

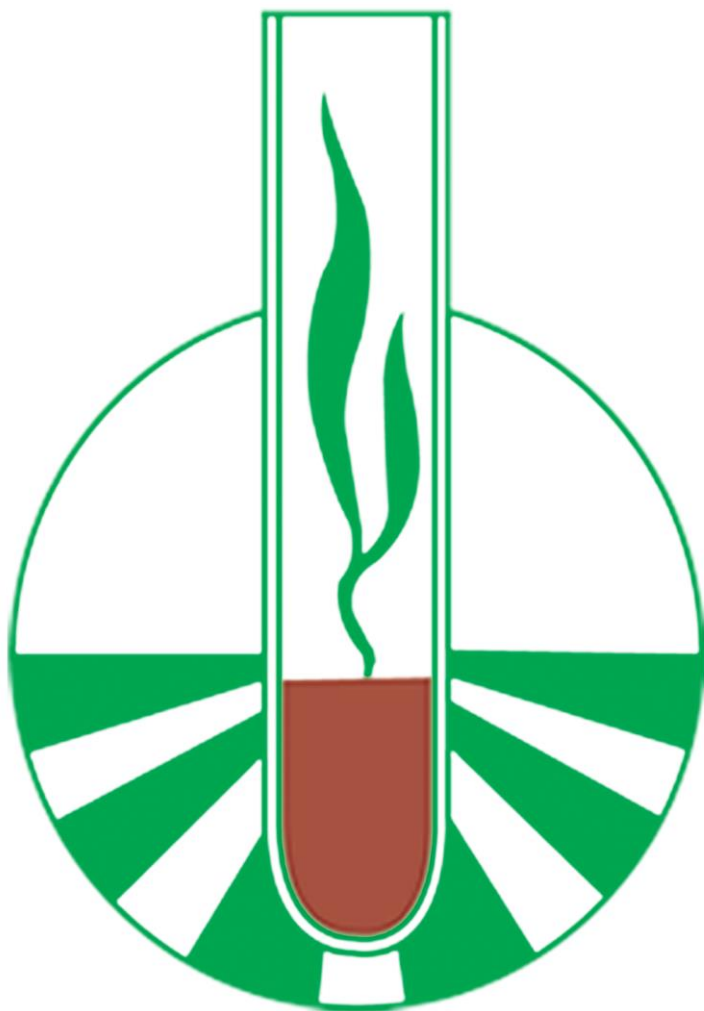
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Screening Durum Wheat Genotypes (*Triticum turgidum* var. durum Desf.) for Soil Acidity Tolerance

Tesfaye Geleta¹ and Tesfaye Balemi²

¹Debre Zeit Agricultural Research Center (DZARC), ²Ethiopian Institute of Agricultural Research (EIAR)

Abstract

The production and productivity of durum wheat is threatened by different biotic and abiotic stresses in different parts of the country. Soil acidity associated with Al toxicity is one of the limiting a biotic factor for the production of durum wheat. A pot experiment was conducted at Debre Zeit Agricultural Research Center in 2020. A total of 102 durum wheat genotypes were grown with and without lime treatment to screen the genotypes for tolerance to soil acidity. The treatments were laid out in Completely Randomized Design (CRD) with two replications. The results of the experiment showed that shoot and root growth were enhanced under lime treated than untreated conditions. Significant variations were observed among the durum wheat genotypes for shoot fresh and dry weight, root fresh and dry weights, relative shoot and root yield, root to shoot ratio, and root volume under both limed and unlimed conditions. Genotypes, that showed consistently better performance based on various growth parameters used for screening purposes such as shoot and root growth parameters under un-limed condition were selected as acid soil tolerant. Accordingly, genotypes 81, 24, 2, 71, 90, 74, 70, 6, 18, 102, 17, 98, 4, 60, 96, 99, 15, 62, 32, 93, 91, 77, 30 and 75 were identified as consistently acid soil tolerant. Among these, thirteen of them (81, 71, 90, 70, 6, 98, 4, 99, 15, 91, 77, 30, and 75) were Ethiopian land races, two of them (2 and 60) were ICARDA materials, four of them (18, 102, 96 and 62) were CIMMYT materials, two of them namely, Tesfaye and Asasa (32 and 93) were Ethiopian improved varieties, and three of them (24, 74 and 17) were Debre Zeit Agricultural Researcher Center durum wheat breeding program advanced lines. Thus, the identified acid soil tolerant durum wheat released varieties can be recommended for acid soil affected areas while the rest tolerant genotypes can be used as parental lines in durum wheat breeding program to develop tolerant varieties for acid soil prone areas of Ethiopia.

Keywords: Acid soil tolerance, Durum wheat, Lime application, Relative shoot yield, Root Volume, shoot dry weight,

Introduction

Durum wheat (*Triticum turgidum* var. durum Desf) is among the oldest traditional and the most diversified

crop species in Ethiopia (Mengistu *et al.* 2016). Ethiopia is a center of diversity and hosts rich genetic resources of tetraploid wheat (Tsegaye and Berg 2006), which can be used for

different breeding objectives. The production and productivity of the crop is currently threatened by different biotic and abiotic stresses in different parts of the country. Soil acidity associated with Al toxicities, soil erosion and soil nutrient depletion are among the major constraints that limits durum wheat productivity in developing countries including Ethiopia (Tolera *et al.* 2006). Currently, Agricultural Transformation Agency estimated that about 43% of the total arable land of Ethiopia is affected by soil acidity (ATA, 2013).

Soil acidification is the result of a complex set of processes caused both naturally and by human activity (Amede *et al.*, 2019). Soil acidity highly reduces crop productivity due to deficiencies of basic cations, reduced phosphorus availability and toxicities of Aluminum and Manganese. Eyasu (2016) also reported that 80% of Nitisols in Ethiopia is originally highly acidic. Amelioration of acid soils using lime remains challenging for sustainable and profitable durum wheat production due to the bulkiness nature and high transportation costs. Although limited work on genetic variability for aluminium resistance, (Stodart *et al.*, 2005) has been reported in tetraploid wheat, it was hypothesized that use of large number of genotypes from different sources and evaluation for acid soil tolerance to be an alternative option for identification of tolerant genotypes targeting acid prone environment in order to expand wheat area and production. Thus, the

objective of this study was to screen durum wheat genotypes for acid soil tolerance and responsiveness to lime application.

Materials and Methods

Study area

Lath house experiment was carried out at Debre Zeit Agricultural Research Center which is located at 8° 44' N and 38° 58' E and an altitude of 1900 m above sea level. The center is located at 47 km south eastern Addis Ababa and is characterized by a mean annual rainfall of 851 mm and mean maximum and minimum temperature of 28.3°C and 8.9°C, respectively.

Experimental treatments and design

About 102 durum wheat genotypes obtained from different sources (twenty-six land races, 15 released varieties, 12 breeding lines, 34 CIMMYT and 15 ICARDA materials) were grown with and without lime (Appendix Table 1). The treatments were laid out in a Completely Randomized Design with two replications.

Soil sampling and analysis

Soil samples were collected from Midakegn District, West Shoa Zone, Oromia Regional State, in Ethiopia where soil acidity is a serious problem for crop production. The collected soil sample was air-dried and roots, sands and other impurities were separated from the soil. Soil analysis was done for both lime treated and untreated

samples for major soil chemical properties at Debre Zeit agricultural research center Soil Laboratory. Soil pH and electric conductivity (EC) were measured with soil extract at a soil/deionized water ratio of 1:2.5 (w/v) using a digital pH meter and electric conductivity meter respectively.

Exchangeable acidity Al^{3+} , was determined using 1N KCl Extraction-titration method Cation exchange capacity (CEC), using by ammonium acetate method, and organic carbon content, by Walkley and Black methods (Walkley and Black, 1934). Total nitrogen was determined by Kjeldahl Method, available phosphorus using Olsen's method (Olsen *et al.*, 1954) and aluminum saturation was calculated as the ratio of exchangeable aluminum to the CEC.

Lime amount determination

The amount of lime required for a kilogram of soil to raise the soil pH to a level suitable for the growth of crops was determined in a separate incubation experiment following a procedure described in Fekadu *et al.* (2017). The soil for the incubation experiment was treated with 5, 10, 15, 20, 25 and 30 grams of lime per kilogram of soil and incubated for 45 days in two replications. The level of pH and electric conductivity was determined using potentiometrically with a digital pH meter in the supernatant suspension of 1:2.5 soils to water ratio and conductivity meter, respectively.

Planting and crop management

The homogenized soil sample was prepared and two kilograms of soils were filled in the plastic pot of five kilograms capacity. A total of 408 pots were filled with soils where 204 pots were treated with lime and the other 204 pots were left untreated. Ten seeds of durum wheat genotypes were sown into lime (CaCO_3) treated and untreated pots. The same amount of nitrogen (N) fertilizer (0.304 gram per 2 kilograms of soil) in split half at the time of sowing and half at tillering stage in the form of urea. Phosphorus (P) fertilizer (0.33 gram per 2 kilograms of soil) was applied to all the treatments at the time of sowing in the form of triple superphosphate (TSP). Thinning was done after the seedlings were establishment to maintain uniform number of plants in each pot. The pots were watered at field capacity throughout the growing period of the crop.

