Mean performance and genetic variability of maize single crosses

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Maize is one of the high priority crops to feed the ever increasing population in Africa, however, its production is limited by shortage of high-yielding varieties coupled with biotic and abiotic stresses. This study was initiated to evaluate mean performance, estimate genetic variability, estimate heritability and genetic advance for maize single crosses. Fifty entries, consisting of 48 F_1 single crosses made from 24 inbred lines and two testers using line x tester design and two commercial check hybrids were used in the study. The experiment was conducted using an alpha lattice design with two replications at Ambo and Holeta Agricultural Research Center. Analysis of variance revealed the existence of significant genetic variation among genotypes for all studied traits except for plant aspect (PA). Location x entry interaction for most of the traits was not significant which suggests hybrid performance was consistent across the tested locations. Crosses L23 x T1 and L11 x T1 were the best performing genotypes for grain yield and some yield related traits. From analysis of genetic variability, ear height showed moderate GCV (10.71%) and PCV (11.24%) values whereas grain yield, ear per plant and ear aspect revealed medium PCV. Moderate to medium values of PCV and GCV indicated the existence of variability for such characters. However, for effective selection, the extent of heritability and genetic advance should be known. Accordingly, plant height and ear height revealed high heritability and genetic advance and so, selection may be effective for these characters. In conclusion, the genetic variability among crosses could be used in developing inbred lines via selection and the crosses with better performance could be used as single cross variety or as parents for synthetic variety.

Keywords: genetic advance, genetic variability, maize, single cross, variability

Gemiddelde Prestasie en Genetiese Veranderlikheid van Enkelkruisingmielies: Mielies is een van die hoëprioriteitgewasse om die steeds groeiende bevolking in Afrika te voed, maar die produksie daarvan word beperk deur 'n tekort aan hoëopbrengsvariëteite tesame met biotiese en abiotiese stremming. Hierdie studie is begin om gemiddelde prestasie te evalueer, genetiese veranderlikheid te beraam, en oorerflikheid en genetiese vooruitgang vir enkelkruisingmielies te beraam. Vyftig inskrywings bestaande uit 48 F1-enkelkruisings gemaak van 24 ingeteelde lyne en 2 toetsers wat lyn x toetser-ontwerp gebruik asook 2 kommersiële kontrolebasters is in die studie gebruik. Die eksperiment is met behulp van alfa-roosterontwerp met twee herhalings by Ambo en Holeta-Landbounavorsingsentrum uitgevoer. Variansieanalise het die bestaan van beduidende genetiese veranderlikheid tussen genotipes vir alle bestudeerde eienskappe aan die lig gebring, behalwe vir plantaspek (PA). Ligging x inskrywingsinteraksie vir die meeste van die eienskappe was nie beduidend nie, wat daarop dui dat basterprestasie konsekwent was oor getoetste liggings heen. Kruisings L23 x T1 en L11 x T1 was die bes presterende genotipes vir graanopbrengs en sommige opbrengsverwante eienskappe. Volgens die ontleding van genetiese veranderlikheid het kophoogte matige GCV-waardes (Engelse afkorting vir *genotypic coefficient of variation*, oftewel genotipiese variasiekoëffisiënt) (10,71%) en PCV-waardes (Engelse afkorting vir *phenotypic coefficient of variation* oftewel fenotipiese variasiekoëffisiënt) (11,24%) getoon, terwyl graanopbrengs, koppe per plant en kopaspek medium PCV aan die lig gebring het. Matige tot medium waardes van PCV en GCV het op die bestaan van veranderlikheid vir sulke eienskappe gedui. Vir effektiewe seleksie moet die omvang van oorerflikheid en genetiese vooruitgang egter bekend wees. Gevolglik het planthoogte en kophoogte hoë oorerflikheid en genetiese vooruitgang geopenbaar en dus kan seleksie effektief wees vir hierdie eienskappe. Ten slotte, die genetiese veranderlikheid tussen kruisings kan gebruik word in die ontwikkeling van ingeteelde lyne deur middel van seleksie en die kruisings met beter prestasie kan as enkelkruisingvariëteit of ouers vir sintetiese variëteit gebruik word.

Sleutelwoorde: genetiese vooruitgang, genetiese veranderlikheid, mielies, enkelkruising, veranderlikheid

Introduction

Maize (Zea mays L, 2n = 2x = 20), a member of the grass family Gramineae (Poaceae), is one of the oldest cultivated crops. Maize is predominantly cross-pollinated by wind, but self-pollination is also possible (Sleper & Poehlman, 2006). The crop is grown over a wide range of environmental conditions.

Maize is the most important crop worldwide and the basic trade product recurring ingredient for millions of people in Sub-Saharan Africa (Nzuve, et al., 2013). It has also become the most important staple food in rural Ethiopia (Tsedeke, et al., 2015). The crop has significant importance worldwide as human food, industrial raw material and animal feed. Approximately 88% of maize produced in Ethiopia is consumed as food, both as green and dry grain (Tsedeke, 2015). Maize is one of the strategic crops for the achievement of food security. Prasanna et al. (2001) noted that the crop is a vital source of calories, protein, and some important vitamins and minerals to billions of people worldwide, particularly in Africa, South America and Asia.

Genetic improvement in traits of economic importance along with maintaining a sufficient amount of variability is always the desired aim in maize breeding programmes (Hallauer, 1973). Dudley and Moll (1969) and Welsh (1990) noted information on the nature and magnitude of genetic variability greatly helps in formulating sound crop breeding programmes. If the character expression of two individuals could be measured in an environment exactly identical for both, differences in expression would result from genetic control and hence such variation is called genetic variation (Welsh, 1990). Several genetic variability studies have been conducted on different crop species based on quantitative and qualitative characteristics to decide on genetically distant parents for hybridisation (Hailegiorgis, Mebrahtom & Tsige, 2011). Grzesiak (2001) observed considerable genotypic variability among various maize genotypes for different traits. Bernardo (1995) and Ihsan, Khalil & Hidayat-ur-Rahman (2005) also reported significant genetic differences for morphological parameters for maize genotypes. This variability is a key to crop improvement (Welsh, 1981). Improvement of crops requires creation and introduction of genetic variation, inbreeding coupled with selection and extensive evaluation of breeding materials at multiple locations to identify adapted and stable genotypes with desirable agronomic traits. Heritability is a measure of the correspondence between breeding value and phenotypic values (Falconer & Mackay, 1996). Allard (1960) used the term "heritability" to specify the genetic portion of the total variability.

In Ethiopia, maize improvement started half a century ago (Mosisa, et al., 2002). Several promising genotypes of east African origin were introduced and evaluated at different locations. In order to improve the genetic diversity of local germplasm, it is important to know the extent of already existing genetic variations in the material. Finally, the study aimed to evaluate the mean performance, estimate genetic variability in maize and estimate the heritability and genetic advance under selection for maize single cross hybrids.

