



Genetic variability of improved maize varieties (*Zea mays* L.) for acidic soil tolerance under contrasting environments in Assosa, Ethiopia

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ABSTRACT

Maize is the second most widely grown food cereal crop cultivated in the world and consumed in various form of as part of diets of human and animals. However, its production and productivity is affected by biotic and abiotic stresses among which, soil acidity is the key factor. This field experiment was conducted to estimate the genetic variability of maize for yield and yield related traits, and determine the association of traits with grain yield at Assosa and Bambasi districts during the 2017 main cropping season. The experiment consisted of limed and unlimed soil as main plots and 21 maize varieties as the sub-plots arranged in a split plot design with 3 replications. Highly significant ($P < 0.01$) differences were observed among maize varieties in yield and yield related-traits at both locations. Moderate to high genotypic coefficient variation, heritability and genetic advance as the percentage of mean values were observed for stalk biomass, ear biomass, diameter and length, and grain yield at both locations. Highly significant phenotypic and genotypic correlations were observed between thousand seed weight and number of kernels per row, thousand seed weight and ear diameter, and number of kernels per row. The yield was highly significant and positively associated with above stalk biomass, ear biomass, thousand seed weight, and number of kernels per row at both locations at the genotypic and phenotypic level. The phenotypic and genotypic correlation and path coefficient analysis of harvesting index, above ground biomass, ear biomass, number of ears harvested per plot, number of rows per ear, and ear length and these traits also showed a direct effect on yield. The highest yield in t/ha was obtained from variety BH547 (3.04) and (7.35) at Assosa and Bambasi, respectively. Additionally, higher yield was recorded from SPRH1, BH661 and BH546 varieties at both locations. Therefore, farmers could use the above varieties in the acidic soil until other advanced varieties are developed, but the exact significant impact and duration of lime management in the acidic soil for maize needs further investigations.

1. INTRODUCTION

Maize (*Zea mays* L., $2n=2x=20$), the third most important cereal crop universally following wheat and rice, occupies a pivotal role in the world's economy and is second among cereals for human consumption after wheat (Muli *et al.*, 2016). It is a main source of income for smallholder farmers in Africa in general and in Ethiopia in particular. In addition, it is a source of raw materials for the food industry (Smale *et al.*, 2013; Tekeu, 2015). The CSA (2017) report revealed that, even though maize is still the first among cereals in production in Ethiopia, its annual average productivity increment is very low and only about 0.3 t/ha annually. This is due to biotic stresses mainly diseases such as Grey Leaf Spot, Turicum Leaf Blight, Common Leaf Rust, Maize Lethal Necrosis and Maize Strike Viruses, insect pests primarily maize stem borer, weevil and fall army worm, and parasitic weeds critically striga hermontica, and abiotic stress especially drought, soil acidity and poor soil N and P content in are critical (Tolera *et al.* 2018).

The mid-altitude sub-humid agro-ecology is the highest potential for maize production in Ethiopia (Gemechu *et al.*, 2016). In Benishangul Gumuz Region, maize is also the second most prominent crop next to sorghum in area under production and the first in its productivity. However, maize is a diversified crop in the world and is extensively influenced by the environment and genetic variation (Peiffer *et al.*, 2013). The efficiency is endangered by several biotic and abiotic stresses. Soil acidity is the second major challenge next to drought worldwide which strongly affects, about 30% of the earth's total area and over 50% of the arable lands in the world (Malekzadeh *et al.*, 2015). Aluminum toxicity is among the mitigating factor for production in acid soils, accounted more than 40% of the arable lands and constraint about 67% of crop production on the overall acid soil in the world (Ermias *et al.*, 2013). In Ethiopia, about 40% of total arable land is highly affected by acidic soil (Taye, 2007). In Benishangul Gumuz Region, critically Assosa and Bambasi districts, highly affected by soil acidity (Daniel and Tefera, 2016).

Grain yield, is a multifaceted trait together influenced by several constituents inherited and environment (Krishnaji *et al.* (2017). The genetic variation for tolerance to soil acidity among different genotypes and traits may exist (Mutimaamba *et al.*, 2017). Genetic variances in adaptation to acid-soil are due to the variances among crop species and the genotypes within the species (Silva *et al.*, 2016). The knowledge of acquiring genetic variability that exists within and among the given crop species for trait improvement is imperious in plant breeding.

Genetic advancement of crops for quantitative traits needs reliable estimation of heritability with variance components are the imperative detecting and quantifying the variability in the genotypes (Sesay *et al.*, 2016). Enumerating the genetic variability in agronomic

traits has an inviolable role for designing the breeding programs of crop improvement (Bello *et al.*, 2012). On acid soil, Al-sensitive crop species could be exchanged by Al-tolerant species that able to maintain the productivity. Inbreeding schemes variations within a species in acidic soil are enhanced by Al-tolerant varieties. Al-tolerance levels of barley, sorghum, and wheat inherited by one or few genes whereas in maize is quantitatively inherited (Famoso *et al.*, 2011; Kochian *et al.*, 2015).

Heritability together with high genetic advance provides a clue on the quantity of a particular trait transferred to the consecutive generations (Sadaiah *et al.*, 2013). The proficiency in which genetic variability that can be exploited by selection depend on the heritability complied with the genetic advance (Ali *et al.*, 2013). Genetic variation and the associated quantitative inheritance for soil-acidity tolerance in maize with various traits can be improved through DNA marker-based breeding (Yang *et al.*, 2013; Mutimaamba *et al.*, 2017). Trait association also plays an indispensable role to identify and select the target trait through correlation coefficients. Phenotypic and genotypic correlation coefficients are imperative to facilitate selection of promising genotypes and important traits (Silva *et al.*, 2016). Partitioning of the total correlation coefficient values to direct and indirect effect for the grain yield is very crucial to identify the cause and effect of most influential trait through path coefficient analysis using the formula of Dewey and Lu (1959) and with statistical package developed by Doshi (1991). Therefore the objectives of the study were to estimate the genetic variability in maize varieties for yield and yield related traits, and to determine the association of traits with grain yield and direct and indirect effects.

2. MATERIALS AND METHODS

2.1. Description of experimental sites

The experiments were carried out at Assosa Agricultural Research Center (AsARC) and Bambasi District (Aamba-16 kebele) on farmer's field in the 2017 main cropping season. AsARC is located about 680 km away from Addis Ababa in the North West direction in Benishangul Gumuz Regional State at 10°2'24.19"N latitude and 34°34'19.16" E longitude with 1541 to 1553 m.a.s.l. The area receives mean annual rainfall of 1165.97mm with the minimum and maximum temperature of 14.9-27.97°C with 5.02 soil pH value found under strong acidic. The second site Bambasi District (Amba 16 kebele) was situated 25km far from Assosa town in the South West direction by 9°56'18.06"N and 34°39'42.95"E latitude and longitude, respectively at 1440m.a.s.l. The mean annual rainfall is about 1373.3mm with minimum and maximum

temperature of 13.1 and 30.4 °C, respectively and 4.8 soil pH.

Meteorological data obtained from Assosa Meteorological Service Center which is located 3.5 km from AsARC for both sites. Both testing sites have Unimodal rainfall pattern and usually occurs between May and November. The dominant type at both study sites was Nitisol with low in N and P content. Agriculture is the starting point livelihood source of managing their life. Sorghum, maize, *teff*, finger millet, soybean, groundnut, haricot bean, sesame and Niger seed are very common crops in the region. These two districts were selected as a study site because of their popularity

for crop productivity, especially in maize which is extensively affected by soil acidity.

