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Full Length Research Paper

Genetic diversity of Ethiopian durum wheat (*Triticum durum* Desf) landrace collections as reveled by morphological markers

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Knowledge of the extent and pattern of genetic diversity within and among populations is crucial to identify useful breeding materials and design appropriate collection and conservation strategies. Genetic diversity of 160 durum wheat (*Triticum durum* Desf) accessions was studied using 15 morpho-agronomic traits. The field studies for morphological characterization were undertaken at Adadi Maryam and Ginchi locations using randomized complete block design with two replications. The average linkage technique of clustering produced a more understandable portrayal of the 160 durum wheat accessions and released varieties by grouping them into seven clusters with inter-cluster D2 values ranged from 13.72 to 235. The highest genetic distances (253) was observed between cluster five (improved varieties) and cluster three accessions. The minimum genetic distance (13.72) was observed between cluster one and two both are landrace collections. Five of the 15 principal components accounted for more than 76.98% of the total variation in the Ethiopian durum wheat genotypes. The first principal components accounted for 32% of the total differences. In this study, there is a moderate genetic diversity between landraces collected from Tigray, Gonder, and Wello. Landraces from these areas can be used as a source of important pre-breeding material for future breeding programs.

Key words: Landraces, durum wheat varieties, genetic distances, correlation, genetic diversity, morphological characters.

INTRODUCTION

Durum wheat (*Triticum durum,* 2n=4x=28) is a monocotyledonous crop of the Gramineae family grown in Ethiopia since antiquity (Feldman, 2001). Zohary (1970) considered Ethiopia as the center of origin for the crop, whereas Purseglove (1975) reported the existence of adequate genetic diversity in landraces of durum wheat grown in the country. However, it is controversial that Ethiopia is the center of origin for durum wheat because of the absence of ancestral forms and wild relatives, which rule-out the proposition that Ethiopia is the center of origin (Pecetti et al., 1992). In Ethiopia, durum wheat (*T. durum* Desf.) is mostly planted on heavy black clay soils (vertisols) of the highlands between 1800 and 2800 m above sea level (masl) (Tesemma et al.,

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1991). It is the main source of semolina for the production of pasta, couscous, burghul, and other local end-use products, but also provides many beneficial traits, including resistance to rust diseases, environmental stability, yield potential, and high quality for bread wheat improvement.

Durum wheat is predominantly grown in central, northwestern and northeastern parts of Ethiopia (Tesemma et al., 1991; Bechere et al., 2000; Gashaw et al., 2007) for different purposes, mainly for its resistance to biotic and abiotic stresses, and better flour and food quality, competitive ability to weeds and straw production. Durum wheat was once the only crop grown in most of the wheat-producing areas of Ethiopia until very recently when it was overtaken by the adoption of improved bread wheat varieties (Tsegaye and Berg, 2007).

There is no doubt that plant breeding is considered one way to confront the challenge of bridging the widening gap between the demand and supply of food grain crops in Ethiopia. The inception of wheat (*Triticum aestivum* and *T. durum*) breeding in Ethiopia dated back to the early 1960s, and, as a result of the efforts made hitherto, many improved varieties have been developed and released to farmers. Ethiopia, as a center of diversity for durum wheat, has plenty amount of germplasm resources, which are essential for breeding programs as a source of genes for different traits. Assessment of the genetic diversity and identify the area with the highest genetic diversity, therefore, the crucial step to use the genetic resources in the breeding program.

Wheat is grown dominantly grown in Ethiopia since antiquity. Even though durum wheat is grown in many areas of the country, the production is very low compared with other crops due to biotic and abiotic stresses (Faris, 2011). To overcome these stresses, using improved resistant varieties and agronomic practices are the major ones. Most of the improved varieties become out of production in a very short time after release due to the low level of resistance to frequent disease Stem rust because of the appearance of new aggressive pathogen races (Singh et al., 2011) and drought. To increase the tolerance of durum wheat varieties to biotic and abiotic stresses crossing of genotypes distant genetic backgrounds is the major and safe option. Mostly genotypes selected from distant parents can resist stresses. Assessment of extent and pattern of genetic diversity is, therefore, a crucial step to equip wheat breeding programs. Therefore, this study aims to assess the genetic diversity of Ethiopian durum wheat landraces and identifying regions with high genetic diversity.

MATERIALS AND METHODS

One hundred and forty-one durum wheat germplasm accessions collected from various eco-geographical zones of Ethiopia and nineteen released varieties were evaluated in this study. The genotypes were all received from the Ethiopian Biodiversity Institute, whereas the released varieties were obtained from Debre Zeit Agricultural Research Center. The germplasm accessions were initially collected from the major durum wheat producing zones of Oromia, Tigray and Amhara regions including Arsi, Bale, West Shewa, East Shewa, Harergie, Semen Shewa, North Gonder, South Gondar, South Wello, North Gojam, South Gojam, Northern Tigray, Central Tigray, and Eastern Tigray (Table 1). The germplasm accessions and released varieties tested in this study are, hereafter, treated as genotypes for experimental purposes.

F Test locations

The genotypes were evaluated at two locations, Ginchi and Adadi, in Ethiopia during the year 2015. The locations were assumed to represent the major durum wheat production areas of Ethiopia. The detailed descriptions of the test locations in terms of geographical position, mean annual rainfall, mean annual temperature, and soil characteristics are shown in Table 2.

Experimental design and layout

The seed rate for a plot of one row 1 m long was 6 g. The spacing between rows was 30 cm. A blanket basal application of nitrogen and phosphorus fertilizer has applied to all plots at the recommended rate of the Ethiopian wheat research program N_2: P_2O_5 Ginchi (64:46) and Adadi (60:69), respectively. All other crop management practices were applied uniformly to all plots as required so that the test genotypes could express their full genetic potential for the traits under consideration. The experiment was laid down in a randomized complete block design (RCBD) with two replications. The genotypes were assigned to plots at random within each block. The data will be collected for fifteen agro-morphological traits (Table 3).

Data analysis

The magnitude of genetic distances

Genetic distance analyses: Genetic distances between clusters as standardized Mahalanobis's D^2 statistics was calculated as:

$$D^2_{ij} = (xi - xj)' \, cov^{-1}(xi - xj)$$

where D^2ij = the distance between cases i and j; xi and xj = vectors of the values of the variables for cases i and j; and cov^{-1} = the pooled within-groups variance-covariance matrix. Principal components based on the correlation matrix will be calculated using the same software as in clustering.

The D^2 values obtained for pairs of clusters were considered as the calculated values of Chi-square (χ^2) and were tested for significance both at 1 and 5% probability levels against the tabulated values of χ^2 for 'P' degree of freedom, where P is the number of characters considered (Singh and Chaudhary, 1985).

Patterns of genetic distances

Cluster analysis: The data on quantitative measurements were standardized to a mean of zero and a variance of unity before clustering and principal component analysis to avoid differences in scales used to measure different traits. The grouping of the genotypes into different homogeneous groups based on multiple characteristics was conducted following the average linkage method. Genetic diversity between clusters based on a correlation matrix was calculated based on Mahalanobis's D^2 statistic (Mahalanobis, 1936) using the SAS system software package (SAS Institute, 2002). The important traits in each principal component

Table 1. Description of the test genotypes and released varieties.

Region	Zone	No. of genotypes	Name of genotypes/accession number
Amhara	South Wello	10 (1-10)	Acc. No 231623, 231597, 231600, 222855, 226094, 8185, 8186, 214590, 214550, 213149
Amhara	South Gonder	11 (11-21)	Acc. No. 206573, 222621, 222641, 216614, 222655, 222608, 222613, 7412, 216474, 226951, 222616
Amhara	West Gojam	6 (22-27)	Acc. No. 203750, 203922, 203893, 5487, 208212, 203757
Amhara	East Gojam	11 (28-38)	Acc. No. 208189, 208195, 210821,226833,226844, 231617, 231618, 214515, 8333, 8328, 214517
Amhara	North Gonder	10 (39-48)	Acc. No. 222515, 203840, 5217, 204340, 6856, 216492, 216545, 226207, 226208, 216440
Oromia	North Shewa	11 (49-59)	Acc. No. 208265, 208278, 208286, 208310, 208312, 208317, 208491, 226375, 5679, 5739, 226892
Oromia	Arsi	11 (60-70)	Acc. No.222421, 222422, 222428, 226868, 226356, 7073, 214498, 7022, 226273, 5927
Oromia	Bale	7 (71-77)	Acc. No. 231467, 222324, 222338, 204349, 204370, 227060, 204357
Oromia	Harergie	14 (78-91)	Acc. No. 214503, 203695, 203886, 226180, 226183, 222708, 231471, 203690, 231603, 5730, 203854, 226179, 231606, 231613
Oromia	East Shewa	11 (92-102)	Acc. No. 210808, 5429, 216651, 5314, 203748, 5300, 5248, 5180, 5736, 214313, 226959
Oromia	West Shewa	11 (103-113)	Acc. No.231528, 222457. 222461, 231557, 231526, 214328, 5454, 5144, 6101, 7206, 227020
Tigray	Southern Tigray	10 (114-123)	Acc. No. 214343, 7956, 207854, 206551, 206554, 223257, 226199, 206558, 238113, 226245
Tigray	Central Tigray	10 (124-133)	Acc. No. 238114, 238118, 238121, 238122, 238123, 238124, 238125, 238126, 238136, 238137
Tigray	Eastern Tigray	8 (134-141)	Acc. No. 238127, 238128, 238129, 238130, 238131, 238133, 238134, 238135
Improved varieties		19 (142-160)	Ginchi, Yerer, Worer, Mangudo, Arendato, Assasa, Denbi, Tob, LD-357, Hitosa, Mukye, Killinto, Quamy, Gerardo, Foka, Cocorit, Boohie, Bichena, Meteyaya

that significantly contributed to the variation observed were identified as suggested by Johnson and Wichern (1988).

The clustering of the genotypes was performed by the average linkage method of SAS system software (SAS Institute, 2002). Points, where local peaks of the pseudo F statistic join with small values of the pseudo t2 statistic followed by a larger pseudo t2 for the next cluster fusion, were examined to decide the number of clusters (SAS Institute, 2002). The dendrogram was built using MINITAB 14.

RESULTS AND DISCUSSION

The magnitude of phenotypic diversity

Genetic distances

Genetic distances (D^2) between the clusters of 160 durum wheat genotypes are presented in Table 4. Inter-cluster D^2 values ranged from 13.72 (between clusters C1 and C2) to 253.89 (between clusters C3 and C6) (Table 4). The maximum pairwise generalized squared distances (D^2) were found between clusters C3 and C6. Cluster C3 constituted landraces collected from Tigray and Amhara, whereas cluster C6 constituted of released varieties from (DZARC).

The first most divergent cluster group were clusters C3 and C6 (D^2= 253.89), which constituted local landraces collected from Amhara and Tigray regions and released varieties (DZARC), respectively. Landraces collected from Amhara (south Gonder and Wello) and Tigray (central and eastern) showed high genetic diversity within the location, and landraces fail into distant clusters 1 and 3. On the other hand, the least divergent groups were clusters C1 and C2 (D^2 = 13.72). Most of the landraces collected from the three regions (Amhara, Oromia, and Tigray) were included in the first and second clusters; they have the lowest genetic diversity between them. Within landraces, the highest genetic diversity was observed between cluster three (from south Gonder and central Tigray) and cluster four (Central Tigray). This result showed that all landraces except accession no. 238134 were grouped in the first three clusters, and only it remains accession 238134 solitary at cluster four, and it was the most distantly related to the other genotypes. The landraces/accessions obtained from Tigray, Wello, and south Gonder did not group closer with each other while other accessions from Oromia and the rest of Amhara were group closer.

Patterns of genetic diversity

Cluster analysis

Cluster analysis of the 160 genotypes distinguished them into seven different clusters (Figure 1 and Table 5). Members within a single cluster or in clusters with non-significant distances have closer

Table 2. Description of the test locations in terms of geographical position and Physico-chemical properties of the soils.

Descriptor	Location	
	Ginchi	Adadi Maryam
Latitude	09°30' N	08°31' N
Longitude	38°30' E	38°13' E
Altitude (m a. s. l.)	2200	2383
Mean annual rainfall (mm)	1139	1105
Mean annual temperature (°C)	16.3	16.9
Soil type	Black Vertisol	Light brown
Soil drainage	Poorly drained	Well-drained
Soil pH	6.18	7.62
% clay	65.83	61.19
% silt	20.42	25.91
% sand	13.75	12.66
Organic C(%)	1.30 (low)	1.16
N (%)	0.103 (low)	0.15
P (ppm*)	4.49 (low)	8.70
K (ppm)	2.483 (high)	39.75
PH (H_2O)	6.18	6.32
EC (µs)	547.33	405.63

Source: Keneni et al. (2012).

relationships than genotypes from significantly distant groups. The first cluster (C1, n = 113) had the largest number of genotypes collected from three regions in Ethiopia. Followed by the second cluster (C2, n = 25) was the second-largest in the number of genotypes constituted from all over the areas, the fourth and six clusters, with only a single genotype each, being the least in terms of the number of genotypes (n=1, 1), respectively. The fifth and seventh clusters were taking the third and fourth ranks in terms of numbers of genotypes (n =10 and 8), respectively. Data in the table revealed the following.

Cluster I: The first cluster consisted of 113 landraces collected from the entire regions of collection. Members exhibited medium plant height (107.25 cm) and late mature (126.27) than other clusters. This cluster was relatively better in the number of tillers (7.9) and relatively better in thousand kernels weights (29.83). From the first four clusters made by landraces, cluster three was the highest in harvest index, grain yield, and biomass yield (78.53, 103.67, 129.32), respectively, followed by cluster one (77.29, 96.36, 122.88). In all clusters, cluster one showed medium performance from other clusters.

Cluster II: This cluster had consisted of 25 landraces collected from all regions of collection, which were medium in plant height and relatively late matured (127.22 days) than genotypes of other clusters (Table 6). Genotypes in this cluster were characterized by low harvest index (60.19), grain yield, and biomass yield (46.51, 75.58), respectively. They were medium in grain filling duration (64.55), but they showed the lowest efficiency in grain production (59.61) and had a low rate of biomass production and economic growth (72.01).

Cluster III: Consisted of two landraces collected from the Amhara and Tigray region. It was characterized by the latest maturing (127.83) days), and it needs a more extended grain filling period than others (Table 6). It has disease severity (36.8%) for stem rust disease. Genotypes in this cluster showed the lowest thousand kernel weight (19.93, 103.67, 129.32), respectively, medium in grain yield, and biomass yield. From the clusters made by landraces, this cluster had shown the highest production biomass production (101.51) and economic growth rate (146.87).

Cluster IV: Had only one landrace which was collected from the Tigray region. When we compare its value with the mean of the landraces of other clusters, it had the most extended plant height (117.5), late-maturing (125.75), largest leaf area index (147.75), for stem rust had 39.46% disease severity, the number of tillers per plant (5.25), and harvest index (67.43). This cluster was the least performance cluster in terms of yield, and yield components had a lower rate of biomass production (64.68) and economic growth rate (88.68) than the other clusters.

Cluster V: Consisted of 10 released varieties. They were characterized by the shortest plant height (85.91),

Table 3. Measurements and their description were taken to all genotypes.

S/N	Traits	Description
1	Plant height (PH)	The average height of the plants in cm from the ground level to the tip at maturity excluding the awn
2	Heading date (HD)	The number of days from planting to a stage when 50% of the plants in a plot have produced spikes
3	Maturity date (MD)	The number of days from planting to a stage when 50% of the plants in a plot have reached maturity
4	Stem rust scoring (SR)	Incidence and severity of the disease scored at two times
5	Number of tillers/plant (TPP)	The average number of effective tillers per plant
6	Number of spikelets/spike (SPPS)	The average number of spikes lets per spike from five randomly selected spikes from a genotype
7	Grain yield/plant (GLD)	The weight (in grams of grain yield obtained from randomly selected five plants in a genotype
8	Harvest index (HI%)	The ratio of dried grain yield to the biomass yield and multiplied by 100;
9	Biomass/Plant (BMP)	The total above-ground biological yield (grains and all other parts) in grams per plant
10	Leaf area index at maturity (LAI)	It is defined as the one-sided green leaf area per unit ground surface area (LAI = leaf area /ground area, m^2/m^2)
11	Grain filling period (GFP)	The number of days from the heading to maturity
12	Grain production efficiency (GPE)	Grain filling duration divided by duration of vegetative; period and then multiplied by grain yield
13	Economic growth rate (EGR)	Grain weight divided by grain filling duration and then multiplied by 100);
14	Thousand kernel weight (TKW)	The weight in a gram of 1000 seeds
15	Spike length (SL)	The average length of a spike, in cm from its base to the tip, excluding awns.

Table 4. Pairwise generalized squared distances between seven clusters constituting 160 durum wheat genotypes.

Cluster	Clusters						
	C1	C2	C3	C4	C5	C6	C7
C1	0.00	13.72^{NS}	128.80**	33.35**	60.26**	71.62**	57.35**
C2		0.00	149.94**	35.17**	73.20**	104.32**	45.88**
C3			0.00	149.69**	235.51**	253.89**	231.05**
C4				0.00	101.83**	135.74**	100.55**
C5					0.00	40.54**	29.55*
C6						0.00	75.95**
C7							0.00

* =Significant, **= highly significant and NS = Non significant.

relatively early maturing (124.41), and it required the shortest time for grain filling (60.02). It has exhibited (18.85) for stem rust disease severity. It was the second cluster in grain yield (103.27) performance next to cluster six. This cluster had better performance in harvest index (83.82), grain production efficiency (95.26), biomass production rate (99.61), and economic growth rate (175.56).

Cluster VI: This cluster consisted of only one released variety, characterized by best performance in terms of thousand kernel weight (43.23), harvest index (89.10), grain yield (163.99),

Table 5. Clustering of 160 durum wheat genotypes from different origins into seven clusters using 15 morpho-agronomic characters.

Cluster	No. of genotypes	Sources of genotypes	Origins of genotypes
1	113	Collection	Tigray, Amhara and Oromiya
C2	25	Collection	Tigray, Amhara and Oromiya
C3	2	Collection	Amhara and Tigray
C4	1	Collection	Tigray
C5	10	Released varieties	DZARC
C6	1	Released varieties	DZARC
C7	8	Released varieties	DZARC

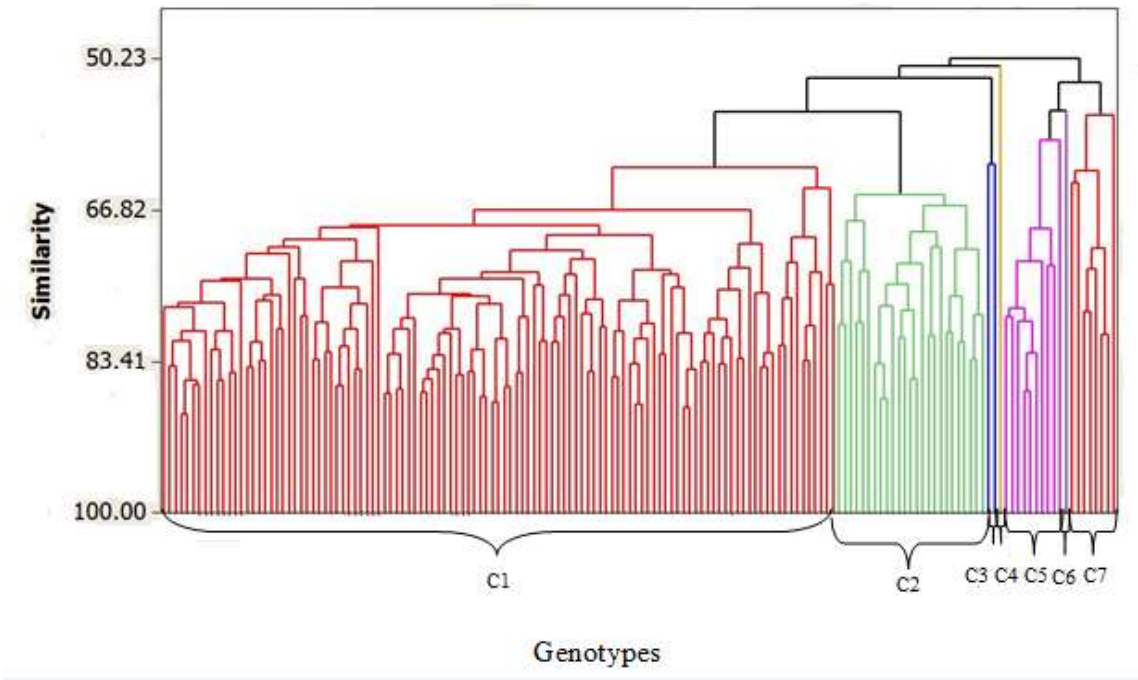

Figure 1. A dendrogram of 160 durum wheat genotypes developed by average linkage method based on Euclidean distance using 15 morpho-agronomic characters.

and biomass yield (183.87). It was resistant to stem rust disease severity (10.80%). It matured early (124.25), and it required a shorter grain-filling period (62.00). It had a relatively short spike length (6.50) with dense spike type. It was also characterized by high grain yield (163.99) and biomass yield production (148.57). The only member included in this cluster, variety Mangudo was better in yield and yield components than other released varieties and landrace collections as well. It was better efficient in grain production, and it had high biomass production and economic growth rate.

Cluster VII: This was the last cluster, which consisted of 8 released varieties. They were small in yield performance than other clusters except cluster two. They were characterized by early maturing (125.86) and short plant height (100.86). They also showed that smaller spike length (8.19) with dense spike shape. It has 26.09% for stem rust disease severity, but it was lower in grain yield and biomass yield (114.17) and also harvest-index. The grain production efficiency, biomass production rate (91.21), and economic growth rate were also lower for this cluster (141. 56).

The local landraces were distributed over clusters C1-C4 but mostly fell into clusters C1 and C2, whereas the released varieties fell into three clusters C5, C6, and C7. Generally, the pattern of distribution of the genotypes from different origins over different clusters was random, showing that there was no clear association between

Table 6. Differences among the seven clusters of 160 durum wheat genotypes for mean performance of 15 characters.