Materials and Method

The experiment was conducted at Ambo and Holeta Agricultural Research Centers of the Ethiopian Institute of Agricultural Research (EIAR) during the main cropping season of 2017. Holeta Agricultural Research Center (HARC) is located in the West Showa zone of the Oromia region, 33 km west of Addis Ababa at 09°04′12″N latitude and 38°29′45″E longitude and an elevation of 2400 m.a.s.l. The centre receives an average rainfall of 1102 mm per annum. The maximum and minimum temperatures of this site are 6 °C and 22 °C, respectively. The centre has nitosols and vertisols soil types with pH of 6.0 (Tamene, et al., 2015). Ambo Agricultural Research Centre (AARC) is located in the West Showa zone of the Oromia region, 114 km west of Addis Ababa at 8°57′N latitude and 37°51′E longitude with an altitude of 2225 m.a.s.l. The site receives an average rainfall of 1115 mm. The maximum and minimum temperatures of this site are 11.7 °C and 25.4 °C, respectively. The soil type of Ambo is clay (heavy vertisols) with a pH of 7.8 (Demissew, 2014).

Experimental Materials

The experiment consisted of 50 maize entries which included 48 testcrosses and two hybrid checks (AMH853-Kolba and AMH851-Jibat). The testcrosses (48) were generated from the crossing of 24 inbred lines (female parents) with two testers (male parents) in line x tester mating design during 2015/2016 cropping season at Ambo Agricultural Research Center. The hybrid checks, AMH851 (Jibat) and AMH853 (Kolba) are released for highland and sub-humid agro ecologies of Ethiopia. They are three-way cross hybrid varieties released by Ambo Agricultural Research Centre, highland maize breeding programme in 2011 and 2015, respectively. They take about 178 days for grain to mature at Ambo and similar environments. Besides, hybrid checks are high yielding, tolerant/resistant to major maize disease in the country and well adapted to the altitude ranging from 1800–2600 m in the highland sub humid agro-ecological conditions of the country (MoANR, 2016).

Experimental Design and Procedure

The experimental materials along with two hybrid checks were grown during the 2016/2017 main cropping season using an alpha lattice design (Patterson & Williams, 1976) with two replications, 10 incomplete blocks and five plots per the incomplete blocks at both locations. Each entry was planted in a single row plot of 5.25 m length with a spacing of 75 cm between rows and 25 cm between plants. Seeds were planted with two seeds per hill and later thinned to one plant at four leaf stage. All agronomic practices were done as per the recommendation of the locations.

Data collected and analysis

Days to 50% anthesis (AD), days to 50% silking (SD), anthesis-silking interval (ASI), ear aspect (EA), plant aspect (PA), grain yield (GY), number of ears per plant (EPP) and thousand kernel weight (TKW) on plot basis. On plant basis, data were collected on plant height (PH), ear height (EH), ear length (EL), ear diameter (ED),

Table I: List and pedigree of parents and hybrid checks used for the study

SN	Line Code	Pedigree	Origion
1	L1	(CML442*/OFP4)-B-4-2-2-BBB-#	AMB16N42-29/AMB16N42-144
2	L2	(CML495*/OFP14)-7-1-5-1-1-BB-#	AMB16N42-107/AMB16N42-144
3	L3	(CML442*/OFP4)-B-17-1-1-BBB-#	AMB16N42-32/AMB16N42-144
4	L4	(CML495*/OFP6)-B-27-1-1-B-#	AMB16N42-142/AMB16N42-144
5	L5	(CML539*/OFP14)-2-1-1-2-2-BB-#	AMB16N42-16/AMB16N42-144
6	L6	(CML442*/OFP4)-B-17-5-1-BBB-#	AMB16N42-36/AMB16N42-144
7	L7	(CML395*/OFP105)-1-1-1-1-1-BB-#	AMB16N42-38/AMB16N42-144
8	L8	(CML395*/OFP105)-1-2-3-1-1-BB-#	AMB16N42-39/AMB16N42-144
9	L9	CML539*/OFP1)-B-11-2-2-BBB-#	AMB16N42-20/AMB16N42-144
10	L10	(CML444*/OFP23)-6-3-1-1-1-BB-#	AMB16N42-44/AMB16N42-144
11	L11	(LPSC7-F96-1-2-1-1-BBB*/OFP9)-3-2-1-1-1-BB-#	AMB16N42-2/AMB16N42-144
12	L12	(CML444*/OFP14)-3-2-4-1-2-BB-#	AMB16N42-47/AMB16N42-144
13	L13	(CML444*/OFP4)-B-4-1-1-BBB-#	AMB16N42-50/AMB16N42-144
14	L14	(CML444*/OFP4)-B-6-1-1-BBB-#	AMB16N42-51/AMB16N42-144
15	L15	(CML537*/OFP106)-6-1-3-1-2-BB-#	AMB16N42-53/AMB16N42-144
16	L16	(CML537*/OFP106)-7-1-2-1-2-BB-#	AMB16N42-56/AMB16N42-144
17	L17	(CML491*/OFP4)-B-10-1-2-BBB-#	AMB16N42-88/AMB16N42-144
18	L18	CML546-#	AMB16N42-61/AMB16N42-144
19	L19	([SYN-USAB2/SYN-ELIB2]-12-1-1-1-B*4-BBB*/OFP105)-4-2-1-1-2-BB-#	AMB16N42-62/AMB16N42-144
20	L20	([CML312/[TUxPSEQ]C1F2/P49-SR]F2-45-3-2-1-BB//INTA-F2-192-2-1-1-1-BBBB]-1-5-1-1 -1-BBB-BBB*/OFP106)-1-2-2-2-1-BB-#	AMB16N42-75/AMB16N42-144
21	L21	([CML444/CML395//DTPWC8F31-1-1-2-2-BB]-4-2-2-1-2-BB-BBB*/OFP105)-1-4-3-3-2-BB- #	AMB16N42-65/AMB16N42-144
22	L22	([CML444/CML395//DTPWC8F31-1-1-2-2-BB]-4-2-2-1-2-BB-BBB*/OFP105)-2-1-1-2-1-BB- #	AMB16N42-66/AMB16N42-144
23	L23	(LPSC7-F71-1-2-1-2-BBB*/OFP2)-B-1-3-2-BBB-#	AMB16N42-8/AMB16N42-144
24	L24	[CML444/CML395//DTPWC8F31-1-1-2-2-BB]-4-2-2-2-1-B*7-B-#	AMB16N42-69/AMB16N42-144
		Tester	
25	T1	FS59	Heterotic group
26	T2	FS67	Heterotic group
		Checks	
27		JIBAT	3-way hybrids
28		KOLBA	3-way hybrids

Source: *Ambo plant protection research center, highland maize breeding program (2017)*

number of kernel rows per ear (KRPE) and number of kernels per row (KPR). Plant aspect and ear aspect were measured in 1 to 5 scales.