2.2. Experimental materials

Twenty one maize varieties were used (17 hybrids and 4 OPVs). Twelve hybrids and four OPVs were collected from Bako National Maize Research Coordinating Center which was developed by National Maize Research Program of EIAR; five hybrids were developed and collected from private seed companies, four from pioneer and one from Seedco (Table 1).

Table1. Maize varieties used in the experiment

S.N	Varieties	Pedigree	Variety type	Year of released	Owner	Maintainer
1	BH-140	SC22/ GuttoLMS	Hybrid	1988	EIAR	Bako NM
2	BH-660	A7033/F7215//142-1-e	Hybrid	1993	EIAR	Bako NM
3	BH-540	SC22/124b-109	Hybrid	1995	EIAR	Bako NM
4	BHQP545	CML161/CML165	Hybrid	2008	CIMMYT	Bako NM
5	BH661	CML395/CML202//1142-1-e	Hybrid	2011	CIMMYT//EIAR	Bako NM
6	BH547	BKL002/CML312/BKL003	Hybrid	2013	EIAR	Bako NM
7	BH546	CML395//CML202	Hybrid	2013	EIAR	Bako NM
8	SPRH1	-	Hybrid	2015	EIAR	Bako NM
9	SBRH1	-	Hybrid	2015	EIAR	Bako NM
10	BHQP548	-	Hybrid	2015	EIAR	Bako NM
11	BH670	A7033/F7215//1447b	Hybrid	2002	EIAR	Bako NM
12	BH543	SC22/124b(109)//CML197	Hybrid	2005	EIAR	Bako NM
13	PHB-3253 (Jabi)	-	Hybrid	1996	Pioneer	Pioneer
14	PHB-30G19 (Shone)	-	Hybrid	2006	Pioneer	Pioneer
15	P2859W (Shala)	-	Hybrid	2011	Pioneer	Pioneer
16	P3812W (Limu)	-	Hybrid	2012	Pioneer	Pioneer
17	Kuleni	OPV	OPV	1995	EIAR	Bako NM
18	Gibe-1	OPV	OPV	2001	EIAR	Bako NM
19	Gibe-2	ZM721	OPV	2011	EIAR	Bako NM
20	Gibe-3	OPV	OPV	2013	EIAR	Bako NM
21	SC627 (Abaraya)	-	Hybrid	2006	Seed Co	Seed Co

Source = From National Maize Research program (Bako)

2.3. Lime application rate

Lime application rate (LAR) was determined based on soil laboratory analysis outcome uniformly on the main plots. The amount of LAR per plot was quantified based on the equation below using exchangeable acidity, mass per 0.15m furrow slice and soil bulk density (Shoemaker et

al., 1961; Lierop, 1983; Hellmuth, 2016). It was applied at a rate of, 2.82 and 3.6 t /ha, respectively, at Assosa and Bambasi. Exchangeable acidity and soil bulk density laboratory result before limed respectively were 2.86 and 3.24 Cmol (+)/ kg, and 1.32 and 1.48Mg/m³, in similar manner for Assosa and Bambasi locations.

$$LR, CaCO_3 (kg/ha) = \frac{cmolEA/kg \text{ of soil} * 0.15 m * 10^4 m^2 * B.D. (Mg/m^3) * 1000}{2000}$$

Where LR = lime rate, EA = Exchangeable acidity, BD= Bulk Density.

2.4. Experimental design and management

The experiment was laid out in split plot design with three replications. Limed and unlimed levels as the main plots whereas 21 maize varieties as the sub-plots at both locations. The main plots were separated by 1.5m apart and 2m between replications. All varieties were planted within each main plot at each replication. Each variety was planted two seeds per hill and later thinned two weeks after germination to one seedling per station. Each plot had two rows 5.1m long with planting space 0.75m and 0.3m between rows and plants, respectively, within row equivalent to a planting density of 44,444 plants ha⁻¹. Sub-plot and main-plot sizes were 1.5 m X 5.1m and 5.1m X 33m, respectively.

Planting was done a month after limed when there was ample moisture in the soil. Diammonium phosphate (DAP) and urea were applied at the rate of 150 and 200kg ha⁻¹ at both sites, respectively. DAP was applied at planting whereas urea was split applied 1/3 at planting together with DAP to increase the level of N used as a starter for seed germination and the remaining 1/3 two weeks after germination at thinning and 1/3 at flower

initiation stage. Weeds were controlled manually three times at the 2nd, 4th and 6th weeks after seed emergence. All other management practices were applied uniformly for all experimental plots.

2.5. Data Collection

Crop data- Plant height (PH), ear height (EH), number of ears per plant (NEPP), ear length (EL) and diameter (ED), number of rows per ear (NRPE), number of kernels per row (NKPR), thousand seed weight (TSW), root length (Rle), root volume (RV), root to shoot ratio (RSR) and root biomass (RBM) were collected from plants in the middle rows. Data such as days to anthesis (DA), days to silking (DS), anthesis-silking interval (ASI), days to maturity (MD), number of ears harvested per plot (NEHPP), above ground biomass yield, ear biomass, harvest index, and grain yield were collected replication per plot. Harvest index (HI) was calculated for each plot as the ratio of grain yield to the total aboveground biomass yield (t/ha) x 100. The grain yield was converted to t/ha using the formula standardized to 15% moisture developed by CIMMYT (1988);

$$\text{Grain yield t/ha} = \frac{\text{Field weight } \frac{\text{kg}}{\text{plot}} \text{ at harvesting} * (100 - \text{GMC}) * (0.8 * 10,000)}{1000 * (100 - 15) * (\text{HPA})}$$

Where, GMC = Grain Moisture Content at Harvesting, HPA = harvested plot area (m²), 0.8 = Shelling Coefficient and 85% = Standard Value of Grain Moisture at 15%.

Disease data

Maize streak virus (MSV), Turicum leaf blight (TLB), Phaeosporia leaf spot (PLS) and gray leaf spot (GLS) disease data were recorded using 1-5 scales subjectively following Badu-Apraku *et al.* (2012). 1 = slight infection, less than 10% of the ear leaf covered by lesion, 2 = light infection 10-25% of the ear leaf covered by lesions, 3 = moderate infection, 26-50 % of the ear leaf covered by lesions which lead premature death of the plant and light cobs, 4 = heavy infection, a large number of lesions on leaves below the top ear, 51-77 % of moderate to large number of leaves above the top ear death. 5 = very heavy infection, 76-100% of the ear covered by lesions and cause the premature death of the plants and cobs.

2.6. Data Analyses

2.6.1. Analysis of variance

Data analysis was carried out using SAS software version 9.0 (SAS, 2002). The generated data on yield and yield-related components were subjected to analysis of Variance (ANOVA) procedure using a general linear model (GLM). F-test was used to test whether the traits of the two locations data fit the assumption of homogeneity rule to be combined or not. Based on this test, traits could not be obeyed the rule and combined (larger EMS/smaller EMS) values of each trait of location were greater than the F-tabulated value at 5% which violated homogeneity rule and separate analysis was used. The existence of significant difference among the varieties and other agronomic traits; mean comparison was done using Duncan Multiple Range test (DMRT) at 5% probability level. The main effect and sub plot interactions were non-significant and the analysis was mainly done on the sub plot factor (varieties), rather lime factor.