Data collection and analysis

The above ground plant parts were collected 80 days after planting and their fresh were weighed and recorded for each plots. The samples were further oven dried to record shoot fresh and dry weight. Moreover, root to shoot ratio and relative shoot and root yield were calculated. Root to shoot ratio was calculated by dividing the root weights for the corresponding shoot weights, while the relative shoot/root yield was calculated by dividing shoot/root weight of the lime untreated treatment for the corresponding lime treated treatment

and multiplying by 100. Data were subjected to analysis of variance using the GLM procedure of SAS software version 9.3 (Anonymous, 2004) to see if each parameter was affected by lime treatments and wheat genotypes.

Result and Discussion

Determination of lime requirement for the experimental soil

According to the classification of soil pH ranges reported by Obi *et al.* (2017), the present soil under study before lime treatment was classified as strongly acidic. Pre-experimental soil treatment with different levels of lime application increased the pH of the experimental soil. Accordingly, the application of 10-gram lime per kilogram of soil raised the soil pH to a level suitable for the growth of crop plants while use of 15 to 30 gram lime per kilogram of soil did not show significant changes on pH of the soil (Figure 1).

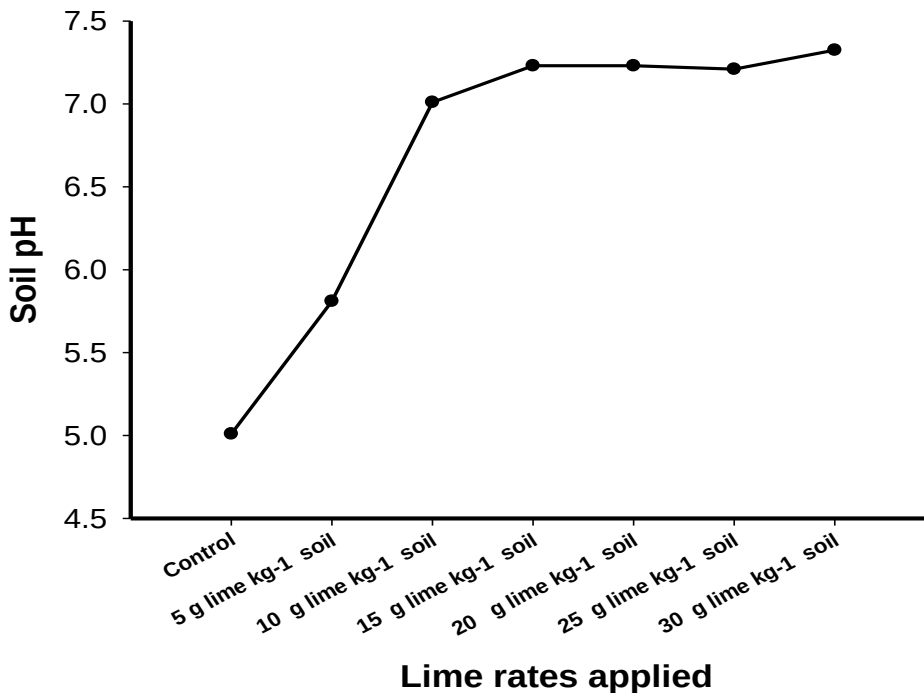


Figure 1: Changes in soil pH under different levels of lime application for the experimental soil samples

Effect of lime application on soil chemical properties

The results indicated that soil pH, available phosphorus, electrical conductivity, cation exchange capacity, exchangeable acidity, total nitrogen and organic matter content significantly responded to the application of lime (Table 1). However, lime application reduced the exchangeable and saturation of Al in the soil (Table 1). This might be due to Al ion neutralization in the soil through the hydrolysis reaction of the liming material added to the soils. PH of the soil was 5.01 and 7.01 for the limed and without treatment

respectively (Table 1). These indicates that amelioration of acid soil with lime improved the most important soil chemical properties and make the soil more suitable for crop production. The findings of Sisay and Balemi (2014) and Obi *et al* (2017) showed that reclamation of acid soil using lime increased the soil pH from 5.2 to 6.8. The probable reason for increasing soil pH could be due to ionization of hydrogen and supply of calcium and magnesium in the soil and phosphorus and nitrogen availability could also be enhanced there by accelerating organic matter decomposition due to lime application.

Table 1: Chemical properties of the experimental soil under lime treated and untreated conditions

Soil chemical properties	Lime untreated soil	Lime treated soil
pH	5.01	7.01
Available phosphorus(mg/kg/soil)	11.7	12.1
EC (ds/m)	0.049	0.087
CEC (cmol(+)/kg	19.3	26.8
Exchangeable Al (meq/100g soil)	0.24	0.1
Aluminum saturation	1.24	0.37
Exchangeable acidity (meq/100g soil)	10.9	21.7
Total nitrogen	0.097	0.125
OM (%)	2.74	3.65

Traits considered for the screening

Soil acidity affects crop growth, development and grain yield. It affects from primarily root elongation to the growth of above ground parts of the crop. In the current study shoot fresh weight, shoot dry weight, root fresh weight, root dry weight, relative shoot yield, and relative root weight and root volume were measured to screen and

identify durum wheat genotypes tolerant to acid soil condition. Similarly, Ma *et al*, (2004) measured root and shoot biomass yield at early stage to identify and rank barley cultivars for acid soil tolerance. Similarly, Sisay and Balemi (2014) recommended that shoot weight, root weight, root volume, relative yield and total p uptake as an important trait for

screening barley cultivars for acid soil tolerance.

Shoot fresh weight

Durum wheat genotypes significantly ($P<0.001$) varied in shoot fresh weight (SFW) under both lime treated and untreated soil conditions (Table 2). This indicates that durum wheat genotypes responded differently to lime application. The results presented in figure 2 showed that, based on SFW parameter, genotypes such as 6, 49, 2,

81, 71, 70, 37 and 34 were classified as highly tolerant to soil acidity as well as responsive to lime application, while the genotypes 87, 78, 89, 36, 47, 76,7 and 9 were grouped into acid intolerant and non-responsive(Figure 2). Generally, SFW of durum wheat genotypes was lower under lime untreated than lime treated soil condition, which could be attributed to toxicity and deficiency of some nutrients which are essential to plant growth.

Table 2: Analysis of variance (ANOVA) for mean square values of the evaluated traits of durum wheat genotypes influenced by lime application

Source of variations	Df	SFW	SDW	RFW	RDW	RV	RSR
Genotypes	101	0.34**	0.043**	0.29**	0.0075**	0.497**	0.038**
Replications	1	0.05NS	0.00005NS	0.021NS	0.0004NS	0.056NS	0.012NS
Type(a and b)	1	90.78**	14.75**	15.37**	0.694**	16.288**	1.523**
Genotypes*Type	101	0.16**	0.021**	0.093**	0.0025**	0.177**	0.011**
Error	203	0.04	0.006	0.009	0.0003	0.026	0.005
Total	408						
Grand mean		1.19	0.64	0.77	0.15	1.18	0.36
R-square		94.8	94.4	96.6	96.2	94.1	87.1
CV		16.4	16.9	12.5	12.1	13.7	18.9

Where, a=lime treated, b=lime untreated, SFW=Shoot fresh weight, SDW=Shoot dry weight, RFW=Root fresh weight, RDW=Root dry weight, RV=Root volume and RSR=Root to shoot ratio

Supporting the present result, Sisay and Balemi (2014) also found similar result on shoot fresh weight of barley genotypes grown in soils treated with lime and without lime. Moreover, Malede *et al.* (2020) reported the presence of significant genotypic variation among soybean varieties for soil acidity tolerance and observed a 16.7 % increase in average shoot fresh weight under liming than without liming.

Shoot dry weight

The result of the present study revealed that the shoot dry weight of durum wheat genotypes was significantly affected by liming, genotypes and their interaction (Table 2). Under un limed soil condition, genotypes 102, 49, 81, 43, 32, 24, 39, 37, 62, 70 and 56 had significantly higher shoot dry weight compared to genotypes 47, 78, 36, 87, 1 and 12 which produced lower shoot dry

weights (Figure 3). Therefore, genotypes with significantly higher shoot dry weights under lime untreated soils condition were considered as acid tolerant whereas those with lower shoot dry weight under unlimed soil condition are categorized as acid intolerant when shoot dry weight is

considered as parameter for ranking the genotypes for acid soil tolerance. On the other hand, under limed soil condition, genotypes 49, 101, 6, 2, 48, 44, 39, 81, 43, 32 and 102 showed significantly higher shoot dry weight compared to genotypes 77, 79, 75, 23, 83 and 36 (Figure 3).