The data collected was analysed by PROC GLM procedure using SAS statistical package (SAS institute, 2014). Location, replication and blocks were considered as random and entry/genotype as fixed factors with statement of RONDOM and TEST option. The significance of mean squares for entries and location in combined analysis were tested against the mean squares for their corresponding interaction with location as error term, while their interaction with location was tested against their corresponding pooled error.

Variance components were computed to identify genetic variability among single crosses of maize. Error (σ^2 e), genotypic (σ^2 g) and phenotypes (σ^2 p) variances were calculated from expected mean squares of analysis of variance by adopting the formula suggested by Hallauer and Miranda (1988). Then, the phenotypic (PCV%) and genotypic coefficient of variation

(GCV%) were estimated. GCV and PCV values were categorised as low (0–10%), moderate (10–20%) and high (20% and above) values as indicated by (Deshmukh, Basu & Reddy, 1986).

Broad sense heritability across location was computed for all traits based on the formula given by Falconer and Mackay (1996). Expected genetic advance under selection for each trait at selection intensity of 5% was computed using the procedure given by Allard (1960). GA = K.h²b.σp, where: GA= Expected genetic advance, k = the standardised selection differential at 5% selection intensity (K = 2.063), σp = Phenotypic standard deviation, h²b = Heritability in broad sense.

Results and Discussion

The analysis of variances for yield and yield-related traits for the combined location are presented in Table II. Significant differences were detected between the two locations for all of the studied traits except for ear length, indicating that the two locations differed in the environmental conditions thus causing

variation. Entry differences were significant (p < 0.01 or p < 0.05) for all traits except for plant aspect (Table II). Entries differed in their performance from one location to another for variables like grain yield, plant and ear height, ear diameter and thousand kernels as entry x location interaction was significant. Gudeta, Dagne & Habtamu, (2015) also found significant entry x location interaction for grain yield, thousand kernels weight and ear height for different maize genotypes. Beyene et al. (2011) and Murtadha et al. (2016) also reported significant entry x location interaction effect for some yield and its components in maize and indicated the presence of wide variability with regard to tested entry and locations. The result showed that location played a significant role in the variation of these traits. If significant genotype x location interaction mean squares existed, different genes involved in controlling the traits show the inconsistency of the genes over locations (Dagne, 2008). The interaction of entry with location suggests further evaluation of the genotypes across a greater number of locations to minimise environmental effect from computation genetic variance.

Mean Performance

The mean performance of 50 entries which include 48 crosses and two standard checks were evaluated across location for grain yield and yield-related traits as presented in Table II. Across location, the overall mean grain yield was 7.54 t ha⁻¹ ranging from 4.64 (L13 x T1) to 10.17 t ha⁻¹ (L23 x T1). Out of 48 crosses, two crosses namely L23 x T1 (10.17 t ha⁻¹) and L11 x T1 (9.50 t ha⁻¹) significantly out yielded the hybrid checks AMH853 (Kolba, 7.78t ha⁻¹) and AMH851 (Jibat, 7.68t ha⁻¹). Most of the crosses with the highest grain yield involved FS59 as one of the parents thereby indicating that FS59 and inbred lines could be from different heterotic groups for this trait.

Across locations, mean values of days to 50% anthesis, days to 50% silking and anthesis- silking interval ranged from 100 (Jibat) to 108.75 d (L13 x T1), 101.75 (Jibat) to 110.75 d (L17 x T1) and

-1.50 d (L12 x T2) to 2.25 (L18 x T1) with overall mean of 104.53, 105.29 and 0.63d, respectively (Table III). However, all crosses were not significantly earlier to the hybrid checks which are in agreement with the findings of Elmyhum (2013) and Demissew (2014). Crosses L9 x T2, L11 x T2, L12 x T2, L18 x T2 and L21 x T2 had narrower ASI than hybrid checks. Due to frost problems and climate change, breeders should concentrate on developing early flowering maize varieties with high yield.

Overall means for plant and ear height were 251.25 and 136.66 cm ranging from 207.5 (L18 x T2) to 292.5 cm (L5 x T1) and 109.75 (L24 x T2) to 183.75 cm (L12 x T1), respectively. Twenty (20) and eight (8) crosses showed significantly shorter and taller plant height over Kolba (259.25 cm) and Jibat (258.50 cm). Twenty six (26) and eleven (11) crosses had significantly lower ear placement compared to Kolba (144.75cm) and Jibat (135cm), respectively. Most of the lines crossed with FS67 had shorter plant and ear height which indicates that FS67 had the tendency to reduce plant stature. Furthermore, high yielding crosses were taller in plant and ear height. Al-Tabbal et al. (2012) suggested that tall genotypes excelled in capacity to support kernel growth through stem reserve mobilisation. In contrast, Abadassi (2015) reported that reduced plant and ear height could be important in decreasing the problem of lodging, increasing physiological efficiency and facilitating harvesting activity. As a result, the variety with medium plant height and ear placement could be affordable.

The overall mean values of the number of ears per plant, ear length and ear diameter were 1.7, 15.47 cm and 4.32 cm ranging from 1.25 cm (L8 x T2) to 2.20 cm (L23 x T1), 12.50 (L9 x T2) to 18.25 cm (L15 x T2), and 4.67 (L10 x T1) to 3.96 (L7 x T2), respectively. Seventeen crosses and one cross (L15 x T1) showed significantly higher ears per plant and longer ear length over Kolba (AMH854), respectively. The crosses that had higher grain yield were also prolific, which indicates that an increasing

Table II: Analysis of variance for yield and yield-related traits of 48 testcross and two hybrid checks evaluated at Holeta and Ambo, 2017

