain yield were recorded in the range of high (>20%) value. PCV was higher for ear height (37.5%) than all other characters followed by grain yield (34.9%). This implies that the phenotypic variations regarding the tested inbreed lines through the overhead characters are moderate to high. Comparable result was also pragmatic [7,17,20]. This indicates the phenotypic variation between the studied inbreed lines is high on these characters.

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 plot at harvest were low. Plant and ear height, plant and ear aspect, and number of ears harvested in a plot were observed medium. While higher GCV value was obtained for grain yield (Table 3). The present investigation was revealed similar outcomes like El-Nagouli et al. and Taimur et al. who confirmed that yield was openly influenced by ear height [19,21]. Ferdoush et al. also reported that lower GCV values were recorded for DA and medium for EH [20]. This pronouncement is also agreed to some extent with the exploration of Muchie and Fentie [17].

It is obviously clear that heritability explained inconceivable sense to the breeder, as its quantity describe the accuracy with which an inbreed line can be conventional via its phenotypic expression. Traits like plant height, plant aspect, and number of ears harvested in a row, and grain yield were revealed moderate heritability convoyed with moderate to high GCV and PCV with genetic advance at the percentage of mean values which indicates that highest potential heritability is due to additive gene effects on behalf of these characters and trait selection could be in existence in first generations (Table 3). The moderate level of heritability explained that these traits were moderately influenced via environmental pressure. Hence, assortment can be doing well on the middle of phenotypic expression of these traits in various plants during concern humble selection techniques. Moderate to high heritability was explained and reported for plant height, ear height and grain yield by Bello et al. and Ferdoush et al. [7,20]. However, Muchie and Fentie revealed that high heritability may not always indicate a high genetic gain, heritability will be proficient shared with genetic advance at the percentage of mean via detecting the critical pressure for identifying better parent of inbreed lines [17].

Genotypic and Phenotypic Correlations

The association study indicates the nature and level of relationship presented among couples of traits. Correlation is also determined that point to characters to be considered to enhance the yield. Days to 50% pollen shedding exhibited significant positive genotypic and phenotypic association with days to silking (r_g = 0.91 and r_p=0.88).The genotypic

Table 3: 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	σ²P	σ²g	σ²e	PCV (%)	GCV (%)	h²(%)	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
Yld	**4.38** ± 1.127	2.7 - 8.2	2.33	1.06	1.27	34.86	25.74	54.53	1.72	39.21

NB: DA= days to 50% of male flower pollen shading in the plot, DS= days to 50% of the female emerging silk (2 to 3 cm), PH= plant height (cm), EH= ear height (cm), PA = plant aspect and EA= ear aspect (1 to 5 scaling), RL= root lodging (counting if <40º inclined in the ground), NP= number of plants at harvest in a plot (counting), NE= number of ears harvested in a plot (counting and Yld= grain yield (t/ha), PCV=phenotypic coefficient of variation, GCV= genotypic coefficient of variation, GA=genetic advance, h²=heritability

and phenotypic association of grain yield with plant height (r_g= 0.43 and r_p=0.38), ear height (r_g=0.44 and r_p= 0.44) and number of ears harvested (r_g= 0.46 and r_p= 0.47) also exhibited positive and significant. 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 positive and significantly associated with ear height both at the genotypic and phenotypic level (r_g=0.86 and r_p=0.8) while plant and ear height negatively and significantly associated with CLR and TLB both at the genotypic and phenotypic level where as the remaining traits are not significant. In general in this investigation grain yield (t/ha) showed some involvement explained positive and highly significant correlation with PH, EH, NE and NP whereas DA and DS, TLB and CLR indicated negative and strong significant association at the genotypic and phenotypic level (Table 4). This result is similar with the previous investigation of and Taimur et al., Mhoswa et al. and Ferdoush et al. [19,20,22]. Therefore this association is able to be applied as a bench mark for trait selection if comparable study will be accomplished in the prospect by means of extra morphological characters.