Character	Cluster							Grand mean
	C1	C2	C3	C4	C5	C6	C7	
Plant Height (PHT)	107.25	107.72	108.75	117.5	85.91	90.00	88.89	100.86
Heading Date (HD)	62.86	62.39	56.83	62.00	63.95	62.25	63.19	61.92
Maturity Date (MD)	126.97	127.22	127.83	125.75	124.41	124.25	124.56	125.86
Leaf Area Index (LAI)	96.95	92.86	101.50	147.75	77.87	72.33	84.98	96.32
Stem Rust first score (SR)	30.43	30.73	36.80	39.46	18.85	10.80	15.56	26.09
Number of tillers/ plant (TIL)	7.9	8.18	8.92	5.25	7.61	7.00	8.56	7.63
Thousand Kernel Weight (TKW)	29.83	25.42	19.93	24.54	27.21	34.23	30.3	27.35
Harvest Index (HI)	77.29	60.19	78.53	67.43	83.82	89.10	64.34	74.39
Grain Yield (GLD)	96.36	46.51	103.67	56.88	103.27	163.99	55.7	89.48
Biomass Yield (BM)	122.88	75.58	129.32	81	123.27	183.77	83.36	114.17
Grain Filling Duration (GFD)	64.1	64.55	71	63.75	60.02	62.00	60.61	63.72
Spike length (SL)	9.71	9.82	10.33	9.75	5.64	6.50	5.61	8.19
Spike lets Per Spike (SLPS)	20.25	20.08	18.83	16	17.07	17.75	19.75	18.53
Grain Production Efficiency (GPE)	99.89	49.06	159.75	60.45	95.26	165.03	53.75	97.60
Biomass Production Rate (BPR)	97.23	59.61	101.51	64.68	99.61	148.57	67.29	91.21
Economic Growth Rate (EGR)	151.37	72.01	146.87	88.68	175.56	264.88	91.57	141.56

Table 7. Clustering pattern of Durum wheat genotypes from different locations over seven clusters based on the mean performance of 15 response characters at two locations.

Origin	No. of genotypes	No. of genotypes in each cluster						
		C1	C2	C3	C4	C5	C6	C7
North Shewa	11	9	2	-	-	-	-	-
Arsi	11	8	3	-	-	-	-	-
Bale	7	5	2	-	-	-	-	-
West Harergie	3	3	-	-	-	-	-	-
East Harergie	11	9	2	-	-	-	-	-
East Shewa	11	10	1	-	-	-	-	-
West Shewa	11	11	-	-	-	-	-	-
South Wello	11	8	-	3	-	-	-	-
South Gonder	11	10	-	1	-	-	-	-
West Gojam	6	6	-	-	-	-	-	-
East Gojam	11	9	2	-	-	-	-	-
North Gonder	9	8	1	-	-	-	-	-
Southern Tigray	10	5	5	-	-	-	-	-
Central Tigray	10	9	-	1	-	-	-	-
Eastern Tigray	8	4	3	-	1	-	-	-
Released Varieties	19	-	-	-	-	10	1	8

geographic sources of origin and genetic diversity.

Landraces collected from West Shewa, West Harergie, and West Gojam zones showed limited phenotypic diversity in that their members were entirely grouped only into cluster C1. The landraces collected from the other zones, except for genotypes from Central Tigray, Eastern Tigray, South Gondar, and South Wello, which were either distributed over distantly divergent or more than two clusters, fell into the first two clusters (C1 and C2) with a non-significant distance. The detailed distribution of the genotypes over the clusters is shown in Table 7.

Principal component analysis

Five of the 15 principal components accounted for more

Table 8. The Eigenvalues and vectors of the correlation matrix for 17 traits of 160 *Triticum turgidum* L. landraces of Ethiopia.

Parameter	PRIN1	PRIN2	PRIN3	PRIN4	PRIN5
Eigen value	5.60	3.19	1.67	1.31	1.14
% variance	32.91	20	9.7	8	6.2
Cumulative	32.91	52.93	62.71	70.77	76.98
Character			**Eigenvectors**		
Plant Height (PHT)	-0.069	0.358	0.141	0.124	-0.156
Heading Date (HD)	-0.003	-0.222	0.497	0.248	0.413
Maturity Date (MD)	-0.072	0.315	-0.237	0.027	0.434
Leaf Area Index (LAI)	-0.054	0.303	0.201	0.231	-0.026
Stem Rust score (SR)	-0.119	0.353	0.291	-0.247	-0.089
Tillering (TIL)	-0.062	0.037	0.014	-0.302	0.560
Thousand Kernel Weight (TKW)	0.116	-0.060	-0.143	0.558	-0.255
Harvest Index (HI)	0.348	0.053	0.009	-0.073	0.115
Grain Yield (GLD)	0.416	0.083	0.037	-0.027	0.047
Biomass Yield (BM)	0.403	0.094	0.062	-0.008	0.016
Grain Filling Duration (GFD)	-0.048	0.377	-0.517	-0.156	0.012
Spike length (SL)	-0.075	0.418	0.102	0.294	-0.087
Spike lets Per Spike (SLPS)	-0.017	0.150	-0.137	0.505	0.443
Grain Production Efficiency (GPE)	0.384	0.184	-0.129	-0.080	-0.038
Biomass Production Rate (BPR)	0.405	0.069	0.076	-0.013	-0.018
Economic Growth Rate (EGR)	0.414	0.014	0.124	-0.012	0.061

PRIN1, PRIN2, PRIN3, PRIN4 and PRIN5 = Principal components 1, 2, 3, 4 and 5 respectively.

than 76.98% of the total variation in the Ethiopian durum wheat genotypes. The first principal component accounted for 32% of the overall differences, and the corresponding value for the second principal component was 20% (Table 8). The first two principal components (PRIN1 and PRIN2) contributed about 52.93% of the total variation. Generally, the traits included in the first principal component had small effects of individual contribution (-0.089 to 0.416) to the difference in PRIN1, but characters with relatively higher positive weights of eigenvectors in PRIN1 include grain yield, economic growth rate, biomass production rate, biomass yield, and harvest index. Selection based on these characters may be effective because of the higher comparative variability. Other characters like days to heading and the number of spikelets per spike had smaller negative/ positive eigenvector values contributed the least share to the total variation of genotypes in the first principal component. Spike length, grain filling duration, plant height, stem rust scores, and leaf area index had a relatively higher positive contribution to the second principal component. Different characters also contributed to the variation in the third fourth and five principal components (PRIN3 PRIN4, and PRIN5), but the component accounted for relatively smaller total differences of 9.7, 8, and 6.2%, respectively.

Characters with relatively higher positive weights of Eigenvectors in PRIN1 include Grain yield, Economic growth rate, biomass production rate, biomass yield, and harvest index. Breeding programs should target those characters to improve the yield and its components as well. Besides this, Eigenvectors of stem rust scores, maturity date, spike length, and plant height had relatively large negative weights on this component. Breeding efforts may need to simultaneously focus on the genetic manipulation of these characters to reduce the disease infection and length of maturity time. Heading date and spikelets per spike with smaller negative and positive effects respectively were contributing the least to the variation of genotypes in the first principal component.

Spike length, grain filling duration, plant height, stem rust scores, and leaf area index had a relatively significant positive effect on the differentiation of the population in the second principal component. Heading date and thousand kernel weight had negative effects, but others were positive effects. Two characters, namely economic growth and thousand kernel weight with small positive and negative effects respectively, contributed least to the variation of genotypes in this component.

DISCUSSION

The magnitude of genetic diversity

The minimum inter-cluster distance was observed

between clusters C1 and C2. It indicated that members of these clusters were closely related and, therefore, the crossing of genotypes from these two clusters may not produce a high level of heterotic expression in the F1's with broad-spectrum of variability in segregating (F2) populations (Allard. 1960). On the other hand, the maximum inter-cluster distance between clusters C3 and C6 indicated that the members of these clusters were most divergent. Hence, the crossing of genotypes from these clusters may be successful in terms of producing higher heterotic expression in the first filial generation and better variability in the segregating generations thereof. Parents for hybridization could be selected based on the large inter-cluster distance for isolating useful recombinants in the segregating generations (Allard, 1960). Increasing parental distance implies a greater number of constraining alleles at the desired loci, and then to the extent that these loci recombine in the F2 and F3 generations following a cross of distantly related parents, the greater will be the opportunities for successful selection for any character of yield interest (Ghaderi et al., 1984; Gashaw et al., 2007).

The first most divergent cluster group were clusters C3 and C6 (D^2= 253.89), which constituted local landraces collected from Amhara and Tigray regions and released varieties, respectively. Maximum genetic recombination and variation in the subsequent generation are expected from crosses that involve parents from the clusters characterized by maximum distances. Crosses between the landraces and introduced genotypes constituted in different clusters are expected to provide relatively better genetic recombination and segregation in their progenies (Singh et al., 2014). On the other hand, the least divergent groups were clusters C1 and C2 (D^2 = 13.72). Therefore, crossing from those parents with small genetic distance will not give us higher segregation.

Patterns of genetic diversity

Clustering

Genetic diversity using cluster mean analysis by Euclidean dissimilarity dendrogram has also been reported previously in other studies by (Ali et al., 2013; Shahryari et al., 2011; Aharizad et al., 2012; Ahmadi et al., 2012; Degwoine and Alamrew, 2013; Mengistu and Pè, 2016). The dendrogram elaborates on the relative magnitude of resemblance among the genotypes as well as the clusters (Singh et al., 2014). Based on agro-morphological traits, the tetraploid wheat landraces and improved varieties were clustered into seven cluster groups consisting of 1 up to 113 accessions. Most of the landraces collected from the three regions were grouped into cluster one, which contained 113 landraces. This indicated that the genetic diversity of Ethiopian durum wheat shows some reduction, or there is a duplication of germplasms in Ethiopian collection. This may be due to the fast rate of replacement of landraces with new, improved bread and durum wheat varieties in the country to overcome the yield loss caused by frequent wheat rust disease epidemics. Faris (2011) reported similar results on the reduction of genetic diversity of Ethiopian tetraploid wheat landraces.

On the other hand, the current result is contrary to the previous studies conducted by Yifru et al. (2006), Negassa (1986), Teklu and Hammer (2008) and Mengistu et al. (2015). Who reported the presence of high genetic diversity in Ethiopian durum wheat landrace collections, and they found similar patterns repeatedly in their study. Besides, Hamrick and Godt (1989) indicated that self-pollinating species maintain high genetic diversity at their polymorphic loci and that most of the variation is found among accessions of landrace collections. Additionally, Mengistu et al. (2015) analyzed the genetic diversity of 274 landraces by using eight qualitative and three quantitative traits scored for 2740 plants and analyzed for genetic diversity and reported that Ethiopian durum wheat landraces are very diverse both within and among districts of origin and altitude classes. Also, Mengistu and Pè (2016) reported higher genetic diversity in EBI collections of durum wheat landraces.

Based on the cluster analysis, some landraces from the same places of origin fell into different clusters and *vice versa.* There was no correspondence between geographic and genetic distances, that is, germplasms, collected from the same geographic area were placed into different cluster groups, and those obtained from different geographic regions were placed into the same cluster. Similar results were found from previous works by Gashaw et al. (2007). Landraces and improved varieties formed different cluster groups; this may be due to the distant genetic background between the improved varieties and landraces. Most of the improved varieties used for this study have CIMMYT and ICARDA backgrounds. Similar results were found by Mengistu and Pè (2016), who analyzed Durum wheat genotypes consisting of 265 farmers' varieties and 24 improved varieties. These analyses displayed larger genetic diversity than in those improved varieties.

On the other hand, Mengistu et al. (2015) also reported that separate cluster formation of improved varieties from the landraces. Landraces collected from Wello, South Gonder, and Eastern Tigray showed better genetic diversity than others, this might be due to low gene flow because of slow seed exchange in these areas. Landraces of these three locations (Wello, South Gonder, and Eastern Tigray) showed much similarity than others. They fell into clusters 1 and 3 similarly. On the other hand, landraces collected from Shewa, Arsi, and Bale failed to separate into different clusters. They were grouped in the first and second clusters without showing significant genetic distances. It might be due to the

highest rate of reduction of durum wheat production in these areas, and there is a high chance of replacement of durum wheat by improving bread wheat varieties because of the proximity of the national wheat research coordinating center. Similar findings of the low level of genetic diversity of Arsi and Bale and Shewa locations were reported by the previous studies (Tessema et al., 1991, Bechere et al., 2000; Mengistu et al, 2015).

The clustering of various districts of origins appeared to follow a propinquity-based trend, representing a higher probability of germplasm exchange among farmers in neighboring regions than among those in the distant areas (Faris, 2011). This trend may explain the clustering of North Gonder with West Gojam and of West Shewa with North Shewa in the same cluster. However, the clustering of mutually distant districts could be due to the introduction of germplasm from one to the other, either formally or informally, sometimes long ago. For instance, the clustering of Arsi and East Tigray landraces in one sub-cluster and Bale and South Gonder in the other sub-cluster may be due to such movements. Faris (2011) also suggested germplasm exchange among non-proximal farmers as an explanation for the clustering of landraces from Arsi and Wollo, mutually distant regions, in their study. Bayush et al. (2007) reported that lumping of species together from larger areas not only affects the clustering pattern but may bias estimates of diversity.

Principal components

The first two principal components (PRIN1 and PRIN2) contributed about 52.93% of the total variation. Therefore, characters with relatively larger absolute values of eigenvector weights in PRIN1 had the highest contribution to the difference of the genotypes into clusters. As it is normally assumed that characters with larger absolute values closer to unity within the first principal component influence the clustering more than those with lower absolute values closer to zero (Chahal and Gosal, 2002). In consequence, the traits included in the first principal component had small effects of individual contribution (-0.089 to 0.416) to the variation in PRIN1. Therefore, the differentiation of the accessions into different clusters was dictated by the cumulative effects of many characters (Keneni et al., 2013). Landraces grouped in similar clusters showed the same pattern in the principal component analysis by failing in a similar quadrant. Similar results were found by Mengistu et al. (2015) and Ratiba et al. (2012).

Conclusion

Based on the results of this study, we can conclude that there is a moderate genetic diversity between landraces collected from Tigray, Gonder, and Wello. Landraces of these areas can be used as a source of essential genes for future breeding programs.

On the other hand, minimum genetic diversity was found between landraces of Shewa, Arsi, and Bale, and this might be due to high gene flow between these areas as they are nearby geographically. Moreover, improved varieties showed high genetic diversity with landraces, but they have profound differences between them. In general, the selection of parent materials from germplasms collected from areas that have wider genetic diversity would be useful to incorporate essential genes underlying different traits like yield and resistance for biotic and abiotic stresses.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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Participatory maize hybrid evaluation for different cropping systems in the central rift valley in Ethiopia

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This study was conducted at research and farmers' field. Seven new promising and three standard checks in total ten hybrid varieties were planted and evaluated in 2013 main season. At research field, the genotypes were tested under sole and inter cropping in two replications and each genotype was planted in two rows using spacing 0.75 cm and 0.30 cm between consecutive maize rows and between plants, respectively. However, at on-farm, the genotypes were tested on two farmers' field each genotype planted in three rows solely under sole cropping. Hawassa-Dume common bean genotype was used for intercropping purpose and planted between two consecutive maize rows. The common bean was planted with 10 cm spacing between plants. Farmers were invited to evaluate planted genotypes at hard dough stage of the crop. The objective the study was to screen maize hybrids under both sole and inter cropping systems at research field and sole crop at farmers' field and finally to select hybrids that best fit cropping systems for grain yield and other important traits. The results of the analysis showed that genotypes varied significantly for yield and other traits. The highest yields were observed for genotype-1 (10.6 t/ha) and genotype-3 (10.3 t/ha). However, at Hawassa Research Station, the standard checks varieties (BH-546 and BH-547) performed better compared with other genotypes under sole cropping system. The land equivalent ratio (LER) for genotypes ranged between 1.05 and 1.41. The highest LER was observed for genotype-1 (1.41) followed by the standard check (BH-546) (1.34). This study highlighted the need for testing genotypes for their compatibility to intercropping system.

Key words: Inter-cropping, land equivalent ratio, sole-crop, cropping-system, *Zea mays* L.

INTRODUCTION

Maize (*Zea mays* L.) is the second most widely cultivated crop grown by smallholder farmers under rainfed condition in Ethiopia. Maize yield in Ethiopia vary considerably across seasons and locations making smallholders livelihoods vulnerable to climate variability. Maize and common bean are two of the leading crops in their respective category of cereals and pulses in southern Ethiopia. Accordingly, maize and common bean occupy 33 and 42% of the area devoted to cereals and pulses, respectively (CSA, 2017).

Intercropping systems play an important role in subsistence and food production in developing countries (Tsubo and Walker, 2002). It is most widely practiced in countries where arable land is scarce and also

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Table 1. Hybrid maize genotypes used for on-station and on-farm experiments in the 2013 cropping season in Ethiopia.

No.	Pedigree	Code	Type	Seed color
1	X1264DW1-2-1-1-1-1/7215//CML312	Genotype-1	TWH	White
2	SC22/124b (109)//Gibe1-91-1-1-1	Genotype-2	TWH	White
3	Kuleni-320-2-3-1-1/DE-78-Z126-2-2-1-1((g)//CML312	Genotype-3	TWH	White
4	DE-78-Z126-2-2-1-1(g)/CML312//IL'OOE-1-9-1-1-1-1-1	Genotype-4	TWH	White
5	DE-78-Z126-2-2-1-1purple/Gibe1-91-1-1-1//lcm395	Genotype-5	TWH	White
6	CML395/CML202//DE-78-Z126-2-2-1-1green	Genotype-6	TWH	White
7	CML395/CML202//CML464	Genotype-7	TWH	White
8	BH-543	Genotype-8 (Check1)	TWH	White
9	BH-546	Genotype-9 (Check2)	TWH	White
10	BH-547	Genotype-10 (Check3)	TWH	White

TWH=Three-way hybrid.

contributes to biodiversity and food security (Mushagalusa et al., 2008). Land scarcity is one of the constraints facing small farmers in Ethiopia. In the southern Ethiopia, 40% of farmers have an average land holding of 0.1 to 0.5 ha with a further 30% having 0.51 to 1 ha (CSA, 2017). This led farmers to use multiple cropping mainly intercropping to increase yield per unit area and reduce the risk from crop failure due to climate change.

Maize-common bean intercropping is an integral part of the cropping system in small-holder farmers expecting better yield and weed suppression (Getahun and Tenaw, 1990), provides balanced diet compared to the predominant cereal monoculture and gives high total productivity compared to sole crops of bean and maize (Walelign, 2014; Workayehu, 2014). However, all varieties released so far in the country were evaluated under monocropping system and has not been tested for intercropping system at early stage of breeding. Selection of genotypes both under sole and intercropping systems is of paramount importance to enhance yield and varietal adoption in the region. Therefore, the objective of this study was to identify best performing hybrids for sole and intercropping systems in the southern part of Ethiopia.

MATERIALS AND METHODS

The experiment was conducted under rain-fed condition at Hawassa Research Station (located at 07°03′71″ N, 38°30′88″ E, and 1689 masl elevation) and on-farms (Farm 1: 07° 79′43″ N, 37° 04′ 31″ E and 1696 masl elevation; Farm 2: 07° 78′ 28″ N, 37° 04′ 31″ E with elevation of 1692 masl) during 2013 main rain season in Ethiopia. These areas are characterized by bimodal rainfall received between March and September, and by mean annual maximum and minimum temperatures of 27.3 and 12.6°C, respectively.

Ten three-way hybrid maize genotypes of medium maturity group (140-160 days) including three check varieties were used and planted at Hawassa experimental field under sole mono-cropping and intercropping with haricot bean (Table 1). In addition, the genotypes were planted on two farmers' field under sole cropping system only at Hawassa-Zuria district in 2013. Common bean variety (Hawassa-Dume), well adapted to Hawassa, was used for the experiment. In the maize-bean intercropping treatment, bean was planted at the same time as maize, between maize rows. The experiment was laid down on randomized complete block design with two replications. Each genotype was planted on 7.65 m^2 and 11.475 m^2 areas at on-station and on-farm, respectively. A 75-cm row to row spacing and 30-cm plant to plant spacing was used for maize while haricot bean was planted between the rows of maize with 10-cm plant to plant spacing. Common bean was planted on the same date with maize. Morphological (plant and ear height), reaction to diseases (common rust, turcicum leaf blight and gray leaf sport), agronomic (number of ears per plant and grain yield) traits were measured for maize while only yield of common bean was measured for this study.

All treatments received fertilizer rates of 110 kg N and 46 kg P_2O_5 ha^{-1} for maize and 46 kg P_2O_5 and 37 kg of N ha^{-1} for common bean recommended for Hawassa research field. Nitrogen was used in the form of Urea while phosphorus was applied in the form of DAP. For maize, all the phosphorous and a third of nitrogen was applied at planting while the remaining 2/3 was side dressed between 25 and 35 days after emergence (V5-V8 stage). For common bean, both phosphorus and N were applied at planting.

Besides, farmers participated in evaluating and making their own selection using their own criteria. Plants from the whole plots were hand harvested at physiological maturity. Ears were shelled, grain weight and grain moisture content were measured, and yield was adjusted for 12.5% grain moisture content. However, for common bean, yield was adjusted to 10% grain moisture content. In both seasons, farmers participated in setting selection criteria and evaluating maize genotypes.

Grain yield, plant height (PH), ear height (EH), gray leaf spot (GLS), turcicum leaf blight (TLB), common leaf rust (CLR) and ear per plant (EPP) were analyzed as randomized complete block design in SAS program (version 9.0) (SAS, 2002).

Land equivalent ratio was computed as in Adu-Gyamfi et al. (1997) (Equation 1).

$$LER = ((Ym/Ysm) + (Yb/Ysb))$$

where Ym and Yb were grain yields of intercropped maize and bean; Ysm and Ysb were grain yields of sole cropped maize and bean.

RESULTS AND DISCUSSION

Yield and yield components

At on-station, the highest yields 10.7 and 10.7 t/ha were

Table 2. Mean plant height (cm), ear height (cm), gray leaf spot (GLS), turcicum leaf blight (TLB), common leaf rust (CLR), ear per plant (EPP) and grain yield (t/ha) of maize genotypes tested under sole cropping at Hawassa Research Station in 2013 cropping season.

Genotype	PH	EH	GLS	TLB	CLR	EPP	Yield
Genotype-1	266^{a}	136^{ab}	1.7^{bc}	2.5^{a}	2.0^{a}	1.08^{bc}	9.4^{cde}
Genotype-2	240^{abcd}	134^{ab}	2.0^{abc}	2.5^{a}	1.8^{a}	1.15^{abc}	10.2^{abc}
Genotype-3	250^{abc}	130^{ab}	2.0^{abc}	2.5^{a}	1.8^{a}	1.20^{abc}	10.7^{a}
Genotype-4	233^{cd}	126^{ab}	2.0^{abc}	2.3^{a}	2.3^{a}	1.03^{c}	8.6^{e}
Genotype-5	228^{d}	127^{ab}	2.2^{ab}	2.5^{a}	2.3^{a}	1.16^{abc}	10.3^{abc}
Genotype-6	234^{cd}	121^{b}	2.0^{abc}	2.5^{a}	2.3^{a}	1.17^{abc}	9.6^{bcd}
Genotype-7	254^{abc}	139^{ab}	2.5^{a}	2.3^{a}	2.3^{a}	1.23^{abc}	9.5^{bcde}
BH-543	247^{abcd}	138^{ab}	2.2^{ab}	2.5^{a}	2.3^{a}	1.31^{ab}	9.1^{de}
BH-546	244^{bcd}	125^{ab}	2.0^{abc}	2.5^{a}	2.0^{a}	1.38^{a}	10.4^{ab}
BH-547	256^{ab}	142^{a}	1.5^{c}	2.5^{a}	2.3^{a}	1.23^{abc}	10.7^{a}
Mean	246	132	2.0	2.5	2.1	1.19	9.9
CV (%)	3.82	6.33	12.35	6.80	15.87	8.73	4.25
R^2	0.85	0.63	0.75	0.44	0.44	0.66	0.85
LSD	21.3	18.9	0.6	0.4	0.8	0.24	1.0

Columns with the same letter are not significantly different at P < 0.05.