Traint	L, df=1	Re(L)df=2	B(L*R) df=36	Ent df=49	Ent*L df=49	Error df=62	Mean ± SE(m)	CV%	R²
GY	8,38*	0,03	1,29	4,41*	2,63**	1.1	7,53± 0,52	13.9	0,86
AD	14162.4**	24.23**	2,96	13.33**	2,77	3.18	104,52±0,89	1,71	0,99
SD	18489.6**	19.34**	2,60	15,66**	2,51	3.31	105,15±0,91	1,73	0,99
ASI	0,63**	0,001	0,005	0,007*	0,005	0,004	1,2± 0,03	5,52	0,86
PH	574,6**	779,0**	161,6	1631,89**	237,4*	139,1	251,07±5,9	4,70	0,93
EH	5724.5**	398,33**	45,04	943.11**	85,85*	54,64	136,66±3,7	5,41	0,95
EPO	0,07**	0,0002	0,001	0,004**	0,0007	0,002	0,54±0,02	7,33	0,79
EPP	1,49**	0,007	0,03	0,13**	0,05	0,03	1,70±0,09	10.18	0,86
EA	0,78*	0,91**	0,13	0,43**	0,19	0,13	3,12±0,18	11.56	0,84
PA	2,88**	0,75*	0,15	0,20	0,14	0,20	3,30±0,22	13,69	0,70
EL	1,69	8,82**	0,98	3,61**	1.21	0,81	15,47±0,45	5,82	0,88
ED	1,62**	0,004	0,03	0,10**	0,03**	0,03	4,32±0,09	3,84	0,86
KRPE	10,76**	0,58	0,63*	1,21**	0,47	0,37	12,86±0,3	4,74	0,86
KPR	19.22*	25.22**	7,43*	8,51**	6,50	4.22	32,3±1,03	6,37	0,83
TKW	193827.8**	27.26	743,1	3102.2**	1603.9*	947,3	305,0±15,39	10.09	0,90

Grain yield (GY), Days to 50% anthesis (AD), days to 50% silking (SD), anthesis-silking interval (ASI), plant height (PH), ear height (EH), number of ear per plant (EPP), ear aspect (EA), plant aspect (PA), ear length (EL), ear diameter (ED), number of kernel rows per ear (KRPE) and number of kernels per row (KPR) and thousand kernel weight (TKW)

Table III: Mean performances of 48 testcrosses and two hybrid checks of maize for yield and yield-related traits for combined data, 2017

SN	ENTRY	GY	AD	SD	ASI	PH	EH	EPO	EPP	EA
		t/ha	days	days	days	cm	cm	ratio	no	1-5 scale
1	L1xT1	8.16	102,75	103,75	1.00	278,25	159,75	0,57	1,96	2,88
2	L1xT2	7,77	102,50	102,25	-0,25	243,50	128,75	0,53	1,95	2,88
3	L2xT1	8,59	105,00	105,25	0,25	254,75	133,50	0,53	1,83	3,63
4	L2xT2	5,85	102,25	103,25	1.00	214,75	116.00	0,54	1,82	3,75
5	L3xT1	5,48	107,25	109,25	2.00	260,25	143,75	0,55	1,69	3,13
6	L3xT2	6,90	107.00	108.00	1,25	231,00	122,00	0,53	1,64	3,25
7	L4xT1	7,64	102,50	104,25	1,75	274,75	151,25	0,55	1,70	2,75
8	L4xT2	7,20	102.00	103.00	1.00	248,25	126,00	0,51	1,42	2,75
9	L5xT1	8,96	103.00	103,50	0,50	292,50	162,00	0,55	1,77	2,38
10	L5xT2	7,49	101,75	102,25	0,50	262,50	134,75	0,51	1,84	3,25
11	L6xT1	7,79	104,25	103,75	-0.50	264,25	147,00	0,56	1,79	2,63
12	L6xT2	6,02	103,75	103,75	0.00	232,75	129,50	0,56	1,73	2,50
13	L7xT1	6,38	106,75	108,75	2.00	265,25	152,50	0,58	1,59	3,75
14	L7xT2	6,94	108.00	108.00	-0,25	223,50	130,00	0,58	1,79	3,63
15	L8xT1	9,00	104,75	106,75	2.00	266,00	144,00	0,54	1,84	2,88
16	L8xT2	6,08	104,25	105,00	0,75	214,00	111,50	0,52	1,25	3,38
17	L9xT1	8,47	101,75	103,00	1,25	260,00	131,50	0,51	1,96	3,63
18	L9xT2	7,45	103,00	101,75	-1,25	243,25	123,50	0,51	1,82	3,25
19	L10xT1	7,79	107,25	108,50	1,25	289,25	166,25	0,57	1,66	2,75
20	L10xT2	8,55	105,25	105,25	0.00	241,25	124,25	0,52	1,66	2,63
21	L11xT1	9,50	106,50	107,75	1,25	277,00	161,25	0,58	1,81	4.00
22	L11xT2	8,56	106,00	105,25	-0,75	232,50	129,75	0,56	1,72	3,50
23	L12xT1	8,53	107,50	107,50	0.00	280,75	183,75	0,66	1,81	3,75
24	L12xT2	7.21	105,75	104,25	-1,50	239,00	131,50	0,55	1,69	2,88
25	L13xT1	4,64	108,75	110.00	1,25	243,50	130,75	0,54	1,51	3,13
26	L13xT2	7,24	104,50	104,75	0,25	229,25	115,50	0,50	1,54	3,25
27	L14xT1	8,78	107.00	108,25	1,25	286,25	159,25	0,56	1,84	2,88
28	L14xT2	6,96	107.00	107,75	0,75	241,25	125,75	0,52	1,63	3,13
29	L15xT1	9,05	106.00	107.00	1.00	275,00	157,25	0,57	1,70	2,75
30	L15xT2	8,48	104.00	105,25	1,25	236,25	125,50	0,53	1,77	2,88
31	L16xT1	8,86	102,25	103,00	0,75	290,00	170,75	0,59	1,75	3,25
32	L16xT2	6,22	105,75	105,75	0.00	222,50	125,00	0,56	1,78	3,50
33	L17xT1	7,06	103,50	104,50	1.00	281,25	156,00	0,55	1,66	3,13
34	L17xT2	7,83	103,50	110,75	-0,25	234,75	129,25	0,55	1,87	3,25
35	L18xT1	7,59	102,50	104,75	2,25	262,00	143,50	0,55	1,40	2,75
36	L18xT2	5,86	103,75	102,50	-1,25	207,50	112,25	0,54	1.31	2,75
37	L19xT1	6,72	103,75	104,75	0,75	266,75	142,00	0,53	1,65	3,13
38	L19xT2	6,09	105,00	105,50	0,50	217,25	125,25	0,58	1,52	3,13
39	L20xT1	8,39	103,50	104,75	1,25	272,50	150,50	0,55	1,66	2,88
40	L20xT2	7.15	104,75	105,00	0,75	220,50	120,00	0,55	1,39	3,50
41	L21xT1	6.12	106,75	107,75	1.00	261,75	147,00	0,56	1,44	3,25
42	L21xT2	6,59	103,00	102,00	-1.00	251,25	136,50	0,54	1,59	3,13
43	L22xT1	7,51	107,50	108,50	1.00	262,00	132,00	0,50	1,92	3,13
44	L22xT2	7.23	105,00	105,50	0,50	218,75	116,00	0,53	1,66	3,38
45	L23xT1	10.17	103,50	104.00	0,50	260,00	138,25	0,53	2,20	3,13
46	L23xT2	8.20	103,75	104,25	0,50	231,50	109,75	0,48	2,11	3,13
47	L24xT1	7,56	103,50	105,00	1,50	260,25	131,50	0,51	1,81	3,13
48	L24xT2	8,56	104,75	104,25	-0,25	238,75	109,75	0,46	1,92	2,88
49	Kolba	7,78	101,75	103,00	1,25	259,25	144,75	0,56	1,54	2,88
50	Jibat	7,68	100.00	101,75	1,75	258,50	135,00	0,52	1,48	2,88
	Mean	**7.54**	**104.53**	**105.29**	**0.63**	**251.56**	**136.66**	**0.54**	**1.71**	**3.12**
	Cross mean	**7.53**	**104.68**	**105.41**	**1.50**	**251.25**	**136.53**	**0.54**	**1.72**	**3.13**
	Maximum	**10.18**	**108.75**	**110.75**	**2.25**	**292.50**	**183.75**	**0.66**	**2.20**	**4.00**
	Minimum	**4.64**	**100.00**	**101.75**	**-1.50**	**207.50**	**109.75**	**0.46**	**1.25**	**2.38**
	LSD (5%)	**1.48**	**2.52**	**2.57**	**1.82**	**16.67**	**10.45**	**0.06**	**0.25**	**0.51**