Genotypic and Phenotypic Path Coefficient Analysis

Genotypic path coefficient analysis: As it's presented in Table 5 the coefficient of strength of mind (R^2) of path analysis model was equivalent to 0.77, characterizing that 77% of the variation in the dependent variable grain yield in the model is explained by the variables used in the causal table. Days to 50% silk emerging (pc=-0.5382) had the highest significant negative direct effect on grain yield which is similar with previous reported by Bello while plant height (pc=0.18) and ear height (pc=0.296), number of ears harvested (pc=0.22) explained moderate to high positive significant effect on the grain yield [23]. Days to 50% silk emergence, plant and ear height had also strong indirect cause on the grain yield via number of ears harvested (Table 5). This shows that the association coefficient with grain yield is due to the continuation of these traits. It is also indicated that, plant height had the highest moderate indirect positive effects on grain yield via ear weight (pc = 0.25). However, it's palpable that other variables could have causes on grain yield. In this cram, days to flowering, plant and ear height, number of gears harvested in a plot come into view to be the important traits that might be consider during selection for high yield, since have highly significant genotypic and phenotypic associations with grain yield.

Phenotypic path coefficient analysis: Days to 50% silk emerging (pc = -0.36) had also the highest significant negative direct effect followed by turcicum leaf blight (pc=-0.25) on the grain yield while ear height (pc=0.26), number of ears harvested in a plot (pc=0.21), number of plats at harvest (pc= 0.13) and plant height (pc= 0.05) had moderate to medium significant positive effect on the grain yield. The positive direct cause of EH on grain yield was also related via Akbar et al., Sreckov et al. and Silva et al. [24-26]. Surrounded by the morphological characters, there was high, positive and significant association between all combinations of traits (Table 6). Consequently, the character NE, PH, EH and NP, which have high association with most, morphological characters, are preferable for selection since of the reserves point in time and employment in the measurements, as well of its precision. Generally this investigation shows that the dependent variable grain yield is mainly affected through the direct cause on an independent variable and its indirect cause via additional yield attributed characters.

Table 4: 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	Yld
DA		0.88***	0.07	0.01	-0.20	-0.03	-0.35**	0.08	0.24*	0.39**	-0.33***	-0.4978**
DS	0.91***		0.14	0.13	-0.23	-0.09	-0.25*	0.11	0.20	0.36	-0.37	-0.4804**
PH	0.13	0.20		0.80***	-0.35**	-0.47***	0.20	0.33	-0.25*	-0.22	0.11	0.38496**
EH	0.07	0.20	0.86***		-0.37***	-0.43***	0.27*	0.28*	-0.32**	-0.22	0.07	0.44366**
TLB	-0.28	-0.29	-0.55***	-0.48*		0.36***	0.21	0.17	0.35***	0.21	-0.10	-0.3141**
CLR	-0.07	-0.13	-0.63***	-0.59**	0.37		-0.19	-0.12	0.20***	0.11	-0.19	-0.278**
NP	-0.39	-0.30	0.21	0.31	0.33	-0.33		0.41**	-0.08	-0.11	0.21	0.32412**
RL	0.08	0.14	0.54***	0.51*	0.06	-0.40	0.52		0.07	0.07	-0.08	-0.0484
PA	0.24	0.19	-0.31	-0.36	0.40	0.13	0.05	0.12		0.48	-0.26*	-0.5185
EA	0.41*	0.37	-0.27	-0.29	0.21	0.16	-0.03	0.13	0.49*		-0.21	-0.5418**
NE	-0.39	-0.44*	0.01	-0.05	-0.15	-0.20	0.19	-0.06	-0.16	-0.11		0.47294**
Yld	-0.58**	-0.58**	0.43*	0.44*	-0.32	-0.37	0.33	-0.02	-0.51*	-0.60**	0.46*	

NB: DA= days to 50% of male flower pollen shading in the plot, DS= days to 50% of the female emerging silk (2 to 3cm), PH= plant height (cm), EH= ear height (cm), TLB= Turcicum leaf blight (1 to 5 scaling), CLR= Common leaf rust, (1 to 5 scaling), PA = plant aspect and EA= ear aspect (1 to 5 scaling), RL= root lodging (counting if <40º inclined in the ground), NP= number of plants at harvest in a plot (counting), NE= number of ears harvested in a plot (counting and Yld= grain yield (t/ha).

Table 5: Genotypic Path Coefficient analysis Result 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)
Days to 50% anthesis pollen shading	**0.06768**	-0.4898	0.022933	0.020754	-0.02991	-0.086	-0.08565	**-0.58****
Days to 50% silk emerging	0.061586	**-0.5382**	0.035282	0.059296	-0.02368	-0.07761	-0.09663	**-0.58****
Plant height (cm)	0.008798	-0.10765	**0.17641**	0.254974	0.038637	0.056635	0.002196	**0.43***
Ear height (cm)	0.004737	-0.10765	0.151711	**0.29648**	0.044869	0.06083	-0.01098	**0.44****
Plant aspect (1-5 scale)	0.016242	-0.10227	-0.05469	-0.10673	**-0.1246**	-0.10278	-0.03514	**-0.51***
Ear aspect (1-5 scaling)	0.027747	-0.19915	-0.04763	-0.08598	-0.06107	**-0.2098**	-0.02416	**-0.6****
Number of ears harvested (counting)	-0.02639	0.236827	0.001764	-0.01482	0.019942	0.023073	**0.21961**	**-0.58****

Table 6: Phenotypic path coefficient analysis result in 2019 main season at Pawe Agricultural Research Center.