Table 3. Mean plant height (cm), ear height (cm), gray leaf spot (GLS), turcicum leaf blight (TLB), common leaf rust (CLR), ear per plant (EPP) and grain yield (t/ha) of maize genotypes of maize genotypes tested under inter-cropping at Hawassa Research Station in 2013 cropping season.

Genotype	PH	EH	GLS	TLB	CLR	EPP	Yield
Genotype-1	268^{ab}	141^{abcd}	2.3^{a}	2.5^{ab}	2.3^{ab}	1.19^{ab}	10.3^{ab}
Genotype-2	264^{abc}	148^{abc}	1.8^{ab}	2.8^{a}	2.0^{a}	1.05^{b}	8.2^{c}
Genotype-3	277^{a}	155^{a}	2.0^{ab}	2.5^{ab}	2.5^{a}	1.29^{ab}	10.1^{ab}
Genotype-4	255^{bcd}	139^{abcd}	2.3^{a}	2.75^{a}	2.3^{ab}	1.13^{ab}	9.1^{abc}
Genotype-5	245^{d}	137^{bcd}	2.0^{ab}	2.5^{ab}	2.0^{b}	1.12^{ab}	9.3^{abc}
Genotype-6	251^{cd}	135^{cd}	2.0^{ab}	2.25^{b}	2.0^{b}	1.11^{ab}	9.4^{abc}
Genotype-7	244^{d}	131^{d}	2.3^{a}	2.5^{ab}	2.0^{b}	1.29^{ab}	9.3^{abc}
BH-543	264^{abc}	152^{ab}	2.3^{a}	2.5^{ab}	2.0^{b}	1.27^{ab}	8.7^{bc}
BH-546	267^{ab}	133^{cd}	1.5^{b}	2.5^{ab}	2.0^{b}	1.31^{a}	10.4^{a}
BH-547	257^{bcd}	155^{a}	2.3^{a}	2.5^{ab}	2.0^{b}	1.27^{ab}	10.3^{a}
Mean	259	143	2.1	2.5	2.1	1.20	9.5
CV (%)	2.59	5.10	14.08	6.76	7.10	9.03	7.53
R^2	0.84	0.76	0.62	0.64	0.75	0.60	0.72
LSD	15.2	16.4	0.7	0.4	0.3	0.25	1.6

Columns with the same letter are not significantly different at P < 0.05.

observed for Genotype-3 and check variety BH-547, respectively while the least yield was observed for Genotype-4 (8.6 t/ha) (Table 2). However, yield under intercropping was highest for BH-546 (10.4 t/ha) and BH-547 (10.2 t/ha) with the least yield observed for Genotype-2 (8.2 t/ha) (Table 3). Maize yields generally at on-farm were lower than on research station with the highest yield 8.9 t/ha observed for BH-547 while the least yield was observed for Genotype-1 (6.9 t/ha) (Table 4). When combined over locations and cropping systems, the highest maize yield was observed for BH-547 (10.0 t/ha) while the least was observed for BH-543 (8.3 t/ha) and Genotype-4 (8.5 t/ha) (Table 5). The highest average maize yield was observed from sole cropping system at on-station while mean yield at on-farm was only 7.6 t/ha (Tables 2 and 4). Maize yields of check varieties were comparable or higher than the genotypes evaluated in this experiment. For instance, BH-547 performed better consistently across cropping systems compared with other genotypes (Tables 2 to 5). This is consistent with higher yields recorded for BH-546 and BH-547 by Seyoum et al. (2019) at Hawassa and Bako, high

Table 4. Mean plant height (cm), ear height (cm), gray leaf spot (GLS), turcicum leaf blight (TLB), common leaf rust (CLR), ear per plant (EPP) and grain yield (t/ha) of maize genotypes of maize genotypes tested under sole cropping at on-farm in the 2013 cropping season.

Genotype	PH	EH	GLS	TLB	CLR	EPP	Yield
Genotype-1	211^{a}	104^{a}	2.3^{a}	2.5^{c}	2.0^{ab}	1.05^{a}	6.9^{b}
Genotype-2	210^{a}	103^{a}	2.0^{a}	2.8^{bc}	2.3^{ab}	0.98^{ab}	7.7^{ab}
Genotype-3	214^{a}	104^{a}	2.5^{a}	2.7^{bc}	2.3^{ab}	0.95^{ab}	8.4^{ab}
Genotype-4	190^{c}	87^{b}	2.0^{a}	3.0^{ab}	2.3^{ab}	0.98^{ab}	7.7^{ab}
Genotype-5	189^{c}	94^{ab}	2.5^{a}	3.3^{a}	2.5^{a}	0.96^{ab}	7.9^{ab}
Genotype-6	189^{c}	90^{ab}	2.0^{a}	2.8^{bc}	1.8^{ab}	0.87^{b}	7.3^{ab}
Genotype-7	203^{abc}	102^{ab}	2.3^{a}	2.5^{c}	1.8^{ab}	1.03^{a}	7.3^{ab}
BH-543	195^{bc}	98^{ab}	2.5^{a}	2.5^{c}	2.0^{ab}	0.91^{ab}	7.2^{ab}
BH-546	209^{ab}	96^{ab}	1.5^{a}	2.5^{c}	1.5^{b}	1.02^{a}	6.9^{ab}
BH-547	200^{abc}	103^{a}	2.0^{a}	2.8^{bc}	2.5^{a}	1.01^{ab}	8.9^{a}
Mean	201	98	2.2	2.7	2.1	0.97	7.6
CV (%)	3.13	6.63	22.9	6.84	16.94	6.55	11.8
R^2	0.83	0.65	0.45	0.82	0.65	0.81	0.78
LSD	14.0	15.0	1.1	0.4	0.8	0.14	2.0

Columns with the same letter are not significantly different at P < 0.05.

Table 5. Mean plant height (cm), ear height (cm), gray leaf spot (GLS), turcicum leaf blight (TLB), common leaf rust (CLR), ear per plant (EPP) and grain yield (t/ha) of maize genotypes of maize genotypes combined data across cropping systems (sole and inter cropping) tested at Hawassa research field and on-farm in the 2013 cropping season.

Genotype	PH	EH	GLS	TLB	CLR	EPP	Yield
Genotype-1	248^{a}	127^{abc}	2.1^{ab}	2.5^{bc}	2.1^{ab}	1.10^{bcd}	8.8^{abc}
Genotype-2	240^{ab}	128^{ab}	1.9^{ab}	2.7^{ab}	2.0^{ab}	1.06^{cd}	8.7^{bc}
Genotype-3	247^{a}	130^{b}	2.2^{a}	2.6^{abc}	2.2^{ab}	1.14^{abcd}	9.8^{ab}
Genotype-4	226^{cd}	117de	2.1^{ab}	2.7^{ab}	2.3^{a}	1.05^{d}	8.5^{c}
Genotype-5	221^{d}	119^{cde}	2.3^{a}	2.8^{a}	2.3^{a}	1.08^{bcd}	9.1^{abc}
Genotype-6	225^{cd}	115^{e}	2.0^{ab}	2.5^{bc}	2.0^{ab}	1.05^{d}	8.7^{bc}
Genotype-7	234^{bc}	124^{bcd}	2.3^{a}	2.4^{c}	2.0^{ab}	1.18^{ab}	8.7^{bc}
BH-543	235^{bc}	129^{ab}	2.3^{a}	2.5^{bc}	2.1^{ab}	1.16^{abcd}	8.3^{c}
BH-546	240^{ab}	118de	1.7^{b}	2.5^{bc}	1.8^{b}	1.23^{a}	9.2^{abc}
BH-547	238^{ab}	133^{a}	1.9^{ab}	2.6^{abc}	2.3^{a}	1.17^{abc}	10.0^{a}
Mean	235	124	2.1	2.6	2.1	1.12	8.99
CV (%)	3.99	5.9	17.15	8.03	13.57	8.88	11.19
R^2	0.95	0.94	0.56	0.67	0.59	0.80	0.75
LSD	11.	9	0.4	0.2	0.3	0.12	1.2

Columns with the same letter are not significantly different at P < 0.05.

potential maize growing environments.

Under sole cropping at on-station, sole cropping at farmer's field, and in combined analysis, the best check was BH-547 based on grain yield performance whereas for inter-cropping the best check was BH-546 (Tables 2 to 5). This corroborates with the previous finding that BH-546 had erectophyl leaf arrangement and intercepted more radiation under high planting density at Hawassa (Seyoum et al., 2019). This highlights the need for breeding maize genotypes that can yield higher both under sole and intercropping systems in the region where maize-common bean intercropping is a common practice. The highest intercrop common bean yield was observed for BH-543-common bean intercropping albeit maize yield was the least among check varieties indicating BH-543 had less competitive advantage. The average plant and ear heights were shorter at on-farm, 201 cm and 98 cm, respectively, compared with the corresponding average plant height (246 cm) and ear height (132 cm) for sole cropping system at on-station (Tables 2 and 4). This could be because crops at on-station received better management and hence good growth (taller) and higher

yields. The number of ears per plant varied significantly among genotypes with the highest number of ears per plants (1.38) for BH-546, consistent under sole and intercropping systems (Tables 2 and 3). High yield observed for BH-546 could in part be due to higher number of ears per plant (prolificacy) and hence higher grain number and ultimately yield. On the other hand, genotypes with the least number of ears per plant, Genotype-4 and Genotype-6 had lower yield compared to other genotypes (Table 5). According to Assefa et al. (2018), high number of ears per plant as characteristics of modern hybrids compared with old hybrids. This highlights the need to consider genotypes with higher yield and yield components under different cropping systems to enhance maize yield.

Genotype disease tolerance

Maize genotypes responded differently to the most common maize foliar diseases GLS, TLB and CLR. BH-546 had better tolerance to GLS compared with check variety and the other new hybrids under both cropping systems, sole at on-farm, intercropping systems at Hawassa on-station and in combined analysis (Tables 3 to 5) whereas BH-547 check variety had better tolerance to GLS under sole cropping at Hawassa research field (Table 2). However, no significant difference among genotypes for response to GLS was observed at on-farm (Table 4). This could be due to the sporadic nature of the disease where it infests when all the susceptible host and favorable environmental conditions are met. Tewabech et al. (2012), have reported higher infestation of maize genotypes at Hawassa maize research site, consistent with this finding. Genotypes-1, 3 and 4 have shown high sensitivity to common leaf rust disease under intercropping condition at Hawassa. Similarly, Genotype-5 and BH-547 had high common rust diseases score at the on-farm. On the other hand, highest TLB infestation was observed for Genotypes-2 and 4 under the intercropping and for Genotype-5 at the on-farm condition while the least was observed for Genotype-1, 7, BH-543 and BH-546 (Tables 2 to 5). Foliar diseases such as GLS and TLB are the most maize yielding limiting factors in the region that causes as high as 36% yield losses depending on time of disease onset, disease severity and on hybrid maize susceptibility and yield potential (Tewabech et al., 2011, 2012). This indicates the need for evaluating genotypes for the most common foliar diseases before release in Ethiopia.

Land equivalent ratio

The overall LER was evaluated to derive land benefits associated with intercropping of maize genotypes and the bean variety Hawassa-Dume. The LER in intercrops ranged from 1.05 to 1.41. LER greater than 1 suggests that there is greater land area requirement for the monoculture system or greater relative yield for intercropping of maize genotypes with common bean variety Hawassa-Dume. For instance, LER of 1.41 observed in this study for genotype-1 indicates that there is 41% requirement for the monocropping system or 41% greater relative yield for the intercropping of genotype-1 and Hawassa-Dume. Previous studies on maize common bean intercropping in Ethiopia reported high LER of intercropping system (Walelign, 2014; Tolera et al., 2005; Assefa et al, 2016). For instance, Daniel and Legesse (2019) reported the highest LER (1.95) from maize genotype (BH-540) combined with common bean genotype Hawassa-Dume. However, all maize genotypes in this study had >1 LER indicating that the land productivity will be greater when genotypes are planted in intercropping than monocropping (Table 6). This study highlights that varieties selected based on monocropping performance may not necessarily do well under intercropping system. O'Leary and Smith (1999) reported the need for testing genotypes under intercropping if corn-bean intercrop is desired. Similarly, Masuka et al. (2017) suggested that for any breeding program, it is important to regularly assess the improvements and monitor the efficiency of the breeding program by considering different breeding methods.

Conclusion

The results of this study showed significant variation among genotypes for yield and other traits. Although genotypes used in this study were developed for monocropping system, some genotypes had higher LER indicating that they are compatible to inter-cropping system. For instance, Genotype-1 demonstrated higher compatibility to the intercropping system providing an opportunity for farmers to grow under both cropping systems. In regions with maize commonly grown as an intercrop, it is of paramount importance to evaluate maize genotypes for their compatibility to intercropping system at early stage of genotype evaluation. Some morphological traits such as canopy architecture and tolerance to high planting density could be considered for varietal selection. The results of this study highlight the need for participatory varietal selection where farmers' criteria could also be met for fast-track release and better adoption of maize varieties.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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Table 6. Land equivalent ratios for genotypes tested in 2013 under sole and inter-cropping.

Genotype	Sole maize yield (t/ha)	Intercropped maize yield (t/ha)	Sole beans yield (t/ha)	Bean yield under inter crop (t/ha)	LER
Genotype 1	9.41	10.26	5.43	1.76	1.41
Genotype 2	10.18	8.17	5.43	1.32	1.05
Genotype 3	10.71	10.12	5.43	1.27	1.18
Genotype 4	8.64	9.13	5.43	1.27	1.29
Genotype 5	10.26	9.27	5.43	1.59	1.20
Genotype 6	9.6	9.36	5.43	1.89	1.32
Genotype 7	9.49	9.25	5.43	1.36	1.23
BH-543	9.1	8.7	5.43	1.99	1.32
BH-546	10.4	10.44	5.43	1.83	1.34
BH-547	10.65	10.34	5.43	1.51	1.25

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Multi-environment trial and spatial analysis for yield performance of sorghum [*Sorghum bicolor* (L.) Moench] hybrids in dry lowland sorghum growing areas of Ethiopia

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Sorghum is one of the most widely preferred and cultivated crops in Ethiopia. It is grown for food and feed components. In the developed world, exploitation of heterosis in most crops (Maize, Sorghum, Rice, etc.) is high. There is a clear need to develop sorghum hybrids in Ethiopia to improve their livelihood by increasing sorghum production and productivity. One of the strategies for increasing sorghum yield is through the exploitation of heterosis because sorghum hybrids are high yielder than OPV lines. Properly selected sorghum hybrids can help growers to increase yield, use less water, reduce lodging losses, increase feed quality, and manage maturation time. In Ethiopia, the National Sorghum Research Program runs a multiple technology development work in Ethiopia with the collaboration of International and National Institutions and Universities. One of the oversea collaborative Universities is Purdue University and the Sorghum program received sorghum hybrids to evaluate their performance across sorghum growing dry lowland areas. A total of 35 sorghum hybrid genotypes were introduced and evaluated at six sorghum growing lowland areas of Ethiopia including two recently released hybrid check in 2014. Based on the experimental data submitted to national variety releasing committee, candidate 9187 has been approved for farmers and commercial seed producers in 2018; it is named ESH-5. This hybrid variety is released with a merit of seed color, over all agronomic performance, head shape and yield superior to the recently released hybrid check by 11% yield advantage.

Key words: Hybrid, heritability, sorghum, stability.

INTRODUCTION

Sorghum [*Sorghum bicolor* (L.) Moench] is an African-domesticated diploid C4 cereal crop. It is an extremely productive, dry-resistant C_4 grass used for grain, forage, sugar and biomass cultivation (Casto et al., 2018). It has

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a chromosome of 2n=20 and a ~800 Mb genome size (Paterson et al., 2009; Mace et al., 2013) . Sorghum is a predominantly self-pollinated short-day crop with the degree of spontaneous cross-pollination reaching in some instances up to 30%, depending on the form and type of panicles. It is an indigenous crop of Ethiopia mostly cultivated with low rainfall areas, low soil fertility and high temperature conditions in extremely varied settings. In Ethiopia, sorghum develops from lowland regions that receive reduced rainfall and have elevated altitude temperatures characterized by low temperatures and greater rainfall levels (Mindaye et al., 2015).

Sorghum is the world's fifth largest cereal crop and third largest dry land crop in Ethiopia cultivated by 6 million smallholder farmers in over 1.9 million hectares of soil with 25% area coverage from cereal crops; sorghum contributed 17% of cereal production (Maize, Teff and Wheat) which is about 51.7 M quintals of production (CSA, 2018).

Most sorghum cultivars released in Ethiopia are open-pollinated, but hybrids could offer yield and seed production advantages. Hybrids have confirmed the yield advantage in comparison to the pure line types (Mindaye et al., 2015), although, the genetic foundation for the extended energy is not widely known. The complementarity among alleles of the parental lines is cautioned to have vast contribution (Han et al., 2016). Improvement of high yielding and stable performing hybrid is the key riding element to interact the personal seed sectors and commercialize sorghum in Ethiopia (Wagaw, 2019). The F1 hybrid in sorghum is derived as a result of healing of male fertility while male sterile (A line) crossed with line confers restorer gene (R strains). The male sterile A line is maintained *via* crossing with an isogenic line by B line (Kidanemaryam et al., 2018). Sorghum hybrid improvement research in Ethiopia has been achieved for longer than 4 decades. Even though, the technology has no longer been exploited due to the predominance of the conventional cultivation of sorghum that is relying on the lengthy maturing excessive biomass producing sorghums along with lack of strong value chain and week extension system (Tadesse et al., 2008).

Hybrids evolved from the breeding program and introduced sorghum hybrids from overseas institutions were evaluated for sterility response, biomass production and grain yield performance within the dry lowland sorghum growing areas in Ethiopia for a long period of time; there is a huge evaluation of oversea hybrid genotypes. The primary hybrids designated through the name ESH-1 and ESH-2 have been released in 2009 having 28% grain yield advantage in comparison of OPV and ESH-3 and ESH-4 (red sorghum hybrid) were released for lowland areas with merit of seed color and grain yield in 2012 and 2016 respectively. In 2018, one early maturing seeded sorghum hybrid (ESH-5) was released for end users, among the imported hybrid genotypes to evaluate their performance; from Purdue University executed under this experiment.

Five sorghum hybrids with the ESH series were released and registered for production under dry lowland sorghum growing areas of Ethiopia; but, due to the problems of seed manufacturing, the observation of hybrids ESH-2 and ESH-3 was tough and additionally had confined preference *via* farmers. The hybrids were proven on farmers' field and demand became valid for ESH-1 hybrid within the lowlands of Tigray, North Shewa and West Hararghae areas. Considering this demand ESH-5 was brought by the National Sorghum Research Program to the areas demanding for it.

Exploiting the locally tailored and farmers favored sorts for hybrid improvement could be very important to be beneficial to tap the genetic sources and address the created demand for farmers. Past studies using Ethiopian sorghum landraces have shown excessive yielding hybrids of 7.2 t ha^{-1} with the most excessive determined heterosis up to 60% (Mindaye et al., 2015). Additionally, the demand found out the capability of hybrids for the intermediate and highland environment. But, development of seed determines viable for hybrid seed production with the tall and overdue maturing restorer lines and adapted to the highland and intermediate environment could be a concern for these environments. Due to the latest intervention to illustrate sorghum hybrids for farmers and seed growers there is a growing demand for sorghum hybrids. Efforts have been made to apply the nearby landraces for hybrid improvement and primarily based on their flowering response; within the F1 hybrids 670 restorer traces and 156 B lines were identified by the National Sorghum Program. The restorer strains getting used for the male determine inbred line improvement and the conversion of the B lines as seed discern being underway. To date, the National Sorghum Research Program evolved six seed female and male parents named by MARC1A to MARC6A being used for hybrid improvement.

In Ethiopia, sorghum breeding has been mostly restricted to germplasm characterization using phenotypic traits and exotic sorghum hybrid parental lines. There is also an increment in developing hybrid parental lines from the local available sorghum lines. Even though, there is a high level of genetic diversity and the potential of local developed inbred liens for hybrid cultivar development has not yet been exhaustively assessed. Although, evaluation and verification of introduced hybrid genotypes across environments in dry lowland areas is pertinent to feed the fast-growing population with high yielder and stable cultivars in the resource limited areas. The behavior of hybrids can be exploited to maximize fertilization and grain production in the sorghum hybrids. In this experiment introduced sorghum hybrid genotypes were evaluated over location to evaluate and exploit their yield performance and stability to verify for farmers and seed growers under moisture stress areas of Ethiopia.

Table 1. Testing location description.

Location	Longitude	Latitude	Altitude in m.a.s.l.	Soil type	Rain fall in mm	Minimum T°	Maximum T°
Kobo	39°38'E	12°09'N	1513	Vertisol	678	14.8	32
Miesso	39°21'E	8°30'N	1470	Vertisol	571	16	31
Shiraro	39°9'E	14°6'N	1179	Vertisol	615	20.4	34
Shewarobit	39°93'E	10°35'N	1500	Vertisol	713	17.7	33
Humera	$40^0$9'E	9°16'N	750	Vertisol and fluvisol	590	26.7	40.8
Erer	$42^0$15'E	9°10'N	1297	Vertisol	778	17°C	37°C

Source: Center profile assessed from each center (Humera assessed on 19/08/2019).

MATERIALS AND METHODS

The field testing was conducted during the main cropping season of six locations (Kobo, Mieso, Shiraro, Erer, Humera and Shewarobit); they represent the moisture stressed lowland areas of Ethiopia located in the altitude range of 750-1513 m.a.s.l, where sorghum is predominantly grown by small holder farmers (Table 1).

Description of the hybrids (genetic materials)

A total of 37 candidate sorghum hybrid genotypes including one popular released variety (Dekeba) and hybrid variety (ESH-3) as a standard check were evaluated in 2014 at six dry lowland areas of Ethiopia (Table 1). The genotypes (Table 2) were introduced from Purdue University to evaluate their grain yield performance and stability under moisture stressed sorghum growing areas of Ethiopia.

Statistical design

The experiment was conducted at Mieso, Shiraro, Shewarobit and Kobo in 2014. Randomized Complete Block Design (RCBD) was used to lay out the hybrids with two replications in a row- column arrangement to minimize the spatial variability (trends) in estimating the genetic value. Each plot contained two rows of 5 m length separated by 0.75 m. At all locations sowing was done in between last week of June to first week of July when enough rain was received. Plantation was done manually by drilling along the farrow, and population was adjusted by thinning considering 0.20 m as spacing between plants. DAP fertilizer was applied at planting time with the rate of 100 kg/ha and urea was side dressed when the plant reached knee height at 50 kg/ha basis. Weeding was conducted at least three times during the growing period in each of the test sites depending on the level of weed infestation in the experimental plot.