Tabel III: Gemiddelde prestasies van 48 toetskruisings en twee basterkontroles van mielies vir opbrengs en opbrengsverwante eienskappe vir gekombineerde data, 2017 *(vervolg)*

SN	ENTRY	EPP	EA	EL	ED	KRPE	KPR	TKW
		no	1-5 scale	cm	cm	no	no	gm
1	L1xT1	1,96	2,88	13.50	4,25	12.50	28.40	283,48
2	L1xT2	1,95	2,88	14.25	4.12	12.67	29,75	298,90
3	L2xT1	1,83	3,63	15.25	4.31	12.67	33.00	244,20
4	L2xT2	1,82	3,75	14.46	4.17	12.83	31,85	315,28
5	L3xT1	1,69	3.13	15.29	4.12	13.17	31,33	287,83
6	L3xT2	1,64	3,25	14.58	4.31	13.34	29,08	311,68
7	L4xT1	1,70	2,75	16.21	4,64	13.83	34,35	305,70
8	L4xT2	1,42	2,75	16.38	4.31	12.67	34,08	311,63
9	L5xT1	1,77	2,38	15.79	4,34	12.34	32,93	312,13
10	L5xT2	1,84	3,25	15.75	4,35	12.17	31,93	299,40
11	L6xT1	1,79	2,63	15.17	4,43	13.17	32.00	283,05
12	L6xT2	1,73	2,50	14.92	4,39	13.33	31,83	306,70
13	L7xT1	1,59	3,75	16.75	4.20	13.33	32,25	248,35
14	L7xT2	1,79	3,63	16.25	3,96	12.50	33,75	267,60
15	L8xT1	1,84	2,88	16.50	4,33	13.83	33,70	294,20
16	L8xT2	1,25	3,38	16.38	4,34	12.83	32,65	349,50
17	L9xT1	1,96	3,63	15.13	4,30	13.17	31,83	251,70
18	L9xT2	1,82	3,25	12.50	4,39	13.00	27,58	302,00
19	L10xT1	1,66	2,75	15.42	4,67	13.50	33,08	313,70
20	L10xT2	1,66	2,63	17.29	4,50	13.17	33,58	308,05
21	L11xT1	1,81	4.00	13.33	4,58	14.00	29,48	317,73
22	L11xT2	1,72	3,50	14.88	4,45	12.67	33,68	352,73
23	L12xT1	1,81	3,75	16.00	4,56	13.50	33,18	328,80
24	L12xT2	1,69	2,88	16.38	4.30	12.17	34,25	336,90
25	L13xT1	1,51	3.13	13.38	4,50	13.17	32,08	254,83
26	L13xT2	1,54	3,25	14.09	4,34	12.33	31,08	310,40
27	L14xT1	1,84	2,88	17.50	4,46	13.50	34,65	266,50
28	L14xT2	1,63	3.13	15.29	4,41	13.17	30,75	315,90
29	L15xT1	1,70	2,75	16.79	4,36	13.67	34,75	263,38
30	L15xT2	1,77	2,88	18.25	4,38	12,84	33,90	301,33
31	L16xT1	1,75	3,25	15.37	4.31	12.67	32,25	297,30
32	L16xT2	1,78	3,50	14.71	4.13	11,84	30,85	279,38
33	L17xT1	1,66	3.13	16.13	4.15	12.50	32,23	293,98
34	L17xT2	1,87	3,25	14.54	4.16	12.00	30,08	338,38
35	L18xT1	1,40	2,75	15.84	4,52	13.00	34,10	290,05
36	L18xT2	1.31	2,75	15.42	4,32	12.67	31,23	310,70
37	L19xT1	1,65	3.13	14.71	4,22	13.17	33,75	241,13
38	L19xT2	1,52	3.13	14.46	4.01	12.67	29,90	296,50
39	L20xT1	1,66	2,88	15.71	4,49	13,84	34,23	302,88
40	L20xT2	1,39	3,50	16.04	4,53	13.50	32,43	333,73
41	L21xT1	1,44	3,25	14.96	4,57	13.00	29,65	375,28
42	L21xT2	1,59	3.13	16.04	4.31	11.50	32,65	387,08
43	L22xT1	1,92	3.13	15.63	4.13	13.00	30,93	321,43
44	L22xT2	1,66	3,38	15.63	4.08	11.67	32,15	331,65
45	L23xT1	2.20	3.13	15.42	4.19	12.50	32,10	301,90
46	L23xT2	2.11	3.13	15.08	4.16	13.00	34,10	311,85
47	L24xT1	1,81	3.13	16.67	4.04	12.17	33,18	292,08
48	L24xT2	1,92	2,88	15.88	4,25	13.00	34,08	334,15
49	Kolba	1,54	2,88	16.33	4,58	12.34	33,25	364,03
50	Jibat	1,48	2,88	15.08	4,27	12.50	32,93	303,25
	Mean	**1.71**	**3.12**	**15.47**	**4.32**	**12.87**	**32.26**	**305.01**
	Cross mean	**1.72**	**3.13**	**15.46**	**4.43**	**12.89**	**33.09**	**303.81**
	Maximum	**2.20**	**4.00**	**18.25**	**4.67**	**14.00**	**34.75**	**387.08**
	Minimum	**1.25**	**2.38**	**12.50**	**3.96**	**11.50**	**27.58**	**241.13**
	LSD (5%) (5%)	**0.25**	**0.51**	**1.27**	**0.23**	**0.86**	**2.90**	**43.50**

