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Full Length Research Paper

Growth, yield and phosphorus use efficiency of potato varieties propagated from apical rooted cuttings under variable phosphorus rates

Pauline Aarakit*, Josephine P. Ouma and Joyce J. Lelei

Department of Crops, Horticulture and Soils, Egerton University, P. O. Box 536 -20115, Egerton Njoro, Kenya.

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This study determined effect of phosphorus (P) rates on growth, yield and phosphorus use efficiency (PUE) of potato varieties propagated from apical rooted cuttings. Experiments were conducted at Egerton University, Njoro and Kenya Agricultural and Livestock Research organization, Molo, in a split plot arrangement in randomized complete block design with three replicates. Main plot factors were four potato varieties (Shangi, Dutch Robyjn, Unica and Wanjiku) and sub plot factors were four P levels of triple super phosphate (0, 30, 60, 90 kg P ha⁻¹). Data on growth, yield and PUE of potato were collected. Phosphorus rates had significant effect on plant growth and yield. The interaction effects of P rates and varieties on plant survival, plant height, shoot biomass, number of eyes and tuber size was significant. The interaction of Wanjiku and 30 kg P ha⁻¹ gave the highest shoot biomass of 0.42g per plant and large sized tubers (> 60 mm diameter). The main effects of variety and P rates significantly affected days to physiological maturity and marketable tuber yield. Unica variety showed high P uptake and PUE at both study sites. Apical rooted cuttings and 30 kg P ha⁻¹ is recommended in the study areas with similar agro ecological zones.

Key words: Nutrient use efficiency, triple super phosphate, potato, apical cuttings.

INTRODUCTION

Potato (*Solanum tuberosum* L.) is the world's fourth most important food crop after maize, rice and wheat. It is an important source of carbohydrate, protein, vitamins B and C and also minerals. It provides a source of income and is important in food and nutritional security (Islam and Nahar, 2012). Potato is the second most consumed crop in Kenya, after maize (Janssens et al., 2013). It is mainly cultivated by small scale farmers in the highland areas of Kenya at altitudes ranging between 1200 to 3000 meters

above sea level. The area under potato production is 192,341 hectares with average yield of 79,020 tonnes per hectare (FAO, 2018). Smallholder farmers propagate potatoes using seeds saved from the previous season's harvest. Diseases and pests subsequently accumulate and cause losses in production (Tsoka et al., 2012; Muthoni et al., 2013). Propagation of potato from rooted apical cuttings offers an alternative for farmers. They are clean planting materials with ability to regenerate rapidly

*Corresponding authors. Email: paulineaarakit14@gmail.com.

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Variables	September	October	November	December	January
Egerton					
Rainfall (mm)	89.7	161.6	289.4	223.6	83.9
Temperature	20.5	19.3	19.3	18.9	19.6
KALRO Molo					
Rainfall (mm)	79.6	178.4	237.4	198.2	76.8
Temperature	18	19	19	18	19

Table 1. Rainfall (mm) and temperature (°C) of study sites.

and can increase potato yield and quality. They are thus ideal for conservation of potato seed, storage and distribution of the potato germplasm through breeding lines and varieties (Yasmin et al., 2011).

Potato has a high phosphorus (P) demand as compared to other crops (Hopkins et al., 2014). P is important for vine growth, tuber formation, tuber bulking and tuber starch synthesis (Atkinson et al., 2003; Hopkins et al., 2014; Nyiraneza et al., 2017). It has a low P uptake efficiency due to its shallow root system. Majority of roots are found in the top 30 cm of the soil (Mikkelsen, 2014). Differences in the rooting systems and utilization ability of genotypes influence optimum rates to be applied (Fernandes et al., 2014). To get the most benefit from fertilizer application, placement and rate of application is critical. The risk of P losses in surface runoff is higher with very high P concentrations in soil (Mikkelsen, 2014). Application of appropriate rates will also minimize risk of contamination of water sources and reduce production costs (Nyiraneza et al., 2017).

The objective of the study was to determine effect of P rates on the growth, yield and phosphorus use efficiency of potato varieties generated from apical rooted cuttings in potato producing sub-counties of Molo and Njoro located in the Kenyan highlands.

MATERIALS AND METHODS

Study area, soil sampling and analysis

The experiment was conducted during the short rain season of September 2019 – January 2020 in the research fields of Egerton University, Njoro and Kenya Agricultural Livestock and Research organization (KALRO), Molo. Egerton University Njoro (35° 35' E; 0° 23' S) is situated at an altitude of 2200 m above sea level, and receives an annual rainfall amount of 1132 mm (Climatic data.org, 2019). KALRO Molo (35.7373° E; 0.2472° S) is located at 2500 m above sea level, and receives annual average rainfall of 1100 mm to 1500 mm (Climatic data.org, 2019). Egerton site received lower rainfall in October (161.6mm) and higher rainfall amounts in November (289.4 mm) and the average temperature is 19.3°C (Table 1). Molo receive more rainfall in October (178mm) and lower rainfall amount in November (237.4mm) and the average temperature is 19°C (Climatic data.org, 2019).

Soil samples were collected before experimental setup from the two sites for initial characterization of chemical and physical properties. Three soil samples per site were collected using a soil auger from six locations in a zigzag pattern, from three depths (0-15, 15-30, 30-45cm). The soil samples were sealed, labelled and transported to the laboratory. Air dried samples sieved through a 2 mm mesh were subjected to chemical analysis to determine initial values of pH (Mehlich et al., 1962), total nitrogen (N) using Kjeldahl method (Page et al., 1982), total organic carbon by calorimetric method (Anderson and Ingram, 1993), available P (Mehlich et al., 1962) and potassium (K) (Anderson and Ingram, 1993). Samples collected were characterized for the physical properties; soil texture (Anderson and Ingram, 1993) and bulk density using core ring method (Anderson and Ingram, 1993). Soil analysis was done at the National Agricultural Research Laboratories of KALRO Kabete Nairobi.

Treatments and agronomic practices

The experiment was laid out as a split plot arrangement in a randomized complete block design (RCBD) with three replicates. Four potato varieties (Shangi, Dutch Robyjn, Unica and Wanjiku) were the main plot factors and four levels of P (0, 30, 60, 90 kg P ha⁻¹) were subplot factors. Triple super phosphate (TSP) was used as source of P. The plot size was 3.0 m by 2.4 m with a footpath of 1.0 m between plots and replicates.

Land preparation was carried out manually which involved ploughing and harrowing to obtain fine tilth for planting of rooted apical cuttings. The rooted apical cuttings, obtained from Stokman Rozen Company located in Naivasha Kenya, were planted at spacing of 0.75 m between plants and 0.35 m between rows. Triple super phosphate (46% P₂O₅) fertilizer was applied as per the treatment rates in the planting holes and mixed thoroughly with the soil. Recommended doses of urea and potassium fertilizers were applied as follows; Urea (46%) at rate of 50 kg N ha⁻¹, in two splits; two weeks after planting and during the potato vegetative stage prior to flowering and Muriate of potash (60% K2O) at rate of 30 kg K ha⁻¹ as basal fertilizer during planting to supply K. Pests like cut worms were controlled by application of Alpha Cypermethrin (Tata Alpha 10 EC-15ml/20 litres water) immediately after planting. Diseases like late blight was controlled by spraying with protective fungicide Ridomil gold (Metalaxyl 40g/kg + Mancozeb 640g/kg) at dose of 40 gms/20 litres water fortnightly until plants attained 50% physiological maturity. Manual weeding was done at two weeks after planting and during crop growth. Earthing up was carried out during tuber initiation to protect tubers from direct sunlight.

Data collection

Growth measurements

Plant survival per plot was determined fourteen days after planting, by manual counting. Three tagged plants in the two middle rows were used for measuring growth parameters. The number of stems

 Table 2. Analysis for soil physical and chemical properties of experimental sites.

Variables		Egerton site	е	Molo	(KALRO)	Site	
Soil depth (cm)	0-15	15-30	30-45	0-15	15-30	30-45	
Soil pH	5.78	5.90	6.06	5.69	5.05	5.00	
Total nitrogen (%)	0.29	0.21	0.18	0.22	0.16	0.15	
Total organic carbon (%)	2.99	2.27	1.89	2.36	1.79	1.66	
Available P (ppm)	25	25	30	30	25	25	
Potassium (%)	1.94	1.70	1.64	1.50	0.96	0.92	
Soil physical properties							
Soil texture class	SCL	SCL	SCL	SCL	SCL	SC	
Sand (%)	56	56	54	54	52	52	
Silt (%)	16	16	14	14	14	12	
Clay (%)	28	28	32	32	34	36	
Soil bulk density (g/m ³)	0.913	0.899	0.897	0.872	0.861	0.861	

Key: SCL= sandy clay loam; SC= sandy clay.

arising from the main plant was counted. Plant height was measured, using a ruler, from the base of plant to the apex of the shoot fortnightly; from 14 days after planting (DAP) up to 56 DAP, before flowering of potatoes. Days to attainment of 50% flowering by 50% of the plant population were recorded. Days to physiological maturity was determined when 50% of the plant leaves had turned yellow.

Yield determination

The plants were harvested after three months when they had reached maturity stage. Shoot biomass weight was determined from the fresh weight. Total number of tubers and tuber weight were measured from three hills per plot and the average determined. Tubers were graded into three sizes: large (>60 mm diameter), medium (30-60mm diameter) and small (<30 mm diameter). Marketable tuber yield was determined by counting number of large sized and medium sized tubers. Number of eyes was counted on the randomly selected tubers.

Phosphorus uptake

The third to sixth leaf from the growing tip was sampled two times: 42 days after planting (prior to flowering) and 84 DAP (prior to maturity). Tubers were also sampled after harvesting. Total P concentration (g kg⁻¹) was determined using the Vanadomolybdate yellow method (Okalebo et al., 2002).

The PUE was calculated using the following formula (Fixen et al. 2015);

PUE (kg kg $^{-1}$) =

 $\frac{\text{Yield of fertilized plot in kg -Yield of unfertilized plot in kg}}{\text{total amount of P applied in kg}}$

Statistical analysis

All of the crop data collected were tested for normality and subjected to general linear model procedure analysis using SAS version 9.3 software to generate analysis of variance (ANOVA).

Least significance difference was used to separate treatment means, where F test was significant. Correlation analysis was done to show the relationship between growth parameters and yield of potatoes.

RESULTS AND DISCUSSION

The soil pH was slightly acidic with values varying from 5.78 to 6.06 (Table 2). The soil had adequate nitrogen, moderate organic carbon and potassium. The soils had available P contents of 25 to 30 ppm, which was adequate according to rating by Landon (1991) (Table 2).

Growth of potato

Plant survival

Plant survival was generally higher at 14 to 28 days after planting (DAP) as compared to 42 and 56 DAP (Figure 1). The rooted apical cuttings were acclimatized to the external environmental conditions through hardening them in the screen houses for 30 days before transplanting to the open fields. The ability of the plants to withstand the new environmental conditions increases their ability to survive until maturity. Tsoka et al. (2012) reported that potato plants derived from apical stem cuttings survive better than tissue culture plantlets.

The main effects of P rates on plant survival was significant (P<0.05) at 14 and 28 DAP. Potato plants in treatments 0, 30 and 60 kg P ha⁻¹ recorded the highest survival during these periods. The initial soil analysis showed that the soils were rich in organic carbon, total N and available P with good bulk density and soil texture. These soil properties enhanced the growth of the plants even in the control treatments where P fertilizer was not applied. Phosphorus is a vital nutrient in early crop

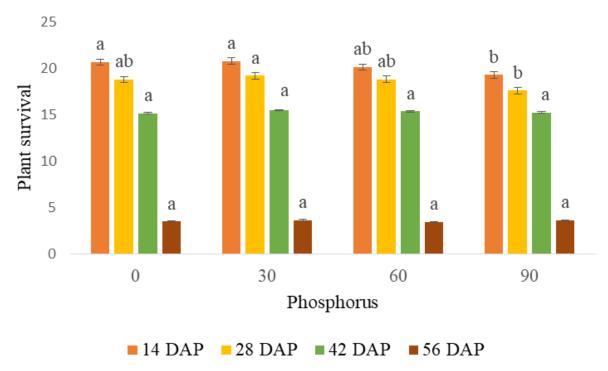


Figure 1. Main effect of phosphorus rates on plant survival of rooted apical cuttings. DAP days after planting, Plant survival (%), Phosphorus rates kg ha-1.

growth and metabolism processes. This is in conformity with the report of Grant et al. (2001), that adequate P application is important for the earliest stages of crop growth. The interaction effect of location and variety on plant survival was significant (P<0.05) at all sampling periods. At 14, 28 and 42 DAP, all varieties at Egerton site had highest survival (Table 3). The differences in survival in the study areas could be attributed to differences in climatic conditions (Öztürk et al., 2010).

Number of stems

The number of stems per plant increased with plant growth. The main effect of phosphorus rates on number of stems was highly significant (P<0.001) at 28, 42 and 56 DAP. The plots in which P was applied at 30, 60, 90 kg P ha 1 recorded significantly higher number of stems per plant compared to the control treatment. The control treatment recorded the least number of stems per plant (Figure 2). The interaction effects of location and P rates on number of stems was significant (P<0.05) at 28 DAP. Phosphorus application rates of 30, 60 and 90 kg P ha⁻¹ at Egerton site recorded higher number of stems of 4.25, 4.17 and 4.25 respectively, as compared to KARLO Molo with 3.75, 3.42 and 4.08, respectively. Application of P enhanced early crop development (Belachew, 2016; Ekelof, 2007). Studies on potatoes grown under field conditions have reported results similar to the present study with least number of stems per plant in control compared to fertilized treatments (Zelalem et al. 2009; Nizamuddin et al., 2003; Alam et al., 2007; Hassanpanah et al., 2009). Rosen and Bierman (2008), Kumar et al. (2012) and Misgina, (2016) reported increased number of potato stems per plant with increase in P rates.

The interaction effect of location and potato varieties on the number of stems per plant were significant (P<0.01) at 28, 42 and 56 DAP (Table 4). At 28 DAP, Shangi and Unica varieties at Egerton had significantly higher number of stems (4.5 and 4.0, respectively). At 42 DAP, Shangi, Dutch Robyjn, Unica and Wanjiku varieties at Egerton site had highest number of stems of 9.92, 9.17, 8.75 and 8.0, respectively. At 56 DAP, all the varieties had higher number of stems at Egerton site as compared to KALRO Molo. The environmental conditions and genetic makeup of varieties might have influenced the plant growth response (Asfaw et al., 2015; Abalo et al., 2003; Kaguongo et al, 2010).