2.6.2. Genetic variance components

Table 2. The formula used for estimating the phenotypic and genetic variance components

No	Variances	Formula	References
1.	Genotypic variance	$\sigma^2 g = \frac{MSg - MSe}{r}$	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	$PCV = \frac{\sqrt{\sigma^2 p}}{\bar{X}} * 100$	Burton and De Vane (1953)
4.	Genotypic coefficient of variation	$GCV = \frac{\sqrt{\sigma^2 g}}{\bar{X}} * 100$	Burton and De Vane (1953)
5.	Heritability (Broad senses)	$H = \frac{\sigma^2 g}{\sigma^2 p} * 100$	Singh and Chaudhary (1985)
6.	Genetic Advance	$GA = \sigma p * H * K$	Johnson <i>et al.</i> (1955)

Where $\sigma^2 p$ = 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, \bar{X} = population mean, H = heritability, GA = Genetic Advance, $K = 2.063$ (selection differential at 5%) and r = number of replications.

2.6.3. Correlation analysis

The phenotypic and genotypic correlation analysis between agronomic traits and grain yield of two variables was done using the formula developed by Singh and Chaudhary in 1985.

$$r_{ph} = \frac{\sigma^2 P_{12}}{\sqrt{(\sigma^2 P_1)(\sigma^2 P_2)}}, r_{gh} = \frac{\sigma^2 g_{12}}{(\sigma^2 g_1)(\sigma^2 g_2)}$$

Where; r_{p12} = phenotypic correlation coefficient between two traits, r_{g12} = genotypic correlation coefficient between two traits, $\sigma^2 P_{12}$ the phenotypic covariance between the two traits, $\sigma^2 P_1$ = the phenotypic variance of the first trait and $\sigma^2 P_2$ = phenotypic variance of the second trait, $\sigma^2 g_{12}$ = the genotypic covariance between the two traits, $\sigma^2 g_1$ = the genotypic variance of the first trait and $\sigma^2 g_2$ = the genotypic variance of the second trait. The calculated phenotypic and genotypic correlation value was tested for their significance using t-test as followed: Phenotypic value was tested for its significance using in which r_{ph} , represent = the

phenotypic correlation coefficient, n = the number of genotypes tested and $SE_{r_{ph}}$, also represent = Standard error of the phenotypic correlation coefficient (Sharma, 1998).

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

The genotypic coefficients of correlations were also tested about their significance using the formula obtained by Robertson (1959) as followed:

$$t = \frac{rg_{xy}}{SE (rg_{xy})}$$

$$SE_{rg_{xy}} = \sqrt{\frac{1 - r_{g_{xy}}^2}{2h_x^2 h_y^2}}$$

Where, h_x^2 = the heritability of trait x and h_y^2 = the heritability of trait y. Calculated "t" value was compared with tabulated "t" value at $(n-2)$ degree of freedom at 5% significance level. Where, n is the number of genotypes tested.

2.6.4. Path coefficient analysis

The path coefficient analysis was done using the formula of Dewey and Lu (1959) and with statistical package developed by Doshi (1991) to identify the most influential trait on the grain yield either directly or indirectly.

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

Where, r_{ij} is association between the independent variable (i) and dependent variable (j) as measured by correlation coefficient; P_{ij} is component of direct effect of the independent variable (i) on the dependent variable (j) as measured by path coefficient and $\sum r_{ik} P_{kj}$ is summation of components of indirect effects of a given independent variable (i) on a given dependent variable (j) via all other independent variables.

3. Results and Discussion

3.1. Analysis of variance

The analysis of variances showed that there were significant and highly significant differences among maize genotypes in all the traits at both locations

3.2. Range and mean of different traits

Wide mean ranges were verified for thousand seed weight (TSW) from 189.33 to 318.67g, ear height (EH), 53.7cm to 93.5cm, plant height (PH), 121.2 cm to 159 cm and yield t/ha (1.623 to 3.43) at Assosa, likewise, yield t/ha (4.42 to 7.35) and PH in cm (144 to 226.5) at Bambasi. The wide range of the most measured traits reinforced the existence of adequate genetic variability among the genotypes in the environment and can be improved till the maximum range value for improving the grain yield (Table 4 and 5). The result is harmony with the finding of Turi *et al.* (2007) that renowned, wide range of variations was detected from kernel weight and grain yield at maize genotypes.

3.3. Phenotypic and Genotypic variations

The genotypic and phenotypic variability that exist in a species is indispensable in developing stress tolerant varieties and designing the breeding platform this was done according to Deshmukh *et al.* (1986) and Sesay *et al.* (2016), report the PCV, GCV, and GA values which were categorized and discussed as low (0-10), moderate (10-20%) and high (> 20%). The phenotypic variance was alienated in to genotypic and environmental variance to estimate the involvement of every to the total variation. Though, phenotypic variances were higher than the genotypic variances for all studied traits at both sites, hence indicate the influence of the environment, especially the soil on these traits (Table 3 and 4) for

Assosa and Bambasi sites, respectively. Comparable findings were detected by Bello *et al.* (2012).

Grain weight, ear biomass (EBM), above ground biomass (ABM), ear (EH) and plant height (PH), days to maturity (DM), days to 50% silking (DS), days to 50% anthesis (DA), 1000-seed weight (TSW), ear diameter (ED), ear length (EL), number of ears harvested per plot (NEHPP), number of kernels per row (NKPR) are variables at both sites which may contribute in the genetic diversity (Table 3 and 4) in both locations. The outcome of the conclusion is similar with the finding of (Muchie and Fentie, 2016; Ferdoush *et al.*, 2017) who identified that those traits are significant and can be contribute genetic diversity impost.

Genotypic coefficient of variation measures the heritable variability with in a trait. In general, the GCV and PCV values found between 2.72%-28.8% and 2.83%-36.2%, correspondingly. The GCV values of PH, GLS, RL, NKPR, SCH, NRPE and EL were observed as moderate whereas EH, TLB, ASI, ABM, RBM, EBM, NEHPP, and grain yield were showed high PCV estimate values which show that the phenotypic variance among the tested maize genotypes with the above traits are moderate (Table 3 and 4) at both Assosa and Bambasi locations, respectively. This finding is in agreement with the result of Azam *et al.* (2014); Muchie and Fentie (2016). Those traits with high heritability, GCV and GA values are governed by additive gene action and can be improved through mass selection technique and similar with the study of Nwangburuka *et al.* (2012). On the contrary, low PCV and GCV share of the total variances were observed from DA, DS, and MD simultaneously at both locations (Table 4 and 5) at both sites indicated that the environment, critically soil acidity highly influenced these traits and comparable with the finding of Vashistha *et al.* (2013); Sesay *et al.* (2016); Muchie and Fentie (2016); Pandey *et al.* (2017) who noted that the lowest PCV and GCV estimate values were recorded from days to 50% anthesis, days to 50% silking and maturity date whereas the highest from grain yield and kernel weight. Dao *et al.* (2017) also conveyed that, the GCV and heritability values of maize traits decreased under stressed condition than optimum condition.

3.4. Heritability estimates

Heritability estimate values are of incredible meaning to the breeder, as the extent shows the precision with which a genotype can be predictable by its phenotypic appearance. According to Singh (2001) traits such as GLS, root bio mass (RBM), root length (Rle) and ED moderate (40-59%), ABM and EBM, moderately high (60-79%), and DA, DS and MD, were detected very high (>80%) heritability estimate values (Table 4 and 5) at both Assosa and Bambasi sites, respectively. Traits including EH, EBM, ABM, and grain yield were observed high GCV and heritability values in both locations revealed that these traits highly influenced by additive genes. Other studied traits which have low heritability

and moderate GAM at both locations revealed that those traits were governed by non-additive gene action and the variation highly attributed by the effect of soil acidity (Table 3 and 4). This finding agreed with Bello *et al.* (2012); Muchie and Fentie (2016) and Pandey *et al.* (2017) prominent that the higher heritability value coupled with the genetic advance for EBM and ABM considered as the genetic parameters for the improvement and selection for higher yield genotypes. From the finding it is clear that high heritability ensures not always show a high genetic achievement, therefore

high heritability and low GA values of AD, SD and MD in the study (Table 4 and 5) indicates these traits are controlled by non-additive genes which need management practice rather than selection to improve the trait performance. This exploration granted with Tilahun *et al.* (2014).