The following agronomic traits were collected and analyzed to identify stable and superior hybrids compared with the standard check:

Days to 50% flowering (DTF)

This is the time between days to emergence to 50% of the plants in a plot reaching half-bloom stage.

Plant height (PHT)

This is the length from the base of the plant to the tip of the panicle in cm.

Grain yield per plot (GY)

This is grain yield in kilogram of plants from the three rows and adjusted to 13% moisture level and converted to t ha^{-1}.

Days to 90% physiological maturity (DTM)

This is the number of days from emergence to the stage when 90% of the plants in a plot reached physiological maturity, that is the stage at which the panicle loses its pigmentation and begins to dry.

Plant aspect (PAS)

Over all agronomic desirability score (drought tolerance, earliness, head exertion and compactness, grain size and shape, thresh ability, disease and insect resistance, etc.) was scored using 1-5 score where 1=excellent and 5=poor.

Statistical analysis

The concurrence of genotypes and populations between testing site was used to allow the trial series to be analyzed as a single MET as of each trial consisting similar hybrids, which is the current best practice method for analyzing field trials for plant breeding programs (Smith et al., 2001). The META for sorghum hybrid included 35 candidate hybrids and 1 hybrid with 1 variety as standard check and run in six environments. Spatial effects were fitted to each trial and then a variance structure was created to produce between trials (environmental) correlations using factor analytic (FA) method (Smith et al., 2001). Heritability (or repeatability) estimates on a line mean basis were calculated for the different environmental (trials) groups according to the method proposed by Ullis et al. (2006).

For each trait, the genotype x environment (GxE) interactions was considered. These interactions were created by considering a pair-wise correlation matrix for the correlations of each pair of trials. The analysis results in a genetic variance for each trial along with a set of loadings that represent FA frameworks can be used to recreate the correlation matrix (Smith et al., 2001). Although the agronomic traits were measured as usual measurement and score, we are confident that the values satisfy an assumption of normality. The genetic correlations between the hybrid trials at the six sites were identified, with a mean genetic correlation between the sites. These results indicated that there was little GxE interaction for the hybrid agronomic trait. In contrast, the genetic correlations between sites for grain yield were indicated (Figure 2, Figure 3 and Figure 5).

Table 2. Descriptions and list of genetic materials evaluated.

SN	Genotypes	Pedigree	Source
1	9035	P9511A/PRL020765	Introduction
2	9203	P-0102105A/TX2737	Introduction
3	9133	PBL984610A/TX2737	Introduction
4	9130	PBL984594-3A/TX2737	Introduction
5	9224	P-0102043A/TX436	Introduction
6	9128	PBL984594-1A/TX2737	Introduction
7	9140	2001-2002-34A/TX2737	Introduction
8	9058	P9511A/PRL020817	Introduction
9	9149	PBL984594-3A/TX436	Introduction
10	9063	P9511A/PRL020962	Introduction
11	9187	PBL984594-3A/PU304	Introduction
12	9228	P-0102105A/TX436	Introduction
13	9227	P-0102028A/TX436	Introduction
14	9136	PBL984724/TX2737	Introduction
15	9190	PBL984610A/PU304	Introduction
16	9061	P9511A/PRL020884	Introduction
17	9186	PBL984594-2A/PU304	Introduction
18	9147	PBL984594-1A/TX436	Introduction
19	9159	2001-2002-34A/TX436	Introduction
20	9204	P-0102008A/TX436	Introduction
21	9142	2001-2002-103A/TX2737	Introduction
22	9036	P9511A/PRL020772	Introduction
23	9205	P9511A/TX2737	Introduction
24	9041	P9511A/PRL020777	Introduction
25	9076	P9511A/TX436	Introduction
26	9229	P-0102032A/TX2737	Introduction
27	9059	P9511A/PRL020839	Introduction
28	9056	P9511A/PRL020811	Introduction
29	9132	PBL984608A/TX2737	Introduction
30	15	HD1	Introduction
31	9161	2001-2002-103A/TX436	Introduction
32	9034	P9511A/PRL020761	Introduction
33	32	P9401	Introduction
34	9062	P9511A/PRL020888	Introduction
35	9144	2001-2002-197A/TX2737	Introduction
36	ESH-3	ICSA15/M5568	MARC breeder seed
37	Dekeba	ICSR24004	MARC breeder seed

The spatial mixed model used for the MET data analysis is written a

$$y = X_\tau + Z_u + e$$

$$= X_\tau + Z_0 u_0 + Z_g\, u_g + e$$

The fixed effect τ includes environmental main effects and trial specific effects for extraneous field variation (Gilmour et al., 1997), u_g is variety effects at each environment with associated design matrix $Z_g{}^{(nxmp)}$ and u_0 comprises additional random effect with design matrixZ_0, and variance matrix G_0.

RESULTS AND DISCUSSION

A visual display of residual variation before spatial adjustment is presented in Figure 1. In large field trials, field variation among and within locations is a substantial source of error, since similar sites can show similar characteristics compared to those that are different. Figure 1 indicates locations of high and low yields in the field. Thus, there is need to include spatial correlation in variance-covariance analysis, to handle location trend

Figure 1. GxE trend of trials for grain yield to show location trend for these hybrids.

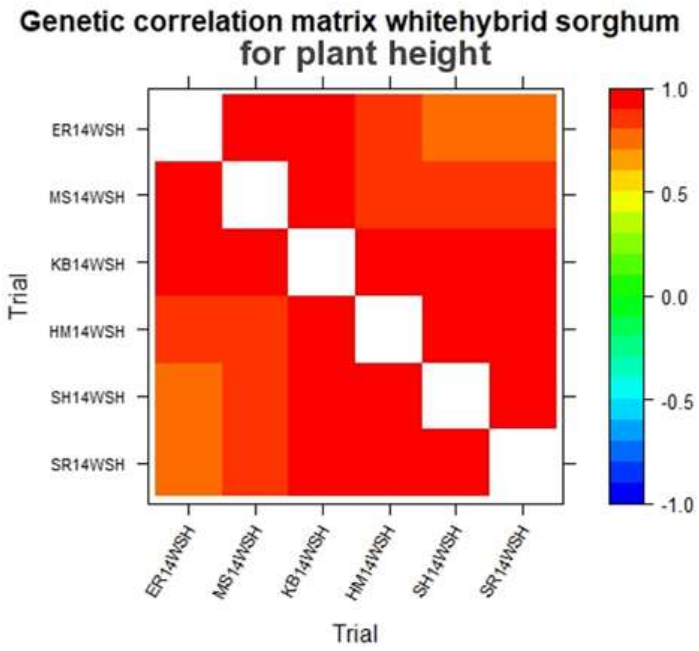

Figure 2. Genetic correlation matrix for plant height across environments.

that extends from one point to the other at the plot and trial level.

The range of trial mean yields among the six trials varied from 1.59 at Humera to 6.39 at Shewarobit (Table 3). The main reason for the lower mean yield at Humera (HM14) is the prevalence of striga infestation in the site

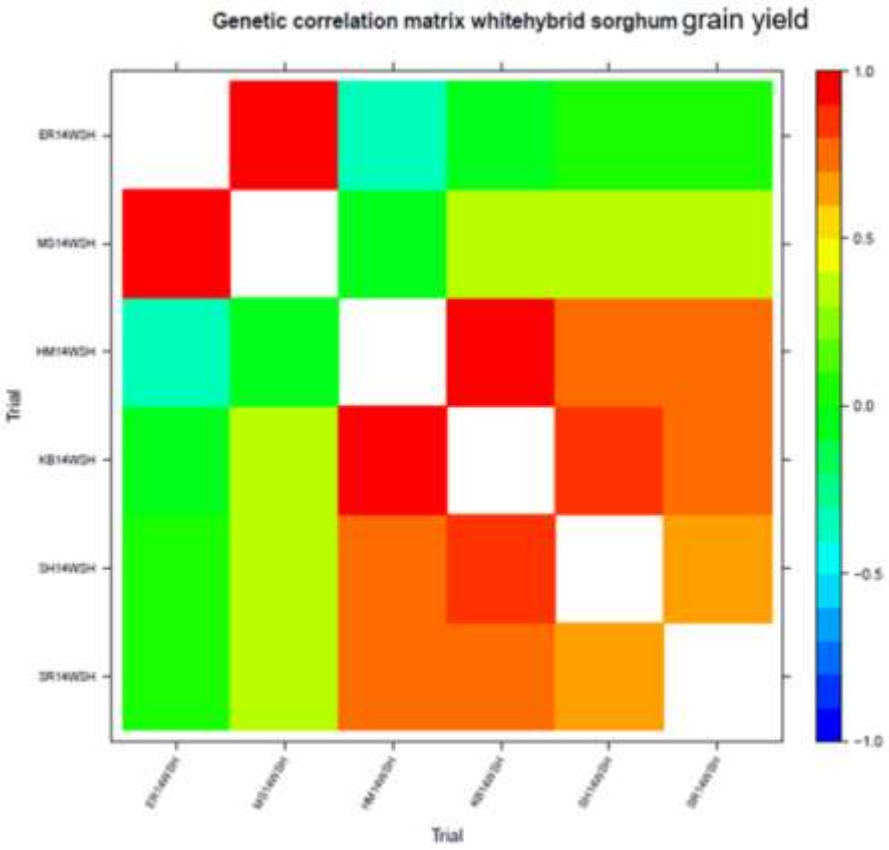

Figure 3. Genetic correlation of trials in respect to their testing sites for grain yield.

Table 3. Over all mean and heritability performance for yield, days to flowering and plant height of hybrids at each of site.

Trial	Grain yield				Days to flowering				Plant height			
	Mean	Genetic σ	Error σ	H_2	Mean	Genetic σ	Error σ	H_2	Mean	Genetic σ	Error σ	H2
ER14WSH	3.61	0.249	1.595	70.61	68.76	5.09	7.97	93.88	129.46	33.21	307.46	90.99
HM14WSH	1.59	0.049	0.156	64.07	47.80	15.80	3.87	92.52	118.93	154.44	118.95	95.83
KB14WSH	4.61	0.058	1.617	65.7	73.27	7.10	2.32	91.72	128.89	247.10	67.83	96.87
MS14WSH	2.94	0.237	0.215	76.75	64.32	3.34	2.00	85.11	115.15	178.76	40.90	93.27
SH14WSH	3.66	0.067	0.539	51.6	63.61	7.96	1.42	94.71	135.41	245.54	108.08	96.24
SR14WSH	6.39	0.245	0.821	59.27	134.14	291.77	91.90	88.18	135.32	298.10	45.42	96.41

during the experiment.

The associated heritability of grain yield varies from 51.6 to 76.75% and averaging 64.67% (Table 3). Heritability for days to flowering and plant height also show a better repeatability ranged from 85.11% to 94.71% with an average of 91.02% of reputability over all testing environments. This indicates that days to flowering is one of the traits that are highly heritable from parent to progenies (Table 3). Similarly, plant height is one of the most preferred traits that researchers need to invest more on to improve grain yield. There is no compromising the biomass component for the framers which is the best input for animal feeding and forage in Ethiopia and other like areas specially where an agrarian life mostly depends on mixed farming system like animal husbandry and cropping. Based on this experiment output, plant height (the main component for biomass production in sorghum) is highly heritable (Table 3) and all the environments are highly correlated (Figure 2) for plant height.

Based on the result, repeatability for plant height ranged from 90.99% to 96.87%, with an overall mean of 94.94% across testing environments. This indicates that taking more samples to measure plant height may not give significant (varied) result different from the result obtained from single observation.

The predicted mean for each of hybrids across testing site ranged from 4.2 to 3.15 t/ha, with an overall mean of 3.8 t/ha of grain yield. Based on the agronomic preference (PAS) and others (PHT, GY and DTF) 9187 named ESH-5 is released over ESH-3 and ESH-4 in 2018. This hybrid variety has a good agronomic preference as compared to ESH-3 and now the outreach system is under way by external funded projects. 9187 has been scored 1.6 followed by the 2nd candidate 9059 rated 1.8 for plant aspect; while the rest of the hybrids scored 2.00 and above (Table 4). Next to molecular aspect (in case of MAS a technology which is used to test the presence of desired gene in early generation), plant aspect (PAS) which encompasses drought tolerance, grain color, farmer preference, thresh-ability, earliness, biomass condition, shattering, tiller capacity, uniformity, lodging, resistance to disease and insect, etc. is the most important technique to identify (evaluate) the genetic materials for a given set of experimental objectives.

The genetic correlations for yield between the six sites varied between -0.371 and 0.933 (average 0.281), indicating the presence of significant amounts of GxE interaction for grain yield and reflecting changes in genotype ranking between sites (Table 4 and Figure 1). The stronger the correlations between trails (locations) indicated that GxE interactions were not as important for this trait and were not causing as much reordering of genotypes between sites (Jordan et al., 2012).

Most of the testing sites are correlated strongly and are not important to test hybrids across the sites since they do not bring change in rank of these hybrids. Trials at HM14 and ER14 were negatively correlated and testing the hybrid will change in rank and might be important to test hybrids in contrast, that is, low correlated (negatively) environments (Figure 3 and 4); whereas ER14 is correlated at zero or null correlation with SR14, SH14 and KB14. MS14 is moderately correlated with SR14, SH14 and KB14. Less angle between biplot lines for trial sites and deep red colored trials showed they are strongly correlated and testing these genotypes in one of them will give reliable information. Locations such as SH, HM and KB, ER and MS, SH and SR are also strongly correlated locations (Figures 3 and 4). As those sites exhibited less angle and strong correlation, selection of the best genotypes based on one of the environments does not change the ranks of the genotypes in another environment.

Among the testing hybrids two of them (9063 and 9058) scored above the standard check variety Dekeba with an average BLUP of 4.2 and 4.19 t/ha of grain yield respectively; while the standard check variety Dekeba predicted 4.1 t/ha grain yield and similar sorghum growing locations.

Graphical explanation of the MET biplot data is commonly used to explain genotype by environment (Figure 3). The plots show that the environment with longest line from the center measures the discriminativeness of that environment when compared with others. For example, ER14WSH and MS14WSH were among the most discriminative environments followed by SR14WSH. This means these environments had considerable contributions in discriminating genetic variations. On the other hand, environments with less distances from the center were those stable environments, hence they explained less genetic variations. In addition, when a specific genotype is close to a given environment, it indicates that the genotype is the winner for that specific environment. That means, that genotype is the best performer for that trial. Hybrid 9187 is the closer genotype to the center of all the locations plot and this genotype is the most stable and winner in all the testing environments. The reason for releasing is being stable and winner across all testing environments.

The other important trait to be considered for the variety to be released and preferred by end users especially by farmers who need to have multiple uses is earliness. Nowadays, one of the cross-cutting issues for agriculture especially for crop farming is climate change when there is lack of enough rainfall to grow a crop. In this case, days to flowering is one of the major important traits to judge a given variety that suits the drought prone years and environments. It can help the breeder (researcher) to give relevant information whether that variety can escape the drought time or not. Mostly days to flowering can tell us the period required to give reasonable yield within the given time span starting from the date to planting. So, days to flowering is repeatable by an average of 91.02% across testing sites.

Conclusion

The hybrid sorghum genetic material is introduced from Purdue University and evaluated as part of an international hybrids' evaluation trial in collaboration with the university. The candidate hybrid has parental line PBL984594-3A/PU304. The parental lines are evaluated based on flowering time and plant height, which has serious implication for large seed production.

Based on the presented data and report one early maturing high yielder hybrid variety is released with good agronomic preference and a merit of seed color, yield and other important parameters with the inclusion of farmer preference mark. The variety is verified mainly for its high grain yield (11% advantage over the hybrid check and 19% over the best OPV check). The candidate variety showed better performance in uniformity and

Table 4. BLUPs for grain yield, days to flowering and plant height performance of the hybrids in specific site and over all locations.

Genotypes	ER14			HM14			KB14			MS14			SH14			SR14			Mean			
	GY	DTF	PHT	GY	DTF	PHT	GY	DTF	PHT	GY	DTF	PHT	GY	DTF	PHT	GY	DTF	PHT	GY	DTF	PHT	PAS
9063	3.89	69.28	133.98	1.82	47.30	130.71	4.95	72.91	144.38	3.50	64.16	127.34	3.95	63.67	150.84	7.09	150.27	142.11	4.2	77.93	138.23	2.31
9058	3.79	69.57	141.41	1.86	47.40	150.30	4.98	71.51	168.92	3.40	63.28	146.91	4.00	63.50	174.91	7.11	166.89	132.94	4.19	80.36	152.57	2.31
Dekeba	4.52	74.25	146.52	1.47	57.44	127.30	4.65	78.29	151.30	3.86	68.67	142.79	3.70	70.86	142.59	6.39	138.43	137.27	4.1	81.32	141.29	2.36
9034	4.36	51.89	120.84	1.51	73.85	134.29	4.66	64.21	121.85	3.68	65.21	137.07	3.70	147.41	137.27	6.66	147.41	133.69	4.09	91.66	130.83	2
9205	3.74	65.87	128.40	1.76	42.63	117.76	4.85	70.68	126.88	3.24	62.34	113.11	3.89	59.73	134.09	6.95	132.34	141.24	4.07	72.27	126.91	2.69
ESH-3	4.18	69.31	137.47	1.51	48.19	144.50	4.64	71.09	160.35	3.51	62.74	138.80	3.72	63.33	168.44	6.65	164.16	114.38	4.04	79.8	143.99	2.14
9132	3.32	66.70	127.56	1.93	45.72	114.57	4.97	71.87	122.97	2.94	63.62	110.32	3.98	61.12	129.76	6.91	124.01	155.96	4.01	72.17	126.85	2.69
9144	3.83	66.21	123.22	1.68	42.65	117.38	4.77	69.27	122.10	3.29	63.22	105.76	3.81	60.27	134.78	6.51	138.85	179.03	3.98	73.41	130.38	2.25
9204	4.09	71.30	130.19	1.49	51.55	108.96	4.59	77.21	120.57	3.41	65.61	111.60	3.65	67.34	122.57	6.41	126.58	159.09	3.94	76.6	125.5	2.38
9133	3.38	66.58	126.47	1.77	43.74	111.23	4.79	71.17	118.81	2.88	63.53	107.16	3.85	61.14	125.43	6.72	128.81	154.61	3.9	72.49	123.95	2.75
9161	3.61	69.65	135.18	1.69	48.81	116.41	4.74	75.25	131.42	3.05	64.76	121.88	3.74	65.10	130.76	6.56	127.72	177.43	3.9	75.22	135.51	2.56
9203	3.51	64.79	126.16	1.73	42.27	115.33	4.77	69.45	123.01	2.97	62.28	109.01	3.81	58.82	131.84	6.60	123.24	152.41	3.9	70.14	126.29	2.5
9130	3.34	67.95	122.36	1.81	47.29	113.20	4.82	72.65	117.17	2.84	64.52	102.42	3.86	62.90	129.03	6.71	125.89	138.25	3.89	73.53	120.41	2.63
9076	3.72	46.39	120.95	1.58	74.13	131.51	4.63	63.90	117.21	3.10	63.32	138.03	3.66	145.21	138.25	6.53	145.21	132.05	3.87	89.69	129.67	2.5
9190	4.31	69.13	126.63	1.32	51.06	108.88	4.44	74.03	117.27	3.53	65.47	106.54	3.57	64.02	123.01	6.06	126.07	128.19	3.87	74.96	118.42	2.13
9035	4.27	52.06	117.33	1.30	75.13	128.02	4.40	65.46	114.89	3.43	65.29	133.89	3.53	126.81	133.69	6.13	126.81	129.10	3.84	85.26	126.15	2.19
9142	3.88	65.56	125.61	1.48	42.48	110.58	4.54	70.80	117.87	3.15	61.95	105.86	3.62	59.73	125.34	6.30	125.76	124.31	3.83	71.05	118.26	2.44
9187	3.63	70.14	126.50	1.61	51.55	110.96	4.64	75.37	118.83	2.99	66.51	107.20	3.70	65.75	125.43	6.45	120.91	108.57	3.83	75.04	116.25	1.69
9228	3.45	69.76	128.50	1.68	48.19	117.60	4.69	74.89	126.53	2.85	65.82	113.03	3.64	64.83	133.44	6.66	132.61	110.67	3.83	76.02	121.63	2.56
15	4.39	50.09	125.61	1.24	75.29	145.48	4.36	66.71	135.21	3.55	65.43	141.32	3.46	130.85	142.11	5.89	130.85	124.20	3.81	86.54	135.66	2.5
9062	3.19	46.82	148.48	1.73	69.58	160.87	4.72	61.60	136.16	2.68	62.27	173.59	3.77	178.30	177.43	6.69	178.30	134.52	3.8	99.48	155.18	2.19
9061	3.37	45.44	133.21	1.70	70.96	143.67	4.71	62.54	124.97	2.83	62.30	152.88	3.72	156.35	154.61	6.40	156.35	134.76	3.79	92.32	140.68	2.5
9186	3.48	70.03	128.67	1.61	50.96	110.24	4.62	75.13	120.08	2.84	66.68	109.90	3.66	65.44	124.06	6.54	124.23	128.91	3.79	75.41	120.31	2.13
9056	3.62	42.26	133.82	1.49	68.67	146.51	4.50	61.69	128.29	2.91	60.62	154.07	3.57	154.12	155.96	6.10	154.12	118.87	3.7	90.25	139.59	2.38
9136	3.27	41.80	100.30	1.67	70.74	107.07	4.66	62.89	99.65	2.65	60.01	111.13	3.69	110.53	108.57	6.28	110.53	130.36	3.7	76.08	109.51	3.13
9128	2.80	47.89	116.38	1.82	73.45	123.77	4.74	65.08	109.70	2.27	63.35	132.47	3.78	128.84	132.05	6.68	128.84	122.86	3.68	84.57	122.87	2.63
9041	3.65	50.66	103.90	1.44	75.28	110.79	4.45	64.27	101.53	2.86	64.67	116.42	3.50	116.67	114.38	6.06	116.67	124.32	3.66	81.37	111.89	2.19
9229	3.31	65.67	124.69	1.57	43.89	110.94	4.54	71.25	117.70	2.61	62.59	104.91	3.62	60.61	126.42	6.33	111.04	121.66	3.66	69.18	117.72	2.69
9059	3.15	44.94	135.87	1.68	71.12	149.74	4.64	62.81	131.09	2.54	61.73	156.89	3.74	149.74	159.09	6.02	149.74	131.36	3.63	90.01	144.01	1.81
9224	3.24	70.00	121.56	1.56	49.60	110.37	4.51	74.33	113.88	2.51	64.22	99.98	3.61	65.48	125.52	6.11	135.77	121.26	3.59	76.57	115.43	2.63
9036	3.57	52.54	121.91	1.38	74.29	128.32	4.37	64.34	110.73	2.77	65.23	140.85	3.42	142.93	141.24	5.99	142.93	133.89	3.58	90.38	129.49	2.5
9147	3.32	51.84	117.68	1.51	76.84	125.43	4.47	66.59	110.46	2.59	67.48	134.93	3.43	138.71	134.76	6.17	138.71	124.31	3.58	90.03	124.59	2.56
9140	3.12	41.97	101.40	1.54	70.93	106.01	4.47	63.39	96.82	2.40	59.26	113.09	3.54	107.85	110.67	6.03	107.85	131.61	3.52	75.21	109.94	3.44
9149	3.35	52.41	114.11	1.46	77.58	121.48	4.42	66.52	108.27	2.55	67.89	129.61	3.45	124.90	128.91	5.89	124.90	133.17	3.52	85.7	122.59	2.75
9159	3.16	48.53	107.53	1.48	75.72	117.65	4.41	64.65	108.80	2.38	64.28	120.42	3.50	114.71	118.87	6.12	114.71	125.37	3.51	80.43	116.44	3
9227	3.45	49.43	115.60	1.36	75.68	125.36	4.32	65.32	112.27	2.61	65.81	132.03	3.35	130.48	131.61	5.99	130.48	143.61	3.51	86.2	126.74	2.5
32	3.13	49.32	116.80	1.23	74.60	123.00	4.10	66.16	108.03	2.09	65.69	133.30	3.09	137.94	132.94	5.26	137.94	171.83	3.15	88.61	130.98	3