Plant height

Plant height increased with time at both sites. The results showed that the interaction effect of study sites and P rates on plant height was significant (P<0.05) at 28, 42 and 56 DAP (Table 4). The P application rates of 30, 60 and 90 kg P ha⁻¹ at 28 and 42 DAP in KARLO, Molo and 56 DAP in Egerton resulted in significantly higher

16.50±0.73^d

13.17±0.86^e

18.58±0.92^{cd}

17.50±0.95^{cd}

3.53

15.47

0.0222

			Plant sur	vival (%)	
Location	Variety	14 DAP	28 DAP	42 DAP	56 DAP
Egerton	Shangi	22.92±0.57 ^{ab}	22.42 ±0.70 ^a	22.08 ± 0.73^{a}	22.08±0.86 ^{ab}
	Dutch R	23.17 ± 0.51^{a}	22.17±0.78 ^{ab}	21.42±0.78 ^{ab}	21.42±0.84 ^{ab}
	Unica	23.50 ± 0.19^{a}	22.92 ± 0.42^{a}	22.50 ± 0.34^{a}	22.67 ±0.26 ^a
	Wanjiku	22.33±0.53 ^{ab}	21.58±0.63 ^{ab}	19.92±0.84 ^{bc}	19.67±0.86 ^{bc}

18.75±0.83^{cd}

 13.67 ± 0.87^{t}

18.67±1.01^{cd}

19.92±1.15^{bc}

18.61

16.35

0.0136

17.00± 0.90^d

 13.33 ± 0.89^{e}

18.83±0.94^{cd}

18.00±1.00^{cd}

15.32

16.90

0.0044

Table 3. Interaction effect of study sites and potato varieties on potato survival of rooted apical cuttings.

21.08±0.50^{bc}

 $13.42 \pm 0.86^{\circ}$

20.25±0.55^{cd}

20.17±0.86^{cd}

20.23

11.57

<.0001

Shangi Dutch R

Unica

Wanjiku

Means within a column with the same superscript are not significantly different at P>0.05, ± values indicates the standard deviation; DAP= Days after planting.

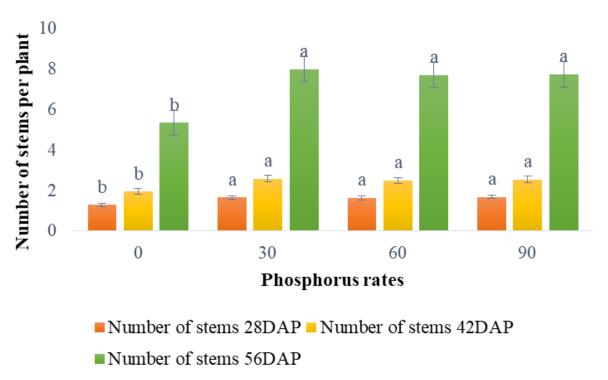


Figure 2. Main effect of P rates on number of stems per potato plant. Key: DAP = days after planting, Phosphorus rates kg ha-1.

(P<0.05) plant heights.

KALRO M

Mean

C.V. (%)

P Value

Phosphorus boosts the metabolic activity of the plants during the early growth stages that encourage stem elongation (Ekelof, 2007; Birtukan, 2016). This result agrees with the work of Firew et al. (2016), Belachew, (2016) and Misgina (2016), who reported increases in height of potatoes with increase in the amount of P applied.

The results showed that the interactive effect of location and variety on plant height was significant (P<0.05) at 14, 28, 42 and 56 DAP (Table 4). Shangi variety at KARLO Molo had significantly (P<0.05) higher height at 14 and 28 DAP. At 42 DAP, significantly higher (P<0.05) plant heights were observed in Shangi Unica and Wanjiku varieties at KARLO Molo. At 56 DAP Shangi variety recorded the highest plant height of 34.82cm at Egerton

Table 4. Interaction effect of study sites and potato varieties on number of stems per plant and plant height (cm) of potato.

Study sites	Variety		Number of stems			Plant he	eight (cm)	
		28 DAP	42 DAP	56 DAP	14 DAP	28 DAP	42 DAP	56 DAP
Egerton	Shangi	4.50±0.29 ^a	9.92±0.34 ^a	10.67±0.26 ^a	6.61±0.28 ^b	7.25±0.39 ^b	15.70±1.04 ^{bc}	34.82±1.90 ^a
J	Dutch Robyjn	3.67±0.31 ^{ab}	9.17±0.79 ^{ab}	10.75±0.76 ^a	3.71±0.13 ^d	4.58±0.16 ^f	11.19±0.92 ^{cd}	23.58±2.08 ^{bc}
	Unica	4.00±0.33 ^{ab}	8.75±0.41 ^{ab}	9.17±0.27 ^{ab}	5.38±0.24 ^c	5.47±0.19 ^{def}	12.06±0.92 ^{cd}	24.67±1.67 ^b
	Wanjiku	3.00±0.28 ^b	8.00±0.54 ^{bc}	9.42±0.50 ^a	6.53±0.15 ^b	5.81±0.19 ^{de}	9.89±0.72 ^d	22.35±1.68 ^{bc}
KALRO	Shangi	3.25±0.39 ^b	6.50±0.84 ^{cd}	7.67±0.89 ^{bc}	7.17±0.19 ^a	9.25±0.67 ^a	22.09±3.14 ^a	22.76±3.16 ^{bc}
	Dutch Robyjn	3.50±0.29 ^b	5.17±0.64 ^d	5.25±0.59 ^d	3.84±0.18 ^d	4.84±0.22 ^{ef}	11.99±1.35 ^{cd}	12.18±1.30 ^d
	Unica	3.25±0.39 ^b	5.83±0.41 ^d	6.42±0.40 ^{cd}	3.95±0.11 ^d	6.03±0.34 ^{cd}	18.29±1.61 ^{ab}	18.79±1.61 ^c
	Wanjiku	3.00±0.39 ^b	6.83±0.71 ^{cd}	7.75 ± 0.70^{bc}	5.71±0.11 ^c	6.92±0.57 ^{bc}	20.67±2.53 ^a	21.22±2.47 ^{bc}
P value		0.0094	0.029	0.0007	< .0001	0.0025	0.0025	0.0017
C.V (%)		19.38	11.76	18.53	12.17	12.89	14.34	12.31
Mean		3.52	2.69	8.38	5.36	6.26	3.79	4.63

Means within a column followed by the same superscripts are not significantly different at P>0.05. DAP (days after planting).

study site. The soil organic matter, which was moderate in both sites, releases plant nutrients slowly, hence providing nutrients over a longer period for crop growth; improves water holding capacity of the soils and acts as pH buffer (Kumar et al. 2012).

Days to 50% flowering

The main effect of P rates on days to 50% flowering of potato was significant (P<0.05). The plots with 90 kg P ha⁻¹ flowered at 56 DAP as compared to plots with 0, 30, 60 kg P ha⁻¹ that flowered at 57 DAP. This contradicts the findings of Zelalem et al. (2009) and Misgina et al. (2016). They reported that increased P rates delayed the days to 50% flowering of potato plants.

The interaction effect of location and variety significantly (P<0.001) influenced days to 50% flowering (Table 5). Shangi flowered faster at both KALRO Molo site and Egerton site; after 45 days

and 49 days, respectively. Unica almost took the same days to flower at both the study sites with difference of one day only. Dutch Robyjn and Wanjiku flowered three days earlier at Egerton site as compared to KALRO Molo study site. The differences in the number of days to 50% flowering could be due to varietal differences in period to maturity due to genetic makeup and response to the environmental conditions (Kaguongo et al. 2010).

Days to 50% physiological maturity

The results showed that the main effect of P rates on days to 50% physiological maturity was not significant (P<0.05). The study soils had sufficient initial P levels, hence the non-significant differences. On the contrary, Zelalem et al. (2009) and Misgina (2016) reported delayed days to 50% physiological maturity of the potato plants with increased P rates. They attributed this

to sustained physiological activities of the plants excessive accumulation of photosynthetic assimilates that lead to continued photosynthesis and growth of the plants.

The main effects of variety and location on days to 50% physiological maturity were highly significant (P<0.01). Shangi variety attained 50% physiological maturity earlier followed by Unica then Dutch Robyn and lastly Wanjiku variety. The differences in the days to physiological maturity could be due to varietal differences, whereby Shangi and Unica are early maturing while Dutch Robyjn and Wanjiku are medium maturing varieties.

Phosphorus uptake and use efficiency of Potato

Phosphorus uptake prior to flowering

The interaction effect of location and variety on

Table 5. Interaction effect of study sites and potato varieties on shoot biomass, days to flowering, number of tubers, tuber weight, size of tubers and number of eyes.

Study sites	Varieties	Shoot biomass per plant	Days to flowering	Number of tubers per plant	Tuber weight per plant	Large size >60 mm	Medium size (30–60 mm)	Small size (<30 mm)	Number of eyes per tuber
	Shangi	0.31±0.02b	49.17±0.11e	19.67±0.87b	1.10±0.05°	11.67±0.31b	12.17±0.34b	13.50±0.51b	11.42±0.26°
-	Dutch Robyjn	0.14±0.01e	63.67±1.22b	18.58±0.98b	0.76 ± 0.05 ^d	12.50±0.29b	10.92±0.34c	16.25±0.33a	14.75±0.60b
Egerton	Unica	0.27±0.01°	58.00±0.54d	15.50±0.57°	1.30±0.07b	11.58±0.60b	8.58±0.15d	2.92±0.48e	8.75±0.49d
	Wanjiku	0.47±0.01a	57.33 ± 0.36 ^d	25.92±0.79a	1.44±0.05a	18.25±1.10a	14.42±0.57a	11.83±0.83°	19.00±1.14ª
	Shangi	0.27±0.01°	45.00 ± 0.25 ^f	10.25±0.78e	0.32±0.03 ⁹	4.75± 0.30e	5.17± 0.34 ^f	10.08±0.51d	4.67±0.28e
	Dutch Robyjn	0.12±0.01e	66.17 ± 0.58a	7.42±0.66 ^f	0.20 ± 0.02^{h}	0.92± 0.19 ^f	1.00± 0.259	13.67±0.36b	1.58±0.34 ^f
KAL DO	Unica	0.21±0.01d	$59.83 \pm 0.75^{\circ}$	6.17±0.41 ^f	0.47 ± 0.02^{f}	9.50± 0.60°	6.58± 0.15e	2.00±0.44e	9.25±0.52d
KALRO	Wanjiku	0.30±0.01 ^b	60.58 ± 0.77°	13.08±0.87d	0.63±0.04e	7.58 ± 1.00^{d}	9.33± 0.56d	13.50±0.84b	7.92±1.13 ^d
	Mean	0.25	57.46	14.57	0.77	9.59	8.52	10.46	9.66
	C. V. (%)	`11.50	3.70	12.86	16.68	2.73	3.68	3.05	5.02

Means within a column followed with the same superscripts are not significantly different at P >0.05.

phosphorus uptake prior to flowering stage (leaves sampled at 42 DAP) was significant (P<0.01). Dutch Robyin variety at Egerton study site and KARLO, Molo, and Unica variety at KALRO, Molo had high P uptake. Shangi and Wanjiku varieties showed lower P uptake at both study sites. The interaction of varieties and P rates on P uptake was significant (P<0.01). Phosphorus rate of 30 kg P ha⁻¹ and Unica variety recorded the highest P uptake (0.36%) followed by Dutch Robvin variety and rates of 60, 90, 30, 0 kg P ha⁻¹ with 0.30, 0.30, 0.29 and 0.27% P uptake, respectively. The variety Wanjiku grown with 90 kg P ha⁻¹ applied and Shangi variety grown without P (0 kg P ha⁻¹) showed the least P uptake of 0.18 and 0.17 %, respectively.

The interaction of study sites and varieties on phosphorus use efficiency was significant. Potato varieties with high PUE recorded the highest marketable tuber yield. This could be attributed to the ability of the varieties to acquire P from the soil and utilize it for biomass accumulation and

yield. Wanjiku and Unica variety had high P acquisition and utilization ability which led to increase in yield as in conformity with the findings of Nyiraneza et al. (2017). This results also agrees with findings (Bayuelo and Ochoa, 2014; Fernandes et al., 2014; Wishart et al., 2013) that reported that differences in phosphorus utilization efficiency is influenced by cultivar characteristics such as root weight, root length and diameter.

Phosphorus availability in the soil is affected by the soil pH and is more available at slightly acidic soils (Hopkins et al., 2014). The soil pH at the study sites was at a range of 5.0 to 6.21 which might have favoured availability of phosphorus to the potato crops. This availability made the acquisition of phosphorus by the plants easy and led to increased phosphorus use efficiency and increased yield. This result is in conformity with findings of Hopkins et al. (2014), Rosen et al., (2014) and Thornton et al. (2014), who reported that soil pH affects the availability of phosphorus in the soil.

Phosphorus uptake prior to maturity

The main effect of P rates on P uptake was significant (P<0.01). Phosphorus rates of 30 and 90 kg P ha⁻¹ recorded higher P uptake values of 0.43% and 0.41%, respectively. The control treatment 0 kg P ha⁻¹ recorded higher P uptake than 60 kg P ha⁻¹ with values of 0.39% and 0.37%, respectively. The main effect of variety on P uptake was significant (P<0.001). Unica variety recorded the highest P uptake value of 0.47% followed by Dutch Robyjn Wanjiku and Shangi varieties with values of 0.39%, 0.38% and 0.37%, respectively.

The main effect of location on P uptake by the potato tubers was significant (P<0.05). The tubers at Egerton recorded higher P content of 0.18% as compared to KALRO Molo with a value of 0.11%. The study soils were slightly acidic (5.0 to 6.21) and had moderate carbon levels; these chemical properties favoured the availability and assimilation of applied P (Hopkins et al., 2014;

Thornton et al., 2014; Rosen et al., 2014; Blake et al., 2000; Benbi and Brar, 1994).

Phosphorus use efficiency

The main effect of P rates on PUE was significant (P<0.001). The potato crops grown with application of 30 kg P ha 1 recorded the highest PUE of 239.79 kg kg followed by 60 kg P ha⁻¹ (126.40 kg kg⁻¹) and 90 kg P ha⁻¹ (73.45 kg kg⁻¹). These results agree with findings of Nyiraneza et al. (2012), who reported that PUE was higher in fertilized plots. The effect of interaction of location and varieties on PUE was significant (0.01). Higher values were observed with Unica variety at Egerton study site (284.88 kg kg⁻¹) and Wanjiku variety at KALRO, Molo (218.7 kg kg⁻¹). The differences in PUE amongst the varieties could be attributed to differences in rooting traits. Bayuelo and Ochoa (2014), Fernandes et al. (2014) and Wishart et al. (2013) similarly reported that phosphorus utilization efficiency was influenced by cultivar characteristics such as root weight, root length and diameter (Kawakami and Iwama., 2012).

Yield of Potato

Plant shoot biomass

The interaction between study sites and varieties on plant shoot biomass was highly significant (P<0.001). Wanjiku variety at Egerton study site registered the highest shoot biomass followed by Shangi and Wanjiku at Egerton and KARLO Molo, respectively (Table 5). The interaction effect of P and varieties on plant shoot biomass was significant (P<0.01). Wanjiku and Dutch Robyjn varieties registered the highest and lowest plant shoot biomass across all P treatments respectively (Table 6). Higher shoot biomass for Shangi and Wanjiku varieties could be attributed to genetic makeup that supports vegetative canopy development and shoot biomass accumulation (Shunka et al., 2017). Zelalem et al. (2009) reported an increase in potato biomass weight after application of N, P and K fertilizers.