In general, traits studied at both locations recorded low GCV and GAM values indicated that variations among the studied traits and the genotypes were highly influenced by the environment, intensely by the soil.

Table 3. Variance components of mean grain yield and other related traits at Assosa in 2017 main season

Traits	Mean \pm SE	Range		σ^2_p	σ^2_g	σ^2_e	PCV (%)	GCV (%)	H (%)	GA	GAM (%)	CV (%)	R ² (%)
		Min.	Max.										
DA	87.24 \pm 1.3	81.50	91.83	13.68	11.14	2.54	4.24	3.83	81	6.21	7.12	1.8	79
DS	90.81 \pm 1.35	85.33	96.50	14.64	11.91	2.73	4.21	3.80	81	6.42	7.07	1.8	80
MD	148.39 \pm 0.94	145.83	155.50	17.61	16.27	1.34	2.83	2.72	92	8.00	5.39	0.8	91
PH	139.10 \pm 13.41	121.20	159.00	376.07	106.27	269.80	13.94	7.41	28	11.30	8.13	11.8	59
EH	69.20 \pm 7.91	53.70	93.50	289.00	195.10	93.90	24.57	20.18	68	23.68	34.21	14.0	75
GLS	2.38 \pm 0.27	1.92	2.75	0.18	0.07	0.11	17.87	11.25	40	0.35	14.60	13.9	56
MSV	1.73 \pm 1.42	1.42	2.25	0.14	0.04	0.10	21.46	11.44	28	0.22	12.58	18.2	52
TLB	2.71 \pm 0.33	1.92	3.33	0.36	0.19	0.17	22.04	16.10	53	0.66	24.28	15.0	63
ASI	3.57 \pm 0.63	2.67	4.67	0.85	0.26	0.59	25.83	14.35	31	0.59	16.44	21.5	48
ABM	8.62 \pm 1.15	6.4	10.4	3.81	2.41	1.4	25.6	20.36	63	2.54	33.4	15.8	70
RBM	0.30 \pm 0.04	0.25	0.39	0.005	0.002	0.003	22.95	15.54	46	0.07	21.71	16.9	64
EBM	2.33 \pm 0.35	1.7	3.5	0.71	0.27	0.26	36.2	28.8	63	1.1	47.2	21.9	71
RV	0.03 \pm 0.0	0.02	0.03	0.00005	0.00002	0.00002	26.57	18.54	49	0.01	26.69	19.0	65
Rle	25.15 \pm 2.61	19.75	29.42	17.18	6.93	10.25	16.48	10.47	40	3.45	13.72	12.7	52
RSR	0.19 \pm 0.02	0.16	0.23	0.0013	0.0004	0.001	19.44	11.02	32	0.02	12.88	16.0	54
TSW	248.25 \pm 30.36	189.33	318.67	3153.04	1770.67	1382.37	22.62	16.95	56	65.05	26.20	15.0	62
NKPR	32.98 \pm 3.16	29.07	39.50	22.49	7.48	15.01	14.38	8.30	33	3.26	9.87	11.7	59
SCH	29.37 \pm 2.18	26.17	31.67	10.24	3.11	7.13	10.90	6.00	30	2.00	6.82	9.1	56
NEHPP	25.83 \pm 3.39	22.00	32.83	27.50	10.28	17.22	20.31	12.41	37	4.04	15.66	16.1	57
NRPE	13.92 \pm 1.74	12.20	17.17	5.62	1.06	4.56	17.03	7.41	19	0.93	6.65	15.3	49
EL	14.50 \pm 1.24	11.88	17.27	4.92	2.62	2.30	15.29	11.15	53	2.43	16.78	10.5	74
ED	3.88 \pm 0.21	3.63	4.37	0.13	0.07	0.06	9.41	6.78	52	0.39	10.07	6.5	73
GYld	2.160 \pm 0.339	1.623	3.043	4.097	2.372	1.725	29.63	22.55	58	7.64	35.39	19.2	84

DA=Days to 50% of plants Shade pollen, DS=Days to 50% Silk emerged (2-3cm silk length), MD=Maturity Date, PH=Plant Height, EH=Ear Height, GLS= Gray Leaf Spot, MSV=Maize Streak virus, TLB=Turcicum Leaf Blight, ASI=Anthesis Silking Interval, ABM=Above Ground Biomass (t/ha), RBM=Root Bio mass (g/plot), RV=Root Volume (cm³), Rle=Root Length (cm), EBM= Ear Biomass (t/ha), RSR=Root to Shoot Ratio, TSW=Thousands Seed Weight (g/plot), NKPR=Number of Kernels Per Row, SCH=Stand Count at Harvest, NEHPP=Number of ears harvested per plant, NRPE=Number of Rows Per Ear, EL=Ear Length (cm), ED=Ear Diameter (cm), GYld= Grain Yield (t/ha).

Table 4. Variance components of mean grain yield and other related traits at Bambasi in 2017 main season

Traits	Mean± SE	Range		σ^2_p	σ^2_g	σ^2_e	PCV (%)	GCV (%)	H (%)	GA	GAM (%)	CV (%)	R ² (%)
		Min.	Max										
DA	81.88±1.47	77.50	88.67	20.7	17.4	3.2	5.55	5.10	84	7.91	9.66	2.2	84
DS	85.47±1.62	81.00	92.67	23.2	19.3	3.9	5.63	5.13	83	8.22	9.62	2.3	83
MD	145.05±1.17	140.8	154.3	31.2	29.1	2.1	3.85	3.72	93	10.71	7.39	1.0	92
GLS	2.07±0.24	1.67	2.33	0.1	0.032	0.1	16.78	8.61	26	0.19	9.09	14.4	58
PLS	2.00±0.23	1.67	2.25	0.1	0.023	0.1	15.80	7.58	23	0.15	7.48	13.9	62
TLB	2.47±0.25	1.833	2.83	0.4	0.113	0.09	26.54	13.58	26	0.35	14.28	12.3	73
ABM	12.2±0.75	10.1	15.9	8.4	5.2	3.2	23.8	18.7	62	3.69	30.3	14.7	83
EBM	5.8±0.6	4.2	8.3	4.1	2.6	1.5	28.17	22.4	63	2.64	36.7	17.1	84
PH	184.89±10.33	144.0	226.5	771.9	611.7	160.2	15.03	13.38	79	45.27	24.48	6.8	79
EH	93.18±8.85	61.17	129.3	688.5	571.0	117.5	28.2	25.64	83	44.74	48.01	11.6	82
ASI	3.57±0.63	2.67	4.67	0.9	0.3	0.6	25.83	14.35	31	0.59	16.38	21.5	48
RBM	0.44±0.07	0.33	0.54	0.012	0.004	0.007	24.47	14.82	37	0.08	18.44	19.5	71
RL	31.49±3.07	26.50	36.33	27.6	13.5	14.1	16.69	11.67	49	5.29	16.79	11.9	61
RSR	0.17±0.02	0.14	0.21	0.001	0.001	0.001	20.24	15.09	56	0.04	23.13	13.5	60
NKPR	41.41±2.93	37.27	46.37	20.7	7.8	12.9	11.00	6.76	38	3.54	8.54	8.7	54
NEHPP	29.10±4.34	24.00	40.33	50.9	22.6	28.3	24.53	16.36	44	6.52	22.42	18.3	59
NRPE	14.03±1.24	12.17	16.33	4.4	2.0	2.3	14.86	10.16	47	2.00	14.29	10.8	53
SCH	27.40±2.92	21.00	32.5	22.8	10.0	12.8	17.42	11.55	44	4.31	15.74	13.0	65
EL	18.36±1.3	15.67	21.43	7.5	5.0	2.5	14.92	12.14	66	3.73	20.30	8.7	69
ED	4.43±0.36	3.89	5.17	0.4	0.2	0.2	14.13	10.04	50	0.65	14.66	9.9	58
GYld	5.443±0.75	4.42	7.35	21.76	13.34	84.3	27.10	21.22	61	18.59	34.15	16.9	85