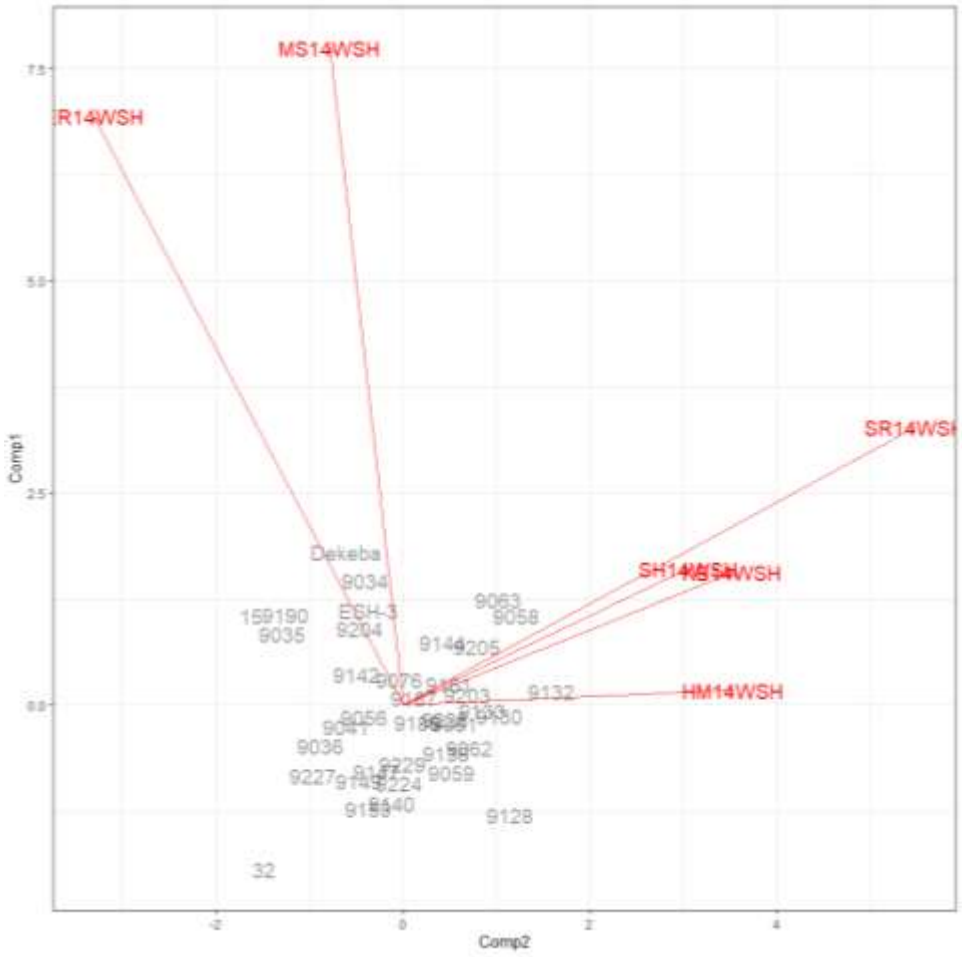

Figure 4. GxE biplot of candidate hybrids.

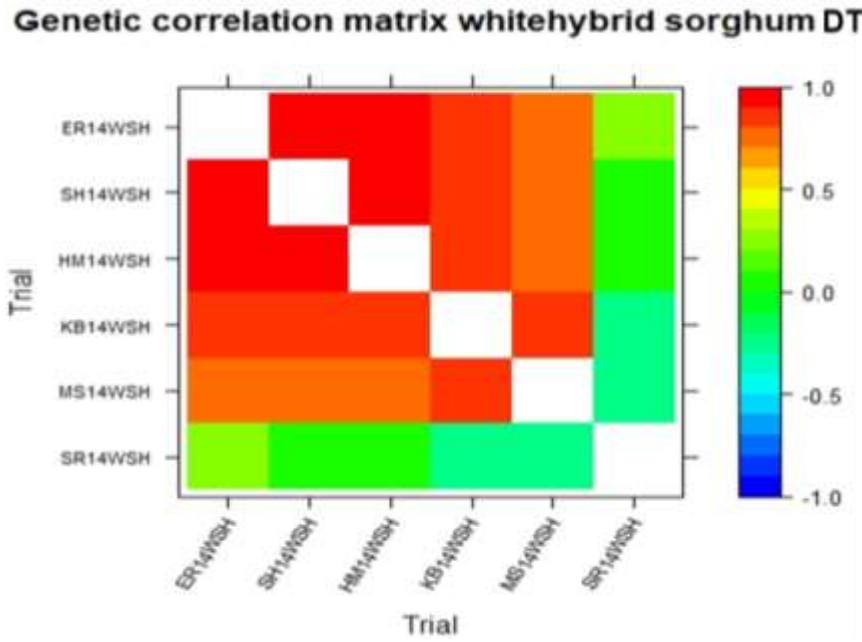

Figure 5. Genetic correlation of hybrids for their days to flowering.

stability in areas where moisture is a limiting factor. The variety is preferred mainly for best overall plant aspect, excellent grain and better yield over the check. Over all agronomic desirability score (includes drought tolerance, earliness, head exsertion and compactness, grain size and shape, threshability, disease and insect resistance, etc.) was measured using 1-5 score where 1 is excellent and 5 is poor. The candidate 9187 recorded the best overall score value of 1.69 on average while the standard checks scored 2.14 and 2.36.

The candidate variety was stable across all the testing locations, mostly in the area where the growing of sorghum is characterized by water moisture deficient and different biotic and abiotic constraints. This variety is verified in favor of these factors. An ideal sorghum hybrid is 175-180 cm tall and flowers in 68-70 days. Whereas, this hybrid has a plant height of 116.25 cm and flowering time of 75 days on average. Such hybrids generally yield 10-32% higher than OPV varieties. The current variety has 19 % yield advantage over OPV check. Across the environments, hybrid yield should be more stable than yield of OPV varieties. This study confirms that the verified hybrid variety is stable across the test environments for grain production.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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Assessment of indigenous knowledge associated with Sorghum (*Sorghum bicolor L. Moench*) seed selection and the seed quality attributes in Fafen Zone of Somali Region, Ethiopia

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Understanding agro-pastoralist's indigenous knowledge associated with sorghum seed selection, seed systems, and seed quality management will help to devise strategies for enhancing the food and feed security in crop-livestock mixed farming system. With this intention, indigenous knowledge practices of on-farm sorghum seed selection and evaluation of the seed quality were surveyed, which ultimately contributes to sorghum genetic diversity maintenance in the agro-pastoral production system. Here, semi-structured interviews, focus group discussions and sorghum field observation were used. A total of 30 agro-pastoralists were interviewed and 16 seed samples were collected from traditional storage. It was observed that six local varieties of sorghum were the dominantly maintained and cultivated by agro-pastoralists of the study area. Among local varieties '*Elmi jama'* is the predominated area allocated for sorghum production in both districts. Agronomic performance (drought resistance, stock borer, and bird resistance) and straw yield were highlighted as important criteria for making decisions to select sorghum to be used for seed selection and maintenance. Over 90% of the informants grow a local variety of sorghum by mixing early and late maturing varieties on the same plot of land to mitigate the risk of moisture shortage and/or drought season. Seed quality assessment from Gursum district showed better germination potential with an average of 86.99%. This research offers the status of seed selection practices and seed quality status in agro-pastoral context and recommends the way forward to enhance sustainability of sorghum seed maintenance.

Key words: Agro-pastoralist, local variety, seed maintenance, seed quality, sorghum, crop-livestock system

INTRODUCTION

Sorghum is an important traditional and multi-purpose cereal crop grown by smallholder farmers of Ethiopia (Girma et al., 2019a). Ethiopia is recognized as a center of origin and diversity (Girma et al., 2019b), and immensely contributed to global sorghum genetic pool. Linked to sorghum domestication in this area, the crop has several uses for the community and no part of this plant is ignored. The leaves were used as fodder, stalks

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mainly used for fuel, fencing and roofing materials in rural areas. In the lowland areas characterized with moisture stress with marginal soil, sorghum is well adapted under drought condition and considered as a model crop (Kidanemaryam, 2019). Most importantly, sorghum grow in a wide range of agro-ecologies, particularly in the moisture stressed areas of Ethiopia (Abebe et al., 2020) where other crops could least survive. Sorghum is a strategic crop in the eastern part of Ethiopia (Mekbib, 2006). The ecology was characterized with shortage of moisture and farmers livelihoods were strongly dependent on crop livestock mixed production systems.

Although sorghum is the third important crop next to *teff* and maize in Ethiopia, the yield is below the world average. The sorghum worldwide average yield is 1314 kg/ha; developed countries is 3056 kg/ha and that of developing countries is 1127 kg/ha. The Ethiopian national average yield account for up to 2000 kg/ha (EIAR, 2014). One of the reasons for low yield productivity was related to seed delivery system.

In Ethiopia, sorghum formal seed industry is not developed yet (Eltayeb and Sana, 2010). Due to the fact that seed is an essential input in farming and most of the farmers in marginal agro-ecologies solely rely on local seed system, this study explored the indigenous on-farm seed selection, maintenance and seed physiological quality attributes.

MATERIALS AND METHODS

The assessment was conducted in Jijiga and Gursum districs of Fafen Zone, Somali Regional State in 2013/2014 cropping seasons. The districts received mean annual rainfall ranges from 380.1 to 756 mm and the mean temperature during the growing period in the area ranges from 20.1 to 22.5°C. Target areas were characterized to the warm semi-arid to cool and humid agro-climatic zone. The altitude is between 500 and 2500 m.a.s.l. The average annual temperature ranges from 27.5-18°C, the average annual rainfall ranges from 200 to 1400 mm, and the potential evapo-transpiration were estimated to be from 1438 to 2099 mm (Oromia Water Works Design and Supervision Enterprise - OWWDSE, 2012).

Sampling procedure

Multi-stage purposive random sampling procedure was followed from higher to lower administrative levels, with agro-pastoralists being sampling units. Eight sorghum producing villages and 16 farmers/agro-pastoralists were selected for interview. The interview was conducted between August to October 2014 using pretested semi structured questionnaires administered by trained enumerators and researchers. Researchers and agro-pastoralists observed sorghum field and assessed the sorghum plant selection criteria, particularly for seed purposes.

A four-stage sampling procedure has been used to select potential areas of sorghum production Somali region. It involves the selection of administrative regions, zones, districts and villages.

First stage: From Fafen Zone, two sorghum producing districts (Jijiga and Gursum) were purposively selected.

Second stage: From selected districts, two villages were purposively selected based on the area allocated for sorghum crop production.

Third stage: Within each of the two selected villages, at least two major sorghum producing villages were selected randomly by considering the proportional area planted by sorghum in the villages.

Fourth stage: From selected villages, sixteen experienced sorghum producer agro-pastoralist's were selected.

Seed quality analysis

Sorghum stored for seed propose was collected from local stores and analyzed for physical and physiological quality parameters. One kilogram of sorghum seed was collected from farmers/agro-pastoralists stores using sample bag. The seed is submitted to Jigjiga University Dryland Crop Science Laboratory for physical and physiological evaluation.

Physical purity test

Each working sample was divided into two 350 g portions for physical purity analysis. The components were separated into pure seed and inert matter and each component was weighed using analytical balance. Finally, the percentage composition of the seed lot was calculated based on the weight of each component.

$$\text{Purity percentage} = \frac{\text{Weight of pure seed}}{\text{Total weight of sample}} \times 100$$

Physiological quality test

For germination test, forty-eight seeds were placed on moistened filter paper in the Petri-dishes. Seeds in Petri dishes were placed on working board at room temperature. First and final counts were made on 5 and 9 days after planting.

$$\text{Germination percentage} = \frac{\text{Number seeds germinated}}{\text{Number seeds on tray}} \times 100$$

Statistical analysis

The average value of panicle length, panicle weight, seed physical purity and physiological quality test were calculated and illustrated in table form.

RESULTS AND DISCUSSION

Indigenous folk names associated with sorghum seed selection

In the target study areas, sorghum is known by the collective folk name '*harur*'. This study has identified six sorghum landraces predominantly produced in the Jijiga and Gursum district of the Somali region (Table 1). Each local landrace are their own specific varietal names and help the farmers to describe, identify and distinguish. The agro-pastroalists have particular names and identify the cultivars with local names such as '*Eilmi-jama'*, '*Wogera*',

Table 1. Study location and list of sorghum landraces owned by interviewed agro-pastoralists.

District	Kebelle	Village	Local name	Altitude (m.a.s.l)
Gursum	Kuramatana	Kontame	Elmi-jama, Wegera, Asse	1721
	Kumijaro	Guta	Elmi-jama, Dongae, Asse	1523
	Kuramatana	Hajje	Elmi-jama, Dongae	1761
	Kumijaro	Aliwal	Elmi-jama, Dongae, Ahmednasir, Wagara, Asse	1517
Jigjiga	Haroreys	Debeleweyni	Elmi-jama, Adengab	1842
		Kutle	Elmi-jama, Asse	1784
	Turuad	Wollego	Elmi-jama, Asse	1763
	2nd Turuad		Asse	1761

Source: Own Survey (2014).

'*Asse*', '*Dongae*' and '*Ahmednasir*'. Sorghum field observation with the key informants and researchers identified that the landraces folk names given were linked to distinct morpho agronomic attributes such as plant height, days to maturity, seed color and bird resistance. Furthermore, the folk names were related to the original source of the material, morphology, end use and name of the person who introduced it to the particular location.

Nevertheless, vernacular names may not always correspond to botanical distinctiveness, although they are quite often descriptors used for variety identification. This indicates that the farmers understand crop genetic diversity on the farm and the value associated to it, and such folk names are extremely useful (Liu, 2013). In our study, the agro-pastoralists classified the sorghum local varieties by seed color, grain head, panicle type, bird resistance and days to maturity. The target communities' practices agro-pastoral production system which relies both on livestock and crop farming, and the sorghum dynamic classification is an indicator for recognition that the significant contribution of the crop is as human food and livestock feed security. Sorghum is widely grown in the Fafen valley of of Gursum districts; particularly in Kumijaro area. This study covers the altitude range of 1517-1842 m.a.s.l (Table 1). Despite the variation in altitude and sorghum cultivars and agronomic practices, six varieties were showed wide adaptation across the elevations studied.

Crop and varietal mixture (poly-cultivar)

In our study, we identified that the agro-pastoral communities have special planting calendar for sorghum landraces. Through field observation and key informants' interview, we noted that there was special linkage between sorghum seed maintenance and planting. For instance, every agro-pastoralists were maintaining an average of 2-5 sorghum cultivars per household. In our view, these practices can be considered as climate change coping strategies practiced at small-scale level. Similarly, Yemane et al. (2009) reported that the North Ethiopia farmers manage different crop landraces as a climate change coping mechanism. In this study, we noted that the indigenous seed selection was complimented with the need to mitigate the risks of drought by planting diversity of sorghum on a single farm. Using this kind of indigenous knowledge, the agro-pastoralists minimize on-farm micro-environment associated risk such as insect damage, diseases protection, and drought, and hence obtain biomass and biological yield, at the same time prolong varietal stability (Altieri and Merrick, 1987). The sorghum farming communities had established varietal mixtures sorghum production strategy.

The varietal mixture prepared based on different days to maturity was a key indigenous strategy implemented by the agro-pastoralists to cope with the biotic and abiotic stress existing in the study areas.

On the other hand, the reasons for using intra-specific varietal mixture were agronomic and gastronomic followed by different secondary uses (feed, fuel wood). Such strategy was commonly practiced in Sub-Saharan Africa and particularly in Ethiopia for other crops such as legumes (Ruelle et al., 2019). Varietal mixture composition was made in order to meet the differential food grain preferences of household members. The agronomic reasons for the use of varietal mixture include stable yield, reduced lodging, diverse maturity groups for minimization of moisture stress risk, confusing birds attack and improved soil fertility utilization. The gastronomic reasons were taste, baking quality, digestibility and diversity of diet. The different secondary uses were feed, fuel wood and construction materials. Several previous studies have shown that many farmers prefer sorghum due to its cultural practices and end uses (Barnaud et al., 2007; Missihoun et al., 2012; Muui et al., 2013; Mekbib et al., 2009).

Dynamics of on-farm seed selection

In each cropping season, the household head is the

Table 2. Local varieties and corresponding seed quality parameters.

Local variety	Seed characteristics	Farmers target	Maturity period (month)
Elmi-jama	White	High yielder and bird resistance	6
Ahmed Said	Red seed colour	Low yield and bird resistance	4
Wagara	Pure white and large head panicle	High yielder and not bird resistance	5
Asse	Red color and	Low yield and bird resistance	3
Adengab	White	Low resistance	5.5

Table 3. Sorghum seed selection based on panicle length and panicle weight.

Kebele	Village	Local name of sorghum	Panicle length (cm)	Panicle weight (g)
Haroresa	Debelweyni	Elmi-jama	12.5	43.39
Haroreys	Gutale	Elmi-jama	11.5	89.17
Aliwalle	Dinga	Ahmed seid	10.83	75.43
Kuramatana	Kontame	Elmi-jama	22	151.6
Welago	Turuad	Elmijama	12.5	96.59
2nd Turuad	Turuad	Adengab	12.5	157

decision-making unit (mainly the household head) a cultivar which type and how much seeds of a given variety apply to a plant. Seed selection take place at different times, for instance, prior to the harvest, at the time of harvest, after the harvest, at different places e.g. in the field, at a drying or storage facility, or in the home. Table 2 illustrates the farmers' on-farm seed selection parameters for each local variety. Likewise, Bellon (1996) reported how farmers decided to maintain a pool of genetic resources since the beginning of crop domestication. The quality parameters such as seed color, bird resistance and days to maturity were the main on-farm seed selection criteria. On top of this, the on-farm selection practices of agro-pastoralists were found to include leaf main vein colors (white, yellow, reddish brown), ever green stalk indicator for drought tolerance and uses as fodder, bent panicle indicator for bird resistance, healthy stalk indicator for tolerance to stalk borer. Interestingly, agro-pastoralists in the study areas have had enormous indigenous experience on diversity of sorghum seed selection and promoting local sorghum varieties for a decade. The farmers were found to be practicing several crop improvements approaches such as introduction, simple mass selection, modified mass selection, modified bulk selection, and pure line selection. This indicates that, the sorghum agro-biodiversity in the study area is highly dynamic and strongly associated with livestock production. This revealed the significance of local knowledge and suggests the consideration of small scale-farmers interests in seed system improvement (Berg,1993; Seboka and Hintum van, 2006).

The seed selection diversity criteria detected in these study villages has paramount significance for the establishment of on-farm conservation programmes; however, it should be well analyzed using biodiversity indices. Similarly, diversity of local variety maintenance practices was reported in Alamata and Raya-Azebo woredas at nothern Ethiopia by Yemane et al. (2009) and in eastern Ethiopia by Mekbib et al. (2009). Teshome et al. (2007) reported that farmers in south Welo were using intra- and inter-specific crop diversities in their field, and as a result, over 30 different sorghum landraces were found in a single field. This practices could also allow the farmers to exploit different microclimates and derive multiple nutritional values and harvest security in times of unpredictable environmental stress. This finding was in agreement with previous report of Brush and Meng (1998), in which crop mixture is purposively practiced for cultural reasons, tastes, gifts, local identity, and for market preference.

Sorghum yield indicators used for seed selection

It was known that the selection of local varieties for seed is usually based on several criteria. Among these, panicle length and panicle weight are predominantly used in our study area. Panicle length and panicle weight were sorghum yield components strongly correlated with sorghum yield. It was obvious that the agro-pastoralists recognized the importance of these traits and included it in their seed selection criteria. The highest panicle length was observed for 'Elmi-jama' grown in Kuramatana, whereas that of panicle weight was observed for 'Adengab' grown at 2nd Turuad (Table 3). Both local varieties have a characteristic of long days to maturity with availability of soil moisture (Table 2). The majority of respondent farmers had begun selection before harvesting for a number of traits such as big and long

Table 4. Physical purity of sorghum seed samples obtained from agro-pastoralist storage.

District	Parameter	
	Physical purity (%)	Hundred seed weight (g)
Gursum	84.58	3.51
Jijiga	89.92	2.78

panicles, early maturing types, straw quality, disease free and good tiller capacity. They also exercise based on indicators selection of morpho-types from other farmers' field through careful day-to-day observation of plant morphology at farmers' field and obtain access by making an agreement before harvesting. A number of characters are also mentioned upon which farmers focus when selecting individual plants after harvesting and during storage, such as yield, bigger seed size and colour.

Sorghum seed system in the target area

This study reveals that the informal seed system is dominantly operated in the area. The sorghum seed used for planting could be either own saved or seed obtained from relatives and from other informal networks. The informal seed exchange system enhances the resilience of sorghum production to unpredicted weather such as increased temperatures and diminished rainfall occurring in the areas which resulted in crop failures. In the study areas, seed production was observed as an integral part of grain production. Seed quality controls were also purely informal and solely based on belief and trust between farmers.

The farmers and agro-pastoralists in the study area also obtained seeds from various sources, such as exchange, neighbours and market, through payment in cash. The flow of seeds of named varieties from nearby spatial scales and villages was evident in this study. For instance, there was much similarity between the names of sorghum varieties grown in both Jijiga and Gursum districts and even eastern Ethiopia (Mekbib et al., 2009), and as the areas are close to one another, the informal seed exchange as part of the local network might cause similarity of sorghum local names. For instance, in bad seasons where drought and birds attack led to crop damage, seed saving may totally fail and seeds may be obtained through market networks with reliable source.