GY = grain yield, AD = anthesis days, AD = silking days ASI = anthesis silking interval, PH = plant height, EH = ear height, EPO = ear position, EPP = ear per plant, EA = ear aspect, PA = plant aspect, EL= ear length, ED = ear diameter, KRPE = kernel row per ear, KPR = kernel per row, TKW = thousand kernel weight.

number of ears per plant might improve grain yield. Eight crosses revealed significantly wider ear diameter than Jibat (4.24), but none of the crosses had better ear diameter than Kolba (4.58). The mean value of the number of kernel rows per ear ranged from 11.5 (L21 x T2) to 14 (L11 x T1) with an overall mean value of 12.87. Nine crosses, namely L11 x T1, L20 x T1, L18 x T1, L4 x T1, L15 x T1, L10 x T1, L14 x T1, L20 x T2 and L12 x T1 exhibited a significantly larger number of kernel rows per ear than the hybrid checks (Table III). The number of kernels per row and thousand kernels weigh ranged from 27.58 (L9 x T2) to 34.75 (L15 x T1) and 241.13 (L19 x T1) to 387.08 gm (Kolba) with overall mean values of 32.26 and 305.01 gm, respectively.

Crosses such as L11 x T1 and L23 x T1 showed better performance over hybrid checks for more than one trait. Higher performance of certain crosses over hybrid checks regarding a number of traits was probably caused by using inbred lines from genetically diverse material. Crosses that revealed higher grain yield could be used for across location breeding programmes to improve grain yield and other traits of interest. Hence, hybrids that exhibited a narrow anthesis silking interval, medium plant and ear height, more prolifically, higher number of kernel rows per ear and ear length could be used as sources of favourable genes for improvement of these traits. Several authors (Dagne, et al., 2010; Zerihun, 2011; Girma, et al., 2015; Amare, et al., 2016) also reported that crosses showed better performance than the best hybrid check in their studied materials.

Estimates of Genetic Components

The estimates of phenotypic and genotypic variance, genotypic (GCV) and phenotypic coefficient of variation (PCV), heritability, genetic gain and genetic advance in percentage of mean (GA) for different characters are given in Table IV. Genetic variance ranged from 0 for ear position to 374.58 for thousand kernels weight and for the same traits phenotypic variance ranged from 0 to 775.55. The GCV values ranged from 1.55% for anthesis days to 10.71% for ear height while PCV values ranged from 1.75% for anthesis days to 13.94% for grain yield. According to Deshmukh et al. (1986) PCV and GCV values greater than 20% are regarded as high and values between 10% and 20% to be medium, whereas values less than 10% are considered to be low. Accordingly, ear height showed moderate GCV (10.71%) and PCV (11.24%) values whereas grain yield, ear per plant and ear aspect revealed medium PCV. The medium values of PCV and GCV indicated the existence of variability for such characters, and selection may be effective based on these characters. However, anthesis days, silking days, anthesis silking interval, plant height, ear position, plant aspect, ear length, ear diameter, number of kernel rows per ear, number of kernels per ear and thousand kernels weight showed low genotypic and phenotypic coefficient of variation. Similarly, Nigus (2018) also reported low values for both coefficient of variation for days to 50% anthesis, days to 50% silking, plant height, ear diameter, ear length, number of kernel rows per cob and number of kernels per row.

In this study, PCV values were relatively greater than GCV for all traits. Similarly, Yusuf (2010) also reported higher phenotypic

coefficients of variations than the genotype coefficient of variations for all studied traits. But GCV and PCV values were slightly different for the characters like anthesis days, silking days, plant height, ear height, ear position, ear length, ear diameter and number of kernel rows/ear, indicating a high contribution of genotypic effect for phenotypic expression of these characters. This finding was in confirmation of Tadesse et al. (2018) for days to 50% silking, days to 50% anthesis, plant height and kernel rows per ear. In other traits, there are wider gaps between estimate of PCV and GCV which showed the distinct contribution of environmental factors in genetic expression. Similarly, Mallikarjuna et al. (2011) reported higher estimates of PCV than estimates of GCV for all studied characters and the role of the environment in character expression. Genotypic coefficient of variance provides information on the genetic variability present in quantitative characters in the base population, but it is not possible to determine the amount of the variation that was heritable only from the genotypic coefficient of variance. Burton & Devane (1953) noted that GCV, together with heritability estimates, would give the best picture of the amount of advance to be expected from selection.

Heritability estimates are helpful in predicting the expected progress to be achieved through the selection process. Estimates of heritability in the broad sense ranged from 23.62% for the number of kernels per row to 90.90% for ear height (Table IV). Heritability values greater than 80% are very high, values from 60–79% are moderately high, values from 40–59% are medium and values less than 40% are low (Singh, 2001). Accordingly, the estimates of heritability for anthesis silking interval, plant aspect and number of kernels per row were low and for silking days, ear height, plant height and ear position were very high. The heritability values for gain yield, ear aspect and thousand kernels weight were medium while anthesis days, ear per plant, ear length, ear diameter and number of kernel rows/ear revealed moderately high heritability. The traits revealed that high heritability indicated the small contribution of the environmental factors to the phenotype, and selection for such characters could be fairly easy due to the high additive effect. High estimates of broad sense heritability have also been reported by Bello et al. (2012) for day to silking, plant height and ear height and Mahmood et al. (2010) for days to silking and plant height and suggested the possibility of effective selection for genetic improvement of these traits.

The amount of genetic improvement that would result from the selection of individual genotypes might not be indicated through heritability alone. So, knowledge on heritability, coupled with genetic advance, will be more useful. Genetic advance (GA) under selection referred to the improvement of characters in genotypic value for the new population compared with the base population in one cycle of selection at given selection intensity (Singh, 2001). Genetic advance (GA) is important to predict the expected genetic gain from one cycle of selection. Estimates of GA values for all characters studied are displayed in Table II. The estimate of genetic advance for plant height (35.61 cm), ear height (28.79 cm) and thousand kernels weight (27.75 gm) suggests the presence of a broader genetic base for these traits. For instance, whenever we select

the best 5% heavy kernel weight genotypes as parents, the new offspring could be improved by 27.75 g TKW. The traits with high genetic gain indicate the better scope for their selection for genetic improvement whereas traits with low genetic gain signifies there is no significant genetic variability in these traits and may not be useful in future breeding programmes. High heritability estimates together with high estimates of genetic advance expected in the next generation plant height and ear heights indicate the preponderance of additive gene action for the expression of these traits which is fixable in subsequent generations. Heritability due to non-additive gene action could result in a low genetic advance whereas, heritability due to additive gene action would be associated with higher genetic advance (Mallikarjuna, et al. 2011). This also implies that a larger proportion of phenotypic variance has been attributed to genotypic variance, and reliable selection could be made for these traits on the basis of phenotypic expression. On the other hand, days to 50% silking and anthesis, ear position, number of ears per plant, ear length and ear diameter showed high heritability but low genetic advance which implies non-additive gene action dominated and selection for traits may not be effective. A similar finding was reported by Begum et al. (2016) for day to 50% anthesis, days to 50% silking and ear diameter.