DA=Days to 50% of plants Shade pollen, DS=Days to 50% Silk emerged (2-3cm silk length), MD=Maturity Date, PH=Plant Height, EH=Ear Height, GLS=Gray Leaf Spot, PLS=Phaeosporia leaf spot, TLB=Turcicum Leaf Blight, ASI=Anthesis Silking Interval, ABM=Above Ground Biomass (t/ha), RBM=Root Bio mass (g/plot), RL=Root Length (cm), EBM= Ear Biomass (t/ha), RSR=Root to Shoot Ratio, NKPR=Number of Kernels Per Row, SCH=Stand Count at Harvest, NEHPP=Number of ears harvested per plant, NRPE=Number of Rows Per Ear, EL=Ear Length (t/ha), ED=Ear Diameter (t/ha), GYld= Grain Yield (t/ha).

3.6. Trait associations

Improving a target trait can be achieved by indirect selection via other traits that are more related and heritable makes easy for selection. Therefore selection strategy needs to know the interrelationship of traits among themselves and with the target trait. Hence trait association plays an indispensable role to identify and select the target trait through the analysis of correlation coefficients.

3.6.1. Phenotypic and genotypic correlations of grain yield and agronomic traits

In this investigation various traits show s positive significant ($P \leq 0.01$) association with the grain yield (t/ha) with ear biomass, 1000-seedweight, above ground biomass, number of kernels per row and number of ears harvested per plot at the genotypic and phenotypic level (Table 5 and 6) at both Assosa and Bambasi sites , respectively. The study revealed that the association can be used as base for selection these traits which may have direct and/or indirect contribution improving stress tolerance and increasing the yield potential positively. This finding is in the harmony of Hefny (2011); Atnafua and Rao (2014) and Pandey *et al.* (2017) who noted that the grain yield was highly and significantly correlated with 100-seed weight, number of kernels per row, ear length and plant height while negatively correlated with days to 50% silking emergence.

However, it is non-significant anthesis silking interval negatively correlated with grain yield which indicate improving varieties with short ASI may be imperative under stressed condition to escape the stress and this is strongly agreed with the finding of Dao *et al.* (2017) who reported that ASI had negative low correlation with grain yield under stressed conditions, but contradicted with Aminu and Izge, (2012) who reported that ASI was significant and positively correlated with grain yield.

3.6.2. Correlation among yield related traits

Days to 50% silk emergence had strong positive significant association genotypic and phenotypic with days to 50% anthesis in a plot and with maturity date at both locations. This finding is in line with Taimur *et al.* (2011) and Sadaiah *et al.* (2013) stated that days to 50% silk emergence is positively and significantly associated with days to 50% plants pollen shading, but the report contradicted with this result that negative genotypic correlations were reported between DS and PH, DS and EH, DS and EL, DA and PH, DA and EH, DA and EL. The outcome of Bambasi partially contradicted with Wannows *et al.* (2010) who conveyed that DS positively correlated with NKPE, but positively and significantly correlated with ED, EH and PH. This finding is also strongly agreed with the finding of Hefny (2011) who stated those days to 50% silking and anthesis strong and significant positively associated with each other at the phenotypic and genotypic level.

Ear biomass per plot (EBM), highly significant and positively correlated with plant height and above ground bio mass (Table 5 and 6) at Assosa and Bambasi sites, respectively. The finding is similar with Taimur *et al.* (2011) indicated that EBM significantly and positively correlated with plant height which resulted positive contribution for yield improvement of maize.

Ear length (EL) highly significant and positively associated with ear bio mass, 1000-seed weight and number of kernels per row at the genotypic and phenotypic level in both sites (Table 5 and 6). This outcome is related with the previous studies (Wannows *et al.*, 2010 and Sadaiah *et al.*, 2013) who reported that EL exhibited significant positive genotypic association with NKPR, seed weight and EBM. These traits had positive contribution under acidic soil.

Ear diameter (ED) had significant and positive genotypic and phenotypic association with 1000-seed weight and ear length which had substantial positive involvement for yield. The finding is in agreement with Yoseph *et al.* (2013), at the genotypic level significant and positive association was observed between ED and 1000-seed weight.

Plant height significantly and positively correlated at the genotypic and phenotypic level with maturity date at both sites. The outcome is comparable with Bello *et al.* (2012) stated that plant height had positive significant association with maturity date. Ear height significantly and positively correlated at the genotypic and phenotypic level with days to 50% plants in the plot shade pollen, days to 50% of plants in the plot silk emergence, maturity date and plant height. It also significantly and positively associated with ABM, EBM, TSW and EL (Table 5 and 6). This result is also comparable with Carpici and Celik (2010); Wannows *et al.* (2010); Cancellier *et al.* (2011); Sadaiah *et al.* (2013) and Silva *et al.* (2016) who reported that EH, positively and significantly correlated with PH at the genotypic level and also NRPE and ED at the phenotypic level.

Generally, the inter association among traits is crucial for designing effective selection for maize improvement in acidic soil. The higher magnitude of genotypic correlation than their phenotypic correlation coefficients of traits advocating a strong inherent association subsists for the traits studied and phenotypic selection may be gratifying. Therefore during selection for the development of acid soil tolerant varieties in maize, it is better to give especial attention for those traits which showed positive significant phenotypic and genotypic connotations with in traits and among the genotypes related to the grain yield.

Table 5. Genotypic (above) and phenotypic (below) diagonal correlations among 16 traits of maize varieties at Assosa in 2017 main cropping season

Traits	ABM	EBM	TSW	NKPR	NEHPP	NEPP	NRPE	EL	ED	Yld
ABM		0.716**	0.362	0.584**	0.649**	0.432	-0.038	0.485*	0.478*	0.716**
EBM	0.464**		0.774**	0.658**	0.5203*	0.312	0.112	0.696**	0.841**	0.998**
TSW	0.355**	0.402**		0.445*	0.389	0.244	-0.003	0.571**	0.641**	0.759**
NKPR	0.311**	0.366**	0.218*		0.674**	0.587**	0.064	0.724**	0.579**	0.661**
NEHPP	0.439**	0.312**	0.381**	0.127		0.834**	-0.027	0.626**	0.359	0.4935*
NEPP	0.263**	0.321**	0.207**	0.15	0.794**		-0.168	0.493*	0.178	0.286
NRPE	-0.002	0.142	-0.013	0.283**	-0.082	-0.077		0.018	0.363	0.107
EL	0.356**	0.464**	0.368**	0.590**	0.345**	0.240**	0.206**		0.786**	0.686**
ED	0.363**	0.572**	0.293**	0.603**	0.151**	0.105	0.311**	0.732**		0.835**
Yld	0.442**	0.997**	0.369**	0.355**	0.294**	0.319**	0.144	0.440**	0.562**	