Number of tubers

The main effect of P rates on number of tubers was highly significant (P<0.01). Treatments did not significantly influence tuber numbers. The initial soil analysis showed that the study soils had adequate levels of total N and moderate levels of organic carbon. This in addition to applied P could have promoted the growth and photosynthesis rate of the plants and tuber formation. Chala et al. (2017) and Zelalem et al. (2009) reported increase in growth of potato plants due to application of

P. Mona et al. (2012) also reported increase in the number of potato tubers per hill with increasing amounts of NPK fertilizers applied in the soil. The results of the study showed that the interactive effect of location and potato varieties on the number of tubers was highly significant (P<0.01). The highest number of tubers was registered with Wanjiku variety followed by Unica and Shangi at Egerton study site. Wanjiku variety had more stems and this could have contributed to the increased number of tubers. The correlation between the number of tubers and number of stems was positive (Table 7). The rate of vegetative growth of the variety contributes to high number of stems which correlates with the number of tubers formed (Belachew, 2016; Chala et al., 2017).

Tuber weight

The main effect of P rates on tuber weight was highly significant (P<0.001). The P rates of 30, 60 and 90 kg P ha⁻¹ recorded tuber weights of 19.30 kg, 19.84kg and 18.88 kg ha⁻¹, respectively. These were not significantly different, but higher than the control treatment (0 kg P ha 1) which recorded tuber weight of 15.55 kg ha⁻¹. The results of the study showed that interaction of location and varieties on tuber weight was highly significant (P<0.01). Wanjiku variety recorded heaviest tubers at Egerton study site while Dutch Robyjn variety registered the lowest tuber weight at KALRO Molo (Table 5). The study soils had moderate amounts of organic matter content and adequate total N and this contributed to tuber weight. The factors that affect tuber weight are variety, location, organic matter content and total nitrogen (Zelalem et al., 2009). In a study on growth, nutrient uptake and dry matter partitioning in potato plants under different combinations of potassium, nitrogen and phosphorus, Jenkins and Mahmood (2003) reported that the response of potatoes to single deficiencies may be influenced greatly by levels of other nutrients. Misgina (2016) reported that increase in tuber weight can be associated with adequate photosynthetic products translocated to the reproductive structures.

Size of tubers

The result of the study showed that the interaction effect of location and varieties on size of tubers was significant (P<0.001). Wanjiku variety at Egerton study site recorded the highest number of large (>60mm diameter) and medium sized tubers (30-60mm diameter). Dutch Robyjn at Egerton site registered the highest number of small sized tubers (<30mm diameter) followed by Shangi at Egerton and Wanjiku at Molo. Unica variety had the least number of small sized tubers at both the study sites (Table 5). The differences in size of tubers could be attributed to environmental factors like soil moisture,

Table 6. Interaction effect of varieties and phosphorus rates on potato biomass, number of eyes and size of tubers.

Varieties	P rates (kg ha ⁻¹)	Shoot biomass per plant	Number of eyes per tuber	Large size >60 mm	Medium size (30-60 mm)	Small size (<30 mm)
	0	0.30 ± 0.04^{bc}	6.67 ± 1.50 ^d	6.83 ± 1.58 ^{cd}	7.50 ± 1.57 ^{cd}	13.00 ± 0.77 ^b
Ol	30	0.31 ± 0.01^{bc}	8.67 ± 1.50^{cd}	8.83 ± 1.58^{bcd}	9.17±1.58 ^{bcd}	12.67 ± 0.80^{b}
Shangi	60	0.26 ± 0.01^{cd}	8.67 ± 1.50^{cd}	8.83 ± 1.58^{bcd}	10.17±1.58 ^{bc}	12.50 ± 0.85^{b}
	90	0.28 ± 0.01^{cd}	8.17 ± 1.58 ^{cd}	8.33 ± 1.54^{bcd}	7.83 ± 1.58^{cd}	9.00 ± 0.77^{c}
	0	0.16 ± 0.02 ^{ef}	6.83 ± 2.61 ^d	6.00 ± 2.39 ^d	5.00 ± 2.10 ^d	16.17 ± 0.60^{a}
Dutch Robyjn	30	0.14 ± 0.01^{ef}	8.33 ± 3.14^{cd}	7.17 ± 2.63^{cd}	7.17 ± 2.32^{cd}	14.00± 0.63 ^b
	60	0.11 ± 0.01 ^f	7.00 ± 2.84^{d}	6.33 ± 2.69^{d}	6.33 ± 2.25^{cd}	14.00 ± 0.63^{b}
	90	0.10 ± 0.01^{f}	10.50 ± 3.21 ^{bcd}	7.33 ±2.69 ^{bcd}	5.33 ± 2.25^{d}	15.67±0.67 ^a
	0	0.21 ± 0.01 ^{de}	6.50 ± 0.22^{d}	7.33 ± 0.49^{bcd}	7.33 ± 0.49^{cd}	4.67 ± 0.42^{d}
l laiss	30	0.26 ± 0.01^{cd}	11.00 ± 0.26^{bcd}	11.17±0.60 ^{abcd}	8.00 ± 0.45^{cd}	1.33 ± 0.33^{e}
Unica	60	0.24 ± 0.02^{cd}	9.00 ± 0.26^{cd}	11.33±0.49 ^{abcd}	7.67 ± 0.49^{cd}	1.17 ± 0.31 ^e
	90	0.24 ± 0.02^{cd}	9.50 ± 0.22^{cd}	12.33± 0.49 ^{abc}	7.33 ± 0.49^{cd}	2.67 ± 0.33^{e}
	0	0.36 ± 0.04^{ab}	7.50 ± 2.46^{cd}	7.33 ± 2.25 ^{bcd}	10.17±1.14 ^{bc}	10.50 ± 0.43 ^c
\\\ ::'!	30	0.42 ± 0.04^{a}	17.17 ± 2.47 ^a	15.67 ± 2.40^{a}	10.17±1.14 ^{bc}	12.50 ± 0.43^{b}
Wanjiku	60	0.37 ± 0.05^{ab}	15.83 ± 2.63^{ab}	15.83 ± 2.47^{a}	12.67±1.20 ^{ab}	17.17 ± 0.48^{a}
	90	0.39 ± 0.04^{a}	13.33 ± 2.43 ^{abc}	12.83 ± 2.47 ^{ab}	14.50 ± 1.12 ^a	10.50± 0.43°
Mean		6	9.59	8.52	10.46	9.66
C.V. (%)		11.55	5.02	2.73	3.68	3.05

Means within a column with the same superscript are not significantly different at P>0.01, ± values indicates the standard deviation.

rainfall and varietal differences. Egerton study site received higher amounts of rainfall and warmer temperatures which led to improved photosynthesis and dry matter accumulation in the tubers. According to the study by Otroshy (2006), changes in day and night temperatures were reported to reduce the number of mini tubers formed per cutting. The interaction effect of P rates with potato variety on size of tubers was highly significant (P<0.001). Wanjiku and Unica varieties with 30, 60 and 90 kg P ha⁻¹ registered the highest (P<0.001) number of large sized tubers and medium size tubers (Table 6).

Phosphorus application leads to increase in formation of medium size tubers (Gitari et al., 2018) and large size tubers (Belachew, 2016). Combination of 0 and 90 kg P ha⁻¹ with Dutch Robyn produced small sized tubers. Similar results were obtained with Wanjiku variety grown with 60 kg P ha⁻¹. The high numbers of small sized tubers resulted in lower yields. Phosphorus plays several plant functions including photosynthesis and transformation of sugars and starches. It also increases accumulation of assimilates that are converted into carbohydrates in tubers which increases tuber size (Chala et al.,

2017; Merga, 2018).

Number of eyes

The results of the study showed that interaction effect of location and varieties on the number of eyes was highly significant (P<0.001). Wanjiku variety grown at Egerton study site had the highest number of eyes followed by Dutch Robyjn then Shangi and Unica in that order. These varieties recorded least number of eyes at KALRO Molo site (Table 5). The interaction of P rates and

PAR	NS	PLH	BW	NT	TW	LST	MST
PLH	0.711***						
BW	0.21*	0.39***					
NT	0.67***	0.51***	0.49***				
TW	0.58***	0.60***	0.59***	0.79***			
LST	0.51***	0.41***	0.42***	0.68***	0.70***		
MST	0.59***	0.47***	0.48***	0.76***	0.69***	0.66***	
MKTY	0.52***	0.36**	0.35**	0.67***	0.60***	0.94***	0.68***

NS = number of stems per plant, PLH = plant height, BW = biomass weight, NT = number of tubers per plant, TW = tuber weight, LST = large sized tubers, MST = medium sized tubers and MKTY = marketable tuber yield.

varieties significantly (P<0.05) influenced the number of eyes. The interaction of 30, 60 and 90kg P ha⁻¹ with Wanjiku recorded highest number of eyes (Table 6). The size and shape of tubers affected the formation and number of eyes. Wanjiku had higher number of large and medium size tubers which correlated with high number of eyes on tubers. The higher the number of eyes in tuber is the higher the quality of the seed. New potato plants sprout and grow from eyes. Lung'aho et al. (2006) reported that farmers selected seed potato based on the number of eyes as it is related to number of stems produced which correlates with yield. In this study the correlation between number of stems and yield was positive (Table 7).

Marketable tuber yield

The main effect of P application rates on marketable tuber yield was significant (P<0.05). Application rates of 30, 60 90 kg P ha⁻¹ recorded the highest marketable tuber yields of 9.6, 9.5 and 10.25 tubers per hill, respectively. These values were however not significantly different but higher than the control (0 kg P ha⁻¹), with 9.25 tubers per hill. Increasing P rate to 90 kg P ha⁻¹ caused a 10 % increase in the marketable tuber vield. The marketable tuber yield was positively and highly correlated with large sized tubers, and medium sized tubers. The main effect of varieties on marketable tuber yield was significant (P<0.001). Shangi recorded the highest number of marketable tubers followed by Wanjiku and Dutch Robyjn with 10.66, 9.87 and 9.54, tubers per hill, respectively. The least was observed for Unica with 8.58, tubers per hill. Varieties have different P requirements and P uptake which influences P utilization by the plants (Tein et al. (2014). The main effect of study sites on marketable tuber yield was significant (P<0.01). KALRO Molo site registered the highest marketable tuber yield of 9.83 tubers as compared to Egerton study site with 9.5 tubers. This may be attributed to specific site conditions in Molo that favoured to higher marketable tuber yield. The subsoil in Molo site was sandy clay which improves water holding capacity and sustains soil moisture that supports tuber bulking. The prevailing factors of environment, rainfall and soil moisture determine the yield of the crop (Chala et al., 2017).

CONCLUSION

The application of P fertilizer enhances growth and yield of potato varieties propagated from rooted apical cuttings. Application rate of 30 kg P ha⁻¹ gave optimum yields, with higher PUE under the study conditions and is recommended. Rooted apical cuttings of Wanjiku, Shangi and Unica varieties can be used by the farmers for potato propagation in order to obtain high yield of potatoes in the study areas and other areas of similar agro ecological zones.

Further studies on the effect of P rates on the growth of potatoes propagated from rooted apical cuttings in comparison with the conventional tubers are recommended.

CONFLICT OF INTEREST

The authors have not declared any conflict of interest.

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Full Length Research Paper

Standard heterosis and heterotic grouping of highland adapted maize (*Zea Mays L.*) inbred lines in Ethiopia

Dufera Tulu^{1*}, Demissew Abakemal¹, Zeleke Keimeso¹, Tefera Kumsa¹, Worknesh Terefe², Legesse Wolde² and Abenezer Abebe²

¹Ambo Agricultural Research Center, Ambo, Ethiopia. ²Holeta Agricultural Research Center, Addis Ababa, Ethiopia.

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The current study was initiated to estimate the magnitude of standard heterosis for grain yield and yield related traits in a line x tester hybrids and to classify the inbred lines into different heterotic groups. Fifty entries consisting of 48 testcrosses developed from 12 inbred lines and 4 testers using line x tester design and two commercial check hybrids used in the study. The experiment was conducted using alpha lattice design with two replications at Ambo and Holeta Agricultural Research Center in 2018 cropping season. Analysis of variance revealed highly significant mean squares due to genotypes for all traits. Site variance showed highly significant mean squares for all traits except ear height. Genotype x site interaction was significant for grain yield, days to silking, bad husk cover and ear aspect. Cross L11 x T4 exhibited maximum standard heterosis over the checks (Kolba and Jibat) for grain yield followed by L9 x T4. In addition, these hybrids showed negative standard heterosis for plant height and ear aspect. The study also proposed eight inbred lines to be assigned to one of the different heterotic groups (A and B). The current study revealed that extensive works needs to be done in broadening the genetic base for highland maize breeding program to develop higher yielding varieties for the target areas.

Key words: Heterotic grouping, Inbreed lines, standard heterosis, testers.

INTRODUCTION

Maize (*Zea mays* L.) is an important food security crop in the developing world, especially in sub-Saharan Africa (SSA) and Latin America. In Africa, maize is produced on a total area of 40.7 million ha; with the production of 81.9 million metric tons. This is about 20.64% of the total maize area of the world and 7.13% of the global production respectively (FAOSTAT, 2019). Lack of congruence between the proportion of production and the

cultivated area is due to the low productivity of maize in Africa (≤ 2t ha⁻¹) as compared to a global average of 5.8 tons ha⁻¹. Increasing Maize production and productivity in African countries like Ethiopia, is of significant importance due to uncertainties in future food supply because of great challenge of rapidly increasing population. Ethiopia currently leads east African countries in maize production (9.6 million metric tons) and Productivity (4.2 tons ha⁻¹)

*Corresponding author. E-mail: duferatulu@gmail.com.

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Table 1. Description of testing locations.

Location	Altitude (masl)	Rainfall (mm)	Temp (°C	C)	Latitude	Longitude	Soil type	
	Aititude (illasi)	Kaiiliali (IIIII)	Min	Max	Latitude	Longitude		
Ambo	2225	1050	10.4	26.3	8°57'N	38°7'E	Black vertisol	
Holeta	2400	1102	6	22	09°04'N	38°29'E	Nitosols and vertisols	

^{*}Rainfall and Temp; were taken as averages of many years for each locations.

(FAOSTAT, 2019). Among the cereal crops, maize contributes the greatest share (28.5%) to the total annual crop production in Ethiopia (CSA, 2020).

Maize is cultivated in all of the major agro-ecological zones in Ethiopia. The maize production in the highland agro-ecology of Ethiopia is characterized by low productivity because of limited germplasm sources and improved varieties adapted to the agro-ecology. This calls for the development of suitable maize cultivars to increase productivity in this agro-ecology. In Ethiopia the national average grain yield increased from about 1.6 ton ha⁻¹ in 1990 (Worku et al., 2012) to 4.2 tons ha⁻¹ in 2019 (FAOSTAT, 2019). Increased yields are in part due to improved agronomic practices and increased inputs, but increased yields could not have been realized without genetic improvements (Abate et al., 2015).

This shows the presence of high potential to increase production and productivity. Information on heterosis is important in the development of maize inbred lines. Heterosis manifestation is dependent on genetic divergence of the two parental varieties (Hallauer and Miranda, 1988). Krivanek et al. (2007), declared that heterosis and combining ability are prerequisites for developing economically viable hybrid maize varieties. Assignment of maize genotypes to their respective heterotic groups has been the key to the economic success of the crop as it has allowed the exploitation of heterosis (Troyer, 2006), particularly for grain yield.