Genetic advance as a percentage of the mean (GAM) ranged from 2.05% to 21.07% for anthesis silking interval and ear height, respectively (Table IV). According to Johnson, Robinson & Comstock, (1955), the value of genetic advance as percentage of the mean is categorised as low (< 10%), moderate (10–20%) and high (> 20%). The GAM of ear height is classified as high and grain yield (11.61%), plant height (14.18%), number of ears per plant (13.46%) and ear aspect (12.10%) classified as moderate and the rest classified as low. Nigus (2018) also reported low

GMA for day to 50% silking, ear diameter, number of kernel rows per ear and kernels per row. High heritability estimates along with the high genetic advance as per mean is usually more helpful in predicting gain under selection than heritability alone (Johnson, et al. 1955).

Conclusion

Analysis of variance revealed the presence of significant variation among the genotypes for all studied traits except for plant aspect. Mean square of entry x location interaction for most of the studied traits was non-significant, indicating that hybrid performance was consistent across locations. Nevertheless, genotype x location interaction was significant for some traits, suggesting further evaluation of selected genotypes over a number of locations. Several better performing maize crosses were identified for most of the studied traits. L11 x T1 and L23 x T1 crosses showed better mean performance over hybrid checks for yield and some yield-related traits. Crosses that revealed higher grain yield could be used for across location breeding programmes to improve grain yield and other traits of interest. The analysis of variability signifies that phenotypic selection for most of the studied traits will be effective. As plant and ear height revealed high heritability coupled with high genetic advance selection may be effective for these three traits.

Acknowledgments

Table IV: Estimation of variance and coefficient of variation, heritability, genetic advance and genetic advance of mean (%) for yield and yield-related traits in maize genotypes

Trait	$\bar{\chi}$	σ^2_g	σ^2_e	σ^2_{g1}	σ^2_p	h2b	GCV (%)	PCV (%)	GA	GAM (%)
GY	7,5	0,45	0,28	1,18	1,10	40,36	8,86	13,94	0,87	11,61
AD	104,5	2,64	0,80	0,99	3,33	79,22	1,55	1,75	2,98	2,85
SD	105,2	3,29	0,83	0,84	3,92	83,97	1,72	1,88	3,43	3,26
ASI	1,2	0,00	0,00	0,00	0,00	28,57	1,86	3,49	0,02	2,05
PH	251,1	348,62	34,78	101,31	407,97	85,45	7,44	8,04	35,61	14,18
EH	136,7	214,32	13,66	36,10	235,78	90,90	10,71	11,24	28,79	21,07
EPO	0,5	0,00	0,00	0,00	0,00	82,50	5,32	5,86	0,05	9,97
EPP	1,7	0,02	0,01	0,02	0,03	61,54	8,32	10,60	0,23	13,46
EA	3,1	0,06	0,03	0,08	0,11	55,81	7,85	10,51	0,38	12,10
PA	3,3	0,02	0,05	0,05	0,05	30,00	3,71	6,78	0,14	4,19
EL	15,5	0,60	0,20	0,50	0,90	66,48	5,01	6,14	1,30	8,42
ED	4,3	0,02	0,01	0,01	0,03	70,00	3,06	3,66	0,23	5,29
KRPE	12,9	0,19	0,09	0,19	0,30	61,16	3,34	4,28	0,69	5,40
KPR	32,3	0,50	1,06	2,72	2,13	23,62	2,19	4,52	0,71	2,20
TKW	305,0	374,58	236,83	683,54	775,55	48,30	6,35	9,13	27,75	9,10

Dates

Reference

Abadassi, J., 2015, Maize agronomic traits needed in tropical zone. *International Journal of Science, Environment and Technology* 4(2), 371–392.

Allard, R.W., 1960, Principles of plant breeding. John Willey and Sons. Inc. New York, 485.

Al-Tabbal, J.A. & Al-Fraihat, A.H., 2012, Genetic variation, heritability, phenotypic and genotypic correlation studies for yield and yield components in promising barley genotypes. *Journal of Agricultural Science* 4(3), 193. https://doi.org/10.5539/jas.v4n3p193.

Aly, R.S. & Hassan, MM., 2011, Combining ability of grain yield and yield components in maize. *Egypt. J. Plant Breed* 15(5), 149–161.

Amare, S., Dagne, W., Sentayehu, A., 2016, Test cross performance and combining ability of elite highland maize (Zea Mays L.) Inbred Lines at Jimma, South West Ethiopia. *International Journal of Trend in Research and Development* 3(2), 13–26.

Begum, S., Ahmed, A., Omy, S.H., et al., 2016, Genetic variability, character association and path analysis in maize (Zea mays L.). *Bangladesh Journal of Agricultural Research* 41(1), 173–182. https://doi.org/10.3329/bjar.v41i1.27682.

Bello, O.B., Ige, S.A., Azeez, M.A., et al., 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. https://doi.org/10.5923/j.plant.20120205.01.

Beyene, Y., Mugo, S., Gakunga, J., et al., 2011, Combining ability of maize (Zea mays L.) inbred lines resistant to stem borers. *African Journal of Biotechnology* 10(23), 4759–4766.

Burton, G.W. & Devane, D.E., 1953, Estimating heritability in tall fescue (Festuca arundinacea) from replicated clonal material 1. *Agronomy Journal* 45(10), 478–481. https://doi.org/10.2134/agronj1953.00021962004500010005x.

Dagne, W., Vivek, S., Birhanu, T., et al., 2011, Combining ability and heterotic relationships between CIMMYT and Ethiopian maize inbred lines. *Ethiopian Journal of Agricultural Sciences* 21(1-2), 82–93.

Dagne, W., 2008, Genotypic variability and combining ability of quality protein maize inbred lines under stress and optimal conditions. PhD Dissertation Presented at University of the Free State, South Africa. 300p.

Demissew, M., 2014, Genetic diversity and combining ability of selected quality protein maize (QPM) inbred lines adapted to the highland agro-ecology of Ethiopia. PhD dissertation presented at University of KwaZulu-Natal, Republic of South Africa.178p.