Traits	DA	DS	PH	EH	TLB	CLR	NP	EA	NE	Yld
DA	**-0.0367**	-0.3162	0.00364	0.00178	0.04946	-0.0001	-0.0455	-0.0852	-0.0688	**-0.4978****
DS	-0.0325	**-0.3578**	0.00716	0.03536	0.05606	-0.0004	-0.0322	-0.0794	-0.0767	**-0.4804****
PH	-0.0027	-0.0518	**0.04945**	0.21086	0.08601	-0.0023	0.02593	0.04754	0.02196	**0.38496****
EH	-0.0002	-0.048	0.03958	**0.26348**	0.09269	-0.0021	0.03437	0.0497	0.01425	**0.44366****
TLB	0.0073	0.08057	-0.0171	-0.0981	**-0.249**	0.00177	0.02755	-0.0456	-0.0215	**-0.3141****
CLR	0.00099	0.03131	-0.0233	-0.1143	-0.0894	**0.00493**	-0.0245	-0.0237	-0.04	**-0.278****
NP	0.01303	0.08993	0.01	0.07059	-0.0535	-0.0009	**0.12828**	0.02415	0.04256	**0.32412****
EA	-0.0142	-0.1284	-0.0106	-0.0592	-0.0514	0.00053	-0.014	**-0.2211**	-0.0433	**-0.5418****
NE	0.01226	0.13307	0.00527	0.01821	0.02596	-0.001	0.02648	0.04648	**0.20617**	**0.47294****

NB: DA= days to 50% of male flower pollen shading in the plot, DS= days to 50% of the female emerging silk (2 to 3 cm), PH= plant height (cm), EH= ear height (cm), TLB= Turcicum leaf blight (1 to 5 scaling), CLR= Common leaf rust, (1 to 5 scaling), EA= ear aspect (1 to 5 scaling), NP= number of plants at harvest in a plot (counting), NE= number of ears harvested in a plot (counting and Yld= grain yield (t/ha).

Conclusion

In conclusion high genetic variability among extensively grown maize inbreeds lines at Pawe agricultural research center is a perquisite in order to have more varietal improvement. The result recommended that there is sufficient prospect for better exploitation of the intended maize inbreeds for careful preferred characters in maize improvement programs as variability subsisted evaluated twenty three maize inbreed lines. Bearing in mind, all the characterA7033, CML197 and CML202 are promising lines among the studied in breeds. Positive significant direct effects of plant and ear height and number of ears harvested in each plot on grain yield can be attributed to better soil nutrient and carbon assimilation for photo synthesis which could have built up in each ear size and numbers hence providing higher grain yield. Accordingly, this might be element of an excellent selection index of identifying best male and female parents for yielding advancement maize. Indirect effects also contribute important role on influencing the yield prospective of inbreeds.

The result of the experiment showed that barley varieties were showed a significant difference both at individual location and combined mean effects. Varieties were highly affected by environments and their interaction which show the selective adaptation to specific location and wider adaptability that favoring their production. Generally, HB1307 and Bentu were the best varieties that showed the stability of these varieties as well as higher yield advantage over the local check. Therefore, these two varieties are recommended as improved varieties and demonstrated on farmers' field for further scaling up.

Acknowledgements

References

1. Abate T, Shiferaw B, Menkir A, Wegary D, Kebede Y, et al. Factors that transformed maize productivity in Ethiopia. *Food Secur*. **2015**, 7(5):965-981.

2. Tsedeke A, Bekele S, Abebe M, Dagne W, Yilma K, et al. Factors that transformed maize productivity in Ethiopia. *Food Sci*. **2015**.

3. Yaregal D, Firew M. Genetic variability of improved maize varieties (*Zea mays* L.) for acidic soil tolerance under contrasting environments in Assosa, Ethiopia. *Greener J Agric Sci,* **2018**, 8(12):332-350.