Farmers/agro-pastoralists in the study area use their own farmer-saved seeds (unless unpredicted factors such as drought cause complete crop failure) although they may obtain seeds through exchange, gift or purchase. On the other hand, farmers' practice of exchanging seed lots for the same named varieties across different large spatial scales has been noted in a number of studies (Almekinders et al., 1994), though an assessment of the direction of the seed flow, the structure of the genetic diversity within the landraces as well as the ethno-botanical knowledge associated with the landraces at respective sites is deemed important for better understanding and utilization of the landraces. Moving landraces within and/or across similar ecological zones could be a powerful way of improving yield production stability. Seed exchange network can be established as a means of facilitating access to locally adapted sorghum genetic resources. However, this may require the establishment of mini-community seed banks (satellite seed banks) designed and managed by farmers themselves. The satellite community seed banks could facilitate mobilizing masses of useful local germplasms at faster rate and can reduce transaction costs.

In our study, majority of the farmers/agro-pastoralists responded to retain their produce and depend on their own seeds; however, during bad season, exchange seeds and sources of named varieties in kinds, either from neighbours, relatives and markets exists along with seed aid. This was probably due to lack of modern varieties that suits their local environment or farmers criteria and that were the main reasons causing reluctance to use and rather stick to their own genetic resources adapted to their locality.

From the focus group discussion, it was noted that women farmers play the leading role in cleaning of stored seeds. The main storage systems used were plastic bags, storage jars and underground pits. However, underground pit storage is mainly used for grains, even though few farmers are storing part of their seed with farmers witnessing severity of mold damage. In our previous study, we identified that the underground storage pit affected the seed quality attributes including germination and market preference (Mulu and Belayneh, 2016). Interesting seed storage practices explored in our study includes mixing sorghum seed with common bean seed to confuse the pests and minimize the damage from storage pest.

Physical seed purity analysis

The physical purity and hundred seed weight of local varieties seeds obtained from storage were illustrated in Table 4. The physical purity of seeds obtained from Jigjiga district (89.92%) was higher than the one collected

Table 5. Germination percentage of sorghum seed samples collected from on farm storage.

District	Villages	Germinated (n=48)	Germination (%)
Gursum	Kuramatana	41	85.42
	Adade	39	81.25
	Adade2	42	87.50
	Welago	29	60.42
	Adade	43	89.58
	Kuramatana2	20	41.67
		Mean	86.99
Jijiga	Tururwad	29	60.42
	Haroreys	18	37.50
	Tururwad 2nd	35	72.92
	Haroreys 2nd	6	12.50
		Mean	35.77

from Gursum district (84.58%). Conversely, higher hundred seed weight was observed for Gursum districts. The physical purity analysis indicated that the contamination with panicle residue appeared to be the major impurity observed in the study samples.

Physiological quality

Seed germination of seeds varied across the districts. Seed samples collected from Gursum exhibited relatively better germination (86.99%) than those obtained from Jigjiga districts (35.77%) (Table 5). However, germination percentage of seeds produced in Jijiga district systems did not fulfil the national standard set (85%) for sorghum seed in Ethiopia. Germination percentages of seed samples collected from different villages were considered; those from Adade (89.58%), Adade (87.5%) and Kuramatana (85.42%) fulfilled the national seed standard whereas none of those seed samples were collected from Jijiga districts (35.77%). Seed samples that had not shown germination percentage was 90%. About 66% of the seed samples had a germination capacity of within 80% for Gursum district. Nonetheless, if more than one quarter of seeds planted by farmers is not viable, then this poses a threat to food security in the region and should be an area of concern. More so, it is not usually true that all seed lots exceeding “the critical minimum germination” are equally good in the eventual test of quality and emergence in the field. This is because, the lower the germination, the poorer the performance since deterioration has occurred even though all lots met the minimum germination recommendation. While it is sometimes possible to compensate for reduced germination by increasing sowing rates so as to achieve a desired population as practiced by many farmers in the district, a point is reached where there can be deleterious effects on yield and quality.

The results of seed quality test reveal that more than one quarter of sorghum seeds used for planting were inadequate in quality parameters including physical seed quality and physiological germination test. This proportion of seed with inadequate quality can lead to poor crop stand and generation of inferior seed quality.

Conclusion

Indigenous seed selection practiced in Fafen Zone has been contributing to enhancement of sorghum genetic resources pool. The contributions of farmers/agro pastoralists are critical to the conservation, use and enhancement of biodiversity. The two districts farmers managed to maintain more than six locally named varieties. Many of the sorghum local varieties are exquisitely fitted to the specific niches and highly associated with the livelihood of the crop livestock farming systems. However, the seed quality is very poor and below national standard. Furthermore, seed quality comprised of more quality aspects and, therefore, it is recommended that further research has to be conducted on storage, seed health and genetic aspects to enable the clarification of the extent to which seed quality affects crop production. In order to make indigenous sorghum seed selection sustainable, it is imperative to take farmer seed selectors as partners in the research extension programs and improve the seed storage mechanisms.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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Characters association and path coefficient analysis of orange fleshed sweetpotato [*Ipomoea batatas* (L.) Lam.] genotypes evaluated in Hawassa, Ethiopia

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The experiment was conducted to assess associations between root yield and yield- related traits of orange-fleshed sweetpotato genotypes to identify traits that have maximum effect on root yield of sweetpotato to make possible selection. Twenty-four Orange Fleshed Sweetpotato genotypes were evaluated in 2017 main cropping season at Hawassa Agricultural Research Center using a Randomized Complete Block Design (RCBD) with three replications. Data were collected from 12 traits, and then subjected to analysis of variance (ANOVA), correlations and path coefficient analysis. The estimation of characters associated revealed that storage root yield was positively and significantly associated with roots number per plant, root length, root girth, harvest index at both genotypic and phenotypic levels. Some of the traits showed a highly significant ($p<0.01$) positive genotypic and phenotypic correlations while the other traits showed significant negative correlations. The genotypic correlation coefficients were higher than phenotypic correlation coefficients in magnitude indicating fairly strong inherent association between the characters studied. Path analysis revealed that roots number per plant, root girth and harvest index had positive direct effects on storage root yield at both phenotypic and genotypic levels. Based on the results of current study, traits that showed a positive direct effect on storage root yield could be used as the best predictors of storage root yield in sweetpotato improvement program.

Key words: Character association, correlation coefficients, path coefficient, sweetpotato.

INTRODUCTION

Orange fleshed sweetpotato [*Ipomoea batatas* (L.) Lam.] is a rich source of β-carotene and has a large potential in fighting against vitamin A deficiency (VAD) in human diet in developing countries (Chassy et al., 2008; Burri, 2011). Previous reports by WHO (2009) and Tsegaye et al. (2010) indicated that VAD is a serious public health problem happening mainly among children and women of childbearing age in Ethiopia. In this regard, orange-fleshed sweet potato (OFSP) is an invaluable crop for fighting against vitamin A deficiency in sub-Saharan Africa countries like Ethiopia (Tumwegamire et al., 2004; Low et al., 2009; Gurmu et al., 2015). Storage roots are

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commonly the edible part of sweetpotato. Since the storage root yield is a complex trait with low heritability, it requires the knowledge on the nature and magnitude of correlations between important traits to make possible direct or indirect selection for improvement of the crop (Gurmu et al., 2017). In sweetpotato, root flesh colour directly correlates with root β-carotene content, where root dry matter content negatively correlated with root β-carotene content (Gurmu et al., 2017). The authors also explained the importance of having knowledge on the number of traits to be evaluated and magnitude of their correlations for indirect selections. More to the point, correlation analysis provides information about the degree of relationship between important plant traits and is also a good index to predict yield response in relation to the change of a particular character. When higher numbers of variables are considered in correlation, the association becomes more complex.

Path coefficient analysis is a reliable statistical technique which provides means not to quantify the interrelationships of different yield components but also indicates whether the influence is directly reflected in the yield or takes some other pathway for ultimate effects (Dewey and Lu, 1959). Therefore, this research was conducted to demonstrate the association among various characters and identify traits that have maximum effect on root yield of orange fleshed sweetpotato genotypes.

MATERIALS AND METHODS

Description of the experimental site

The experiment was conducted during the 2017 under rain-fed condition at Hawassa Agricultural Research Center (HwARC). HwARC is located in Hawassa city ($7^0$04´N, $38^0$31´E, 1700 m above sea level with the average annual rain fall of the area 1141 mm, minimum/maximum air temperature is 13.1/27.1^{0}C respectively), the capital of Southern Nations, Nationalities, and Peoples' Regional State (SNNPRS), in the southern part of Ethiopia. The soil is volcanic in origin and is classified as Vitric Andosol which is suitable for sweetpotato production.

Experimental materials

Twenty four orange fleshed sweetpotato genotypes were used for the study, among which two released varieties in Ethiopia included as checks (Kulfo and Tula). The four genotypes are advanced lines from HwARC crosses and the rest are introduced varieties from Kenya, Uganda and Mozambique. The description of the genotypes is shown in Table 1.

Experimental design and field management

The experiment was arranged in Randomized Complete Block Design (RCBD) having three replications. There were three blocks each consisting 24 plots. A plot size was 7.2 m^2 with 3 m long and 2.4 m width. Each plot consisted four rows (ridges), with ten plants per a row. The spacing between rows and between plants within row was 60 and 30 cm, respectively. The spacing between blocks was 2 m. Ten holes per row and 40 per plot were prepared and one vine cutting (plant) of 30 cm length was planted in each hole of the row (ridge). The trial was planted on 8 August, 2017. All plots received the recommended cultural practices uniformly and no fertilizer was applied. Replanting was done to substitute the dead vine after one week of planting. Hilling up was done after fourth week of planting and all plots were kept weed free by regular weeding and cultivation. Harvesting was done on 28 December, 2017 after sweetpotato leaves changed to yellowish color. Two central rows were used for data recording by excluding the two plants grown at both ends of the row and the two border rows.

Data collection

The data were recorded on the following parameters: vine length (cm), vine inter-nodal length (cm), mature leaf length (cm), vine girth (mm), petiole length (cm), ground coverage (%), number of storage roots per plant, storage root length (cm), storage root girth, aboveground fresh weight (t ha^{-1}), marketable yield (t ha^{-1}), unmarketable yield (t ha^{-1}), total storage root yield (t ha^{-1}), sweetpotato virus disease (SPVD), predominant skin colour, predominant flesh colour , β-carotene content, root dry matter content (RDMC), and harvest index (HI).

$$\text{Harvest Index} = \frac{\text{Economical Yield}}{\text{Biological Yield}} \times 100$$

$$\text{Yield per hectare in tones} = \frac{\text{Yield per net plot (kg) x 10,000}}{\text{Net area of the plot (m}^2\text{) x 1000}}$$

Data analysis

Correlation analysis

Phenotypic and genotypic correlations were computed following the method described by Singh and Chaudhary (1985) as:

$$r_g = \frac{Ccovx.y}{\sqrt{\sigma^2 gx.\sigma^2 gy}}$$

$$r_p = \frac{Pcovx.y}{\sqrt{\sigma^2 px.\sigma^2 py}}$$

where r_p and r_g are phenotypic and genotypic correlation coefficients, respectively; Pcovx.y and g covx.y are phenotypic and genotypic covariance between variables x and y, respectively; σ2px and σ2gx are phenotypic and genotypic variances for variable x and y, respectively.

$$\text{SE (rp)} = \sqrt{\frac{1-r^2p}{n-2}}$$

where n is the number of genotypes tested, r2p is phenotypic correlation coefficient, SE (rp) = standard error of phenotypic correlation.

The calculated phenotypic correlation values were tested for its significance using t-test:

$$t = \frac{rp}{SE(rp)}$$

The calculated "t" values were compared with the tabulated "t" value at (n-2) degree of freedom at 5% level of significance. Where n is number of genotypes.

$$\text{SErgxy} = \sqrt{\frac{1-r^2gxy}{\text{h2x}} . \text{h2y}}$$

The coefficients of correlations at genotypic levels were also tested for their significance by the formula described by Robinson and Comstock (1955) indicated as follows:

Table 1. List of genotypes used for the study.

No.	Genotypes	Source	Status	Year of release
1	Ukr/Eju-10	HwARC cross	Advanced line	Not yet released
2	Ukr/Eju-13	HwARC cross	Advanced line	Not yet released
3	Res/Tem-14	HwARC cross	Advanced line	Not yet released
4	Res/Tem-23	HwARC cross	Advanced line	Not yet released
5	Jewel	CIP-Kenya	Released abroad	1995
6	Carrot Dar	CIP-Kenya	Released abroad	1995
7	Maputha-1	CIP-Kenya	Released abroad	1995
8	Vita	CIP-Uganda	Released abroad	2007
9	Kabode	CIP-Uganda	Released abroad	2007
10	Naspot-12	CIP-Uganda	Released abroad	2013
11	Naspot-13	CIP-Uganda	Released abroad	2013
12	Tainung-15	CIP-Kenya	Released abroad	1995
13	Carrot C	CIP-Kenya	Released abroad	1995
14	Mayai	CIP-Kenya	Released abroad	1995
15	Kyoyabwerere	CIP-Kenya	Released abroad	1995
16	RW11-4743	CIP-Kenya	Released abroad	1995
17	Tomulabula	CIP-Kenya	Released abroad	1995
18	Wagabolige	CIP-Kenya	Released abroad	1995
19	Melinda	CIP-Mozambique	Released abroad	2011
20	Cacilia	CIP-Mozambique	Released abroad	2011
21	Gloria	CIP-Mozambique	Released abroad	2011
22	Jane	CIP-Mozambique	Released abroad	2011
23	Kulfo	Ethiopia	Released in Ethiopia	2005
24	Tula	Ethiopia	Released in Ethiopia	2005

HwARC = Hawassa Agricultural Research Center, CIP = International Potato Center.

$$t = \frac{rgxy}{\text{SErgxy}}$$

where h2x = Heritability of trait x and h2y = Heritability of trait y, SErgxy= standard error of genotypic correlation for character x and y. All the analysis was done using SAS software version 9.0.

Path coefficient analysis

Path coefficient analysis provides an effective way of finding out direct and indirect sources of correlations and identifies the most reliable yield contributing traits. It is computed using the method suggested by Dewey and Lu (1959) using Microsoft Excel 2010. Thus, correlation coefficient of different characters with storage root yield was partitioned into direct and indirect effects adopting the following formula:

riy = r1ipi + r2p2 +…+ r1ipi +…rnipn

where riy is correlation of ith character with storage root yield; r1iPi is indirect effects of ith character on storage root yield through first character; rni is correlation between nth character and ith character; n is number of independent variables; Pi is direct effect of ith character on storage yield; Pn is direct effects of nth character on storage root yield.

Direct effect of different component characters on storage root yield was obtained by solving the following equations:

(riy) = (pi) (rij); and (pi) = (rij)-1(r1ipi)

where (Pi) is matrix of direct effect; (rij) is matrix of correlation coefficients among all the nth component characters; (riy) is matrix of correlation of all component characters with storage root yield; (r1iPi) is indirect effect of ith character on storage root yield through first character.

RESULTS AND DISCUSSION

Genotypic and phenotypic correlations

Phenotypic and genotypic correlation coefficient between root yield and its 12 component traits in all possible combinations are presented in Table 2. Traits such as harvest index r_p=0.82, r_g=0.83, number of roots per plant r_p=0.84, r_g=0.84, marketable root yield r_p=0.91, r_g=0.97, unmarketable root yield r_p=0.49, r_g=0.56 showed a highly significant (P<0.01) and a significant (P<0.05) positive phenotypic and genotypic correlation was observed by root length r_p=0.45, r_g=0.49 while sweetpotato virus disease showed significant (r_p=-0.33 and r_g=-0.34) negative correlations. Root dry matter content, root beta-carotene content and root flesh colour exhibited non-significant correlations. In general, the genotypic correlation coefficients were higher than the phenotypic correlation coefficients in magnitude, indicating fairly

Table 2. Genotypic (above diagonal) and phenotypic (below the diagonal) correlation coefficients among nine traits in 24 OFSP genotypes.

Trait	SPVD	RL	RG	AGFW	HI	RDMC	RBCC	FC	NRP	MRKY	UMRKY	TYLD
SPVD		-0.23^{ns}	-0.21^{ns}	-0.29*	-0.14^{ns}	-0.06^{ns}	0.30*	0.17^{ns}	-0.24*	-0.35*	-0.14^{ns}	-0.34*
RL	-0.20^{ns}		0.12^{ns}	0.36*	0.26*	0.61***	-0.03^{ns}	0.07^{ns}	0.52***	0.44**	0.40*	0.49**
RG	-0.20^{ns}	0.22^{ns}		0.02^{ns}	0.36*	-0.18^{ns}	-0.22^{ns}	0.09^{ns}	0.36*	0.48***	-0.05^{ns}	0.41*
AGFW	-0.25*	0.32*	0. 04^{ns}		-0.45***	0.32*	-0.34*	-0.22^{ns}	0.04^{ns}	0.07^{ns}	0.08^{ns}	0.08^{ns}
HI	-0.16^{ns}	0.23^{ns}	0.31*	-0.43**		-0.14^{ns}	0.16^{ns}	0.25*	0.74***	0.80***	0.51***	0.83***
RDMC	-0.04^{ns}	0.48***	-0.14^{ns}	0.26*	-0.13^{ns}		-0.01^{ns}	-0.10^{ns}	0.07^{ns}	-0.02^{ns}	0.26*	0.05^{ns}
RBCC	0.24*	-0.02^{ns}	-0.16^{ns}	-0.29*	0.15^{ns}	-0.01^{ns}		0.78***	-0.13^{ns}	0.09^{ns}	-0.23^{ns}	0.02^{ns}
FC	0.14^{ns}	0.06^{ns}	0.06^{ns}	-0.09^{ns}	0.20^{ns}	-0.09^{ns}	0.75***		-0.02^{ns}	0.18^{ns}	-0.02^{ns}	0.15^{ns}
NRP	-0.24*	0.53***	0.33*	0.07^{ns}	0.59***	0.04^{ns}	-0.10^{ns}	0.00^{ns}		0.82***	0.47***	0.84***
MRKY	-0.32*	0.44***	0.36*	0.13^{ns}	0.76***	-0.03^{ns}	0.09^{ns}	0.18^{ns}	0.68***		0.34*	0.97***
UMRKY	-0.15^{ns}	0.20^{ns}	0. 08^{ns}	0.02^{ns}	0.46***	0.20^{ns}	-0.19^{ns}	-0.03^{ns}	0.23^{ns}	0.21^{ns}		0.56***
TYLD	-0.33*	0.45***	0. 34*	0.12^{ns}	0.82***	0.03^{ns}	0.02^{ns}	0.15^{ns}	0.67***	0.91***	0.49**	

*, ** and ***denote significant correlations at 0.05, 0.01 and 0.001 probability levels, respectively; ^{ns}Not significant, SPVD = Sweetpotato virus diseases, RL = Root length, RG = Root girth, AGFW= above ground fresh weight, HI = Harvest index, RDMC = Root dry matter content, RBCC = root beta carotene content, FC = Flesh colour, NRP = number of storage roots per plant, MRKY Marketable storage roots yield, UMRKY = Unmarketable storage roots yield, TYLD = Total storage root yield.

strong inherent association between the characters studied.

Total storage root yield had highly significant positive correlations with number of roots per plant, root length, root girth, harvest index, marketable root yield and unmarketable root yield, at both genotypic and phenotypic levels. The increase in positively correlated traits would increase the root yield in sweetpotato plant. The existence of the positive correlation between storage root yield and other traits suggest that the traits could be used as selection criteria for high storage root yield of sweetpotato (Gurmu et al., 2015, 2017; Gasura et al., 2008). Similar results have also been reported by Abdissa et al. (2012) who explained the positive and highly significant correlations among total storage root fresh weight and marketable tuberous root yield, unmarketable tuberous root yield and tuberous root number per plant, indicating the presence of a close relationship among these parameters in sweetpotato. Jha (2012) also reported the positive correlations of root yield per plant with biological yield per plant, harvest index and root diameter. The author suggested that selection for component traits may increase the root yield of sweetpotato. Also, in addition, Yohannes et al. (2010) reported that total storage root yield had significant and positive association with marketable storage root yield and average storage root weight of sweetpotato. The flesh colour and β-carotene content showed a strong positive correlation (r=0.78 and r=0.75), respectively, at both genotypic and phenotypic levels. Thus, the existence of a strong positive correlation between flesh colour and β-carotene content suggests that storage root flesh colour can be used as a selection means of sweetpotato genotypes for high β-carotene content, particularly, during early screening of large progenies (to reduce handling of huge number of genotypes, economize space and other resources). The current results are in line with previous works that have been reported by various authors (Gurmu et al., 2017; Burgos et al., 2009; Vimala and Hariprakash, 2011).

Number of roots per plant had a strong positive association with root length, harvest index and marketable root yield, at genotypic and phenotypic levels. This indicates selection based on these traits would improve the total storage root, since these traits are the most important components of total storage root yield (Tadesse, 2006; Gurmu et al., 2015, 2017). Total storage root yield had negative correlation with SPVD, indicating the damaging effects of diseases severity on the total storage root yield. Similarly, Mekonnen et al. (2014) reported in their previous work a negative correlation between fresh root yield and SPVD with emphasis to the damaging effects of the disease on sweetpotato in Ethiopia. On the other hand, highly significant negative correlation was observed between harvest index and aboveground fresh weight (-0.43). This may signify that a genotype that possesses vigorous vegetative growth tends to produce less storage roots, which in turn imply the presence of competition between the shoots and roots for photosynthates (Tsegaye et al., 2006), a trait contributed to reasonable distribution structure of photosynthates that led to the high root yield of sweetpotato (Chen, 1965).

Genotypic path analysis of various traits on storage root yield

The path-coefficient analysis showed that harvest index and aboveground fresh weight had maximum positive

Table 3. Genotypic direct (bold diagonals) and indirect effects of yield contributing nine traits in 24 OFSP genotypes.