Deshmukh, S.N., Basu, M.S., Reddy, P.S., 1986, Genetic variability, character association and path coefficients of quantitative traits in Virginia bunch varieties of groundnut. *Indian Journal of Agricultural Sciences*.

Dudley, J.W. & Moll, R.H., 1969, Interpretation and use of estimates of heritability and genetic variances in plant breeding 1. *Crop Science* 9(3), 257–262. https://doi.org/10.2135/cropsci1969.0011183X000900030001x.

Elmyhum, M., 2013, Estimation of combining ability and heterosis of quality protein maize inbred lines. *African Journal of Agricultural Research,* 8(48), 6309–6317.

Falconer, D.S. & Mackay, T.F.C., 1996, Introduction to quantitative genetics. 4th Edition, Addison Wesley Longman, Harlow. Harlow, Longman Frankel. 280p.

Girma, H., Sentayehu, A., Berhanu, T., et al., 2015, Test cross performance and combining ability of maize (Zea Mays L.) inbred lines at Bako, Western Ethiopia. *Glob J Sci Front Res,* 15(4), 1–24.

Grzesiak, S., 2001., Genotypic variation between maize (Zea mays L.) single-cross hybrids in response to drought stress. *Acta Physiologiae Plantarium* 23(4), 443–456. https://doi.org/10.1007/s11738-001-0055-4.

Gudeta, N., Dagne, W., Habtamu, Z., 2015, Heterosis and combining ability of highland quality protein maize inbred lines. *Maydica* 60-2015.

Hailegiorgis, D., Mebrahtom M., Tsige G., 2011, Genetic divergence analysis on some bread wheat genotypes grown in Ethiopia. *Journal Central Euphytica Agriculture* 12(2), 344–352. https://doi.org/10.5513/JCEA01/12.2.922.

Hallauer, A.R. & Miranda, J.B., 1988, Quantitative genetics in maize breeding. 2nd ed. Iowa state Universality Press. Pp. 1–680.

Hallauer, A.R. & Sears, J.H., 1973, Change in quantitative traits associated with inbreeding in a synthetic variety of maize. *Crop Sci* 13(3), 327–330. https://doi.org/10.2135/cropsci1973.0011183X001300030012x.

Ihsan, H., Khalil, I.H., Hidayat-ur-Rahman, N.W., 2005, Genotypic variability for morphological traits among exotic maize hybrids. *Sarhad J Agric* 21(4), 599–602.

Johnson, H.W., Robinson, H.F., Comstock, R.E., 1955, Estimates of genetic and environment variability in Soybean. *Agronomy Journal* 47, 314–318. https://doi.org/10.2134/agronj1955.00021962004700070009x.

Mahmood, Z., Malik S.R., Akhtar, R., et al., 2004, Heritability and genetic advance estimates from maize genotypes in Shishi Lusht, a valley of Krakurm. *Int J Agric Biol* 6(5), 790–791.

Mallikarjuna, N.M., Chandrashekhar, H., Shashibhaskar, M.S., et al., 2011, Genetic variability and correlation studies for yield and related characters in single cross hybrids of maize (Zea mays L.). *Current Biotica* 5(2), 157–163.

MoANR. 2016. Plant Variety Release, Protection and Seed Quality Control Directorate, Crop Variety Register, 19: 318p.

Mosisa, W., Tuna, H., Abera, W., et al., 2002, Developing low-N tolerant maize varieties for mid-altitude sub-humid agro-ecology of Ethiopia. Integrated Approaches to Higher Maize Productivity in the New Millennium (No. CIS-4176. CIMMYT)

Murtadha, M.A., Ariyo, O.J., Alghamdi, S.S., 2016, Analysis of combining ability over environments in diallel crosses of maize (Zea mays). *Journal of the Saudi Society of Agricultural Sciences* 17(1), 68–78. https://doi.org/10.1016/j.jssas.2016.01.004.

Nigus, B. 2018. Genetic variability, heritability, correlation and path coefficient analysis for grain yield and yield component in maize (Zea mays L.) hybrids. *Adv Crop Sci Tech* 6(5), 3–9.

Nzuve, F., Githiri, S., Mukunya, D.M., et al., 2013, Analysis of genotype x environment interaction for grain yield in maize hybrids. *Journal of Agricultural Science* 5(11), 75. https://doi.org/10.5539/jas.v5n11p75.

Patterson, H.D. & Williams, E.R., 1976, A new class of resolvable incomplete block designs. *Biometrika* 63, 83–—92. https://doi.org/10.1093/biomet/63.1.83.

Prasanna, B.M., Vasal, S.K., Kassahun, B., et al., 2001, Quality protein maize. *Current Science* 81(10), 1308–1319.

SAS Institute., 2014, Statistical Analysis System Version 9.3, SAS Institute, Inc. Cary, NC, USA

Singh, A.K., Mishra, S.P., Parihar, R., 2018, Studies on genetic variability parameters on grain yield and its yield attributing traits in maize (Zea mays L.), *Int J Curr Microbiol App Sci* 7(9), 1261–1266. https://doi.org/10.20546/ijcmas.2018.709.150.

Singh, B., 2001, Plant breeding principles and methods, 6th ed. Kalyani Publishers, New Delhi, India. 600p.

Sleper, D.A. & Poehlman, J.M., 2006, Breeding field crops (No. Ed. 5). Blackwell publishing.

Tadesse, J., Leta, T., Techale, B., et al., 2018, Genetic variability, heritability and genetic advance of maize (Zea mays L.) inbred lines for yield and yield related traits in southwestern Ethiopia. *Journal of Plant Breeding and Crop Science* 10(10), 281–289. https://doi.org/10.5897/JPBCS2018.0742.

Tamene, T., Gemechu, K., Hussein, M., 2015, Genetic progresses from over three decades of faba bean (Vicia faba L.) breeding in Ethiopia. *Australian Journal of Crop Science* 9(1), 41–48.

Tsedeke, A., Bekele, S., Abebe, M., et al., 2015, Factors that transformed maize productivity in Ethiopia. *Food Security* 7(5), 965–981. https://doi.org/10.1007/s12571-015-0488-z.

Welsh, J., 1981, Fundamentals of plant breeding and genetics. Jhon Weliey & Sons, New York.

Yusuf, M., 2010, Genetic variability and correlation in single cross hybrids of quality protein maize (Zea mays L.). *African Journal of Food, Agriculture, Nutrition and Development* 10(2). https://doi.org/10.4314/ajfand.v10i2.53358.

Zerihun, T., 2011, Genotype x environment interaction and yield stability analysis of maize (Zea Mays L.) in Ethiopia. MSc Thesis Presented at School of Graduate Studies, Jimma University, Ethiopia.