* and ** Indicate significance and highly significance at 5% and 1% probability level respectively. ABM=above ground biomass (t/ha) =, EBM= ear biomass (t/ha) =, TSW= thousand seed weight (g/plot), NKPR=number of kernels per plot, NEHPP=number of ears per plot, NEPP=number of ears per plot, NRPE= number of rows per, Ears = EL=ear length(cm), ED= ear diameter (cm); Yld= grain yield (t/ha)

Table 5 (Continued)

Traits	DA	DS	MD	PH	EH	ASI	Yld
DA		0.981**	0.785**	0.208	0.695**	0.062	0.07
DS	0.958**		0.771**	0.144	0.697**	0.253	-0.006
MD	0.675**	0.657**		0.509*	0.828**	0.062	0.329
PH	0.019	-0.053	0.133		0.633**	-0.29	0.707**
EH	0.366**	0.342**	0.473**	0.731**		0.119	0.35
ASI	0.04	0.324	0.065	-0.246**	-0.025		-0.38
Yld	0.089	0.083	0.205	0.299**	0.255**	0.001	

* and ** Indicate significance and highly significance at 5% and 1% probability level respectively. DA= days to 50% plants shade pollen in the row, DS=days to silking, MD=maturity date, PH= plant height (cm), Era height (cm), ASI = anthesis silking interval, and Yld= grain yield (t/ha).

Table 6. Genotypic (above) and phenotypic (below) correlations among 16 traits of maize varieties at Bambasi in 2017 main cropping season

Traits	ABM	EBM	TSW	NKPR	NEHPP	NEPP	NRPE	EL	ED	Yld
ABM		0.987**	0.675**	0.58	0.815**	0.324	0.086	0.665**	0.409	0.985**
EBM	0.979**		0.670**	0.587**	0.784**	0.323	0.1	0.657**	0.422	0.998**
TSW	0.315**	0.327**		0.651**	0.405	-0.182	-0.095	0.802**	0.611**	0.664**
NKPR	0.457**	0.476**	0.399*		0.278	-0.072	-0.243	0.759**	0.157	0.581**
NEHPP	0.539**	0.528**	0.219*	0.18		0.559**	0.003	0.344	0.097	0.786**
NEPP	0.296**	0.281**	-0.098	0.096	0.602**		0.041	-0.158	-0.095	0.331
NRPE	0.218*	0.240**	0.064	0.031	0.052	0.139		0.063	0.345	0.105
EL	0.5432**	0.543**	0.530**	0.699**	0.257**	0.029	0.156		0.494*	0.647**
ED	0.441**	0.441**	0.463**	0.247	0.207*	0.096	0.523**	0.431*		0.421
Yld	0.978**	0.998**	0.311**	0.464**	0.528**	0.297**	0.238**	0.523*	0.435**	

* and ** Indicate significance and highly significance at 5% and 1% probability level respectively. ABM=above ground biomass (t/ha) =, EBM= ear biomass (t/ha)=, TSW= thousand Seed weight (g/plot), NKPR=number of kernels per plot, NEHPP= number of ears per plot, NEPP=number of ears per plot, NRPE= number of rows per ear = EL=ear length (cm), ED= ear diameter (cm); Yld= grain yield (t/ha).

Table 6 (Continued)

Traits	DA	DS	MD	PH	EH	ASI	Yld
DA		0.989**	0.821**	0.661**	0.754**	-0.055	0.403
DS	0.960**		0.824**	0.657**	0.766**	-0.016	0.365
MD	0.682**	0.680**		0.777**	0.814**	0.144	0.427
PH	0.471**	0.442**	0.637		0.871**	-0.054	0.532*
EH	0.551**	0.532**	0.656	0.835**		0.084	0.386
ASI	-0.019	-0.012	0.097	-0.039	0.013		-0.179
Yld	0.306**	0.271**	0.253**	0.432**	0.387**	0.001	

* and ** Indicate significance and highly significance at 5% and 1% probability level respectively. DA=days to 50% plants shade pollen in the row, DS=days to 50% silking, MD=maturity date, PH= plant height (cm), Era height (cm), ASI=anthesis silking interval, and Yld= grain yield (t/ha).

3. 7. Path coefficient analysis

Path coefficient analysis is very imperative tool that allow partitioning of correlation coefficient values into direct and indirect effects of traits on the dependent variable or the yield. It also helps to assess the cause and effect relationship for effective target trait selection. Finally it provides deciding the most prominent and significant trait influenced the yield either positively or negatively.

Genotypic path coefficient analysis

Genotypic path coefficient analysis of grain yield and yield attributes at both Assosa and Bambasi are presented in Table 7 and 8, respectively. The bolded diagonal under lined values indicated the direct effect of each trait on the grain yield and the other values indicate indirect effects. Ear biomass had the highest significant positive direct effect on grain yield followed by above ground biomass in both locations. Ear diameter, TSW, ABM, EL, NKPR, HI, SCH and RBM had strong indirect effect on the grain yield by ear biomass at Assosa site (Table7), and plant height exhibited strong positive indirect effect on the grain yield by ABM, EBM, TSW, NKPR, NEHPP, and EL (Table 8) which indicates the correlation coefficient with grain yield is due to the exertion of these traits. The negative direct effect of plant height on the grain yield of this finding at Bambasi is similar with the pervious finding Sreckov *et al.* (2011) while partially contradicted with the finding of Kumar *et al.* (2006) and Patil *et al.* (2016) who reported that plant height and EBM showed positive direct effect on the grain yield.

The positive direct effect of root biomass on the grain yield agreed with the findings of Mhoswa *et al.* (2016) and Silva *et al.* (2016) who reported that root dry matter and root fresh weight had positive direct effect on grain yield which directly related with the nitrogen absorption capacity of the crop that helps to afford the nutrient demand of the crop and increasing the yield. Therefore direct selection of these traits is advisable for

improving the grain yield. Generally from this finding, plant height and ear diameter were positively and significantly associated with grain yield, but PH at Bambasi and ED at Assosa showed negative direct effect which means direct selection of these traits can compromise for the grain yield improvement. Above ground biomass, ear biomass, HI, and EL were positive and significantly correlated with the grain yield at the genotypic level for both sites as well as had positive direct effect. This revealed that for improving the grain yield in the acidic soil condition considering these traits will be crucial at the time of selection.

Phenotypic path coefficient analysis

Ear biomass was perceived strong positive direct effect on the grain yield. Ear height and RBM also exerted positive direct effect on the grain yield while PH, TSW, NKPR, NEHPP, and EL exerted negative direct effect on the grain yield at both sites (Table 9 and 10). But these traits had positive indirect effect on the grain yield by other traits. For instance PH exerted positive indirect effect on the grain yield by RBM, EBM, ED, and NEPP at Assosa location (Table 9) and Ear length, NEHPP, NKPR, PH and SCH applied positive indirect effect on the grain yield at Bambasi site (Table 10). Most traits were detected negative direct and indirect effect on the grain yield this may be the impact of soil acidity which influenced those traits. This is in line with the finding of Bello *et al.* (2012) and Krishnaji *et al.* (2017) who reported that EBM exerted strong positive direct effect on the grain yield which indicates this trait has an inviolable contribution for grain yield improvement to be considered during selection for acidic soil tolerant. The diseases including TLB, GLS and PLS were negatively. In general this finding indicate that the direct effect of EBM, RBM, EH and ABM were observed as the main factors for strong association with the grain yield at the phenotypic level. Therefore understanding the direct and indirect effect of traits may be decisive for selection improving the yield under stressed soil condition.