Standard heterosis of highland maize inbred lines for grain yield and yield related traits were conducted for different sets of locally developed and introduced inbred lines (Elmyhum, 2013; Nepir et al., 2015; Shimelis et al., 2019; Abebe et al., 2020; Keimeso et al., 2020). Legesse et al. (2009), also studied the combining ability of highland inbred lines and grouped the lines to heterotic groups using specific combining effects. However, it is always important to generate such information for any new batch of inbred lines and group them to different heterotic groups for further use in developing high yielding hybrid varieties. The objective of the study was to estimate the magnitudes of standard heterosis for grain yield and yield related traits in line x tester hybrids and to classify the inbred lines into different heterotic groups.

MATERIALS AND METHODS

Description of experimental sites

The study was conducted at two locations in the highland sub-

humid agro ecology of Ethiopia, namely, Ambo and Holeta Agricultural Research Centers, in the main cropping season of 2018 (Table 1).

Experimental materials

A total of 50 entries composed of 48 test crosses, formed by crossing 12 highland maize inbred lines with four line testers (known as heterotic testers A and B), and two standard checks (Jibat and Kolba,) were investigated. Prior to this time, Ambo highland maize breeding program and CIMMYT (International Maize and Wheat Improvement Center) had developed the inbred lines from the crosses of elite by elite inbred lines. List and pedigrees of the inbred lines used in the line x tester crosses along with the testers are presented in Table 2. Two of the line testers (T3 and T4) are CIMMYT developed testers and widely used in Ethiopian maize breeding programs, while the other two are locally developed line testers (T1 and T2) commonly used by the highland maize breeding program at Ambo.

Experimental design and field managements

The experimental design was alpha lattice design (0, 1) (Patterson and Williams, 1976) with 5 plots per an incomplete block and 10 incomplete blocks with two replicates. Each entry was planted in a one row 5.25 m long plot with spacing of 0.75 m between rows and 0.25 m between plants within a row. The experimental materials were hand planted with two seeds per hill, which were later thinned to one plant to get the recommended planting density for the testing sites, 53,333 plants per hectare. Planting was conducted on the onset of the main raining season after an adequate soil moisture level was reached to ensure good germination and seedling development. Other agronomic practices were carried out as per the recommendation for the test areas.

Data collection

Data on grain yield and other important agronomic traits were collected on a plot and sampled plants bases. Data collected on a plot basis include days to 50% silking (DS), number of ears per plant (EPP), field weight (FW) (kg/plot), plant aspects (PA), ear aspects (EA) and bad husk cover (HC); while data recorded on sampled plants basis were ear height (EH) (cm) and plant height (PH) (cm). Yield (GY) in t/ha was calculated using CIMMYT fieldbook software (Banziger and Vivek, 2007).

Data analysis

All Data collected for this study were subjected to analyses of variance (ANOVA) using the PROC GLM procedure in SAS® computer program (SAS Institute, 2004). Least significant difference (LSD) was used for mean comparisons. For traits that displayed significant differences among crosses, line by tester analysis was

S/N Lines code Genotype name Source (origin) 1 L1 EIAR- HMBP MH1307001-4-2-1-1 2 L2 EIAR-HMBP MH1307002-3-3-3-1 3 L3 MH1307002-4-1-1-2 EIAR-HMBP 4 L4 MH1307002-4-2-2-1 EIAR-HMBP 5 L5 MH1307002-9-1-1-1 EIAR-HMBP 6 L6 MH1307002-9-2-1-2 EIAR-HMBP 7 L7 MH1307002-10-1-2-1 EIAR-HMBP 8 L8 MH1307002-10-1-2-2 EIAR-HMBP 9 L9 MH1307002-10-1-2-3 EIAR-HMBP 10 L10 MH1307002-10-2-3-2 EIAR-HMBP MH1307002-10-2-3-3 11 L11 EIAR- HMBP

MH1307002-10-3-2-2

HLM0001

HLF0002

CML312

CML395

Table 2. List of highland maize inbred lines and testers used for test-cross formation.

L12

T1

T2

T3

T4

performed to further partition the variances due to crosses into lines, tester and line by tester effects using SAS program (SAS institute, 2004).

12

13

14

15

16

Estimation of standard heterosis

Standard heterosis (SH) in percent was calculated for those traits that showed significant differences among genotypes as suggested by Falconer and Mackay (1996). These were computed as percentage increase or decrease of the cross performances over best standard check as follows:

$$SH(\%) = \frac{F1 - SV}{SV} * 100$$

Where, F1 = mean value of a cross; SV = mean value of standard check variety.

Test of significance for heterosis was done using the t-test. The standard errors of the difference for heterosis were calculated as follows:

SE(d) for
$$SH = \pm \sqrt{2MSE/r}$$

Where, SE (d) is standard error of the difference, MSE is error mean square and r is number of replications and calculated t value was compared against the tabulated t-value at degree of freedom for error.

$$t(standard\ check) = F1 - \frac{SV}{SE(d)}$$

Grouping of inbred lines into different heterotic group

The inbred lines were classified into different heterotic groups based on the results from ANOVA, genotype means and SCA effect for grain yield. Heterotic grouping was determined according to the CIMMYT heterotic classification system as A, B and AB. Depending on the direction of the SCA estimate such that lines displaying

positive SCA with tester A were grouped towards the opposite heterotic group, and vice versa, whereas lines exhibiting positive SCA to both testers were grouped under AB heterotic group (Vasal, 1992). Line by tester analyses was performed for traits that showed significant differences among crosses as suggested by Dabholkar (1999) and Singh and Chaudhary (1985) to partition the mean square due to crosses into lines, testers and line x tester interactions. The following mathematical model was used for the combining ability analysis of individual locations:

EIAR-HMBP

EIAR-HMBP

EIAR-HMBP

CIMMYT

CIMMYT

$$Y_{ijk} = \mu + r_k + g_i + g_j + S_{ij} + e_{ijk}$$

Where, Y_{ijk} = the value of a character measured on cross of line i by tester j in k^{th} replication; μ = population mean; r_k = effect of k^{th} replication; g_i = general combining ability (GCA) effects of i^{th} line; g_j = general combining ability (GCA) effect of the jth tester; S_{ij} = specific combining ability (SCA) of ith line and j^{th} testers such that S_{ij} equals S_{ij} ; e_{ijk} = experimental error for ijk^{th} observation.

The significance of SCA effects were tested by dividing the corresponding SCA values by their respective standard error, to obtain the calculated t values, and comparing the calculated t value with tabular t-value at the error degree of freedom.

RESULT AND DISCUSSION

The combined analysis of variance for grain yield and other related traits are shown in Table 3. The analysis showed highly significant mean squares due to genotypes for all studied traits. This indicates the presence of high genetic variation between the genotypes and the potential to develop high yielding hybrids for the targeted agro-ecology of the country. Similar results have been reported by (Tulu et al., 2018; Abebe et al., 2020). Site variance showed significant mean squares for all traits except for ear height (EH), indicating that the test environments were unique and

^{*}HMBP = Highland Maize Breeding Program.

Source of	Df				Trait			
variance	Di	GY	DS	PH	EH	HC	EPP	EA
Rep(site)	3	3.42*	11.38**	81.80	121.70	53.96	0.01	0.15
Blk(Rep*Site)	36	3.11**	4.96**	290.68*	176.78	13.59	0.04*	0.09
Site	1	84.97**	13744.82**	1404.5**	169.28	43.92*	0.96**	15.96**
Genotype	49	13.65**	26.22**	1072.16**	620.07**	77.61**	0.10**	0.64**
Genotype*Site	49	2.24**	11.04**	200.81	110.68	34.78**	0.03	0.17**
Error	62	0.86	1.80	170.27	126.16	10.93	0.02	0.06
CV		12.07	1.27	6.29	10.49	82.71	12.43	8.30
Grand Mean		7.68	105.95	207.57	107.04	4.02	1.21	3.04
R^2		0.96	0.99	0.90	0.86	0.91	0.89	0.94

Table 3. Combined analyses of variance for grain yield and yield related traits of 48 testcrosses and two hybrid checks evaluated at Ambo and Holeta.

that there is adequate variability among the inbred lines for improvements in the traits. Genotype*site interaction showed significant mean variance for grain yield (GY), days to 50% silking (DS), bad husk cover (HC) and ear aspect (EA), indicating that, the performance of these genotypes were not consistent across sites for the traits. In line with the current findings, Nepir et al. (2017) and Keimeso et al. (2020) reported similar results for GY in their study on other batches of highland adapted inbred lines.

Estimation of standard heterosis

The estimates of standard heterosis over the standard checks were computed for grain yield and yield related traits that showed significant differences among genotypes in combined analysis (Table 4). None of the crosses demonstrated positive significant heterosis over the standard checks (Kolba and Jibat). Standard heterosis (SH) for GY ranged from -66.17% (L8 x T1) to 6.86% (L11 x T4) over Kolba, and -64.39 % (L8 xT1) to 12.49% (L11 x T4) over Jibat. Thirty-seven crosses showed negative and significant standard heterosis over the best hybrid check (Kolba) for grain yield, while three crosses showed positive and non-significant standard heterosis. Similarly, 31 crosses revealed negative and significant standard heterosis over Jibat, while five crosses revealed positive and non-significant standard heterosis for the same trait.

Negative and significant heterosis implies that their respective parents have resemblance and are from same heterotic group or parents are genetically less distant, whereas significantly positive heterosis in most crosses reveals parents are divergent and could be used to develop heterotically responsive hybrids. The result obtained in the study implies that inbreed lines were

crossed to testers with less genetic distant. In contrast to the current findings several investigators (Zeleke, 2015; Nedi et al., 2017; Mesenbet et al., 2016; Abebe et al., 2020) have reported significant standard heterosis for GY in both directions. This may be because of the difference in materials (inbred lines) used in their study.

Estimates of standard heterosis for days to 50% silking (DS) ranged from - 4.08% (L2 x T3) to 6.95% (L2 x T4) and - 2.91% (L2 x T3) to 8.25% (L2 x T4) over standard checks Jibat and Kolba, respectively. Twenty-one testcrosses over Jibat and 27 testcrosses over Kolba showed positive and significant SH for this trait while, only five and one testcrosses revealed negative and significant SH over checks, respectively. Inbreed lines with positive and significant SH for DS can potentially be used in the breeding program to develop late maturing hybrids as compared to the standard checks and vice versa. According to Lekha et al. (2015), both positive significant and negative significant SH for DS and suggested that negative SH is desirable for this trait in maize hybrid development.

The lowest SH for PH and EH were recorded on L4 x T4 (-30.35%, -28.95%) and L8 x T3 (-34.45%, -25.57%) over Jibat and Kolba respectively. Similarly, the highest SH for these traits, were recorded on L1 x T4 (4.05%, 6.14%) and L8 x T4 (11.29%, 26.35%) over standard checks Jibat and Kolba. None of the testcrosses except two over Kolba for EH showed positive and significant SH over both standard checks for both traits, whereas 28 and 16 testcrosses over Jibat, and 22 and four over kolba were revealed to have negative and significant SH for PH and EH, respectively. This implies that, most of the hybrids tested in this study were hybrids with short stature as compared to the standard checks. (Abebe et al., 2020) reported negative and positive significant SH for these traits in their study and suggested that, the negative heterosis for plant and ear height is desirable to

^{* =} Significant at 0.05 probability level; ** = significant at 0.01 probability level; GY = Grain Yield, DS = Days to Silking, PH = Plant Height, EH = Ear Height, HC = Bad Husk Cover, EPP = Ears Per-Plant, EA = Ear Aspect, CV = Coefficient of variation, R² = coefficient of determination.

Table 4. Estimates of standard heterosis (SH) for grain yield and other agronomic traits of 12 maize inbred lines crossed with four line testers in line x tester mating design and evaluated across sites in 2018 main cropping season.

	SH fo	or GY	SH fe	or DS	SH for I	PH (cm)	SH for	EH (cm)	SH for	EPP (#)	SH fo	r HC (%)	SH for	EA (1-5)
Crosses	Kolba	Jibat	Kolba	Jibat	Kolba	Jibat	Kolba	Jibat	Kolba	Jibat	Kolba	Ĵibat	Kolba	Jibat
L1xT1	-30.21**	-26.54**	1.94	0.72	-8.94	-10.73	9.09	-3.92	-18.01	-25.72**	-23.00	-25.05	3.80	-9.12
L1xT2	-20.2*	-16.00	0.00	-1.20	-16.9**	-18.53**	-9.52	-20.31*	-2.26	-11.45	-60.80	-61.87	-0.40	-12.78
L1xT3	-5.93	-0.98	-1.94	-3.12*	-16.45**	-18.1**	-9.58	-20.36*	-1.21	-10.50	57.20	53.07	-11.70	-22.72**
L1xT4	-17.7*	-13.37	7.04**	5.76**	6.14	4.05	25.18*	10.26	-29.36**	-36.01**	28.40	24.99	-10.50	-21.66**
L2xT1	-48.66**	-45.95**	3.88**	2.64*	-7.89	-9.71	5.14	-7.40	-21.43*	-28.82**	134.5**	128.31**	41.5**	23.93**
L2xT2	-35.87**	-32.49**	3.88**	2.64*	-11.01	-12.76*	0.84	-11.18	11.11	0.66	135.4**	129.12**	34.6**	17.87*
L2xT3	-11.68	-7.02	-2.91*	-4.08**	-22.35**	-23.88**	-23.41*	-32.54**	-0.55	-9.90	353.7**	341.7**	18.20	3.46
L2xT4	-22.8*	-18.73*	8.25**	6.95**	4.00	1.95	13.62	0.07	-27.04*	-33.9**	541**	524**	7.30	-6.07
L3xT1	-46.62**	-43.8**	4.13**	2.88*	-12.77*	-14.49*	-2.47	-14.10	-13.59	-21.72*	-55.40	-56.61	22.1*	6.87
L3xT2	-41.15**	-38.05**	3.4*	2.16	-9.88	-11.65*	6.15	-6.51	2.05	-7.55	-49.70	-51.02	34.2**	17.5*
L3xT3	-30.77**	-27.12**	-0.73	-1.92	-13.63*	-15.33**	-19.34	-28.95**	-11.43	-19.76*	32.60	29.04	12.10	-1.86
L3xT4	-19.37*	-15.12	5.83**	4.56**	-5.45	-7.31	6.41	-6.28	-23.95*	-31.1**	320.8**	309.62**	8.30	-5.14
L4xT1	-53.01**	-50.54**	5.58**	4.32**	-14.67*	-16.35**	0.00	-11.92	-21.37*	-28.77**	186.3**	178.68**	36.5**	19.49*
L4xT2	-53.57**	-51.12**	1.94	0.72	-28.95**	-30.35**	-24.57*	-33.56**	-8.83	-17.40	-0.30	-2.92	35.4**	18.54*
L4xT3	-32.16**	-28.59**	-2.18	-3.36*	-10.63	-12.39*	-14.50	-24.7*	-17.74	-25.47**	146.6**	140.1**	12.80	-1.26
L4xT4	-28.08**	-24.29**	6.8**	5.52**	-3.72	-5.62	1.37	-10.72	-30.66**	-37.18**	246.3**	237.11**	8.60	-4.95
L5xT1	-53.85**	-51.41**	4.37**	3.12*	-14.7*	-16.37**	-8.66	-19.55*	-14.70	-22.72*	25.30	22.01	37.6**	20.46*
L5xT2	-38.74**	-35.51**	3.4*	2.16	-10.43	-12.19*	-9.24	-20.06*	-17.33	-25.11**	177.2**	169.85**	25.1**	9.57
L5xT3	-23.26**	-19.22*	-0.73	-1.92	-7.67	-9.49	0.95	-11.09	-10.32	-18.75	-29.40	-31.29	5.60	-7.51
L5xT4	-4.36	0.68	7.77**	6.47**	0.73	-1.26	14.17	0.56	-14.08	-22.16*	419.4**	405.63**	16.10	1.65
L6xT1	-65.43**	-63.61**	3.88**	2.64*	-20.21**	-21.78**	-9.81	-20.57*	-38.7**	-44.47**	-74.70	-75.34	35.7**	18.82*
L6xT2	-44.3**	-41.37**	3.4*	2.16	-8.23	-10.04	3.00	-9.28	-17.25	-25.04**	-71.90	-72.61	33.4**	16.83*
L6xT3	-21.59*	-17.46	-0.73	-1.92	-8.95	-10.74	-21.22	-30.61**	-9.73	-18.22	-81.20	-81.66	-8.10	-19.57*
L6xT4	-38.18**	-34.93**	8.01**	6.71**	3.56	1.52	24.1*	9.30	-41.7**	-47.21**	-90.8*	-91*	-14.10	-24.83**
L7xT1	-57.74**	-55.51**	4.61**	3.36*	-20.87**	-22.42**	0.14	-11.80	-24.0*	-31.16**	-85.8*	-86.22*	37.5**	20.39*
L7xT2	-35.87**	-32.49**	2.18	0.96	-15.34**	-17.01**	-1.60	-13.33	-13.12	-21.29*	85*	80.12	25.3**	9.74
L7xT3	-25.49**	-21.56*	0.97	-0.24	-13.99*	-15.68**	-6.22	-17.40	-12.20	-20.46*	136.6**	130.34**	16.10	1.68
L7xT4	-8.80	-4.00	7.04**	5.76**	-5.15	-7.01	18.61	4.46	-2.95	-12.08	313.8**	302.84**	1.50	-11.12
L8xT1	-66.17**	-64.39**	7.04**	5.76**	-23.03**	-24.54**	-14.96	-25.1*	-26.3*	-33.21**	-100*	-100*	26**	10.30
L8xT2	-34.66**	-31.22**	1.94	0.72	-17.67**	-19.29**	-0.40	-12.27	9.26	-1.02	-76.30	-76.90	27.3**	11.43
L8xT3	-24.28**	-20.29*	0.49	-0.72	-18.98**	-20.57**	-25.6*	-34.45**	-9.63	-18.13	51.50	47.50	3.50	-9.34
L8xT4	-7.23	-2.34	7.04**	5.76**	-9.18	-10.97	26.35*	11.29	-21.3*	-28.74**	136.9**	130.66**	-12.20	-23.12**
L9xT1	-49.49**	-46.83**	2.91*	1.68	-18.95**	-20.54**	-11.78	-22.3*	-26.9*	-33.74**	-76.40	-77.07	24.8**	9.28
L9xT2	-25.86**	-21.95*	1.70	0.48	-20.55**	-22.11**	-7.42	-18.46	20.17	8.87	261.7**	252.15**	31**	14.73