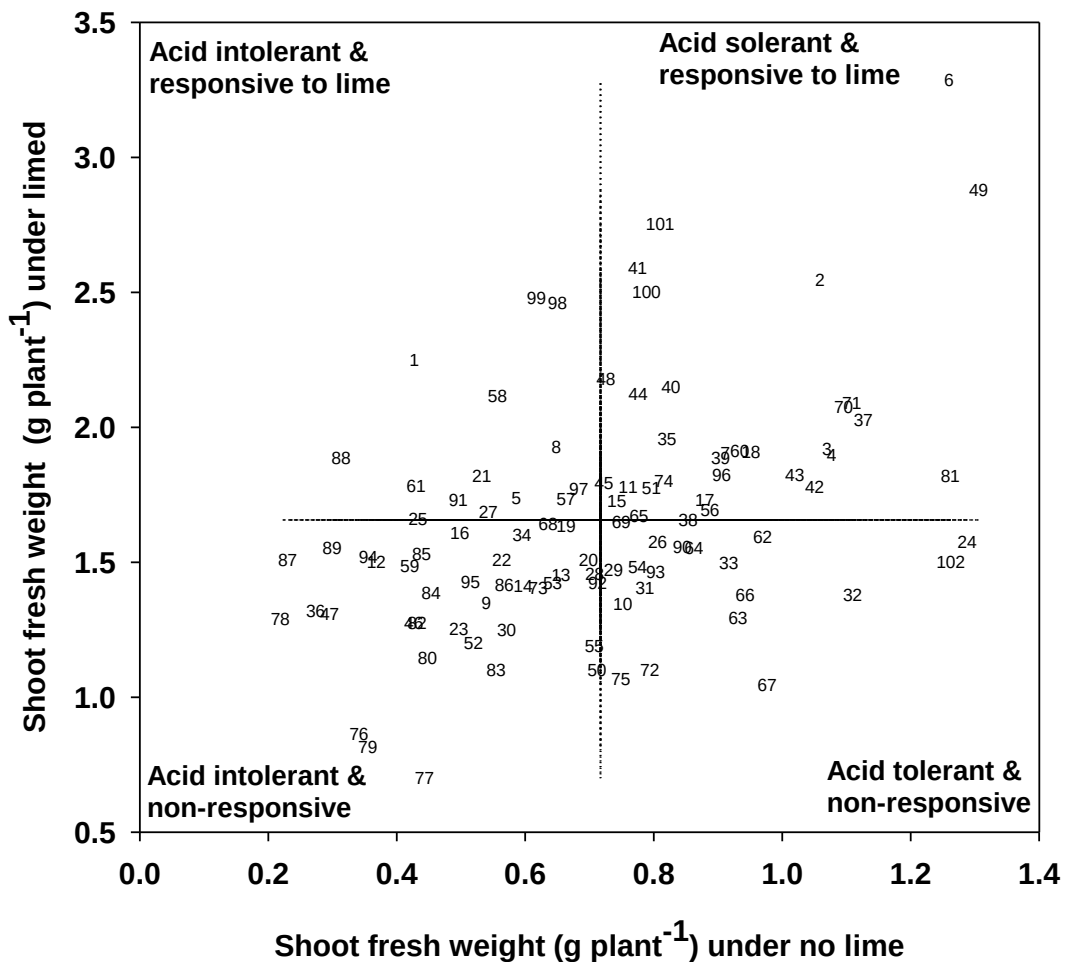


Figure 2: Categorization of acid soil tolerant and intolerant genotypes based on shoot fresh

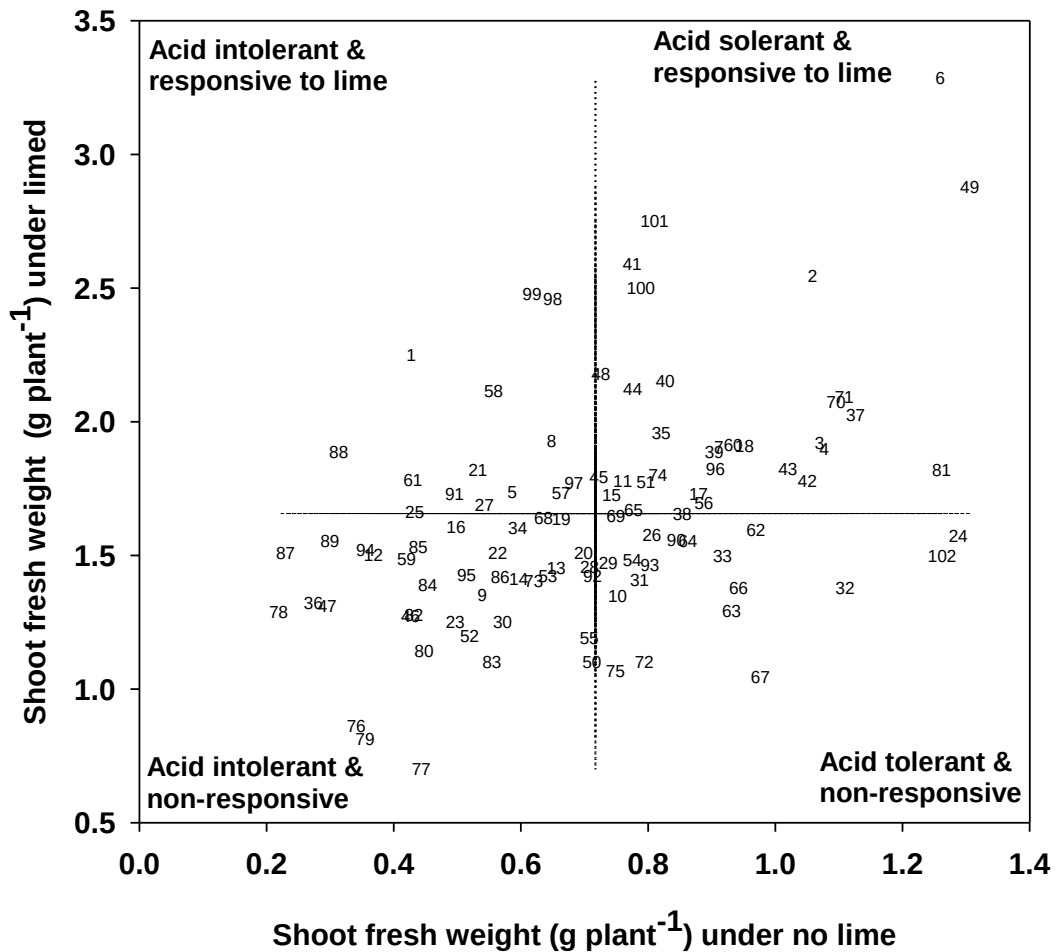


Figure 3: Categorization of acid tolerant and intolerant genotypes based on shoot dry weight

Thus, genotypes having significantly higher shoot dry weight under limed soil condition were regarded as responsive to lime application whereas those genotypes that showed lower shoot dry weight under lime treated soils condition were classified as non-responsive. Taking shoot dry weight as a selection parameter, the genotypes 49, 39, 81, 43, 6 and 102 were found both responsive to liming and tolerant to acid soils. Thus, these genotypes could be used for further evaluation

and hybridization in the future breeding program. In line with this finding Tang *et al.* (2001) reported that shoot weight of Al sensitive wheat genotypes increased by 60% using subsurface liming. Moreover, Arshad *et al.* (2012) suggested that acid soil treatment with wood ash and lime increased shoot dry matter production of barley, canola and field pea crops. In contrast, to the current study, Tang *et al.* (2001) stated that shoot dry weight of Al-tolerant wheat genotype

was not affected by subsurface soil acidity.

Root fresh weight

Analysis of variance showed that root fresh weight was significantly ($P < 0.001$) varied among durum wheat genotypes grown under lime treated and untreated soil conditions (Table 2). The result implies that the genotypes gave higher root fresh weight under lime treated soils condition as compared to the unlimed

soil condition. This might be due to a high concentration of aluminum and manganese which inhibit root growth and development under lime untreated condition. Based on mean values of root fresh weight, about half (49%) of the genotypes were categorized under intolerant and non-responsive to liming and accordingly, genotypes 81, 91, 70, 6, 86, 64 and 41 were among the best performing genotypes under both limed and unlimed soil conditions (Figure 4 and Table 3).

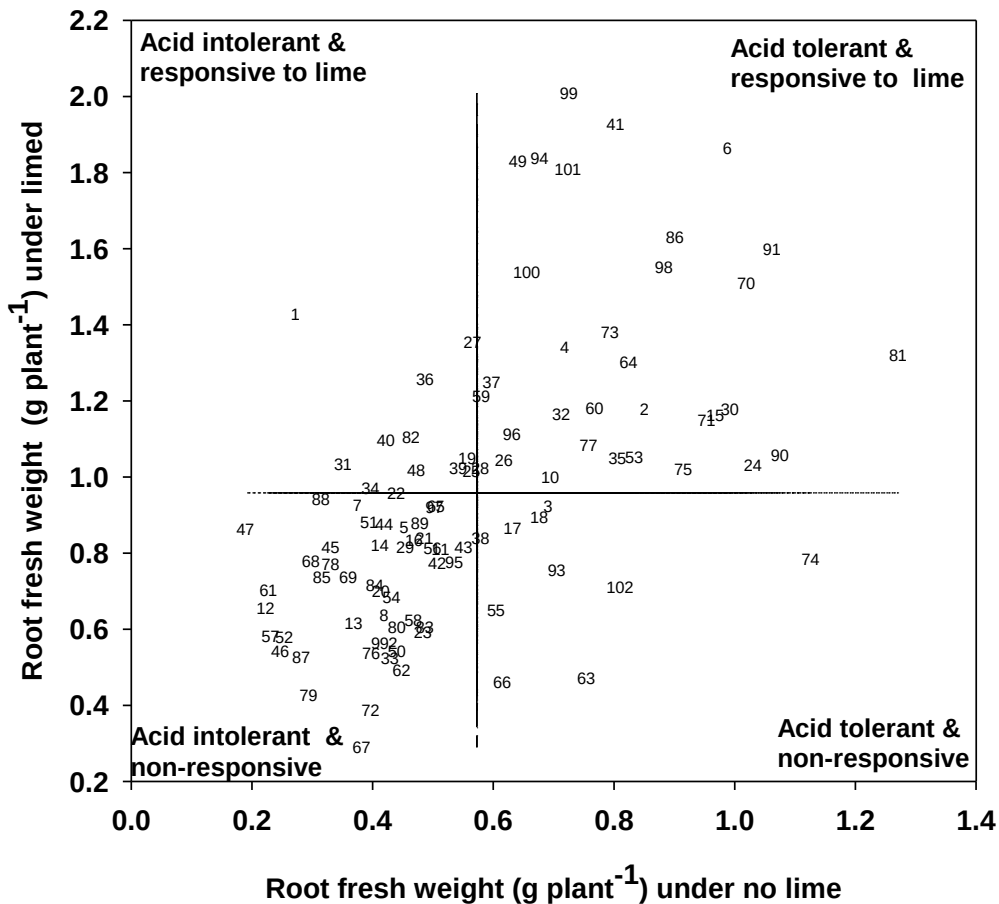


Figure 4: Categorization of acid tolerant and intolerant genotypes based on root fresh weight