Traits	SPVD	RL	RG	AGFW	HI	RDMC	RBCC	FC	NRP	r_g
SPVD	**-0.063**	0.004	-0.013	-0.155	-0.133	-0.001	0.041	-0.012	-0.020	-0.34*
RL	0.014	**-0. 180**	0.007	0.196	0.249	0.013	-0.004	-0.005	0.043	0.49**
RG	0.014	-0.002	**0.060**	0.011	0.348	-0.004	-0.031	-0.006	0.029	0.41*
AGFW	0.018	-0.007	0.001	**0.542**	-0.437	0.007	-0.047	0.015	0.003	0.08
HI	0.009	-0.005	0.021	-0.243	**0.975**	-0.003	0.023	-0.017	0.060	0.83***
RDMC	0.004	-0.011	-0.011	0.171	-0.136	**0.502**	-0.002	0.007	0.006	0.05
RBCC	-0.019	0.001	-0.013	-0.183	0.159	0.000	**0.140**	-0.650	-0.011	0.08
FC	-0.011	-0.001	0.006	-0.121	0.242	-0.002	0.610	**-0.069**	-0.001	0.15
NRP	0.015	-0.010	0.022	0.022	0.6 24	0.002	-0.019	0.001	**0.591**	0.84***

SPVD = Sweetpotato virus diseases, RL = root length, RG = root girth, AGFW= above ground fresh weight, HI = harvest index, RDMC = root dry matter content, RBCC = root beta carotene content, FC = flesh colour, NRP = number of storage roots per plant, rg=genotypic correlation.

direct effects of 0.975 and 0.542, respectively on total storage root yield (Table 2). Harvest index exhibited a negative indirect effect through aboveground fresh weight (-0.243). Thus, the effect of harvest index on total storage root yield was not only due to its direct positive effect but also due to its negative indirect effect by influencing other characters such as aboveground biomass (Tsegaye et al., 2006). These two traits (harvest index and aboveground fresh weight) were also significantly and negatively correlated (rg=-0.43). Similar results have been reported by Gurmu et al. (2017) in their previous study. Traits such as number of roots per plant and root dry matter content exerted positive direct effects on total storage yield with values of 0.591 and 0.502, respectively, at genotypic level. Number of roots per plant also exerted a high positive indirect effect (r=0.624) through harvest index on total storage root yield, because harvest index was the ratio of storage root yield per total plant biomass. Thus, this implies that the higher storage root number and greater proportion of assimilate translocation to the storage root contributed to an increase in the fresh weight and subsequent biomass production (Borhan et al., 2016).

The highly positive indirect effect of number of roots per plant through HI contributed more to its highly significant positive correlation with total storage root yield. RBCC exerted negligible positive direct effect (0.140) on total storage root yield. This trait had highly positive correlation with root flesh color (r=0.78). The existence of a strong positive correlation between flesh colour and Gurmu et al. (2017) β-carotene content in sweetpotato was previously reported by other authors (Burgos et al., 2009; Vimala and Hariprakash, 2011). Gurmu et al. (2017) reported the relationship between flesh colour and β-carotene content in sweetpotato genotypes and observed a high correlation of r=0.76, which is similar to the results of the current study between flesh colour and r=0.61. Hence, root flesh colour can be used as selection criterion for high β-carotene content in sweetpotato genotypes. Root dry matter content was another trait which exerted positive direct effect (0.202) on total storage root yield (Gurmu et al., 2017). Similarly, root length, which exhibited highly significant correlation with total root yield, showed negative direct effect (-0.180) on total storage root yield. Conversely, flesh color, which has no correlation with total storage root yield, exerted negative direct effect (-0.069) on total storage root yield (Table 3). Traits that have negative correlations or no correlations with yield might exert a positive direct effect on yield (Gurmu et al., 2017). The negative correlation observed between SPVD and total storage root yield showed that this trait exerted negative direct effect (-0.063) on total storage yield; implying when SPVD severity increases, the total storage yield tends to decrease. This finding is in agreement with the work of Mekonnen et al. (2014) who reported a negative correlation between storage root yield and SPVD which was expected as SPVD is a damaging disease complex of sweetpotato in Ethiopia.

Phenotypic path analysis of various traits on storage root yield

Similar to the results observed at genotypic level, harvest index showed the maximum positive direct effect (0.94) on total storage root yield at phenotypic level (Table 4). This trait also exerted high negative indirect effect through aboveground fresh weight (-0.256). However, this negative indirect effect was compensated by the highest positive direct effect, ensuring high positive correlation between harvest index and total storage root yield (Tsegaye et al., 2006). Similarly, aboveground fresh weight yield and number of roots per plant also exhibited relatively the highest positive direct effect (0.795, 0.691), respectively, on total storage root yield. Even though, aboveground fresh weight had no correlation coefficient with total yield, it influenced total storage yield indirectly through other character. Thus, aboveground fresh weight and number of roots per plant could be used as indirect selection means for total storage root yield in sweetpotato.

Table 4. Phenotypic direct (bold diagonals) and indirect effects of yield contributing nine traits in 24 OFSP genotypes

Trait	SPVD	RL	RG	AGFW	HI	RDMC	RBCC	FC	NRP	r_p
SPVD	**-0.026**	-0.005	0.000	-0.149	-0.171	0.000	0.025	-0.012	0.003	-0.33*
RL	0.005	**-0.023**	0.000	0.190	0.246	-0.002	-0.002	-0.005	-0.006	0.45***
RG	0.005	0.005	**0.001**	0.024	0.331	0.001	-0.017	-0.005	-0.004	0. 34*
AGFW	0.006	0.008	0.000	**0.795**	-0.459	-0.001	-0.031	0.008	-0.001	0.12^{ns}
HI	0.004	0.005	0.000	-0.256	**0.94**	0.000	0.016	-0.018	-0.007	0.82***
RDMC	0.001	0.011	0.000	0.155	-0.139	**0.201**	-0.001	0.008	0.000	0.03^{ns}
RBCC	-0.006	0.000	0.000	-0.173	0.160	0.000	**0.106**	-0.066	0.001	0.02^{ns}
FC	-0.004	0.001	0.000	-0.054	0.214	0.000	0.080	**-0.089**	0.000	0.15^{ns}
NRP	0.006	0.012	0.000	0.042	0.630	0.000	-0.011	0.000	**0.691**	0.67***

SPVD = Sweetpotato virus diseases, RL = root length, RG = root girth, AGFW= above ground fresh weight, HI = harvest index, RDMC = root dry matter content, RBCC = root beta carotene content, FC = flesh colour, NRP = number of storage rootsper plant, r_p= phenotypic correlation.

Root dry matter content, root beta carotene and root girth also exerted slightly positive direct effect on total storage root yield, with path coefficients of 0.201, 0.106 and 0.001, respectively (Table 4). This is partially in agreement with the report by Gurmu et al. (2017). SPVD, root length and flesh colour showed negative direct effect of -0.026, -0.023 and -0.089, respectively, on total storage root yield. In the current study, at phenotypic level, most of traits showed similar trends of direct and indirect contribution to the total storage root yield as indicated at genotypic level, except the differences in the extent of the contribution (Tables 3 and 4).

Conclusion

This study showed that the presence of extensive genetic variation among sweetpotato genotypes for all traits tested. The existence of the positive correlation between storage root yield and other traits suggests that the traits could be used as selection criteria for high storage root yield of sweetpotato Also, a negative correlation between storage root yield and SPVD severity at both genotypic and phenotypic levels indicated the damaging effects of diseases severity on the storage root yield of sweetpotato. The path analysis revealed that root number per plant, root girth and harvest index had direct positive effect and indirect positive effect through influencing other traits on storage root yield at both genotypic and phenotypic levels. These traits could be used as indirect selection means in sweetpotato storage root yield improvement. Therefore, the traits that showed high positive correlation and direct effects on storage root yield can used as a tool to make possible selection in sweetpotato improvement.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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Association and interrelationship of yield and agronomic characters in coffee (*Coffea* sp L)

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Coffee is an important commodity in the international market. However, little attention is given to it and its breeding research in Nigeria. This has resulted to low production and foreign earning. The information on relationship between yield and yield- related characters is an excellent and significant tool for breeding. The experiment was conducted on Cocoa Research Institute of Nigeria coffee germplasms. The objectives of this study were to determine the genetic relationship and identify traits that have a direct and indirect effect on yield of coffee. A total of 45 coffee genotypes were studied during 2016/2017 cropping season. The data were subjected to correlation coefficients and regression analyses. The result revealed significant (P<0.05) correlation among traits. Weight of seed per tree (actual yield) has strong and positive correlation with trunk height, leaf length, leaf width, stiple arista length, number of flower per axil, number of flower per fascicle, berry width, berry thickness, 100 berry weight, 100 seed weight, and weight of berry per tree. Weight of berry per tree, plant height, number of flower per axil and number of fascicle per node were the predictors and accounted for 94% of the variation observed and therefore be given serious consideration in coffee breeding programmes.

Key words: Coffee, germplasm, yield, characters, correlation, stepwise regression.

INTRODUCTION

Coffee is one of the most economically important beverage crops, and it stands second only to crude oil in terms of international trade on the world market. It is originated from tropical Africa where wild populations occur abundantly in the tropical regions (Berthaud and Charrier, 1988; Maurin et al., 2007). Its production is fundamental in over 50 developing countries for which it is the main foreign currency earner. In many producing countries, besides contributing a tremendous amount to the foreign exchange as main crop, it serves as a main crop for livelihood for millions of people and plays a vital role in their socio-economic life (Orozco Castillo et al., 1994; Agwanda et al., 1997; Carneiro, 1999; Anthony et al., 2001; Steiger et al., 2002). Coffee trees are evergreen which range from shrubs to trees and can grow to a height of 10 m. The stems are orthotropic and developed from aerial part of the stem. The primary branches arise in pairs opposite each other and are subsidiary to the main stem. The sub lateral branches that is, secondary, tertiary and quaternary branches

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developed from primary branches (Coste, 1992; Cliffort and Wilson, 1985). The upper side of leaves is shiny, waxy, spear-shaped, and elliptical with conspicuous vein. They grow on the side of main stem and branches in pairs with buds at the leaf stalk base. Leaf color varies. It can be greenish, yellowish, dark green, bronzed or purple tinged young flush. Leaf can be as long as 40 cm. Some trees are deciduous while others retain leaves for three or more years with a leaf area index of 7-8 for a high yielding variety (Wintgens, 2004; Ngugi and Aluka, 2017).

In developing adapted cultivars of any crop, available genetic resources of the crop are important for its improvement. The significant positive correlation coefficient, genetic advance, variability and heritability are an excellent tool to explore for genotype selection in crop improvement programme (Akbar et al., 2003, Mwenye et al., 2010). Yield is a quantitative trait that is complex because of the influence of a number of characters contributing to yield (Xie, 2015). There is need therefore to understand the interrelationships and the magnitude of characters among themselves and with the yield in order to improve the selection efficiency through a combination of suitable characters (Ahmad et al., 2013). The correlation coefficient is an imperative statistical method to evaluate breeding programs for high yield and to study direct and indirect input of the yield variables (Mohamed, 1999). Correlation may be due to phenotypic, genotypic and environmental factors.

However, traits that are not important could be eliminated through stepwise regression analysis. Stepwise regression proved to be the more resourceful predictive equation for yield (Naser and Leilah, 1993). Therefore, traits that are most important with considerable effects on yield, which is a dependable trait or variable, will be verified. The traits selected through stepwise regression analysis can be used as selection criteria in a breeding programme (Williams et al., 1990; Ogrodowczyk and Warzyniak, 2004; Sabaghnia et al., 2010). Moreover, the stepwise regression model is a technique that is used to estimate the value of a quantitative variable regarding its relationship with one or some other quantitative variables. This relation is such that it is possible to predict other changes using one variable.

Getachew (2019) in his research reported a significant and positive correlation of coffee yield with average internode length on stem, angle of primary branches, number of primary branches, stem diameter, the width of fruit, length of fruit, thickness of fruit and average length of primary branches. Percentage of bearing primary branches, hundred bean weight, leaf length, and canopy diameter also had a positive and significant correlation with coffee yield. Lemi et al. (2017), similarly reported canopy diameter, length of first primary branch, plant height have direct effect that had positive and significant on coffee. Seyoum (2003) reported his findings that the highest direct effect on coffee yield was exerted by length of the longest primary branches and angle of primary branches. All these suggested that selection, using these characters, would be of help in coffee improvement. In order to meet the demand for coffee, there is need for increase in yield per hectare. Therefore, the objectives of the study are to determine the genetic relationship and identify traits that have a direct and indirect effect on coffee.

MATERIALS AND METHODS

Forty-five coffee genotypes from Cocoa Research Institute of Nigeria (CRIN) coffee germplasms located in headquarter in Ibadan, Oyo state and two of her substations (Ibeku, Abia state and Kusuku Mambilla, Taraba state) were used for the study as represented in Table 1. The sites are situated between latitude 5.3130° and 7.3775^{0}N; and longitude 3.9470° and 11.7200°E (Figure 1). The experiment was conducted during 2016/ 2017 cropping season on existing coffee trees. The experimental design was Randomised Complete Block Design. Data were collected from 4 individual plants using a random sampling procedure. Descriptor of Coffee (IPGRI, 1996) was used for data collection. Twenty quantitative characters namely: trunk height (cm), trunk diameter (cm), number of primary branches, leaf length (mm), leaf width (mm), leaf petiole length (mm), stipule arista length (mm), number of flower per axil, number of flower per fascicle, number of fascicle per node, berry length (mm), berry width (mm), berry thickness (mm), seed length (mm), seed width (mm), seed thickness (mm), weight of berry per tree (g), 100berry weight (g), weight of seed per tree (g) (actual yield), and 100seed per tree (g) were scored on the morphology of the 45 genotypes. The quantitative characters were determined by measurement and weighing (Table 2).

Genetic parameters and association among characters

The phenotypic, genotypic and environmental correlation coefficients were estimated using the formula of Miller et al. (1958) thus:

$$r\,(x,y) = \frac{\mathrm{Cov}\,(xy)}{\sqrt{(\sigma x)^2.\ (\sigma y)^2}}$$

Where r(x,y) is either genotypic or phenotypic or environmental correlation between variables x and y; $Cov_{(xy)}$ is the covariance of variables x and y; $(\sigma_x)^2$ is either the genotypic or phenotypic or environmental variance of variable x; $(\sigma_y)^2$ is either the genotypic or phenotypic or environmental variance of variable y.

The significance of the correlation coefficients was tested using the non-directional probability in the software of Lowry (2009). Stepwise regression analysis was performed using SAS software version 9 (SAS Institute Inc. 2004.

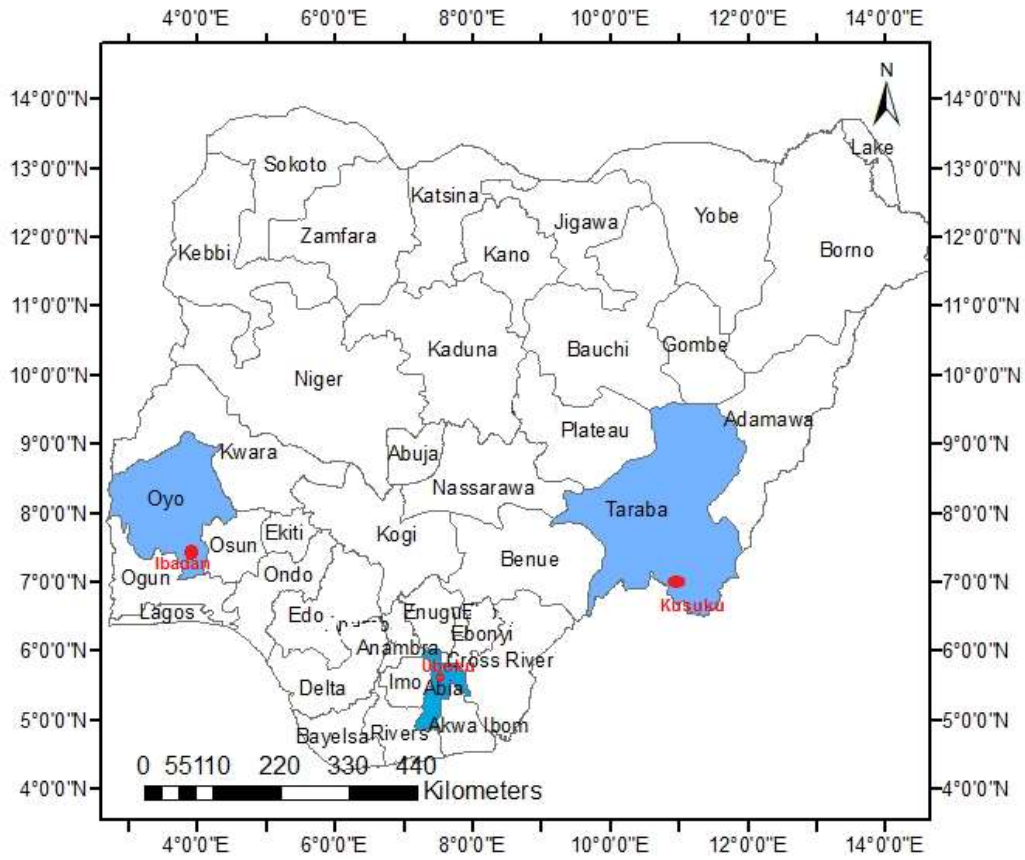
RESULTS

The result of phenotypic correlation coefficient is presented in Table 3. Trunk height had a positive correlation with trunk diameter, number of primary branches, leaf length, leaf width, leaf petiole length, stipule arista length, weight of berry per tree, 100 berry

Table 1. Information on the coffee genotypes**.**

S/N	Code	Germplasm location
1	A81	Ibadan
2	A110	Ibadan
3	C36	Ibadan
4	C96	Ibadan
5	C105	Ibadan
6	C107	Ibadan
7	C108	Ibadan
8	C111	Ibadan
9	D57	Ibadan
10	E1	Ibadan
11	E106	Ibadan
12	M10	Ibadan
13	M53	Ibadan
14	H139	Ibadan
15	T24	Ibadan
16	T204	Ibadan
17	T921	Ibadan
18	T1049	Ibadan
19	W109	Ibadan
20	TG181	Ibeku
21	TG405	Ibeku
22	TG107	Ibeku
23	TG149	Ibeku
24	TG468	Ibeku
25	TG375	Ibeku
26	TG211	Ibeku
27	TG216	Ibeku
28	TG202	Ibeku
29	TG126	Ibeku
30	C Arabica Porto Rico	Kusuku, Mambilla
31	TH-F1 12-2	Kusuku, Mambilla
32	T.992 Padang	Kusuk, Mambilla
33	Porto Rico	Kusuku, Mambilla
34	T.1997 A187	Kusuku, Mambilla
35	TH-F1 5-1	Kusuku, Mambilla
36	T,971 Guadeloupe	Kusuku, Mambilla
37	TH-F1 18-1	Kusuku, Mambilla
38	T.977	Kusuku, Mambilla
39	TH-F1 4-1	Kusuku, Mambilla
40	T.990	Kusuku, Mambilla
41	TH-F1 9-3	Kusuku, Mambilla
42	T.2000 Semper Florens	Kusuku, Mambilla
43	Nicaragua	Kusuku, Mambilla
44	T.1996 Selection Fica Flora	Kusuku, Mambilla
45	TH-F1 32-2	Kusuku, Mambilla

weight, weight of seeds per tree and 100 seed weight (r = 0.33, 0.26, 0.71, 0.80, 0.41, 0. 51, 0.34, 0.49, 0.39, and 0.52 respectively) but negatively correlated with number of flower per fascicle, seed length and seed thickness (-0.23, -0.35 and -0.42 respectively). The trunk diameter had positive significant correlation with number of primary



Ibadan……453 ft
Mambilla, Kusuku….5114 ft
Ubeku…..490 ft

Figure 1. Map of Nigeria showing the three locations where the study were carried out.

branches, leaf length, leaf width, leaf petiole length, stipule arista length and 100 berry weight (0.80, 0.22, 0.25, 0.35, 0.62 and 0.21 respectively) but negative significant correlation with berry width and berry thickness (-0.25 and -0.34 respectively). Number of primary branches had positive correlation with leaf length, leaf width, leaf petiole length, stipule arista length and seed width (0.26, 0.28, 0.46, 0.55, 0.32) but negatively correlated with berry width and berry thickness (-0.26, -0.40). Leaf length had positive significant correlation with leaf width, leaf petiole length, stipule arista length, berry width, weight of berry per tree, 100 berry weight and 100 seed weight (0.90, 0.59, 0.49, 0.24, 0.23, 0.33 and 0.41 respectively) but negative significant correlation with number of flower per fascicle, seed length and seed thickness (-0.26, -0.26 and -0.43 respectively).

Similarly, leaf width had a positive significant correlation with leaf petiole length, stipule arista length, berry width, 100 berry weight and 100 seed weight (0.55, 0.49, 0.24, 0.37 and 0.43 respectively) and negative significant correlation with number of flowers per fascicle, seed length and seed thickness (-0.27, -0.30 and 0.45 respectively). Leaf petiole length had positive significant correlation with stipule arista length and seed width (0.65 and 0.33 respectively) and negative significant correlation with number of flowers per fascicle and number of fascicles per node (-022 and 0.41 respectively). Stipule arista length had a positive significant correlation with weight of berries per tree and weight of seed per tree (0.20 and 0.21 respectively) and negative significant correlation with seed length and seed thickness (-0.20 and -0.33 respectively). Number of flowers per axil positive significant correlation with number of flowers per fascicle, number of fascicles per node, berry length, weight of berries per tree, 100 berry weights, weight of seeds per tree and 100 seed weight (0.20, 0.59, 0.20, 0.31, 0.46, 0.32, and 0.45respectively). Number of flowers per fascicle is positive significant correlation with number of fascicle per node (0.29). Number of fascicles per node had positive significant correlation with berry length, berry thickness, seed thickness, 100 berry weights and 100 seed weight (0.23, 0.25, 0.24, 0.32, and 0.34 respectively).

Berry length had positive significant correlation with

Table 2. Description of the 20 morphological characters used for the study.

S/N	Character	Descriptive value
1	Trunk height	The length from the ground level to the tip of the tree
2	Trunk diameter (cm)	Measured as a diameter of the main stem at five cm above the ground
3	Number of primary branches	Total number of primary branches counted per tree
4	Leaf length	Average of five normal (> node 3 from the terminal bud) leaves, measured from petiole end to apex
5	Leaf width	Average of five normal (> node 3 from the terminal bud) leaves, measured at the widest part
6	Leaf petiole length	Average of five normal (> node 3 from the terminal bud) petioles, measured from the base to the insertion with the blade
7	Stipule arista length	Average of five well-developed stipule arista
8	Number of flower per axil	Average number of flowers counted per axil
9	Number of flower per fascicle	Average number of flowers counted per fascicle
10	Number of fascicle per node	Average number of fascicles counted per node
11	Berry length	Average of ten normal and mature green fruits of each tree measured at the longest part
12	Berry width	Average of ten normal and mature green fruits of each tree measured at the widest part
13	Berry thickness	Average of ten normal and mature green fruits of each tree measured at the thickest part
14	Seed length	Average of ten normal beans of each tree measured at the longest part
15	Seed width	Average of ten normal beans of each tree measured at the widest part
16	Seed thickness	Average of ten normal beans of each tree measured at the thickest part
17	Weight of berry per tree	Weight of mature and riped berries per tree
18	100berry weight	Average of four samples of 100 berry weight of each tree
19	Weight of seed per tree	Weight of green beans harvested per tree
20	100seed weight	Average of four samples of 100 beans weight of each tree

Coffee descriptor (IPGR).

berry width, berry thickness, seed length, seed width, seed thickness and 100 seed weight (0.77, 0.80, 0.65, 0.44, 0.53 and 0.28 respectly). Berry width had positive significant correlation with berry thickness, seed length, seed width, and seed thickness, weight of berry per tree, weight of seeds per tree and 100 seed weight (0.88, 0.53, 0.20, 0.21, 0.32, 0.30, and 0.31 respectively). Berry thickness had a positive correlation with seed length, seed width, seed thickness weight of seed per tree and 100 seed weight (0.49, 0.26, 0.34, 0.23 and 0.27 respectively). Seed length was significantly correlated with seed width and seed thickness (0.35 and 0.69 respectively). Seed width had positive significant correlation with seed thickness, 100 berry weight and100 seed weight (0.63, 0.28, and 0.21 respectively). Weight of berries per tree had positive significant correlation with 100 berry weights, weight of seeds per tree and 100 seed weight (0.48, 0.98, and 0.45 respectively). Also, 100 berry weights had positively correlated with weight of seed per tree and 100 seed weight (0.48 and 0.91 respectively). Weight of seeds per tree had positive correlation with 100 seed weight (0.46).