Table 4. Contd

L9xT3	-15.11	-10.63	-0.49	-1.68	-17.71**	-19.33**	-19.46	-29.06**	-13.5	-21.62*	203.6**	195.55**	13.50	-0.63
L9xT4	4.36	9.85	5.34**	4.08**	-2.08	-4.00	11.89	-1.45	-9.91	-18.39	204.5**	196.45**	-6.60	-18.21*
L10xT1	-33.64**	-30.15**	1.94	0.72	-5.50	-7.36	3.99	-8.41	-12.8	-20.95*	1.10	-1.54	25.3**	9.69
L10xT2	-43**	-40**	2.67*	1.44	-14.84*	-16.52**	-6.98	-18.08	-0.10	-9.50	-75.00	-75.69	33.9**	17.21*
L10xT3	-16.22	-11.80	-1.46	-2.64*	-10.92	-12.67*	-10.75	-21.39*	-10.9	-19.28*	21.50	18.24	-2.30	-14.47
L10xT4	0.09	5.37	5.1**	3.84**	-6.09	-7.94	16.77	2.84	-10.4	-18.78*	161**	154.08**	-2.30	-14.46
L11xT1	-26.23**	-22.34*	1.70	0.48	0.22	-1.75	16.26	2.40	-17.1	-24.94*	-64.00	-64.92	12.60	-1.38
L11xT2	-50.14**	-47.51**	4.13**	2.88*	-10.84	-12.6*	4.77	-7.72	-11.4	-19.76*	-25.90	-27.85	35.7**	18.85*
L11xT3	-21.87*	-17.76	1.21	0.00	-20.1**	-21.67**	-6.43	-17.59	2.28	-7.34	-69.10	-69.87	5.70	-7.48
L11xT4	6.86	12.49	3.88**	2.64*	-0.62	-2.57	12.77	-0.67	-4.52	-13.50	254**	244.6**	-9.70	-20.95*
L12xT1	-39.67**	-36.49**	1.21	0.00	-6.96	-8.79	4.88	-7.62	4.37	-5.45	-85.2*	-85.58*	13.50	-0.64
L12xT2	-52.18**	-49.66**	3.16*	1.92	-17.57**	-19.19**	-6.67	-17.79	8.95	-1.30	-53.20	-54.47	30.7**	14.39
L12xT3	-20.48*	-16.29	-2.18	-3.36*	-14.43*	-16.12**	-8.10	-19.06*	7.49	-2.62	-85.2*	-85.61*	12.20	-1.75
L12xT4	-1.85	3.32	5.34**	4.08**	3.16	1.13	17.96	3.90	10.47	0.08	261.2**	251.64**	8.80	-4.74
SE(d)	0.93	0.93	1.34	1.34	13.05	13.05	11.23	11.23	0.14	0.14	3.31	3.31	0.24	0.24

^{* =} Significant at 0.05 probability level; ** = significant at 0.01 probability level; GY = Grain Yield, DS = Days to Silking, PH = Plant Height, EH = Ear Height, EPP = Ears Per Plant, HC = Bad Husk Cover, EA = Ear Aspect. SE(d) = Standard error of difference.

enable the selection of effective shorter plant, with reduction of lodging and mechanical harvesting.

Regarding bad husk cover (HC) 19 and 20 testcross hybrids showed positive and significant SH over Jibat and Kolba standard checks. On the other hand, five and three testcross hybrids showed negative and significant SH over Jibat and Kolba, respectively. For this trait, negative SH is desirable since materials with negative SH produces tighten husk cover which is important for resisting birds and rotting of ears. This is in agreement to the Tulu et al. (2018), who reported similar result in their study over other batches of inbreed lines. None of the testcross hybrids showed positive and significant SH for EPP over both checks, while 28 and 12 testcross hybrids were showed negative and significant SH over Jibat and Kolba, respectively. Positive SH for this trait implies prolificacy of the hybrids as compared

to the standard checks. In the current study L9 x T2 which showed 20.17% and 8.87% SH over Kolba and Jibat, respectively may be used in the breeding program to develop hybrids with prolific ears. Similar findings have been reported (Abrha et al., 2013; Mesenbet et al., 2016; Abebe et al., 2020) reported similar results with the current findings.

Estimates of SH for ear aspect (EA) ranged from -24.83% (L6 x T4) to 23.93% (L2 x T1) and -14.1% (L6 x T4) to 41.5% (L2 x T1) over Jibat and Kolba, respectively. Testcrosses with negative and significant SH for this trait are in desirable direction, since lower scores are taken as good ear aspect by maize breeders. Standard heterosis is important in maize breeding and is dependent on level of dominance and differences in gene frequency. The manifestation of heterosis depends on genetic divergence of the two parental varieties

(Hallauer and Miranda, 1988). In a maize breeding aimed at developing hybrids, the usage of combining ability of inbred lines and the information on heterosis is an important tool to decide whether the hybrid is selected for promotion or not.

Heterotic grouping

Grain yields averaged over two locations and estimates of SCA effects for the 48 single cross progenies are presented in Table 5. Among the testers, T1 and T2 are locally developed inbred lines by the Ethiopian highland maize breeding program having good combining ability; and have been used as testers in maize breeding for highland sub-humid agro-ecology of Ethiopia. These testers are presents of one of the

1 !	T1 (HGB)		T2 (HGA)		T3 (HGA)		T4 (HGB)		ПС
Line	GY	SCA	GY	SCA	GY	SCA	GY	SCA	HG
L1	7.53	0.65	8.61	0.88	10.15	0.37	8.88	-1.90**	В
L2	5.54	-0.13	6.92	0.41	9.53	0.96	8.33	-1.24*	В
L3	5.76	0.6	6.35	0.34	7.47	-0.58	8.70	-0.36	-
L4	5.07	0.69	5.01	-0.21	7.32	0.04	7.76	-0.52	-
L5	4.98	-0.66	6.61	0.12	8.28	-0.25	10.32	0.79	-
L6	3.73	-0.58	6.01	0.86	8.46	1.26*	6.67	-1.54*	В
L7	4.56	-0.84	6.92	0.54	8.04	-0.25	9.84	0.54	-
L8	3.65	-1.66**	7.05	0.89	8.17	-0.03	10.01	0.8	В
L9	5.45	-1.11	8.00	0.6	9.16	-0.29	11.26	8.0	AB
L10	7.16	0.78	6.15	-1.07	9.04	-0.23	10.80	0.52	Α
L11	7.96	1.55*	5.38	-1.88**	8.43	-0.88	11.53	1.22	Α
L12	6.51	0.71	5.16	-1.48*	8.58	-0.11	10.59	0.89	Α

Table 5. Heterotic grouping of twelve inbreed lines using SCA estimates with four tester lines with defined heterotic groups.

commercial hybrid (Jibat) used as standard checks in this study. Whereas, testers T3 and T4 are CIMMYT inbreed lines with T3 being in heterotic group 'A' and T4 in heterotic group 'B' (Tolesa et al., 1993; Keno et al., 2017). These CIMMYT testers have been used as testers in CIMMYT and other national and international maize breeding programs in the tropics. The heterotic grouping of the locally developed inbred lines in the present study was, therefore, based on using these locally developed and CIMMYT established testers, usingan assumption that SCA and heterosis of two inbred lines from different heterotic groups is greater than those from the same group.

An inbred line expressing negative SCA effect when crossed to a certain tester implies that the line and the tester belong to the same heterotic group, while the reverse is true when the SCA effect is positive (Vasal et al., 1992). As shown in Table 5, L1 and L2 had negative and significant SCA effects when crossed to T4 and showed lowest GY when crossed to T1. This therefore, indicates that L1, L2, T1 and T4 were highly likely to be in the same heterotic group. As a result, L1 and L2 were assigned to heterotic group B. Similarly, L6 and L8 had negative and significant SCA effects when crossed to T4 and T1, respectively. In addition L6 showed positive and significant SCA effect when crossed to T3 which is in heterotic group A. Consequently these inbreed lines were postulated to be in heterotic group B.

L9 had no significant SCA effects when crossed with both heterotic testers. However, all crosses of L9 with testers from both heterotic groups gave considerably high heterosis thus; L9 was postulated to be in AB heterotic group. There were no testers whose cross combination with L10 expressed significant SCA effects in both directions. But the cross combinations of this lines with

T1 and T4 gave higher average grain yield. As a result this line was assigned to heterotic group A. L11 and L12 were showed negative and significant SCA effects when crossed to T2 and they had positive SCA effects and higher grain yield (L11 = 11.53 and L12 = 10.59 tons) when crossed to T4. Consequently, L11 and L12 were postulated to be in a heterotic group. In this study, some inbreed lines (L3, L4, L5 and L7) could not be assigned to any of the heterotic groups developed by CIMMYT because the testers used in our study does not gives us clear cut data to postulate these lines to one of the heterotic group.

Conclusion

The analysis of the current study, revealed the presence of high genetic variation between the genotypes and the potential to develop high yielding hybrids for the targeted agro-ecology of the country. The study also identified some testcross hybrids that have desirable standard heterosis as compared to the standard checks. L9 x T4 and L11 x T4 revealed positive standard heterosis for grain yield over both checks. In addition, these hybrids showed negative standard heterosis for PH and EA, indicating these hybrids can be used in the improvement of these traits. The two crosses identified based on their heterosis over the best standard check, (L9 x T4 and L11 x T4) had T4 as a parent in their pedigrees. This confirms that T4 is genetically distant from the rest of inbred lines and it can be used as parent in hybrid maize breeding for commercial release or for further breeding activities in highland agro-ecologies of the country. The study also proposed eight inbred lines to one of the heterotic groups. Lines L1, L2, L6 and L8 were assigned to HGB,

^{* =} Significant at 0.05 probability level; ** = significant at 0.01 probability level; HGA = Heterotic group A; HGB = heterotic group B; GY = grain yield.

while lines L10, L11 and L12 were assigned to HGA and only line L9 assigned to heterotic group AB. In general, the current study revealed that extensive works should be done in broadening the genetic base for highland breeding program to develop high yielding varieties for the target areas. The information obtained from this study on the heterotic groups of the inbred lines and standard heterosis of the testcross hybrids for different traits would be useful in planning hybrid maize breeding.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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Full Length Research Paper

Genetic variability and correlation of agronomic and malt quality traits in Ethiopian sorghum [Sorghum bicolor (L.) Moench] landraces at Sheraro, Northern Ethiopia

Tamirat Bejiga^{1*}, Berhanu Abate² and Temesgen Teressa¹

¹Melkassa Agriculture Research Center, Adama, P. O. Box 436, Ethiopia.
²School of Plant and Horticultural Sciences, Collage of Agriculture, Hawassa University, Hawassa, P. O. Box 05, Ethiopia.

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Sorghum (Sorghum bicolor (L.) Moench) is a major cereal crop, grown in a wide range of agro-ecology. However, in Ethiopia there are very few high yielding improved sorghum varieties for malting purpose. A field experiment was conducted at Sheraro, sub-site of Mytseberi Agricultural Research Center during the 2017 cropping season. The objectives of the study were to identify sorghum landraces with high grain yield, study phenotypic and genotypic variability and correlation among yield, yield components and malting quality-related traits. In this experiment, 34 landraces and two malt sorghum varieties were evaluated in alpha lattice (6x6) design with three replications. The analysis of variance revealed highly significant variations among landraces in all analyzed characteristics. Among the tested landraces, Gambella 1107 gave the highest grain yield (4.88 ton/ha) followed by varieties Debar (4.28 ton/ha) and Macia (4.03 ton/ha), while the lowest yielding sorghum landraces were ETSL 100575 (0.18 ton/ha), ETSL 100547 (0.28 ton/ha) and ETSL 100738 (0.30 ton/ha). High values for the phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were recorded for grain yield, head length and plant height. High heritability and genetic advance as percent of mean (GAM%) was obtained for plant height, head length, head width, thousand kernel weight and grain yield. Grain yield had highly significant and positive correlations with head width, hectoliter weight and germination energy. The 36 genotypes were clustered into five groups. Cluster I contained the maximum (16) number of accessions and cluster IV contained the minimum (3) number of accessions.