Similarly, Haling *et al.* (2010) demonstrated that root hair length and density were adversely affected by soil acidity. Moreover, they identified that fine root growth was highly reduced in Al sensitive line of wheat and barley while Al-resistant lines maintain root growth under these conditions. Likewise, Caires *et al.* (2008) described that liming improved root growth and it was well correlated with the grain yield of wheat. Moreover, Raman *et al.* (2002 and 2008) reported aluminum resistant wheat and barley varieties possessing a higher root growth as compared to sensitive varieties under acid soil conditions. Generally, root development was lower under unlimed soil than the lime

treated soil, which is in agreement with Whalley *et al.* (2008), who suggested that breeding for resistance to Al is required because soil amelioration by liming is effective only in the upper root zone and susceptible or moderately susceptible cultivars do not develop extensive root systems. In contrary to the present finding, Wayima *et al.* (2019) who evaluated 595 Ethiopian landrace durum wheat accessions in hydroponic by their length of seminal root reported some level of tolerance, however, all of the accessions were rated as aluminum intolerant categories while evaluated by molecular markers.

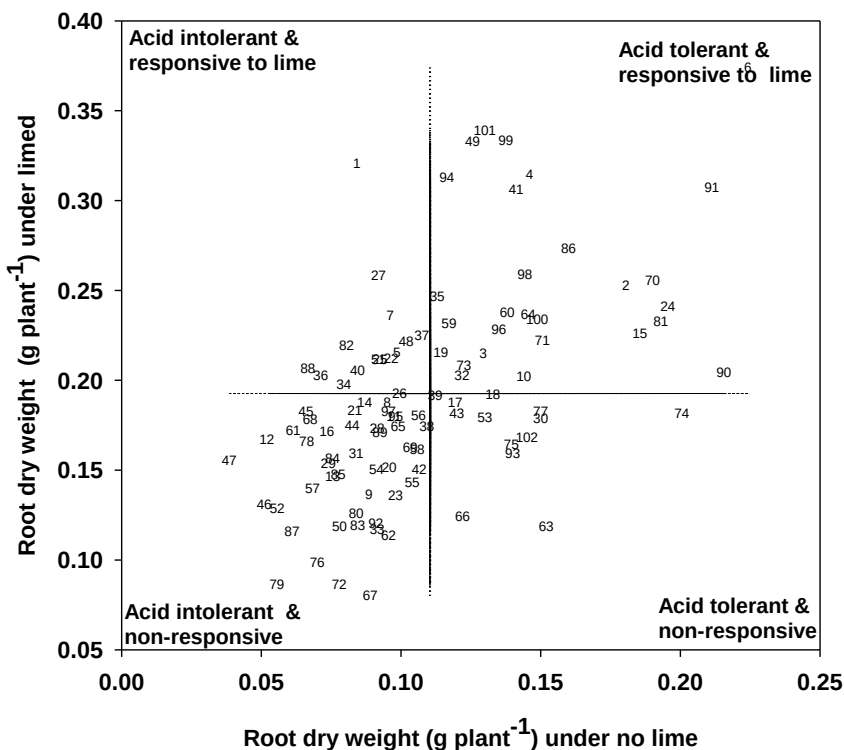


Figure 5: Categorization of acid tolerant and intolerant genotypes based on root dry weight

Root dry weight

The value of root dry weight per plant was significantly ($P<0.001$) affected by the main effects of genotypes, lime application and by their interaction effect (Table 2). Durum wheat genotypes in root dry yield production showed similar performance as that of root fresh yield where majority of them were grouped under acid soil intolerant and non-responsive to lime application category (Figure 5).

However, higher root dry weight was recorded from genotypes grown under lime treated soil condition than the untreated soils and genotypes 6,90,91,74,24,81, 15,70, 2 and 86 were among the good performing in root dry mass production (Figure 5 and Table 3). Incongruent with this study, Baquy *et al.* (2018) reported that shoot and root dry matter is changing with soil pH in maize inbred lines.

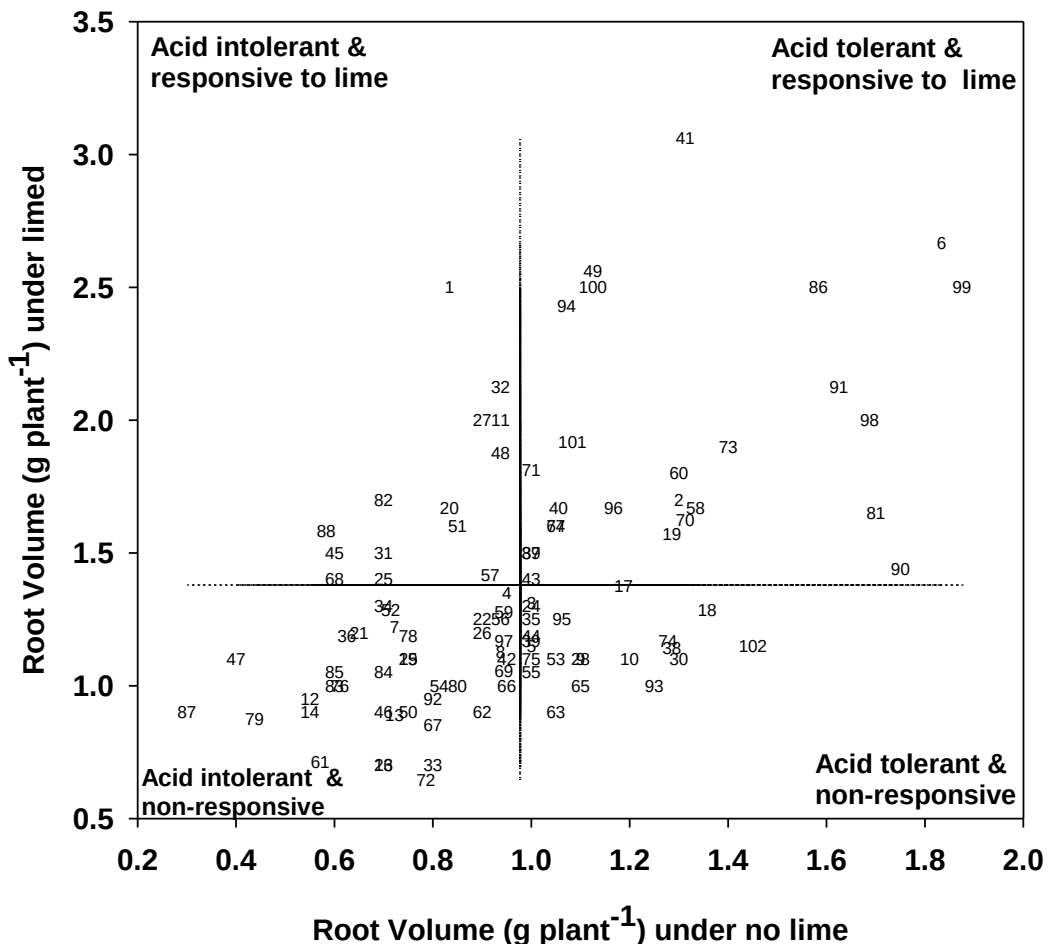


Figure 6: Categorization of acid tolerant and intolerant genotypes based on the root volume

Similarly, Sisay and Balemi (2014) observed differences among barley cultivars in terms of root dry weight under lime untreated and lime treated soil conditions. Additionally, Malede *et al.* (2020) indicated that soil acidity reduced root fresh and dry weight and total dry biomass yield per plant in soybeans.

Root volume

The result of this study revealed that, the mean value of root volume significantly ($P < 0.001$) differed among durum wheat genotypes grown in lime treated and untreated pots (Table 2). Genotypes 6, 99, 98, 91, 81, 90, 73, 41

and 102 had the highest root volume under both lime untreated and limed condition compared to genotypes 87, 47, 79, 61, 14, 12 and 85 (Figure 6). Under lime untreated conditions genotypes 99, 6, 90, 81, 98, 91, 86 and 102 were among the best performing durum wheat genotypes and 41, 6, 49, 1, 86, 99, 100, 94 and 32 were genotypes produced the highest root volume under limed pots. Considering root volume as selection criteria for acid soil tolerant and responsive to lime application, 6, 99, 98, 91, 86 and 41 were the most preferred durum wheat genotypes from the tested materials (Figure 6 and Table 3).