Table 7. Genotypic direct (underlined) and indirect effects of agronomic traits for yield at Assosa in 2017 main cropping season

Variables	PH	GLS	PLS	MSV	TLB	HI	ABM	RBM	EBM	TSW	NKPR	SCH	EL	ED	Yld (r _g)
PH	<u>0.000</u>	-0.046	0.013	0.018	0.018	0.033	0.138	0.015	0.576	-0.023	-0.003	-0.030	0.006	-0.009	0.71**
GLS	0.000	<u>0.071</u>	-0.021	-0.011	-0.026	0.024	-0.179	-0.018	-0.576	0.020	0.004	0.021	-0.008	0.010	-0.69*
PLS	0.000	0.049	<u>-0.030</u>	-0.006	-0.017	-0.001	-0.120	-0.012	-0.466	0.019	0.002	0.010	-0.005	0.007	-0.59*
MSV	0.000	0.030	-0.007	<u>-0.026</u>	-0.015	-0.017	-0.101	-0.010	-0.391	0.023	0.004	0.021	-0.005	0.004	-0.49*
TLB	0.000	0.062	-0.017	-0.013	<u>-0.029</u>	0.019	-0.160	-0.015	-0.530	0.020	0.003	0.020	-0.005	0.007	-0.64*
HI	0.000	0.009	0.000	0.002	-0.003	<u>0.177</u>	-0.032	-0.007	0.451	-0.028	-0.002	-0.002	0.006	-0.014	0.56**
ABM	0.000	-0.065	0.018	0.013	0.024	-0.029	<u>0.196</u>	0.018	0.585	-0.017	-0.004	-0.021	0.007	-0.010	0.72**
RBM	0.000	-0.056	0.016	0.011	0.020	-0.053	0.152	<u>0.023</u>	0.374	-0.014	-0.003	-0.026	0.005	-0.004	0.44**
EBM	0.000	-0.050	0.017	0.012	0.019	0.098	0.140	0.010	<u>0.817</u>	-0.036	-0.004	-0.018	0.010	-0.018	0.99**
TSW	0.000	-0.030	0.012	0.013	0.013	0.108	0.071	0.007	0.632	<u>-0.046</u>	-0.003	-0.012	0.009	-0.014	0.76**
NKPR	0.000	-0.039	0.008	0.014	0.011	0.047	0.115	0.011	0.537	-0.021	<u>-0.006</u>	-0.014	0.011	-0.012	0.66**
SCH	0.000	-0.039	0.008	0.014	0.016	0.011	0.109	0.016	0.386	-0.015	-0.002	<u>-0.038</u>	0.006	-0.008	0.46**
EL	0.000	-0.036	0.009	0.009	0.009	0.072	0.095	0.008	0.569	-0.027	-0.005	-0.016	<u>0.015</u>	-0.017	0.69**
ED	0.000	-0.034	0.010	0.005	0.009	0.117	0.094	0.005	0.687	-0.030	-0.004	-0.014	0.012	<u>-0.021</u>	0.84**

Residual effect (R) = 0.032

PH= Plant Height, GLS = Gray Leaf Spot, PLS = Phaeosporia Leaf Spot, MSV=Maize Steak Viruses, TLB = Turcicum Leaf Blight, HI = Harvesting Index, ABM = Above Ground Biomass, RBM= Root Biomass, EBM = Ear Biomass, TSW = Thousand Seed Weight, NKPR=Number of Kernels Per row, SCH = Stand count at Harvest, EL= Ear length, ED = Ear Diameter and Yld = Grain yield.

Table 8. Genotypic direct (underlined) and indirect effects of agronomic traits for yield at Bambasi in 2017 main cropping season

Variables	PH	GLS	PLS	TLB	HI	ABM	RBM	EBM	TSW	NKPR	SCH	NEHPP	EL	Yld (r _g)
PH	<u>-0.010</u>	0.025	-0.011	-0.008	0.040	0.162	-0.014	0.322	0.021	0.003	-0.016	0.017	0.001	0.53*
GLS	0.007	<u>-0.038</u>	0.015	0.010	-0.067	-0.196	0.010	-0.406	-0.016	-0.002	0.018	-0.022	0.000	-0.69*
PLS	0.007	-0.031	<u>0.018</u>	0.011	-0.057	-0.212	0.010	-0.405	-0.018	-0.002	0.021	-0.027	-0.001	-0.69*
TLB	0.007	-0.030	0.015	<u>0.013</u>	-0.072	-0.243	0.009	-0.486	-0.020	-0.003	0.019	-0.027	-0.001	-0.82*
HI	-0.004	0.023	-0.009	-0.009	<u>0.108</u>	0.241	-0.007	0.524	0.016	0.002	-0.011	0.022	0.000	0.89**
ABM	-0.006	0.025	-0.013	-0.011	0.089	<u>0.294</u>	-0.013	0.583	0.019	0.003	-0.017	0.030	0.001	0.99**
RBM	-0.006	0.015	-0.007	-0.004	0.031	0.151	<u>-0.025</u>	0.287	0.017	0.002	-0.010	0.017	0.000	0.47*
EBM	-0.006	0.026	-0.012	-0.011	0.096	0.290	-0.012	<u>0.591</u>	0.019	0.003	-0.016	0.029	0.001	0.99**
TSW	-0.007	0.021	-0.011	-0.009	0.059	0.199	-0.014	0.396	<u>0.029</u>	0.003	-0.015	0.015	0.001	0.67**
NKPR	-0.007	0.016	-0.008	-0.007	0.052	0.171	-0.008	0.347	0.019	<u>0.005</u>	-0.009	0.010	0.001	0.58**
SCH	-0.007	0.029	-0.016	-0.010	0.050	0.210	-0.010	0.398	0.019	0.002	<u>-0.024</u>	0.026	0.001	0.67**
NEHPP	-0.005	0.022	-0.013	-0.009	0.064	0.240	-0.011	0.463	0.012	0.001	-0.016	<u>0.037</u>	0.000	0.78**
EL	-0.007	0.020	-0.011	-0.010	0.053	0.196	-0.008	0.388	0.023	0.004	-0.014	0.013	<u>0.001</u>	0.65**

Residual effect (R) = 0.045

PH = Plant Height, GLS = Gray Leaf Spot, PLS = Phaeosporia Leaf Spot, TLB = Turicum Leaf Blight, HI = Harvesting Index, ABM = Above Ground Biomass, RBM = Root Mio mass, EBM = Ear Biomass, TSW = Thousand Seed Weight, NKPR=Number of Kernels Per row, SCH = Stand count at Harvest, NEHPP = Number of ears Harvested Per plot, EL= Ear length and Yld = Grain yield.

Table 9. Phenotypic direct (underlined) and Indirect effects of agronomic traits for yield at Assosa in 2017 main cropping season