4. Central Statistical Agency (CSA). Area and Production of major Crops, Addis Ababa, Ethiopia. **2018**.

5. Tyagi SD, Khan MH. Studies on genetic variability and interrelationship among the different traits in Microsperma lentil (Lens culinarisMedik). *J Agricl Biotech Sustain Dev*. **2010**, 2(1):15-20.

6. Sesay S, Ojo D, Ariyo O, Meseka S. Genetic variability, heritability and genetic advance studies in top cross and three-way cross maize (*Zea mays* L.) hybrids. *J Int Inst Trop Agric*. **2016**, 61:1-7.

7. Bello OB, Ige SA, Azeez MA, Afolabi MS, Abdulmaliq SY, et al. Heritability and genetic advance for grain yield and its component characters in maize (*Zea mays* L.). *Int J Plant Res*. **2012,** 2(5):138-145.

8. Singh SK, Singh CM, Lal GM. Assessment of genetic variability for yield and its component characters in rice (*Oryza sativa* L.). *Res Plant Biol*. **2011**, 1(4).

9. CIMMYT. From agronomic data to farmer recommendations. *An Economic Training Manual. Mexico.* **1988,** 79.

10. Burton G, Devane E. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agronomy J*. **1953,** 45:478-481.

11. Singh RK, Chaudhary BD. Analysis in biometrical genetics. *Biomed Genet*. **1985**, 70(3):306-308.

12. Johnson HW, Robinson HF, Comstock RE. Genotypic and phenotypic correlations in soy beans and their implications in selection. *Agronomy J.* **1955**, 47:477-483.

13. Sharma S, Vredenburg H. Proactive corporate environmental strategy and the development of competitively valuable organizational capabilities. *Strateg Manag J.* **1998**, 19(8):729-753.

14. Robertson A. The sampling variance of the genetic correlation coefficient. *Biometrics*. **1959**, 15:469-485.

15. Dewey DR, Lu KA correlation and path-coefficient analysis of components of crested wheat grass seed production 1. *Agronomy J.* **1959**, 51(9):515-518.

16. Doshi SP. Statistical Package for Agricultural Research. *IASRI*, New Delhi. **1991**.

17. Muchie A, Fentie D. Performance evaluation of maize hybrids (*Zea mays* L.) in bahir dar zuria district, North Western Ethiopia. *Int Invent J Agric Soil Sci*. **2016**, 4(3):2408-7254.

18. Mehdi SS, Ahmad N, Ahsan M. Evaluation of S1 maize (*Zea mays* L.) families at seedling stage under drought conditions. *Online J Biol Sci*. **2001**, 1(1):4-6.

19. Taimur M, Khan MAU, Abbas SJ, Zaheer A, Mehran M, et al. Genotypic and phenotypic relationship among maturity and yield traits in maize hybrids (*Zea mays* L.). *Int Res J Agric Sci Soil Sci.* **2011**, 1(8):339-343.

20. Ferdoush A, Haque MA, Rashid MM, Bari MAA. Variability and traits association in maize (*Zea mays* L.) for yield and yield associated characters. *JBAU.* **2017,** 15(2):193-198.

21. El-Nagouly OO, Abul-Fadl MA, Ismail AA, Khamis MN. Genotypic and phenotypic correlations and path analysis in maize and their implications in selections. *Agronomy Abstracts, Madison, Wisconsin, USA*, **1983**, 62-63.

22. Mhoswa L, Derera J, Qwabe FN, Musimwa TR. Diversity and path coefficient analysis of Southern African maize hybrids. *Chilean J Agric Res.* **2016**, 76(2):143-151.

23. Bello OB, Abdulmaliq SY, Afolabi, MS, AndIge, SA. Correlation and path coefficient analysis of yield and agronomic characters among open pollinated maize varieties and their F1 hybrids in a diallel cross. *African J Biotechnol.* **2010,** 9(18):2633-2639.

24. Akbar M, Shakoor MS, Hussain A, Sarwar M. Evaluation of maize 3-way crosses through genetic variability, broad sense heritability, characters association and path analysis. *J Agric Res (Pakistan)*. **2008**.

25. Sreckov Z., Nastasic, A, Bocanski J, Djalovic I, Vukosavljev M, et al. Correlation and path analysis of grain yield and morphological traits in test-cross populations of maize. *Pakistan J Botany.* **2011**, 43(3):1729-1731.

26. Silva TN, Moro GV, Moro FV, Santos DMMD, Buzinaro R. Correlation and path analysis of agronomic and morphological traits in maize. *Rev Ciênc Agron.* **2016**, 47(2):351-357.