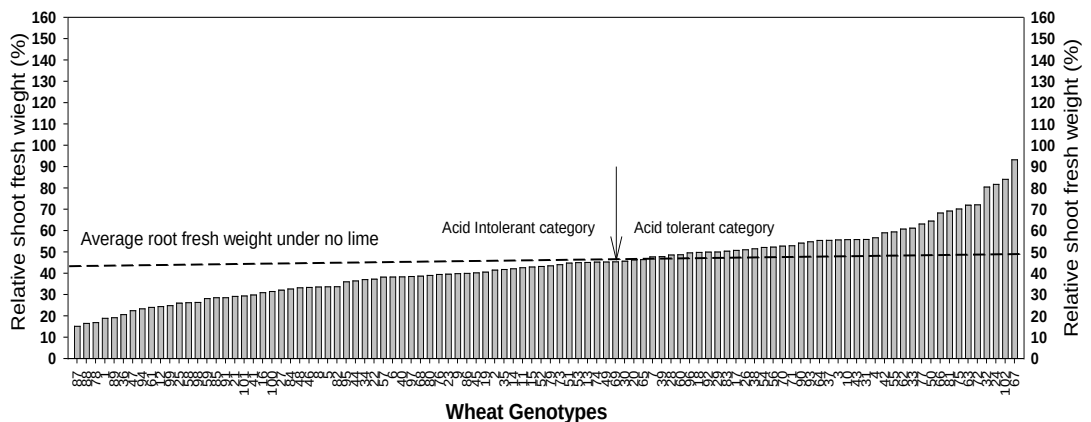


Figure 7: Categorization of acid tolerant and intolerant genotypes based on relative shoot fresh weight

Genotypes evaluated in this study showed a difference in root volume under both lime treated and lime untreated soil conditions demonstrating the existence of genetic variation in acid soil tolerance among the durum wheat genotypes.

Comparable with this result, Sisay and Balemi (2014) reported significant variation between barley cultivars in root volume production under lime untreated soil conditions compared to lime treated soils.

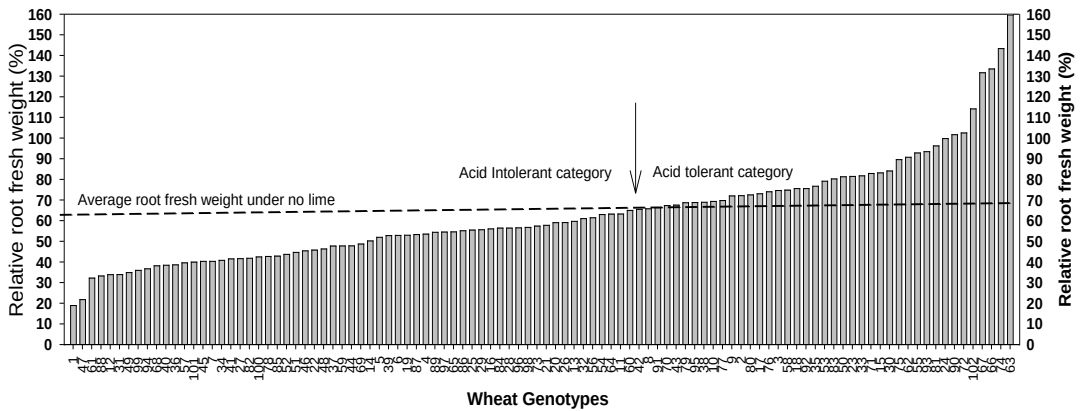


Figure 8: Categorization of acid tolerant and intolerant genotypes based on relative root fresh weight

Relative shoot yield

Relative shoot yield was computed as the yields under no lime soil condition expressed as a percentage of shoot yields under limed conditions for the same treatment. In this study, relative shoot yield varied considerably among the durum wheat genotypes ranging between 15.2% for genotype 87 to 93.3% for genotype 67. A similar observation was made by Tang *et al.* (2003) who stated that the relative yields of wheat genotypes on acid soil ranged from 50 to 89% of yields on lime treated soils. In this study, genotypes such as 102, 24, 32, 72, 63, 75 and 81 had a relative shoot yield of 84.2, 81.8, 80.5, 72.2, 72, 70 and 69.3% which was higher when compared to durum wheat genotypes 88, 78, 1, 89, 36, 47 and 94 in which a lower relative shoot yields of 16.6, 17, 19, 19.3, 20.7, 22.6 and

23.4% were recorded, respectively (Figure 7, Table 3). Genotypes that had a relative yield above the average (36 durum wheat genotypes or 35.3%) can be classified as acid soil tolerant whereas the rest (66 durum wheat genotypes or 64.7%) can be classified as acid soil intolerant categories. However, in this study, relative shoot yield was not a good parameter for comparing genotypes for acid soil tolerance since most of the selected genotypes based on this parameter produced lower shoot yield under lime treated soil conditions. Similar to this observation, Balemi (2011) reported that comparing genotypes with their relative yield without considering their responsiveness is potentially misleading since high relative yield can result from low yield at high nutrient supply for P efficiency in potato cultivars.

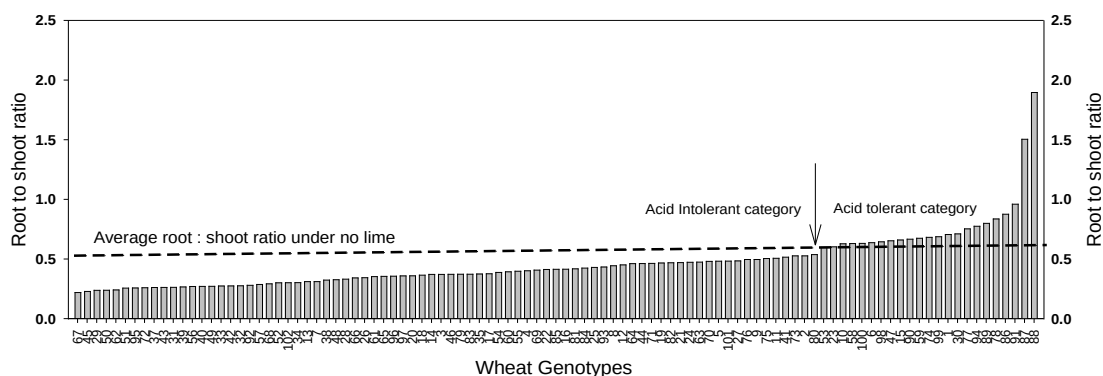


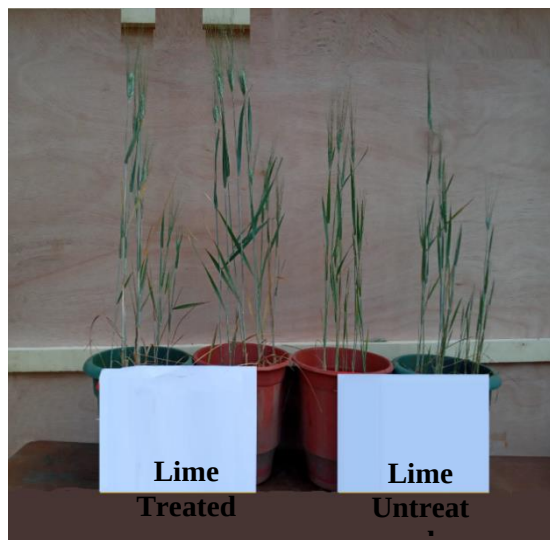
Figure 9: Categorization of acid tolerant and intolerant genotypes based on the root to shoot ratio

Relative root fresh weight

Relative root weight considerably varied among the durum wheat genotypes where 39.2 percent of the tested genotypes were acid soil tolerant while 60.8 percent of the genotypes were categorized as acid soil intolerant group (Figure 8). Variation in relative root yield shows the presence of variability among durum wheat genotypes in terms of acid soil tolerance since most of the genotypes studied were responsive to lime application. Genotypes such as 63, 74, 66, 67, 102, 72, 30, 24, 81, 93, 55, 62, 75, 30, 15 and 71 gave higher relative root weight among which genotypes 81, 24, 30 and 71 were responsive to lime application and best performing under both soil conditions (Figure 8 and Table 3). Parallel with this result, Cosic *et al.* (1994) described that genotypes of durum wheat differed in relative root length and Al tolerance, but the span of the tolerance was relatively narrow.

Root to shoot ratio

The value of root to shoot ratio was highly different among durum wheat genotypes grown under limed and unlimed soil conditions (Table 2). The highest value of root to shoot ratio was recorded from genotype 88 followed by 87, 91, 86 and 78 while the lowest value was obtained from genotype 67 followed by 45, 29, 50 and 62 genotypes. Among the 102 durum wheat genotypes evaluated in this study, only 21 genotypes were categorized under acid soil tolerant based on this parameter (Figure 9). Similar results were reported by Malede *et al.* (2020), Adie and Krisnawati (2016) and Kuswantoro (2015) that, the effects of genotype and genotypes by soil interaction on the root to shoot ratio were highly significant.