Key words: correlation, landraces, malt quality, sorghum and yield.

INTRODUCTION

Sorghum is the third cereal after rice and wheat in India and the second major crops after Maize in Africa (Melese, 2016). The largest grain sorghum producers are the United States, India, Nigeria, Mexico, Sudan and

China (Agrama and Tuinstra, 2003). It is used as a major food grain in semi-arid tropical Africa (Tadesse et al., 2008). In Ethiopia, sorghum is one of the major crops produced and the third important crop in terms of area

coverage and volume of production (CSA, 2015). Generally, cereals contributed 87.48% (about 26,778, 976.40 tons) of the grain crops production of which 16.89% (5, 169, 252, 54 tons) was from sorghum (CSA, 2018). It grows in a wide range of agro-ecologies most importantly in the moisture stressed parts where other crops can least survive and food insecurity is rampant (Asfaw, 2007). It is an indigenous crop second to tef used as injera (leavened local flat bread) making (Geremew et al., 2004). As the prices of tef, a staple cereal food crop of Ethiopia, have been ascended in recent years, sorghum has become the most affordable substitute for low-income society in urban areas. It is also a preferred substitute crop for countryside communities who produce tef as a cash crop (Demeke and Di Marcantonio, 2013).

The amount of genetic variability existing in sorghum is immense (Warkad et al., 2008). Ethiopia and Niger have abundant sorghum genetic diversity and are the largest sorghum producing countries in eastern and western Africa, respectively (Tesfaye et al., 2008). Genetic enhancement in sorghum yield depends on the degree of genetic variability, heritability and genetic advance in the population as well as the nature of the correlation between yield and its components (Jimmy et al., 2017). Correlation coefficients support in deciding the way of selection and number of characters to be looked at in improving grain yield (Jimmy et al., 2017). In droughtstricken lowland sorghum growing parts of Ethiopia, sorghum landraces showed a wide range of genotypic variations in terms of plant traits, which are useful in sorghum breeding program (Beyene et al., 2016). For real use of the genetic stock in crop enhancement, information of mutual correlations among yield, malting quality and yield components are needed (Gobezayohu et al., 2019b). Sorghum landraces are farmer's varieties cultivated for grain production over many years and they are also the basic breeding resources for developing varieties or hybrids (Shiferaw and Yoseph, 2014). The earliness and grain characteristics were the most required characters of the improved varieties sought by farmers (Hailegebrial and Adane, 2018). Demand for malt sorghum will be increased because sorghum is a climateresilient crop and the extent of barley production is not increasing with malt demand. However, using sorghum for brewing is low due to limited availability of improved sorghum varieties and commercial production of malt sorghum in Ethiopia (Tamirat et al., 2020). Hence, it is high time to explore the genetic variability to address the increasing malting sorghum request with advanced malting quality and yield (Gobezayohu et al., 2019a).

Therefore, in germplasm collection and selection, the creation of new genetically dissimilar genotypes from the novel population is possible (Addissu, 2011). Focus on identifying varieties that meet important traits in agricultural and nutrition necessities from the great diversity of sorghums is crucial to insure food security (Dicko et al., 2006). The objectives of this study were to identify sorghum landraces with high grain yield, study phenotypic and genotypic variability and analyze the correlation of yield and malting quality traits.

MATERIALS AND METHODS

Study Site

The experiment was conducted at Sheraro in the Northern Tigray regional state of Ethiopia in 2017. Sheraro is a substation of Mytseberi Agricultural Research Center, located at 14°24'N and 37°45'E, with an altitude of 1028 m above sea level. The location is categorized by hot to warm semi-arid low-land plains, with a monomodal rain pattern between May and September (Hailegebrial et al., 2019). The minimum and maximum temperatures of the site are 18.8 and 32.9°C, respectively and the average rainfall received annually is 677mm. The monthly minimum value of the daily maximum temperature at Sheraro during July, August and September varied from 21 to 26°C, while the minimum value of the daily maximum temperature during March, April, May and June ranged between 26 and 36°C from 1983 to 2016. Increasing day and night temperature, and decreasing total annual rainfall, might affect crop development and yield, requiring heat resilient and drought-tolerant crop genotypes as adaptation strategies (Abadi et al., 2020).

Experimental materials and design

The study was conducted using 34 landraces and two malt sorghum varieties. The landraces were collected by Melkassa Agricultural Research Center from different sorghum growing regional states of Ethiopia: namely, Tigray, Afar, Amhara, Benshangul-Gumuz, Oromia, Southern Nation Nationalities People Regional State (SNNPRS), Dire Dawa city administration and from Ethiopian Institute of Biodiversity (Table 1). The trial was planted in a 6x6 alpha-lattice design with three replications. Each replication consisted of 6 blocks spaced 1 m apart and the distance between replications was 1.5 m. The spacing between rows and between plants was 75 and 15 cm, respectively. The experimental plot area was 7.5 m² having two rows of 5 m length.

Data collection

The data were recorded on seven agronomic traits according to the sorghum descriptors (IBPGR/ICRISAT, 1993) while malting quality parameters were recorded at the Assela Malt Factory.

*Corresponding author. E-mail: tamiratbejiga@gmail.com.

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Table 1. List of sorghum landraces and region of collection.

No	Landrace	Region	No	Landrace	Region
1	ETSL 100974	Afar	19	87BK4250	Oromia
2	ETSL 101650	Amhara	20	05MI5069	Oromia
3	IS 38378	Amhara	21	01MS7013	Oromia
4	ETSL 100141	Amhara	22	ETSL 100710	Oromia
5	IS 38279	Amhara	23	ETSL 101259	Oromia
6	IS 38358	Amhara	24	ETSL 100401	Oromia
7	ETSL 101061	Amhara	25	ETSL 101760	Oromia
8	ETSL 100954	Amhara	26	ETSL 100738	Oromia
9	ETSL 101622	Amhara	27	ETSL 100735	Oromia
10	ETSL 101438	Amhara	28	ETSL 100297	SNNP
11	ETSL 100582	Amhara	29	ETSL 100613	SNNP
12	ETSL 101006	Amhara	30	ETSL 100568	SNNP
13	ETSL 101466	Benishangul Gumuz	31	ETSL 100550	Tigray
14	ETSL 100575	Benishangul Gumuz	32	ETSL 101130	Tigray
15	ETSL 101605	Dire Dawa city Administration	33	ETSL 100547	Tigray
16	ETSL 100759	Dire Dawa city Administration	34	ETSL 100535	Tigray
17	ETSL 101068	Ethiopia institute of biodiversity	35	Debar	Check
18	Gambella1107	Oromia	36	Macia	Check

ETSL=Ethiopian Sorghum Landrace; SNNPRS =Southern Nation Nationalities People Regional State.

Days to flowering (DF)

DF was recorded as the number of days from the date of emergence to the date when 50% of the plants in a plot produce flowers. Plant height (PH): PH in centimeter was measured as an average height from ground level to the tip of five randomly taken plants at maturity per plot.

Days to maturity (DM)

DM was recorded as the number of days from emergence to the stage when grains developed a black layer at the base.

Head Length (HL)

HL was measured in centimeter from the base to the tip of the panicles of five randomly selected plants at the middle of the rows and averaged.

Head Width (HW)

HW was measured in centimeter at the widest part of the panicles of five randomly selected plants and averaged.

Thousand Kernel Weight (TKW)

TKW was measured as the weight of a sample of thousand kernels and the obtained weight was adjusted to 12.5% moisture content.

Grain yield per plot (GY)

GY was expressed in kilogram weight units and adjusted to 12.5% standard moisture content of each accession grain after harvested from each plot. The adjusted yield was converted to ton ha⁻¹. Plot yield adjustment was done based on stand count taken just before harvest and the required plant population per plot using the following equation.

$$\mbox{Adjusted plot yield} = \frac{\mbox{actual plot yield X required plant population}}{\mbox{Actual plant population} \ \pm \ \ensuremath{\frac{1}{2}} \mbox{missing plants}}$$

Plot yield adjustment was done based on actual and standard (12.5%) grain moisture contents of grains using the following equation.

Adjusted plot yield =
$$\frac{\text{plot yield X (100 - actual grain moisture content)}}{100 - 12.5}$$

Germination energy (GE)

The germination energy was estimated by putting a hundred grains on moist double filter paper with 4 ml water in a Petri dish and germinated seeds were counted at 72 h.

Hectoliter weight (HLW)

Hectoliter weight was determined on dockage free samples using a

standard laboratory hectoliter weight apparatus according to method no 55-10 (American Association of Cereal Chemists, 2000).

Extract fine and extract coarse grind

These were investigated at Assella Malt Factory by using the method of the American Society of Brewing Chemists (ASBC, 2008). The extract was measured based on the following procedure a 50.0 gram of milled malt placed in a mash beaker and 200 ml of distilled water was added at 45°C for 30 min. Then, after 30 min, the temperature of the mash was raised to 70°C over a 25 min period. 100 ml of distilled water was added to each mash beaker after a temperature of 70°C was achieved or at 55 min. The scarification rate was started to measure after 10 min of water spray at 65 min. Subsequently, after 65 min, the temperature of the mash was kept at 70°C for 1 h. During the next 115 min of mashing, the temperature of mash was cooled to room temperature within 10-15 min. At 125 min of mashing the mash, the beaker was picked out of the mash bath and dried the exterior well and distilled water was added until the content of the beaker weighed 450.0 gram. The contents of the mash beaker were stirred with a glass rod and immediately poured into the fluted filter paper. The obtained extract was measured for its specific gravity using a DMA density meter and reported in degrees Plato.

$$E \text{ (\%)} = \frac{P * (MC + 800)}{DM(100 - P)} x100$$

Where, E=Extract content of wort in % by weight; Mc=Moisture content of wort taken malt; 800=portion of water added to the mash which is added to the 100-gram malt. DM=dry mass matter (100-Mc)

P=Plato metric reading value of soluble solids (glucose)/density metric reading value.

Total protein content (TPC)

TPC of dry malt was analyzed by using the Kjeldahl method (Kenyan Standards Authority, 1979), nitrogen per cent was calculated from the procedure as V_{HCL} was the volume of HCl in litter consumed to the end point of the titration, V_{HCL} blank was the volume of HCl consumed in a liter to titrate the blank (sample containing all chemicals for Kjeldahl procedure), NHCL is the normality of the HCl that was used; and 14.00 was molecular Weight of Nitrogen.

$$\%Nitrogen = \frac{((VHCL - VHCLblank)X \, NHCL \, X \, 14.00))}{Sample \, weight \, on \, dry \, mass \, basis}$$

Protein Content = $\%N \times 6.25$ (conversion factor) (Kenyan Standards Authority, 1979).

Statistical analysis

The data were subjected to analysis of variance (ANOVA) suggested by (Gomez and Gomez, 1984) using the general linear model (PROC GLM) of SAS software (version 9.0) to assess the difference among the tested landraces. Mean separation was carried out using the least significant difference (LSD).

Estimation of variance components

Environmental variance, genotypic variance and phenotypic variance was calculated based on formulas suggested by Burton and Devane, (1953).

Environmental variance (δ_e^2) = error mean square

Genotypic variance
$$(\delta^2 g) = \frac{MSg - MSe}{r}$$

Phenotypic variance $(\delta^2 p) = \sigma^2 g + \delta^2_e/r$

Where: MSg = mean sum square of genotype, MSe = mean sum square of error and <math>r = number of replications

Estimation of phenotypic and genotypic coefficients of variation

Phenotypic and genotypic coefficients of variations were estimated using the equations suggested by Burton and Devane (1953).

$$PCV = \frac{\sqrt{\sigma^2 p}}{\bar{X}} \ X \ 100 \qquad GCV = \frac{\sqrt{\sigma^2 g}}{\bar{X}} \ X \ 100$$

Where: δ^2 p= the phenotypic variance, δ^2 g= the genotypic variance, \overline{X} = the grand mean for the trait considered, Phenotypic coefficient of variation (PCV) and Genotypic coefficient of variation (GCV).

Estimation of broad-sense heritability

Broad sense heritability (H^2) is the proportion of phenotypic variance explained by genotypic variance Johnson *et al.* (1955).

$$H^2 = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

Where: H^2 = Broad sense heritability, $\delta^2 g$ = the genotypic variance and $\delta^2 p$ = the phenotypic variance.

Estimation of genetic advance and genetic advance as percent of mean

Genetic advance under selection represents improvement in a genotypic value in the selected population with the assumption that 5% of the genotypes were selected. The genetic advance (GA) for selection intensity (K) at 5% was calculated based on the method suggested by Johnson et al. (1955).

$$GA = \frac{K X \sqrt{\sigma^2 p} X \sigma^2 g}{\sigma^2 p}$$

Where, $\delta^2 g=$ genotypic variance, $\delta^2 p=$ phenotypic variance, K= Selection differential (K=2.06 at 5% selection intensity)

The genetic advance as percent of the mean (GAM) was calculated using the following equation.

$$GAM = \frac{GA}{\bar{X}} \times 100$$

	Mean square of agronomic traits									
Trait -	Rep	Genotype	Block (Rep)	Error	CV%					
DF	7.24	93.07**	3.62	3.00	2.14					
PH	3093.28	13382.76**	383.75	384.72	6.56					
DM	2.00	85.09**	10.15	6.04	2.10					
HL	35.6	168.05**	7.76	6.09	10.05					
HW	6.22	12.97**	1.65	1.48	10.39					
TKW	2.24	74.41**	5.92	5.83	8.53					
GY	0.09	3.65**	0.02	0.02	8.47					

Table 2. Mean squares of agronomic traits in 34 sorghum landraces and two checks grown at Sheraro in 2017.

Where, GA=genetic advance and \overline{X} = the grand mean for the trait considered.

Principal component and clustering analysis

Principal components (PCs) with an Eigen value greater than one were used as criteria to determine the number of PCs. Clustering was performed by average linkage method and using the SAS computer software facilities.

RESULTS AND DISCUSSION

The analysis of variance for agronomic traits revealed highly significant variation ($P \le 0.01$) among 34 landraces and two checks for all studied traits (Table 2). This indicated that the landraces were genetically diverse and provides opportunities for improvement through breeding. Sorghum landraces are used as a genetic resource for breeding programs. Girma et al. (2019) noted that Ethiopia and its surroundings countries are considered as the center of origin and diversity for sorghum, and has contributed to global sorghum genetic improvement. The germplasm from this region harbors enormous genetic variation for various traits.

Crop phenology and plant growth

Days to flowering ranged from 67.33 for variety Macia to 102 days for landrace ETSL 100575 with a mean of 80.94 days. Fuad et al. (2018) reported that the earliest days to flowering was Meko variety on two locations with 68.67 and 66.67 days at Fedis and Erer respectively, which was almost similar with Macia variety in the days to flowering. Early maturity is the most required characters of a crop grown by farmers in areas with low rainfall Hailegebrial et al. (2019). The days to maturity ranged from 103.67 for variety Macia to 126 for landrace ETSL 101622 with a mean of 117.29 days.