Table 4 presents the genotypic correlation coefficient. Trunk height had strong, positive correlation with trunk diameter, number of primary branches, leaf length, leaf width, stipule arista length, weight of berries per tree, 100berry weight, weight of seeds per tree and 100 seed weight (0.35, 0.28, 0.75, 0.84, 0.43, 0.53, 0.37, 0.53, 0.38 and 0.55 respectively) but negative significant correlation with number of flowers per fascicle, seed length and seed thickness (-0.64, -0.37 and -0.46 respectively). Similarly, trunk diameter correlated positively with number of primary branches, leaf length, leaf width, leaf petiole length, stipule arista length and 100berry weight (0.97, 0.24, 0.27, 0.39, 0.67 and 0.24 respectively) but exhibited negative and significant correlation with number of flowers per fascicle, berry width and berry thickness (-0.43, -0.30 and -0.39 respectively) . Number of primary branches had a positive correlation with leaf length, leaf width, leaf petiole length, stipule arista length and seed width (0.29, 0.31, 0.52, 0.61 and 0.42 respectively) but negatively and significant correlation with number of flowers per fascicle, beery width and berry thickness (-0.45, -0.28 and -0.45 respectively). Leaf length had a positive correlation with leaf width, leaf petiole length, stipule arista length, berry width, seed width, weight of berries per tree, 100berry weight, weight of seeds per tree and 100seed weight (0.91, 0.60, 0.51, 0.25, 0.20, 0.24, 0.35, 0.20 and 0.45 respectively) and negative correlation with number of flowers per fascicle, seed length and seed thickness (-0.75, -0.28 and -0.46 respectively). Leaf width had positively correlated with leaf petiole length, stipule arista length, berry width, weight of berries per tree, 100berry weight, weight of

Table 3. Phenotypic correlation coefficient among twenty characters of coffee.

Character	TD (cm)	NPB	LL	LW	LPL	SAL	NFA	NFF	NFN	BL	BW	BT	SL	SW	ST	WBT	100BW	WST	100SW
TH (cm)	0.33**	0.26**	0.71**	0.80**	0.41**	0.51**	0.07	-0.23*	0.14	-0.02	0.14	0.01	-0.35**	0.05	-0.42**	0.34	0.49**	0.35**	0.52**
TD (cm)		0.80**	0.22*	0.25*	0.35*	0.62**	0.05	-0.11	-0.04	-0.15	-0.25*	-0.34**	-0.17	0.18	-0.13	0.16	0.21*	0.19	0.07
NPB			0.26**	0.28**	0.46**	0.55**	-0.04	-0.13	-0.06	-0.14	-0.26**	-0.40**	-0.04	0.32	0.04	0.08	0.16	0.13	0.01
LL				0.90**	0.59**	0.49**	0.01	-0.26**	-0.10	0.04	0.24*	0.03	-0.26**	0.17	-0.43**	0.23*	0.33**	0.19	0.41**
LW					0.55**	0.49**	-0.03	-0.27**	0.01	0.05	0.24*	0.04	-0.30**	0.08	-0.45**	0.23	0.37**	0.19	0.43**
LPL						0.65**	-0.16	-0.22*	-0.41**	-0.04	0.05	-0.19	-0.04	0.33**	-0.14	0.09	0.09	0.11	0.12
SAL							0.01	-0.11	-0.13	-0.15	-0.04	-0.16	-0.20*	0.16	-0.33**	0.20*	-0.06	0.21*	-0.09
NFA								0.27**	0.59**	0.20*	0.04	0.10	0.11	0.07	0.16	0.31**	0.46**	0.32**	0.45**
NFF									0.29**	0.07	-0.06	0.00	0.18	-0.14	0.08	0.13	0.05	0.11	0.04
NFN										0.23*	0.07	0.25*	0.15	0.04	0.24*	0.03	0.32**	0.01	0.34**
BL											0.77**	0.80**	0.65**	0.44**	0.53**	0.11	0.18	0.09	0.28**
BW												0.88**	0.53**	0.20*	0.21*	0.32**	0.13	0.30**	0.31**
BT													0.49**	0.26**	0.34**	0.23*	0.09	0.18	0.27**
SL														0.35**	0.69**	0.07	-0.04	0.11	0.03
SW															0.63**	0.00	0.28**	-0.02	0.21*
ST																0.02	0.11	0.02	0.06
WBT																	0.48**	0.98**	0.45**
100BW																		0.48**	0.91**
WST																			0.46**

TH-Trunk height, TD-trunk diameter, NPB-number of primary branches, LL-leaf length, LW-leaf width, LPL-leaf petiole length, SAL-stipule arista NFA-number of flower per axil, NFF- number of flower per fascicle NFN- number of fascicle per node, length BL-berry length, BW-berry width, BT-berry thickness, SL-seed length, SW-seed width, ST- seed thickness, WBT-weight of berry per tree, 100BW-100berry weight, WST-weight of seed per tree, 100SW-100seed weight.
NB: *, **- significance at 0.05 and 0.01 respectively. The values without any asterisk are not significant.

seeds per tree and 100seed weight (0.56, 0.51, 0.25, 0.24,0.40, 0.20 and 0.48 respectively) and negatively correlated with number of flowers per fascicle, seed length and seed thickness (-0.79, -.0.32 and 0.48 respectively).

Leaf petiole length had positive correlation with stipule arista length, number of flowers per axil and seed width (0.67, 0.21, and 0.38 respectively), but negatively correlated with number of flowers per fascicle, number of fascicles per node and berry thickness (-0.67, 0.52 and -0.20 respectively). Stipule arista length was negatively correlated with number of flowers per fascicle, seed length and seed thickness (-0.33, -0.22 and -0.36 respectively) but exhibited positive and significant correlation with weight of berries per tree and weight of seeds per tree (0.22 and 0.23 respectively). Number of flowers per axil had positive and significant correlation with number of flowers per fascicle, number of fascicles per node, weight of berries per tree, 100bery weight, weight of seeds per tree and 100seed weight (0.73, 0.68, 0.36, 0.54, 0.37 and 0.53 respectively). Number of flower per fascicle had positively correlated with number of number fascicles per node, seed length, weight of berries per tree and weight of seeds per tree (0.91, 0.36, 0.35 and 0.30 respectively) and negative correlation with berry width and seed width (-0.23 and -0.68 respectively). Number of fascicles per node had positive correlation with berry thickness, seed thickness, 100berry weight and 100seed weight (0.22, 0.20, 0.37 and 0.40 respectively).

Berry length had positively correlated with berry width, berry thickness, seed length, seed width, seed thickness and 100seed weight (0.76, 0.80,

Table 4. Genotypic correlation coefficient among twenty characters of coffee.

Character	TD (cm)	NPB	LL	LW	LPL	SAL	NFA	NFF	NFN	BL	BW	BT	SL	SW	ST	WBT	100BW	WST	100SW
TH	0.35**	0.28**	0.75**	0.84**	0.43**	0.53**	0.11	-0.64**	0.18	-0.04	0.14	0.00	-0.37**	0.06	-0.46**	0.37**	0.53**	0.38**	0.55**
TD		0.97**	0.24*	0.27**	0.39**	0.67**	0.07	-0.43**	-0.05	-0.19	-0.30**	-0.39**	-0.19	0.19	-0.16	0.18	0.24*	0.21	0.10
NPB			0.29**	0.31**	0.52**	0.61**	-0.04	-0.45**	-0.06	-0.15	-0.28**	-0.45**	-0.03	0.42**	0.05	0.09	0.18	0.15	0.00
LL				0.91**	0.60**	0.51**	-0.01	-0.75**	-0.11	0.05	0.25*	0.02	-0.28**	0.20*	-0.46**	0.24*	0.35**	0.20*	0.45**
LW					0.56**	0.51**	-0.04	-0.79**	0.03	0.05	0.25*	0.04	-0.32**	0.11	-0.48**	0.24*	0.40**	0.20*	0.48**
LPL						0.67**	0.21*	-0.67**	-0.52**	-0.04	0.05	-0.20*	-0.04	0.38**	-0.15	0.10	0.08	0.12	0.11
SAL							0.04	-0.33**	-0.13	-0.16	-0.05	-0.17	-0.22*	0.18	-0.36**	0.22*	-0.07	0.23*	-0.10
NFA								0.73**	0.68**	0.17	-0.02	0.05	0.06	-0.04	0.13	0.36**	0.54**	0.37**	0.53**
NFF									0.91**	0.16	-0.23*	-0.05	0.36**	-0.68**	0.05	0.35**	0.10	0.30**	0.11
NFN										0.14	-0.02	0.22*	0.07	-0.16	0.20*	0.04	0.37**	0.03	0.40**
BL											0.76**	0.80**	0.63**	0.38**	0.52**	0.13	0.17	0.10	0.28**
BW												0.88**	0.51**	0.12	0.18	0.35**	0.10	0.32**	0.32**
BT													0.47**	0.20*	0.31**	0.25*	0.06	0.20*	0.26**
SL														0.25**	0.71**	0.07	-0.08	0.11	-0.02
SW															0.63**	-0.01	0.24*	-0.04	0.17
ST																0.03	0.08	0.02	0.02
WBT																	0.51**	0.99**	0.49**
100BW																		0.52**	0.94**
WST																			0.50**

TH-Trunk height, TD-trunk diameter, NPB-number of primary branches, LL-leaf length, LW-leaf width, LPL-leaf petiole length, SAL-stipule arista NFA-number of flower per axil, NFF-number of flower per fascicle NFN- number of fascicle per node, length BL-berry length, BW-berry width, BT-berry thickness, SL-seed length, SW-seed width, ST- seed thickness, WBT-weight of berry per tree, 100BW-100berry weight, WST-weight of seed per tree, 100SW-100seed weight.
NB: *, **- significance at 0.05 and 0.01 respectively. The values without an asterisk are not significant.

0.63, 0.38, 0.52, and 0.28 respectively). Berry width had positively correlated with berry thickness, seed length, weight of berries per tree, weight of seeds per tree and 100seed weight (0.88, 0.51, 0.35, 0.32, and 0.32 respectively). Similarly, berry thickness was correlated with seed length, seed width, seed thickness, weight of berries per tree, weight of seeds per tree and 1000seed weight (0.47, 0.20, 0.31, 0.25, 0.20 and 0.26 respectively). Seed length was correlated with seed width and seed thickness (0.25 and 0.71 respectively). Seed width was correlated seed thickness and 100berry weight (0.63 and 0.24). Weight of berries tree was correlated with 100berry weight, weight of seeds per tree and 100seed weight (0.51, 0.99 and 0.49 respectively). 100berry weight was correlated with weight of seeds per tree and 100seed weight (0.52 and 0.94 respectively). Weight of seeds per tree was correlated with 100seed weight (0.50). Trunk height had positively correlated with trunk diameter, number of primary branches, stipule arista length and 100seed weight (0.22, 0.22, 0.29 and 0.26 respectively) (Table 5). Trunk diameter had a positive correlation with leaf length and stipule arista length (0.21 and 0.33 respectively). Number of primary branches had positively correlated with stipule arista length (0.23). Leaf length was strongly correlated with leaf width (0.72). Leaf width had negative correlation with seed width (-0.20). Leaf petiole length had positively correlated with 100 berry weight and 100 seed weight (0.23 and 0.21 respectively). Stipule arista length had a negative correlation with number of fascicles per node (-0.21). Number of flowers per axil had positively correlated with

Table 5. Environmental correlation coefficient among twenty characters of coffee.

Character	TD (cm)	NPB	LL	LW	LPL	SAL	NFA	NFF	NFN	BL	BW	BT	SL	SW	ST	WBT	100BW	WST	100SW
TH (cm)	0.22*	0.22*	0.07	0.10	0.12	0.29**	-0.12	-0.09	0.00	0.11	0.15	0.16	-0.06	0.04	0.11	0.02	0.09	0.00	0.26**
TD (cm)		0.12	0.21*	0.16	0.01	0.33**	-0.01	0.07	-0.02	0.04	0.10	0.02	0.01	0.13	0.10	0.01	-0.03	-0.01	-0.13
NPB			0.10	0.06	0.07	0.23*	-0.05	0.01	-0.06	-0.09	-0.15	-0.12	-0.11	-0.06	-0.02	0.03	0.03	0.02	0.05
LL				0.72**	0.03	0.08	0.16	-0.03	-0.10	0.05	0.14	0.05	-0.08	-0.06	0.06	0.06	-0.06	0.03	-0.12
LW					0.03	0.10	-0.06	-0.07	-0.18	-0.01	0.02	-0.01	-0.18	-0.20*	0.01	-0.03	-0.12	-0.06	-0.17
LPL						0.06	0.09	0.01	-0.01	-0.08	-0.04	0.03	-0.06	0.06	0.09	0.05	0.23*	0.06	0.21*
SAL							-0.16	-0.01	-0.21*	0.04	0.05	0.03	-0.03	0.05	-0.06	-0.07	0.04	-0.07	0.00
NFA								0.12	0.41**	0.35**	0.40**	0.40	0.36**	0.39**	0.35**	0.09	0.16	0.15	0.20
NFF									0.08	0.07	0.07	0.07	0.22*	0.14	0.22*	0.05	0.07	0.07	0.00
NFN										0.58**	0.54**	0.54**	0.52**	0.53**	0.47**	-0.03	0.21*	-0.06	0.21*
BL											0.93**	0.87**	0.79**	0.78**	0.62**	-0.02	0.31**	-0.01	0.29**
BW												0.93**	0.75**	0.76**	0.61**	-0.04	0.37**	-0.02	0.31**
BT													0.72**	0.72**	0.64**	-0.09	0.44**	-0.06	0.39**
SL														0.90**	0.58**	0.09	0.39**	0.12	0.36**
SW															0.66**	0.11	0.52**	0.10	0.43**
ST																-0.06	0.48**	-0.07	0.35**
WBT																	0.03	0.90**	0.05
100BW																		0.03	0.75**
WST																			0.13

TH-Trunk height, TD-trunk diameter, NPB-number of primary branches, LL-leaf length, LW-leaf width, LPL-leaf petiole length, SAL-stipule arista NFA-number of flower per axil, NFF- number of flower per fascicle NFN- number of fascicle per node, length BL-berry length, BW-berry width, BT-berry thickness, SL-seed length, SW-seed width, ST- seed thickness, WBT-weight of berry per tree, 100BW-100berry weight, WST-weight of seed per tree, 100SW-100seed weight. NB: *, **- significance at 0.05 and 0.01 respectively. The values without an asterisk are not significant.

number of fascicles per node, berry length, berry width, berry thickness, seed length, seed width, seed thickness and 100 seed weight (0.41, 0.35, 0.40, 0.40, 0.36, 0.39, 0.35 and 0.20 respectively). Similarly, number of flowers per fascicle had a positive correlation with seed length and seed thickness (0.22 and 0.22 respectively). Number of fascicles per node had positively correlated with berry length, berry width, berry thickness, seed length, seed width, seed thickness, 100 berry weight, and 100 seed weight (0.58, 0.54, 0.54, 0.52, 0.53, 0.47, 0.21 and 0.21 respectively).

Berry length had strong a positive correlation with berry width, berry thickness, seed length, seed width, seed thickness, 100 berry weight, and 100 seed weight (0.93, 0.87, 0.79, 0.78, 0.62, 0.31 and 0.29 respectively). Berry width had a strong positive correlation with berry thickness, seed length, seed width, seed thickness, 100 berry weight, and 100 seed weight (0.92, 0. 75, 0.76, 0.61, 0.37 and 0.31 respectively). Berry thickness was strongly positively correlated with seed length, seed width, seed thickness, 100 berry weight, and 100 seed weight (0.72, 0.72, 0.64, 0.44 and 0.39 respectively). Seed length had strong positive correlation with seed width, seed thickness, 100 berry weights and 100 seed weight (0.90, 0.58, 0.39 and 0.36 respectively). Seed width had strong positive correlation with seed thickness, 100 berry weight and 100 seed weight (0.66, 0.52 and 0.43 respectively). Seed thickness had positively correlated with 100 berry weight and 100 seed weight (0.48 and 0.35 respectively). Weight of berries per tree was strongly correlated with weight of seeds per tree (0.90). Also,100 berry weight strongly correlated with 100 seed weight (0.75).

Stepwise regression analysis identifies the best subset of predictors or independent variables and

Table 6. Stepwise regression analysis of independent characters on 100seed weight and weight of seed per tree of coffee.

Dependable character	Model	Independable characters	Partial R^2	Cumulative	Model R^2
100 seed weight	Y= -2.6+0.154+0.269+0.151+0.005-0.014	X1= 100berry weight (g)	0.867		
		X2= Berry length (mm)	0.009	0.879	
		X3= Number of flower per fascicle	0.003	0.882	
		X4= Trunk height (cm)			
		X5=Trunk diameter (cm)	0.002	0.884	
			0.004	0.888	0.888**
Weight of seed per tree	Y=84.833+0.266-31.885+10.315-18.590	X1= weight of berry per tree (g)	0.934	0.934	
		X2= Plant height			
		X3= Number of flower per axil	0.004	0.968	
		X4= Number of fascicle per node	0.003	0.971	
			0.002	0.973	0.973**

** 0.01.

the order in which variables are included in the regression equation. The order tells the relative importance of the predictors, which is the best predictor, second best and so on. The result for 100 seeds weight as dependent variables showed that 100 berries weight, berry length, number of flower per fascicle, trunk height and trunk diameter are the predictors for 100seed weight and accounted for 93% of variation observed. Each trait made a significant contribution to 100seed weight with 100berry weight as best predictor, which accounted for 86% of the total variation (Table 6). Similarly, the result obtained for weight of seed per tree showed that weight of berry per tree, plant habit, number of flower per axil and number of fascicle per node in that order are the predictors and accounted for 94% of the variation observed with weight of berry per tree as best predictor, accounting for 93.4%.

DISCUSSION

Knowledge of correlations among characters is useful in designing an effective breeding programme for any crop. The mutual association among characters is often expressed by the phenotypic, genotypic and environmental correlation (Searle 1961; Ariyo, 1989; Akinyele and Osekita, 2006). Weight of seed per tree which is actual yield is has strong and positive correlation with trunk height, leaf length, leaf width stiple arista length, number of flower per axil, number of flower per fascicle, berry width, berry thickness, 100 berry weight, 100seed weight and weight of berry per tree. According to Getachew (2019), coffee yield was found to have strong and positive association with fruit width and fruit thickness at genotypic level. Gizachew and Hussei (2017) in their findings reported that average yield has positive and significant correlation with 100 bean weight and leaf length. Ermias (2005) also reported strong and positive correlation with plant height. Phenotypic correlation is a composite of genotypic and environmental correlations. There are several reasons for using indirect selection. Sometimes the main character is expressed late, or measurement of the indirect character is much easier than for the direct character. Although yield is not directly correlated with seed length and berry length but has correlation with berry width and berry thickness which in turn have direct correlation seed length (0.51 and 0.47) and berry length (0.76, 0.80). Selection could be made for seed length and berry length during breeding programme resulting to yield improvement.

Moreover, complex plant characters such as yield are quantitatively inherited and influenced by genetic effects, as well as by genotype x environment interaction. Due to these reasons, selections to improve yield directly may be difficult and time-consuming, especially for perennial crops with a long juvenile period such as coffee. Therefore, identification and use of positively correlated characters are appropriate.

From the results obtained, the lower values of phenotypic correlation coefficients (weight of seed per tree with trunk height, weight of berry per tree, 100seed weight and correlation among traits) to the genotypic correlation coefficient values,

indicates that the influence of environmental factors is minimal and lower than the inherent genetic effects. This is in line with the work of Walyaro and Van der Vossen, 1979 where genotypic correlation values were greater than phenotypic values. According to Falconer (1989), linkage effects or pleotropic effect of genes may be the source of significant correlation coefficients among various characters. Negative correlation between two traits implies selection of one trait for improvement will cause decrease in the other trait especially if it is of high magnitude. In this study, number of flower per fascicle had strong negative correlation with leaf length, leaf width and leaf petiole length (-0.75, -0.79 and -0.67 respectively). When the correlation is strong and positive, simultaneous improvements of both traits could be achieved (Rangaswamy, 1995). All flower characters (number of flower per axil, number of flower per fascicle, and number of fascicle per node) and some yield and yield related characters were positively correlated with one another. The implication of this is that selection/breeding for any of the characters is invariably selecting /breeding for others. Moreover, those with high values of correlation show that no matter how many times the trial is repeated, the result will be highly dependent.

Stepwise regression procedure was used to determine the variables that accounted for the majority of total yield variability. At each step, one variable was added to the regression equation. The added variable was the one that included the greatest reduction in the error sum of square. It was also the variable that had the highest partial correlation with the dependent variable for fixed values of those variables already added. Moreover, it was the variable which had the highest F-value. Stepwise regression is, therefore designed to find the most parsimonious set of predictors that are most effective in predicting the dependent variables (Ndukauba et al., 2015).

In order to remove the effect of non-effective characteristics in the regression model of coffee yield, stepwise regression was used in the analysis. 100seed weight and weight of seeds per tree as dependent variable and other traits as an independent variable were considered.

The result suggested that 100 berry weight, berry length, number of flowers per fascicle, trunk height and trunk diameter were the major contributors towards 100seed weight. In contrast, the weight of berries per tree, plant height, number of flowers per axil and number of fascicles per node were the major contributors towards weight of seeds per tree of coffee and should therefore be given serious consideration in coffee breeding programs.

Conclusion

In conclusion, genotypic correlations among characters affecting yield elucidate true relationship as they eliminate the environmental influences. It can be recommended that coffee yield improvement could be accomplished through selections based on these correlations. Consequently, knowledge of associations between yield and its component traits as well as among the component traits themselves can promote the efficiency of selection in coffee breeding programs.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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