Acid Soil Tolerant Durum Wheat Genotype



Acid Soil Sensitive Durum Wheat Genotype

Table 3. Summary of multi-criteria classification of durum wheat genotypes for acid soils tolerance

Parameters	Tolerant Genotypes
Shoot fresh weight	49, 6,81,37,2,70,71,3,4,42,43,18,60,39,96,7,24,10,2,32,17,56,49,35,74,51,62
Shoot dry weight	49,102,81,43,32,4,37,39,62,96,6,56,42,24,70,3,18,51,40,2,66,38,71,17
Root fresh weight	81,91,70,74,90,24,71,15,30,75,2,98,86,64,53,41,77,60,4,32,35,73,99
Root dry weight	6,90,91,74,24,81,15,70,2,86,71,100,98,4,41,99,64,60,96,101, 18, 3, 63, 93,77,75, 102,53
Root volume	6,99,98,91,81,90,73,41, 102,60,2,58,70,19,18,96,17,74,38,30,93,49,100,101,94
Root-shoot ratio	88,87,91,86,78,89,94,77,30,1,99,74,59,90,15,47,98,6,100,58,10
Relative shoot yield	67,102,24,32,72,63,75,81,66,50,77,33,62,55,42,4,31,43,10,3,37,64,93,90,71,70,56,54,38,26,17,83
Relative root weight	63,74,66,67,102,72,90,24,81,93,55,62,75,30,15,71,33,23,50,83,53,35,92,18,58,76,3,17,80,2
Genotypes selected using different traits	81, 24, 2, 71,90, 74, 70, 6, 18, 102, 17 98, 4, 60, 96, 99, 15, 62, 32, 93, 91, 77, 30, 75

Common ≥ 4

Conclusion

Results of the durum wheat genotypes screening experiment for tolerance to soil acidity and responsiveness to lime application showed the presence of considerable variability among the genotypes under lime untreated and treated conditions. Shoot fresh and dry weights, root fresh and dry weights, relative shoot and root yields, root to shoot ratio and root volume were used to screen the genotypes. Genotypes showing superior performance in terms of the most parameters were selected as acid soil tolerant and responsive to lime application. Accordingly, genotypes 81, 24, 2, 71, 90, 74, 70, 6, 18, 102, 17, 98, 4, 60, 96, 99, 15, 62, 32, 93, 91, 77, 30, 75 were identified as consistently acid soil tolerant durum wheat genotypes. Among these, thirteen of them (81, 71, 90, 70, 6, 98, 4, 99, 15, 91, 77, 30 and 75) were Ethiopian land races, two of them (2 and 60) were ICARDA materials, four of them (18, 102, 96 and 62) were CIMMYT materials, two of them namely, Tesfaye and Asasa (32 and 93) were Ethiopian improved varieties, and three of them (24, 74 and 17) were Debre Zeit Agricultural Research Center breeding program advanced lines. Thus, the identified acid soil tolerant durum wheat improved varieties can be recommended for acid soil affected areas and the rest tolerant genotypes can be used as parental lines in the durum wheat breeding program to develop tolerant varieties for acid soil prone areas of Ethiopia. Moreover, the

tolerant genotypes should be further studied using molecular markers to confirm their genetic variation with phenotypic performance and on multi-locations acidic soil areas to investigate for mechanisms of tolerance to soil acidity.

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Appendix Table 1: Description of durum wheat genotypes studied in the trial

No	Genotype Name	Pedigree or Accession number/description
1	CDSS09B00191T-099Y-020M-6Y00M	RBC/7/CMH83.2578/4/D88059//WARD/YAV79/3/ACO89/5/2*S00TY-9/RASCON-37/6/...
2	ICARASHA2	Stj3/Ber/Lks4/3/Ter3
3	CD15DZ_ELT/off/950/2015	YAVA 79/9/ USDA 595/3/D67.3/RABI//CRA/4/ALO/5/HUI/YAV-1/6/ARDENTE /7/HUI/YAV 79/8/...
4	Land race	ETH 208474
5	FIGSDRYWET0144	IRNS382/ID-119026
6	land race	222414
7	land race	236988
8	Breeding pipeline, DWNL p#2	C F4 20 S/4/YAZI-1/AKAKI-4//SOMAT-3/3/AUK/GUIL//GREEN/5/CANELO-9.1//SHAKE-3/...
9	FIGSDRYWET001	OMN87:113/ID-43315
10	Land race	208162
11	CD15DZ_ELT/off//1086/2015	CMH83.2578/4/D88059//WARD/YAV 79/3/AC089/5/2*S00TY-9/RASCON-37/6/1A.1D 5+1.06/...
12	CD15DZ-ELT/off/935/2015	CORDEIRO/9/GUAYACAN INIA/GUANY/8/GEDIZ FG0//GTA/3/SRN-1/4/TOTUS/5/ENTE/MEXI-2//...
13	CD15DZ_ELT/off/994/2015	JUPARE C 2001* 2/RBC/5/MOHAWK/3/GUANAY//TILD-1/LDTUS-4/4/ARMENT //SRN- 3/...
14	DURUM_PANEL_UNIBO-054	D333/GAVIOIA/4/AVETORO//ALUINCO/D/EIOD/ID-MARJANA MOROCCO
15	Land race	202012
16	Ude	CHEN/ALTAR84//JO69
17	2015 offseason DW/F3 DZ #33	Yere/Mova/DZ 2013meh F1 P#9/DZ 2014meh F2 P#9-2
18	CD15DZ-ELT/off/802/2015	GEROMTEL-3/9/GUANCAN INIA/GUANAY/8/GEDIZ FG0//GTA/3/SRN-1/4/TOTUS/5/ENTE/MEXI-2//...
19	CDSS10Y00164S-099Y-030M-5Y-3M-06Y-0B	C F4 20 S/4/YAZI-1/AKAKI-4//SOMAT-3/3/AUK/GUIL//GREEN/5/CANELO-9.1//SHAKE-3/...
20	ICD08-291-0AP	otb4/3/HFN94N-8/Mrb5//Zna-1/4/5+j3//Dra2/Bcr/3/Ter-3
21	CD15DZ-ELT/off/891/2015	GEROMTEL-3/7/ALTAR84/BINTEPE85/3/ST0T//ALTAR84/ALD/4/P0D-11/YAZI-1/5/...
22	DURUM_PANEL_UNIBO-092, ICA#360	ID-DUREX south-western USA, elite
23	CD15DZ_ELT/off/980/2015	ALTAR.84/STINT//SILVER-45/3/GUANAY/4/GREEN-14//YAV-10/AUK/10/CMH79.959/CHEN//...
24	CD15DZ_ELT/off/1103/2015	KOFA/9/USDA595/3/D67.3/RABI//CRA/4/ALO/5/HUI/YAV-1/6/ARDENTE/7/HUI/YAV79/8/...
25	Land race	238498
26	CDSS09B00190T-099Y-036M-18Y-0M	RBC/HUALITA/5/MOHAWK/3/GUANAY//TILO-1/LOTUS-4/4/ARMENT//SRN-3/NIGRIS-4/3/...
27	CD15DZ_ELT/off/1069/2015	CHAM1/4/INRAM-1005//SOMAT-4/INTER/8/3/SOOTY-9/RASOON-37//TILO-1/LOTUS-4/5/...
28	DURUM_PANEL_UNIBO-081	ID-BRAVADUR,SW USA
29	DURUM_PANEL_UNIBO-048	INRA1807 /ID-CHAOUI MOROCCO
30	Land race	8034
31	CD15DZ_ELT/off//248/2015	CF4 20S/4/YAZI-1/AKAKI-4//SOMAT 3/3/AUK/GUIL//GREEN/5/CANELO-9.1//SHAKE-3/...
32	Tesfaye	ARMENT//SRN-NIGRIS-4/3/CANED-9.1/4/TOSKA-26/RASCON-37//SNITSN/5/PLAYERO
33	CD15DZ-ELT/off/889/2015	GEROMTEL-3/7/ALTAR84/BINTEPE85/3/ST0T//ALTAR84/ALD/4/P00-11/YAZI-1/5/...
34	2015 offseason DW/F3 DZ #27	Yerer/UC 1113GPC Lr 19/DZ 2013mehF1P#8/DZ 2014 mehF2 P#8-2