The high yielding Gambella 1107, Debar and Macia genotypes flowered and matured early while landraces 87BK4250, ETSL 101650, ETSL 100141, ETSL 100954 and ETSL 100568 flowered and matured early but gave lower grain yield (Table 3). Days to flowering and maturity determine adaptability and yield potential of sorghum genotypes in areas where the growing period is limited by the availability of adequate rainfall. In this study, early flowering and maturing landraces gave a higher yield than late flowering and maturing landraces. This indicates that Sheraro is not suitable for the production of latematuring sorghum landraces. Geremew et al. (2004) reported that in dry lowland areas, the growing period is short, and highly erratic dry spells may occur at vegetative and grain formation stages of crop growth; therefore, the genotype cultured in these areas should be early maturing.

Plant height ranged from 149 cm for genotype Macia to 386.73 cm for genotype IS 38279 with a mean of 299.174 cm. The highest plant height was recorded from landraces IS 38279, ETSL 100582 and ETSL 100735 while the lowest plant height was measured from Macia, 87BK4250 and Debar (Table 3). Farmers prefer taller landraces to harvest high above-ground biomass for animal feed. However, landraces with tall plant height, flowering and maturing late gave lower grain yield than landraces that had medium plant height. Therefore, landraces with reasonable plant height and early maturity were better than tall landraces in dry lowland areas. As Amare et al. (2019) mentioned plant biomass is a vital trait to sorghum growing farmers and the variety 2005MI5064 is preferred primarily for its tall plant height (190.79 cm). It also has a favorable grain yield (3810.96 kg/ha), with a benefit of 7% over the standard check Melkam.

Yield and yield components

The landraces ETSL 100141, ETSL 101466 and ETSL

^{**=}highly significant at p ≤ 0.01, DF=days to flowering, DM=days to maturity, PH=plant height (cm), HL=head length (cm), HW=head width (cm), TKW=thousand kernel weight (g), GY=grain yield (ton/ha).

Table 3. Mean values of grain yield and other agronomic traits of 34 sorghum landraces and two checks grown at Sheraro, 2017.

Entry	Accession	DF	DM	PH	HL	HW	TKW	GY
1	IS 38378	83.00 ^{dg}	119.33 ^{dj}	355.47 ^{af}	34.13 ^{bd}	9.73 ^{lo}	29.94 ^{ci}	0.71 ^{km}
2	Gambella1107	76.67 ^{jk}	109.33 ^{oq}	209.53 ¹	20.67 ^{kn}	13.87 ^{be}	30.50 ^{ch}	4.88 ^a
3	ETSL 100141	76.00 ^k	115.33 ^{jm}	242.47 ^{jk}	43.80 ^a	11.87 ^{fk}	29.78 ^{ci}	2.35 ^e
4	87BK4250	71.67 ^l	108.00 ^q	159.47 ⁿ	30.13 ^{dg}	10.93 ^{jn}	30.61 ^{ch}	2.64 ^d
5	ETSL 100297	82.00 ^{eg}	112.33 ^{mo}	273.87 ^{ij}	24.07 ^{ik}	8.80°	19.39 ^{op}	0.34 ^{op}
6	IS 38279	83.67 ^{bf}	124.33 ^{ab}	386.73 ^a	18.82 ^{mo}	9.60 ^{mo}	29.56 ^{di}	0.37 ^{op}
7	05MI5069	79.00 ^{hj}	110.67 ^{nq}	208.53 ^l	24.73 ^{hj}	15.47 ^{ab}	33.50 ^{bd}	2.32 ^{ef}
8	01MS7013	79.00 ^{hj}	115.67 ^{im}	194.87 ^{lm}	23.07 ^{il}	16.10 ^a	31.61 ^{cg}	2.73 ^d
9	IS 38358	81.67 ^{eh}	118.67 ^{ej}	349.87 ^{df}	20.67 ^{kn}	12.27 ^{ej}	28.39 ^{gj}	1.51 ^{hj}
10	ETSL 101061	85.33 ^{bd}	122.00 ^{ae}	357.27 ^{af}	13.87 ^{pq}	12.93 ^{ci}	27.06 ^{hk}	0.72 ^{km}
11	ETSL 101068	84.00 ^{be}	118.33 ^{ek}	331.93 ^{eg}	25.60 ^{hj}	10.00 ^{ko}	23.89 ^{kn}	0.40 ^{no}
12	ETSL 101466	77.67 ^{jk}	118.67 ^{ej}	259.40 ^{ij}	36.60 ^b	11.33 ^{im}	32.94 ^{bf}	1.44 ^{hj}
13	ETSL 100710	78.33 ^{ij}	114.33 ^{kn}	223.93 ^{kl}	25.40 ^{hj}	12.00 ^{ej}	22.61 ^{lo}	1.86 ^g
14	ETSL 100550	80.67 ^{gi}	121.00 ^{bg}	257.80 ^{ij}	32.00 ^{ce}	9.33 ^{no}	31.06 ^{cg}	1.31 ^j
15	ETSL 101259	82.00 ^{eg}	112.67 ^{mp}	312.40 ^{gh}	22.07 ^{jm}	9.20 ^{no}	19.44 ^{op}	1.36 ^{ij}
16	ETSL 100401	80.67 ^{gi}	115.67 ^{im}	348.40 ^{df}	14.40 ^{pq}	13.33 ^{ch}	32.33 ^{bg}	2.13 ^f
17	ETSL 101605	81.00 ^{fi}	117.33 ^{fl}	315.60 ^{gh}	13.93 ^{pq}	12.27 ^{ej}	33.61 ^{bc}	2.17 ^{ef}
18	ETSL 100954	76.33 ^{jk}	117.00 ^{gl}	349.33 ^{df}	24.80 ^{hj}	13.87 ^{be}	33.50 ^{bd}	1.53 ^{hi}
19	ETSL 100759	86.00 ^{bc}	123.33 ^{ad}	376.47 ^{ad}	14.07 ^{pq}	12.27 ^{ej}	25.50 ^{jm}	0.78^{km}
20	ETSL 101622	86.00 ^{bc}	126.00 ^a	382.07 ^{ac}	11.73 ^q	13.07 ^{ci}	30.61 ^{ch}	0.81 ^{kl}
21	ETSL 100974	83.33 ^{cg}	119.67 ^{di}	362.20 ^{ae}	17.03 ^{np}	14.80 ^{ac}	33.72 ^{bc}	1.62 ^h
22	ETSL 101438	85.00 ^{bd}	113.33 ^{lo}	259.33 ^{ij}	26.53 ^{fi}	11.53 ^{gm}	30.45 ^{ch}	0.77 ^{km}
23	ETSL 101130	83.67 ^{bf}	122.33 ^{ae}	286.50 ^{ih}	19.57 ^{lo}	11.60 ^{gl}	29.39 ^{ej}	0.83 ^{kl}
24	ETSL 101760	83.00 ^{dg}	121.33 ^{bf}	329.91 ^{fg}	16.80 ^{np}	13.47 ^{cg}	33.33 ^{be}	0.59 ^{mn}
25	ETSL 100582	85.00 ^{bd}	124.33 ^{ab}	385.80 ^{ab}	13.00 ^{pq}	12.67 ^{dj}	35.94 ^{ab}	0.91 ^k
26	ETSL 100613	77.67 ^{jk}	115.67 ^{im}	325.53 ^{fg}	15.60 ^{oq}	14.53 ^{ad}	33.00 ^{be}	2.14 ^f
27	ETSL 100738	80.67 ^{gi}	120.33 ^{bg}	339.60 ^{eg}	30.07 ^{eg}	8.53 ^{op}	21.39 ^{np}	0.30 ^{op}
28	ETSL 100568	76.33 ^{jk}	116.00 ^{hm}	278.73 ⁱ	34.60 ^{bc}	11.47 ^{hm}	18.50 ^p	1.31 ^j
29	ETSL 100547	86.33 ^b	124.00 ^{ac}	216.60 ^{kl}	31.60 ^{ce}	9.80 ^{lo}	28.78 ^{gj}	0.28 ^{op}
30	ETSL 100535	81.00 ^{fi}	121.33 ^{bf}	339.73 ^{eg}	28.40 ^{eh}	11.87 ^{fk}	29.00 ^{fj}	1.40 ^{ij}
31	ETSL 100735	83.33 ^{cg}	120.00 ^{ch}	385.60 ^{ab}	31.60 ^{ce}	8.67°	26.33 ^{il}	0.70^{lm}
32	ETSL 100575	102.00 ^a	124.33 ^{ab}	351.00 ^{cf}	30.53 ^{df}	6.67 ^p	18.89 ^{op}	0.18 ^p
33	ETSL 101006	84.33 ^{be}	119.67 ^{di}	353.87 ^{bf}	36.20 ^b	9.27 ^{no}	23.83 ^{kn}	0.58 ^{mn}
34	ETSL 101650	72.33 ^l	108.67 ^{pq}	335.20 ^{eg}	26.73 ^{fi}	13.60 ^{bf}	38.22 ^a	2.78 ^d
35	Debar	71.67 ^l	107.67 ^{qr}	176.27 ^{mn}	26.13 ^{gi}	12.80 ^{dj}	20.39 ^{np}	4.28 ^b
36	Macia	67.33 ^m	103.67 ^r	149.00 ⁿ	24.67 ^{hk}	12.40 ^{ej}	21.83 ^{mp}	4.03 ^c
Mean		80.94	117.29	299.17	24.55	11.72	28.30	1.53

DF=days to flowering, DM=days to maturity, PH=plant height (cm), HL=head length (cm), HW=head width (cm), TKW=thousand kernel weight (g),GY=grainyield(ton/ha).

101006 had the longest head lengths of 43.80, 36.60 and 36.20 cm respectively, whereas the shortest head lengths were recorded on landraces ETSL 101622 (11.73 cm), ETSL 100582 (13.00 cm) and ETSL 101061 (13.87 cm) (Table 3). Moreover, the largest panicle width was recorded on 01MS7013, 05MI5069 and ETSL 100974 with values of 16.10, 15.47 and 14.80 cm respectively,

while the smallest panicle width was recorded on the landraces ETSL 100575 (6.67 cm), ETSL 100738 (8.53 cm) and ETSL 100735 (8.67 cm). Bhagasara et al. (2017) reported the range of panicle length from 6 to 45 cm and panicle width from 3 to 19 cm of sorghum crop. In this study, landraces with larger width and compacted panicle had high grain yield. Among the tested landraces, ETSL

Trait	Range	Mean	SE	$\delta^2 P$	$\delta^2 g$	δ²e	PCV	GCV
DF	67.33 - 102.00	80.94	0.57	33.0	30.02	3.00	7.10	6.77
DM	103.67 - 126.00	117.29	0.57	32.39	26.35	6.04	4.85	4.38
PH	149.00 - 386.73	299.17	6.91	4717.40	4332.68	384.72	22.96	22.00
HL	11.73 - 43.80	24.55	0.78	60.08	53.99	6.09	31.58	29.94
HW	6.67-16.00	11.72	0.23	5.31	3.83	1.48	19.66	16.70
TKW	18.50 - 38.22	28.30	0.54	28.69	22.86	5.83	18.93	16.89
GY	0.18 - 4.88	1.53	0.11	1.23	1.21	0.02	72.52	71.93

Table 4. Components of variance, phenotypic and genotypic coefficient of variation of sorghum agronomic traits at Sheraro (2017).

DF=days to flowering, DM=days to maturity, PH=plant height (cm), HL=head length (cm), HW=head width (cm), TKW=thousand kernel weight (g), GY=grain yield (ton/ha), SE=standard error, δ^2 P=phenotypic variance, δ^2 g=genotypic variance, δ^2 e=environmental variance, PCV=phenotypic coefficient of variation, GCV=genotypic coefficient of variation.

101650 had the highest thousand kernel weight (TKW) of 38.22 g followed by ETSL 100582 (35.94 g) and ETSL 100974 (33.72 g).

The landraces ETSL 100568 (18.50 g), ETSL 100575 (18.89 g) and ETSL 100297 (19.39 g) had the lowest TKW values (Table 3). The highest value of thousand kernel weight of sorghum in this study is similar to the maximum TKW (36.00 g) reported by Fuad et al. (2018). The average thousand kernel weight was 28.30 g and the result is comparable with 28.37 g reported by Kashiri et al. (2010). Abuajah et al. (2016) reported that genotypes with higher TKW may have more extract potential than genotypes with smaller TKW. Therefore, landraces which had high thousand kernel weight, low in grain protein content and produced high grain yield were preferable for sorghum malt.

The supply of sufficient quantity of grain with acceptable malting quality is important to satisfy the demand of malting industries. Among the tested landraces, Gambella 1107, gave the highest grain yield (4.88 ton/ha) followed by the check varieties Debar (4.28 ton/ha) and Macia (4.03 ton/ha). The lowest yielding landraces were ETSL 100575, ETSL 100547 and ETSL 100738 (Table 3). The landrace, Gambella 1107 was the top yielder followed by varieties Macia, Meko and Melkam at Fedis as reported by Fuad et al. (2018). □

Phenotypic and genotypic variation for agronomic traits

The range, mean, standard error, phenotypic variance, genotypic variance, phenotypic and genotypic coefficient of variations for agronomic traits are presented in Table 4. Days to flowering and maturity, plant height, head length and thousand kernel weight exhibited high phenotypic $(\delta^2 P)$ and genotypic $(\delta^2 g)$ variances. Phenotypic variance $(\delta^2 p)$ and phenotypic coefficient

variation (PCV) were higher than their corresponding genotypic variance (δ^2 g) and genotypic coefficient of variation (GCV), respectively for all the traits recorded (Table 4). This indicates that the expression of these characters was influenced by the environment. Bhagasara et al. (2017) noted the role of environment in the expression of characters that are demonstrated when phenotypic coefficient of variation (PCV) was slightly greater than corresponding genotypic coefficient of variation (GCV).

According to Deshmukh et al. (1986), phenotypic coefficient variation (PCV) and genotypic coefficient of variance (GCV) with values less than 10% are regarded as low, whereas values greater than 20% are considered as high and those between 10 - 20% are accounted medium. Based on the above explanation, high PCV values were recorded for grain yield (72.52%), head length (31.58%) and plant height (22.96%). Bhagasara et al. (2017) reported that estimates of PCV were slightly greater than the corresponding GCV which indicated that the effect of the environment was high. Days to physiological maturity and days to flowering exhibited low PCV of 4.85 and 7.10% respectively, indicating they were less affected by environmental factors (Table 3). Belay and Meresa (2017) reported a relatively high phenotypic coefficient of variation (21.73%) for the grain yield of sorghum. Jimmy et al. (2017) reported high values of PCV for plant height of sorghum.

Grain yield, head length and plant height revealed high GCV of 71.93, 29.94 and 22.00% respectively, whereas low GCV of 4.38 and 6.77% were recorded for days to physiological maturity and flowering, respectively. Belay and Meresa (2017) reported high GCV values (> 20%) for plant height and grain yield of sorghum. Jimmy et al. (2017) reported that GCV measures the variability of any trait due to genetic factors and higher GCV estimates than the PCV estimates of the genotypes showed large variation in phenotypic expression due to genetic factors.

Table 5. Broad sense heritability (H ² %), genetic advances (GA) and genetic
advance as percent of the mean (GAM %) of sorghum Accessions at Sheraro
in 2017.