Variables	PH	EH	GLS	MSV	TLB	HI	ABM	RBM	EBM	TSW	NKPR	NEHPP	NEPP	EL	ED	Yld (r_{ph})
PH	<u>-0.003</u>	0.006	-0.001	0.004	0.000	0.000	-0.009	0.002	0.320	-0.009	-0.001	-0.007	0.003	-0.010	0.004	0.30**
EH	-0.002	<u>0.008</u>	-0.001	0.004	0.000	0.000	-0.011	0.002	0.271	-0.007	-0.001	-0.004	0.001	-0.008	0.003	0.26**
GLS	0.001	-0.002	<u>0.006</u>	-0.006	0.001	0.000	0.009	-0.002	-0.358	0.008	0.001	0.005	-0.002	0.008	-0.004	-0.34*
MSV	0.001	-0.002	0.002	<u>-0.015</u>	0.001	0.000	0.006	-0.001	-0.257	0.012	0.001	0.006	-0.003	0.007	-0.003	-0.25*
TLB	0.001	-0.002	0.003	-0.004	<u>0.002</u>	0.000	0.009	-0.002	-0.242	0.007	0.001	0.006	-0.006	0.005	-0.001	-0.22*
HI	-0.001	0.001	0.000	0.001	0.000	<u>-0.002</u>	0.003	0.000	0.680	-0.008	0.000	-0.003	0.004	-0.009	0.005	0.67**
ABM	-0.001	0.004	-0.002	0.005	-0.001	0.000	<u>-0.020</u>	0.003	0.474	-0.011	-0.001	-0.008	0.006	-0.009	0.004	0.44**
RBM	-0.001	0.004	-0.002	0.005	-0.001	0.000	-0.012	<u>0.005</u>	0.362	-0.009	-0.001	-0.007	0.005	-0.011	0.004	0.34**
EBM	-0.001	0.002	-0.002	0.004	0.000	-0.001	-0.009	0.002	<u>1.021</u>	-0.012	-0.001	-0.006	0.007	-0.012	0.007	0.99**
TSW	-0.001	0.002	-0.001	0.006	0.000	0.000	-0.007	0.001	0.410	<u>-0.031</u>	-0.001	-0.007	0.004	-0.010	0.004	0.37**
NKPR	-0.001	0.002	-0.001	0.004	0.000	0.000	-0.006	0.002	0.374	-0.007	<u>-0.003</u>	-0.002	0.003	-0.015	0.007	0.35**
NEHPP	-0.001	0.002	-0.002	0.005	-0.001	0.000	-0.009	0.002	0.318	-0.012	0.000	<u>-0.018</u>	0.017	-0.009	0.002	0.29**
NEPP	0.000	0.000	-0.001	0.002	-0.001	0.000	-0.005	0.001	0.328	-0.006	0.000	-0.015	<u>0.022</u>	-0.006	0.001	0.32**
EL	-0.001	0.002	-0.002	0.004	0.000	-0.001	-0.007	0.002	0.473	-0.011	-0.002	-0.006	0.005	<u>-0.026</u>	0.009	0.44**
ED	-0.001	0.002	-0.002	0.004	0.000	-0.001	-0.007	0.002	0.584	-0.009	-0.002	-0.003	0.002	-0.019	<u>0.012</u>	0.56**

Residual effect (R) =0.055

PH = Plant Height, EH= Ear Height, GLS = Gray Leaf Spot, MSV= Maize Streak Virus, TLB = Turcicum Leaf Blight, HI = Harvesting Index, ABM = Above Ground Biomass, RBM = Root Biomass, EBM = Ear Biomass , TSW = Thousand Seed Weight, NKPR=Number of Kernels Per row, NEHPP= Number of Ears Harvested Per Plot, NEPP = Number of Ears Per Plant , EL= Ear length, ED= Ear Diameter and Yld = Grain yield of phenotypic correlation coefficient value.

Table10. Phenotypic direct (underlined) and indirect effects of agronomic traits for yield at Bambasi in 2017 main cropping season

Variables	PH	EH	GLS	PLS	TLB	HI	ABM	RBM	EBM	TSW	NKPR	SCH	NEHPP	EL	Yld (r_{ph})
PH	<u>-0.005</u>	0.009	0.003	-0.002	-0.011	0.002	0.024	0.001	0.430	-0.002	-0.001	-0.007	-0.001	-0.009	0.43**
EH	-0.004	<u>0.011</u>	0.003	-0.001	-0.010	0.002	0.021	0.001	0.384	-0.001	-0.001	-0.008	-0.001	-0.008	0.39**
GLS	0.002	-0.004	<u>-0.007</u>	0.003	0.015	0.001	-0.022	-0.001	-0.409	0.001	0.001	0.003	0.000	0.006	-0.41*
PLS	0.002	-0.004	-0.005	<u>0.004</u>	0.015	0.002	-0.019	-0.001	-0.346	0.001	0.000	0.004	0.000	0.006	-0.34*
TLB	0.003	-0.005	-0.005	0.003	<u>0.022</u>	-0.001	-0.030	-0.001	-0.555	0.001	0.001	0.006	0.000	0.008	-0.55*
HI	-0.001	0.002	0.000	0.001	-0.002	<u>0.014</u>	0.023	0.000	0.455	-0.001	0.000	-0.007	-0.001	-0.002	0.48**
ABM	-0.002	0.004	0.003	-0.001	-0.012	0.006	<u>0.055</u>	0.001	0.942	-0.001	-0.001	-0.006	-0.001	-0.008	0.98**
RBM	-0.002	0.004	0.003	-0.002	-0.008	0.001	0.034	<u>0.002</u>	0.610	-0.001	-0.001	-0.003	0.000	-0.006	0.63*
EBM	-0.002	0.004	0.003	-0.001	-0.012	0.007	0.053	0.001	<u>0.962</u>	-0.001	-0.001	-0.006	-0.001	-0.008	0.99**
TSW	-0.002	0.004	0.002	-0.001	-0.007	0.002	0.017	0.001	0.314	<u>-0.004</u>	-0.001	-0.007	0.000	-0.007	0.31**
NKPR	-0.003	0.005	0.003	-0.001	-0.010	0.002	0.025	0.001	0.458	-0.001	<u>-0.001</u>	-0.002	0.000	-0.010	0.46**
SCH	-0.002	0.004	0.001	-0.001	-0.006	0.004	0.016	0.000	0.286	-0.001	0.000	<u>-0.021</u>	-0.001	-0.004	0.28**
NEHPP	-0.002	0.003	0.001	0.000	-0.005	0.008	0.029	0.000	0.508	-0.001	0.000	-0.008	<u>-0.002</u>	-0.004	0.53**
EL	-0.003	0.006	0.003	-0.002	-0.012	0.002	0.030	0.001	0.522	-0.002	-0.001	-0.006	-0.001	<u>-0.014</u>	0.52*

Residual effect (R) =0.032

PH = Plant Height, EH= Ear Height, GLS = Gray Leaf Spot, PLS = Phaeosporia Leaf Spot, TLB = Turcicum Leaf Blight, HI = Harvesting Index, ABM = Above Ground Biomass, RBM = Root Bio mass, EBM = Ear Biomass, TSW = Thousand Seed Weight, NKPR=Number of Kernels Per row, SCH = Stand Count at Harvest, NEHPP = Number of ears Harvested Per Plot, EL= Ear length and Yld = Grain yield.

4. CONCLUSIONS

The analysis of variance showed significant ($P \leq 0.05$) to highly significant ($P \leq 0.01$) differences among the evaluated genotypes and most studied traits at both locations which indicates the existence of variability among the tested genotypes and their traits. Traits restrained in the study shown different ranges of variability, heritability and genetic advance as the percentage of means between two genotypes. Estimation of heritability value together with genetic advance as the percentage of mean value is supplementary and necessary in foresees the heritable advance under selection than heritability only. Moderate to high GCV, heritability and GA as the % of mean were detected from ABM, EBM, ED, EL, and grain yield were governed by additive gene effect in the genotypes whereas the other most studied traits were highly influenced by the environment, judgmentally by soil acidity. For this reason selection of genotypes constructed on these values of traits drive is operative to improve the grain yield in acidic soil. The phenotypic and genotypic association with path coefficient analysis shown that selection based on traits HI, ABM, EBM, NEHPP, NRPE, EL, RBM, TSW, and EL will be also desirable for the improvement of maize grain yield in acidic soil condition. Generally deprived of devising genetic assortment further varietal development is unpredicted. The lime effect was seen in magnitude on yield and yield related traits, but statically it was not significant, it may need further investigation to confirm its residual effect at the acidic soil on maize.

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