No	Genotype Name	Pedigree or Accession number/description
35	Land race	222655
36	Land race	228862
37	CD15DZ_ELT/off/943/2015	LILE/6/CF4 205/4/YAZI-1AKAKI-4//SOMAT3/3AUK/GUIL//GREEN /5/CANELD-9.1//...
38	Werer	1346/LAHN/BICRE/LOUKOS-4
39	FIGSDWHOTCLD009	ETH74::56/ID-79653
40	FIGSDWHOTCLD051	AFG54::17 ID-85521
41	Land race	238498
42	Land race	ETH 2368039
43	ICARASHA2	Stj3/Ber/Lks4/3/Ter3
44	Utuba	Icajihan42) Omruf1/Stojocri2/3/1718/BeadWheat24//Karim
45	CD15DZ_ELT/off/275/2015	CF4 20S/4/YAZI-1/AKAKI-4//SOMAT-3/3/AUK/GUIL//GREEN/5/CANELD-9.1//SHAKE-3/...
46	CD15DZ_ELT/off/1034/2015	CMH83.2578/4/D88059//WARD/YAV79/3/AC089/5/2*S00TY-9/RASCON-37/6/1A.1D 5+1-06/...
47	CD15DZ_ELT/off/1035/2015	CMH83.2578/4/D88059//WARD/YAV79/3/AC089/5/2*S00TY-9/RASCON-37/6/1A.1D 5+1-06/...
48	FIGSDRYWET016	RUSS199/ID-82244
49	2015 Offseason DW/F3 DZ # 20	Yerer/UC 1113GPC Lr 1908001/59/ DZ 2013mehF1P#7/DZ 2014 mehF2 P#7-2
50	Mangudo	MRF1/STJ2/3/1718/BT//KARIM,TUN
51	2015 offseason DW/F3 DZ #77	Mangudo/Mekuye/DZ 2013 meh DW F1 P#20/DZ 2014 meh DW F2 P#19-8
52	Mukiye	STJ3//BICRE/LOUKOS-4/3/TER3
53	Improved variety	Bichena
54	Durum wheat 301/10-Italy	NA
55	FIGSDRYWET134	IRAN931:19
56	QUAMY	FLAMINGO,MEX/CRANE//FLAMINGO/3/HUIT[2837][3589]; TEZONTLE/YAVAROS-79//HUITLE/3/ALTAR
57	2015 offseason DW/F3 DZ #19	Yerer/UC 1113GPC Lr 1908001/59/ DZ 2013mehF1P#7/DZ 2014 mehF2 P#7-1
58	Improved variety	Boohai
59	Land race	208316
60	FIGSDRYWET108	IRNS294/ID-98797
61	CD15DZ_ELT/off/1084/2015	CMH83.2578/4/D88059//WARD/YAV 79/3/ACO89/5/2*S00TY.9/RASCON-37/6/1A.1D 5+1-6/...
62	CD13DZOS F6SR 2013 MS DZLS/97	K0FA/9/USDA595/3/D67.3/RABI//CRA/4/AL0/5/HUI/YAV-1/6/ARDENTE/7/HUI/YAV79/8/...
63	CD15DZ-ELT/off/1032/2015	JUPARE C 2001*2/KHAPLI/5/M0HAWK/4/DUKEM-1//PATKA-7/YAZI-1/3/PATKA-7YAZI-1/11/...
64	Land race	ETH CHEFE-9
65	Durum wheat 301/11-Italy	NA
66	CD15DZ_ELT/off/989/2015	TRIDENT /3*KUCUK/7/CMH83 2578/4/D88059//WARD/YAV 79/3/AC089/5/2*S00TY-9/RASCON-37/6/...
67	AlemTena	Icasyr-1/3/Gcn//Sti/Mrb3
68	CD15DZ_ELT/off/998/2015	JUPARE C 2001*2/RBC /11/PLATA-10/6/MQUE/4/USDA573//QFN/AA-7/3/ALBA-D/5/AVO/HUI/7/...
69	CD15DZ_ELT/off/1000/2015	JUPARE C 2001*2/RBC /11/PLATA-10/6/MQUE/4/USDA573//QFN/AA-7/13/ALBA-D/5/AVO/HUI/7/...

No	Genotype Name	Pedigree or Accession number/description
70	Land race	ETH 203762
71	Land race	ETH 2368039
72	CD15DZ-ELT/off/306/2015	AG 1-22/2*AC089//2*UC1113/3/5*K0FA/5/K0FA/4/DUKEM-1//PATKA-7/YAZI-1/3/PATKA-7/...
73	Land race	236270
74	2015 offseason DW/F3 DZ #70	Mangudo/Mekuye/DZ 2013 meh DW F1 P#20/DZ 2014 meh DW F2 P#19-1
75	Land race	222856
76	CD15DZ-ELT/off/995/2015	JUPARE C 2001*2/RBC/11/PLATA-10/6/MQUE/4/USDA573//QFN/AA-7/3/ALBA-D/5/AV0/HUI/7/...
77	Land race	238531
78	Kilinto	IUMILLO/INRAT-69//BOOHAI/3/HORA/JORRO/4/COCORIT-71[1922][2837]; IUMILLO/INRAT-69//BOOBY/3/HORA/JORRO/4/COCOBAS[1551]; IUMILLO/INRAT-69//BOOHAI/3/HORA/4/COCORIT-71/JORI
79	CD15DZ-ELT/off/1081/2015	CMH83.2578/4/D88059//WARD/YAV79/3/AC089/5/2*S00TY-9/RASCON-37/6/1A.1D5+1-06/...
80	CD15DZ-ELT/off/973/2015	ALAM0:DR/4/ARMENT//SRN-3/NIGRIS-4/3/CANEL0-9.1/5/PLATA-6/GREEN-17//SNITAN/4/...
81	Land race	215411
82	DURUM PANELUNIBO0177 ID-RAZZAK(TUN)	NA
83	CD15DZ-ELT/off/849/2015	NASSIRA/10/PLATA-10/6/MQUE/4/USDA573//QFN/AA-7/3/ALBA-D/5/AV0/HUI/7/PLATA-13/8/...
84	Improved variety DU-2018	CGS
85	Land race	208217
86	Land race	227009
87	CDSS09B00408D-5Y-014B-4Y-5B-9Y-3B-06Y-0B	AG 1-22/2*AC089//2*UC1113/3/5*K0FA/5/K0FA/4/DUKEM-1//PATKA-7/YAZI-1/3/PATKA-7/...
88	2015 offseason DW/F3 DZ #20	Yerer/UC 1113GPC Lr 1908001/59/ DZ 2013mehF1P#7/DZ 2014 mehF2 P#7-2
89	Yerer	CHEN/TEZONTLE/3/GUILLEMOT//CANDEAL-II
90	Land race	238555
91	Land race	236269
92	CDSS09B00203T-099Y-066M-2Y-0M	CIT71/5/MOHAWK/4/DUKEM-1//PATKA-7/YAZI-1/3/PATKA-7/YAZI-1/7/CMH83.2578/4/D88059//...
93	Asasa	CHORLITO/YAVAROS//FREE-GALLIPOLI/3/FREE-GALLIPOLI/CANADIAN-RED/4/FREE-GALLIPOLI/DON-
94	FIGSDRYWET091	PEDRO/5/HUITLE
95	CD15DZ-ELT/off/1239/2015	ETH731::112/ID-90482
96	CDSS09B00067S-099Y-035M-3Y-0M	GER0MTEL-3/8/ST0T//ALTAR84/ALD/3/THB/CEP7780//2*MUSK-4/6/EC0/CMH76A.722//...
97	CD15DZ_ELT/off/1024/2015	STORLOM/3/RASCON-37//TARRO-2//RASCON-37/4/D00003A/5/1A.1D5+1-06/3*Mojo/3/AJAIA-12/...
98	Land race	JUPARE C2001*2/1M/10/KOFA/9/USDA 595 /3/D67.3/RABI//CRA/4/ALD/5/HUI/YAV-1/16/...
99	Land race	222859
100	Improved variety	210817
101	Land race	Foka
102	CD15DZ_ELT/off/1006/2015	208215
		JUPARE C2001*2/RBC/6/STORLOM/3/RASCON-37/TARRD-2//RASCON-37/4/D00003A/5/...

Combining Ability of Maize Inbredlines for Secondary Traits of Adaptation to Multiple Cropping Systems

Alemeshet Lemma*¹ and Firew Mekbib²

¹Melkassa Agricultural Research Center, P.O.Box 436, Adama, Ethiopia; ²Haramaya University
P.O. Box 138, Dire Dawa, Ethiopia; E-mail: alelgc98@gmail.com

Abstract

Selecting genotypes based on secondary has been employed in crop improvements to various managements. However their importance in maize breeding has been limited. This study was conducted to identify high yielding maize hybrids and to study combining abilities of maize inbredlines for secondary traits of adaptations to maize-bean intercropping. Maize genotypes ($G=42$) were planted at two locations in 6×7 α -lattice design as maize-bean intercrop and as sole maize. All data were collected and analyzed for individual Management (M) and Environments (E) followed by across M and E using random model in SAS. Significant G, E, M, Line (L) and Tester (T) effects were observed for most of the traits measured while $L \times T$, $E \times M$, $E \times G$, $M \times G$, $E \times M \times G$, $M \times L$, $M \times T$ and $M \times L \times T$ effect for few. Relative reduction (RR) varied from -11.7% to +5.4%. Stalk diameter (SD), Yield (GY), Leaf area/area index (LA/LAI) and Ear height (EH) of the G decreased opposed to Plant height (PH) and Leaf number (NL) in maize-bean intercropping. Heritability (H^2) ranged from 0.49(LAI) to 0.98(EH). General combining ability (GCA) effects for L varied from -0.77** to 0.89** for GY, -54.07** to 95.4** in leaf area (LA); -23.6** to 25.1** in PH, -1.42** to 2.0** in SD and -0.99** to 1.35** in NL. Four hybrids (Entry: 2, 3, 4 and 18) performed well under sole maize and showed resilience under maize-bean intercropping conditions were recommended for possible release. Five lines (L2, L3, L4, L18 and L19) showed desirable GCA effects across managements were identified to start crossing program.

Keywords: Secondary traits, Line, Tester, Combining Abilities, Management

Introduction

Modern plant breeding majorly focused on developing genotypes targeting superior yield under high input and mono-culture conditions, desirable above ground traits and wider adaptation. However, crops has

been grown under low input, intercropping or conservation agriculture in the tropics though unexplained physiological, edaphic and genetic mechanisms involved (Francis, 1985; Mahajan et al., 1990). In Ethiopia despite the whole maize growing agro-ecologies are characterized as maize

based cropping systems there was neither maize varieties nor breeding programs to developing varieties adapted to maize based cropping systems until recent efforts of testing previously released varieties and developing hybrids that adapt well for both cropping systems (Dagne et al, 2012).