Tuelt		Agronomic traits	
Trait	H ² %	GA	GAM%
DF	90.92	10.76	13.30
DM	81.35	9.54	8.13
PH	91.84	129.95	43.44
HL	89.86	14.35	58.46
HW	72.13	3.42	29.22
TKW	79.68	8.79	31.07
GY	98.37	2.25	146.96

DF=days to flowering, DM=days to maturity, PH=plant height (cm), HL=head length (cm), HW=head width (cm), TKW= thousand kernel weight (g), GY=grain yield (ton/ha).

The PCV was relatively greater than GCV for the traits days to flowering and days to maturity and the difference was low (Table 4). The results showed that the influence of environmental factors for the phenotypic expression of these traits was low. Therefore, the chance of improvement of these traits through selection based on the phenotypic performance of the landraces will be high. High GCV was estimated for characters head length and plant height, revealing that the genotypes have a broad base genetic background as well as good potential for improvement through selection. Similar results were reported by Bello et al. (2007). Belay and Meresa (2017) reported a high phenotypic and genotypic coefficient of variations for grain yield of sorghum. Low GCV and PCV value for days to flowering of sorghum was also reported by Kalpande et al. (2018).

Heritability and expected genetic advance

Estimates of heritability

According to Robinson et al. (1949), broad-sense heritability values greater than 60% are high, 31 to 60% are moderate and 0 to 30% is low. Based on the above heritability range, in this study, high broad-sense heritability was observed for days to flowering (90.92%), plant height (91.84%), and days to maturity (81.35%), head length (89.86%), head width (72.13%), thousand kernel weight (79.68%) and grain yield (98.37%). Similar estimates of heritability were reported by Bello et al. (2007) for panicle length (96%), plant length (93%) and date of flowering (95%) of sorghum crop.

Kalpande et al. (2014) reported that high heritability values were recorded for days to flowering of sorghum. Bello et al. (2007) stated that the characters with high broad-sense heritability would have a positive response

to selection. A high degree of heritability estimates for most of the traits suggested that they were under genetic control and selection could be fairly easy for variety improvement. High estimates of heritability in a broadsense were obtained for days to flowering and plant height of sorghum (Kalpande et al., 2018).

Selection may be considerably difficult for characters with low heritability. In this study high heritability was observed for days to maturity (81.35%) with low genetic advance as percent of the mean (8.13%). Kalpande et al. (2014) and Warkad et al. (2008) indicated that the high heritability estimates of days to physiological maturity of sorghum was accompanied by low genetic advance indicating the significant effect of non-additive gene action where the breeding method like heterosis breeding may be important for these traits to exploit non-additive gene action.

Genetic advance

Genetic advance as percent of mean ranged from 8.13 for days to maturity to 146.96 for grain yield. The genetic advance days to flowering, plant height, days to maturity, head length, head width, thousand kernel weight and grain yield are presented in Table 5. Johnson et al. (1955) classified genetic advance as percent of mean (GAM) values < 10% is low, 10 to 20% is moderate and > 20% is high. Based on the above GAM classified range, days except to flowering and days to maturity of all the characters showed high genetic advance in this study (Table 4). Thus, the improvement of these traits can be made through selection. The days to flowering of sorghum had moderate genetic advance as percent of the mean (Kalpande et al. 2018). This implies improvement of this character in genotypic value for the new population compared with the base population with one cycle of

0.144

Traits	DF	PH	DM	HL	HW	TKW	GY
DF		0.528**	0.722**	-0.146	-0.397**	-0.139	-0.721**
PH	0.576**		0.625**	-0.319**	-0.161	0.144	-0.609**
DM	0.765**	0.700**		-0.148	-0.250**	0.113	-0.733**
HL	-0.158	-0.336*	-0.175		-0.366**	-0.248**	-0.029
HW	-0.441**	-0.194	-0.285	-0.470**		0.536**	0.500**

Table 6. Genotypic (below diagonal) and phenotypic (above diagonal) correlation coefficient of seven sorghum agronomic traits.

-0.281

-0.028

0.592**

0.560**

0.102

-0.779**

selection is not rewarding.

TKW

GΥ

In this study the genetic advance as percent mean for grain yield was 146.96% and heritability was 98.37%. Similarly, Kalpande et al. (2014) has reported a high estimate of heritability together with high genetic advance as percent of the mean for grain yield of sorghum, revealing the influence of additive gene action for this trait. Jimmy et al. (2017) reported that high heritability and high genetic advance as per cent of mean (GAM) due to highly additive gene effect was observed for panicle diameter and grain yield of sorghum. The result indicated high heritability accompanied with high genetic advance was observed in the case of plant height. This indicated that these traits were highly heritable and the selection of superior genotypes is possible to improve these characters (Kalpande et al., 2018; Jimmy et al. 2017). In this study high heritability and low genetic advance were estimated for head width (Table 5). This result is in agreement with the result reported by Chavan et al. (2010) who revealed high heritability combined with low genetic advance for panicle width in sorghum.

-0.144

-0.737**

0.140

-0.638**

Correlations of grain yield and yield-related traits of sorghum landraces

Phenotypic correlations

The phenotypic correlation coefficients between grain yield and other agronomic traits are presented (Table 6). Deshmukh et al. (2018) stated that correlation coefficient helps in defining the way of selection and number of traits to be considered in improving the grain yield. Grain yield had a highly significant (P=0.01) positive phenotypic correlation with head width (0.5). This shows that genotypes with larger panicle width produced high grain yield at Shiraro. Jimmy et al. (2017) reported that the positive association between grain yield and panicle width. This indicated width to use as selection criterion in

sorghum to proportionally increase grain yield of sorghum.

0.15

Highly significant (P=0.01) negative correlation of grain yield was observed with plant height (r= -0.609), days to flowering (r= -0.721) and maturity (r= -0.733). Jimmy et al. (2017) reported that negative significant associations between plant height and grain yield. This shows that sorghum genotypes which are late flowering and maturity with taller plant height produced low grain yield at Sheraro which is characterized by low amount and erratic rainfall. Therefore, early maturing sorghum varieties with reasonable plant height, heavy thousand seed weight and bigger panicle width are required. Abate (2017) reported a similar results from a study conducted at moisture stressed locations of Ethiopia indicating that days to flowering, days to maturity and plant height had a negative relationship with the major yield components including grain yield of sorghum.

Genotypic correlation

Grain yield had highly significant (P=0.01) and positive genotypic correlation with head width (r=0.560), and it had highly significant (P=0.01) negative correlations with days to flowering (r= -0.737), plant height (r= -0.638) and days to maturity (r= -0.779). Thousand kernel weight had significant (P=0.01) and positive correlation with head width (r=0.592). Highly significant (P=0.01) positive correlations were observed between days to maturity and flowering (r=0.765) and between days to maturity and plant height (r=0.700). Kalpande et al. (2014) reported that days to maturity exhibited significant positive association with plant height, and days to flowering and plant height at physiological maturity; while a significant negative association was observed for grain yield. High significant (P=0.01) positive correlation was also obtained between plant height and days to flowering (r=0.576). Abate (2017) reported that days to flowering was

^{**=}highly significant at P=0.01, *=significant (P=0.05), DF=days to flowering, PH=plant height (cm), DM=days to maturity, HL=head length (cm), HW=head width (cm), TKW=thousand kernel weight (g), GY=grain yield (ton/ha).

Traits	HLW	GE	TPC	EFG	ECG	TKW	GY
HLW		0.491**	-0.488**	-0.085	-0.166	0.268*	0.684**
GE	0.541**		-0.369**	0.086	-0.009	0.18	0.507**
TPC	-0.502**	-0.413*		0.128	0.306**	0.115	-0.763**
EFG	-0.1	0.106	0.151		0.916**	0.313**	0.069
ECG	-0.193	0.005	0.352*	0.932**		0.335**	-0.118
TKW	0.266	0.161	0.146	0.318	0.366*		0.119
GY	0.693**	0.569**	-0.792**	0.062	-0.132	0.122	

Table 7. Genotypic (below diagonal) and phenotypic (above diagonal) correlation coefficients between sorghum malt quality parameters and grain yield.

positively and significantly correlated with plant height (r=0.27) of sorghum.

Correlations of grain yield with malt quality related traits of sorghum landraces

Phenotypic and genotypic correlations

Grain yield showed highly significant and positive phenotypic correlations with hectoliter weight (r=0.684) and germination energy (r=0.507) (Table 7). This shows that landraces with high hectoliter weight of seeds produced high grain yield. As Gobezayohu et al. (2019b) reported that grain yield exhibited positive and highly significant phenotypic correlation with hectoliter weight. Highly significant (P=0.01) and negative correlation of grain yield was exhibited with total protein content (r= -0.763). In this study, the results showed landraces with high grain yield had low protein content. Ross et al. (1981) reported similar result protein and grain yield had strong negative genetic correlations. Also, Matthieu et al. (2010) reported that a highly significant negative correlation was observed between mean grain yield and grain protein content in wheat.

Grain yield had highly significant (P=0.01) and positive genotypic correlations with hectoliter weight (r=0.693) and germination energy (r=0.569) (Table 7). These indicated accessions, with high grain yield and thousand kernel weight are better in hectoliter and germination energy. As Gobezayohu et al. (2019b) reported, grain yield showed a positive and highly significant genotypic correlation with hectoliter weight. The results obtained in the study showed high significant and negative genotypic correlations of grain yield with total protein content (r= 0.792).

Principal component analysis

Principal component analysis was executed with the aim

of decrease a large set of phenotypic traits to a more meaningful smaller set of traits and to know which trait is contributing to maximum variability (Kassahun, 2017). The principal components (PCs), with eigenvalues greater than one were considered sufficient for inclusion in the analysis. The largest and the smallest Eigen values were (3.4) and (1.9), correspondingly, and two principal components are found between these Eigen values (Chatfied and Collins, 1980). The first principal component (PC1) alone explained 48% of the total variation, mainly due to variation in days to sorghum flowering, days sorghum maturity, plant height and head width (HW). Traits which contributed more to the second principal component (PC2) accounted for 28% of the total variation and were dominated by head length (HL), head width (HW) and thousand kernel weight (TKW) (Table 8). Mesfin (2016) also reported similar results from their experiment. Generally, a maximum and minimum cumulative contribution is 76 and 48%, respectively.

Cluster analysis

The 34 sorghum accessions along with the two standard checks formed five clusters. The result of the hierarchical cluster analysis indicated that 36 sorghum accessions were grouped into five different clusters with a range of accessions that are categorized based on their similar performance of the trait under study. The clustering pattern indicated the existence of a significant amount of variability among the sorghum landraces. Among the different clusters, the cluster size varied from 3 to 16. The maximum number of accessions was included in cluster I having 16 accessions and the minimum number in cluster IV having 3 accessions. Accession IS 38378, IS 38358, ETSL 101061, ETSL 101068, ETSL 101259, ETSL 100401, ETSL 101605, ETSL 100954, ETSL 100974, ETSL 101760, ETSL 100613, ETSL 100738, ETSL 100535, ETSL 100575, ETSL 101006 and ETSL 101650 were grouped into cluster I, accessions IS 38279, ETSL

^{**=}highly significant at P=0.01, *=significant (P=0.05), HLW=hectoliter weight, GE=germination energy, TPC=total protein content, EFG=extract fine grind, ECG=extract caurse grind, TKW=thousand seed weight, GY= grain yield.

Table 8. Principal component analysis showing the contribution of seven a	agronomic traits in the first seven principal
components among the 36 sorghum Accessions.	

Traits	PC1	PC2	PC3	PC4	PC5	PC6	PC7
DF	0.48	0.02	136	0.57	0.39	0.39	-0.34
DM	0.48	0.18	0.18	0.25	-0.43	0.12	0.67
PH	0.42	0.28	-0.01	-0.75	0.05	0.40	-0.12
HL	-0.05	-0.55	0.69	-0.01	-0.17	0.39	-0.18
HW	-0.31	0.53	-0.01	0.19	-0.58	0.29	-0.41
TKW	-0.09	0.55	0.67	0.06	0.43	-0.21	0.02
GY	-0.50	0.06	-0.14	0.02	0.32	0.63	0.47
Eigenvalue	3.4	1.9	0.727	0.382	0.218	0.199	0.144
Variance	0.48	0.28	0.10	0.05	0.03	0.03	0.02
Cumulative	0.48	0.76	0.86	0.91	0.95	0.97	1.00

DF=days to flowering, PH=plant height (cm), DM=days to maturity, HL=head length (cm), HW=head width (cm), TKW=thousand kernel weight (g), GY=grain yield (ton/ha).

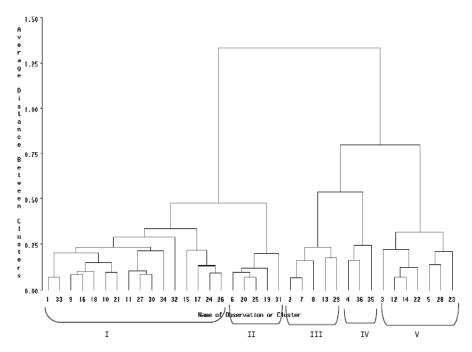


Figure 1. Dendrogram showing clusters using the seven traits of 36 sorghum accessions.

100759, ETSL 101622, ETSL 100582 and ETSL 100735 were grouped into cluster II, accessions Gambella1107, 05MI5069, 01MS7013, ETSL 100710 and ETSL 100547 were grouped into cluster III, accessions 87BK4250 and the two checks Debar and Macia varieties were grouped into cluster IV and accessions ETSL 100141, ETSL 100297, ETSL 101466, ETSL 100550, ETSL 101130 and ETSL 100568 were grouped into cluster V. The two standard checks used in this study were grouped into cluster IV, along with one other sorghum accession that

performed in a similar way for the studied quantitative characters. The grouping pattern of the accessions in the dendrogram showed similarity with the matrix plot. Figure 1 show the dendrogram clusters using the seven traits of 36 sorghum accessions.

Conclusion

A wide range of genetic variability was detected among

sorghum accessions in agronomic characters. This genetic variability of the accessions will encourage breeders to improve the grain yield of sorghum. A total of 34 accessions and two checks were grouped into 5 cluster groups, which consists of 16 accessions for the largest cluster that clearly shows there exists a diversity of the sorghum accessions.

Sorghum genotypes which are late flowering and maturity, along with taller plant height, produced low grain yield at Sheraro; which is characterized with a low amount and erratic rainfall. Therefore, early maturing sorghum varieties with reasonable plant height, heavy 1000 seed weight and bigger panicle width are required. Head width and compactness and reasonable head length had positive contribution to grain yield.

The landrace Gambella 1107 flowered and matured in 77 and 109 days respectively. It had 210 cm plant height, 20.67 cm head length, 13.87 cm head width, 4.88 t/ha grain yield and 30.50 g thousand kernel weight. All these characteristics indicate that the landrace Gambella 1107 has the required agronomic characteristics to be successful. As a result, it can be used in sorghum breeding programs as a source of genes. This landrace might be used in sorghum breeding program for development of high yielding varieties with good malting quality characters in Ethiopia. Further study on sorghum grain yield, yield components and malt quality related traits association should be undertaken across locations and over the years for demonstration of the important traits contribute for grain yield and quality malt.

CONFLICT OF INTEREST

The authors have not declared any conflict of interest

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