Selecting genotypes based on secondary traits have key role in certain stress environments without relying on yield data (Mahajan et al., 1990; Banziger et al., 2000). Unlike drought, heat or low nitrogen stresses, there are no well-defined secondary traits of adaptation to multiple cropping systems. However plant height, maturity days, stalk lodging and leaf area are considered as secondary traits of adaptation (Mahajan et al., 1990; Smith and Zobel, 1991).

Combining ability (CA) studies has been utilized in maize breeding since the realization of heterosis in hybrid breeding (Griffing, 1956). Selecting inbredlines based on secondary traits' CA under stressed environments is correlated to selection under optimum environments based on yield data (Banziger et al., 2000). The secondary traits of adaptation to multiple cropping systems are targeted to improve the efficiency of resource utilization of the component crops and improve productivity of the maize based cropping systems.

Since the launch of Sustainable Intensification of Maize-Legume

Cropping Systems for Food Security in Eastern and Southern Africa (SIMLESA) project in 2010/11 the need of getting compatible maize varieties for different cropping systems became important. However there were no breeding programs for maize compatibility improvement for different cropping systems at the time. Therefore the project had focused on testing the already released maize varieties as the immediate solution and later on to establish breeding programs for maize compatibility to different managements. The project identified that the released maize varieties were not responding well to the different cropping systems (Dagne et al, 2012). They identified Melkassa2 and Nasir as the most compatible with good Land Equivalent Ratio (LER) for the Central Rift Valley while the recently released hybrids like MH130, MH140 and MH138Q were all poor in maize-bean intercropping systems. By the second phase of the project hybrids such as BH546 and BH547 were released for their high yield performance under different cropping systems for mid altitude high potential areas (Dagne et al, 2012). However for drought prone areas, the quest for high yielding maize varieties compatible to different cropping systems remain important. Therefore this study was conducted to identify high yielding maize hybrids compatible to different cropping systems and to study combining abilities of maize inbredlines for yield and some secondary traits of adaptations to maize-bean intercrop systems.

Materials and Methods

Melkassa and Ziway have altitude of 1550 and 1637 masl each with sandy loam and silt soil types and received 870 and 826.8 mm annual rainfall, respectively. The study had 42 maize test crosses and 1 bean variety in 100% maize and maize+50% bean intercrop as per the recommendation by Dagne et al. (2012). Each plot had 2 rows of 4m with spacing of 0.75m x 0.25m. The bean was planted after 25 days of maize planting with spacing of 10cm between plants. All the inbred lines were from CIMMYT. Two single cross testers were ((CML312/CML442 =Tester A) and (CML202/CML395 =Tester B)) used. Melkassa2 and MH130 were used as maize checks whereas Nasir was the bean variety used as the component variety under the maize-bean intercropping experiment. Melkassa2 and Nasir were used in these experiments since the two were the recommended varieties for maize-bean intercropping in the Central Rift Valley Areas. The maize inbred lines were selected based on their drought tolerance genetic background.

A 6x7 α -lattice design (Patterson and Williams, 1976) with two replications were used. Data were collected for Grain Yield (GY), Leaf Area (LA), Plant Height (PH), Ear Height (EH), Stalk Diameter (SD) and Number of Leaves (NL). ANOVA was conducted following Proc mixed procedure of SAS 9.4 (SAS, 2015) and genotypes

were considered as random. The GCA and SCA mean squares were tested against the mean squares of their interactions with locations and managements (Kempthorne, 1957).

Results and Discussions

Mean Performance, Relative Reduction, Variance Components and heritability

Combined analysis across Managements (M) _ revealed that the mean GY of genotypes was 6.1tha⁻¹ and ranged from 4.7tha⁻¹ and 7.3tha⁻¹. The results showed that some entries: (3, 7, 16, 17, 20, 24 and 40) were among the top 20 better performing hybrids affected differently by M (Table 1). Yield loss of -27% (Entry20) were recorded under intercrop conditions while it was the second highest yielder under sole maize. The mean Relative Yield Reduction (RR) recorded due to maize-bean intercrop was -6.5% (Table 1). Overall, 29 genotypes depicted a positive RR value which implied the majority are benefited from their interactions in maize-bean inter-crop system whereas twelve which showed negative RR were negatively affected by the component crop. Among the top ten high yielding hybrids only five of the hybrids (Entries: 2, 3, 4, 18 and 21) remained within the top ten in both cropping systems though significant changes were observed in their rank (Fig.1). The result revealed genotypes depicted

wide range of genetic variability (Table 1). The result showed maize genotypes were different in their adaptation to the different crop management. Similar to this finding, yield loss ranging from -64 to 88.5% was reported from low N stress as contrasted to optimum N level (Dagne, 2008). Davis and Garcia (1983) reported 15 - 30% maize yield loss when maize was inter-cropped with beans, while an increase in maize yield as sole crop was reported (Muraya et al., 2006).

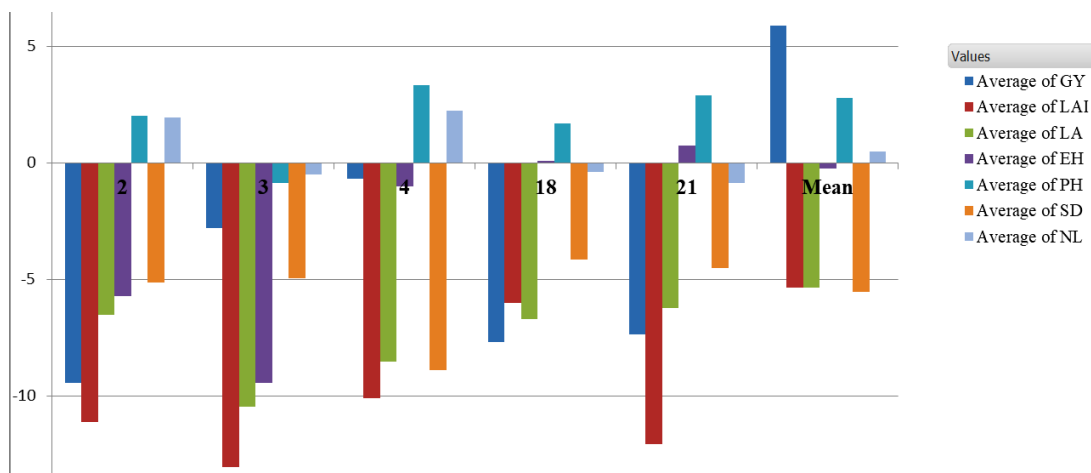
Mean Leaf Area Index (LAI) of maize genotypes were 0.49 and 0.44 whereas the minimum and maximum were between 0.39-0.58 and 0.37-0.50 under sole maize and maize-bean inter-crop conditions respectively with mean Relative Reduction (RR) of -11.4% due to intercropping. Similarly, mean Leaf Area (LA) for them were 867.34cm² and 779.13cm² ranging from 718.45cm²-991.53cm² and 686.64cm²-898.35cm² orderly. Means ear height (EH)/number of leaves (NL) were 111.99cm/111.43cm and of 12.75/12.87 whereas means of plant heights (PH) were 212.17cm and 224.3cm under sole maize and maize-bean intercrop, respectively. Means for stalk diameter (SD) were 21.07mm and 18.86mm for sole maize and

maize-bean inter-crop conditions successively. Relative Reduction (RR) recorded ranged from penalty of -11.7% (SD) due to inter-cropping to increment of +5.4% in (PH) (Table 1 and Fig1). For example minimized LA, LAI, PH and NL in maize varieties are desirable since they allow light penetration and air circulations enhancing photosynthesis in the component crop ultimately enhancing the productivity of the system as a whole (Francis, 1985; Mahajan et al., 1990). It was reported maize genotypes with increased SD resist lodging, on the contrary increased LA, LAI, PH and NL in maize contributed to lodging and ultimately yield loss (Davis and Garcia, 1983; Francis, 1985; Mahajan et al., 1990). The result agreed with previous reports which stated breeding maize for its specific adaptation and compatibility to different maize based cropping systems would improve the productivity of the system as a whole (Francis, 1985; Mahajan et al., 1990) where as others reported negative effects on maize due to maize-bean intercropping or sometimes no significant effects at all (Davis and Garcia, 1983; Francis, 1985; Dagne et al., 2012).

Table1. Combined mean comparison of top ten maize genotypes between crop management systems for GY and secondary traits

Entry	Sole maize						
	GY	LAI	LA	EH	PH	SD	NL
2	8.1	0.50	838.69	99.37	193.20	20.12	11.18
20	7.8	0.50	877.96	97.46	211.27	20.45	11.90
18	7.7	0.53	920.66	103.14	209.46	20.24	12.21
38	7.5	0.49	873.54	98.96	207.81	20.70	12.45
39	7.3	0.50	923.45	88.67	190.12	20.87	12.40
3	7.3	0.52	894.63	116.50	224.51	19.61	13.30
21	7.3	0.51	842.73	109.64	211.26	20.77	12.85
4	7.3	0.49	866.13	123.42	215.79	21.32	12.99
22	7.2	0.44	785.20	110.78	203.06	20.25	12.50
40	7.2	0.50	872.63	100.27	209.94	21.04	12.65
Mean	6.4	0.49	867.34	111.99	212.17	21.07	12.75
Minimum	4.9	0.39	718.45	85.23	190.12	19.06	11.18
Maximum	8.1	0.58	991.53	136.92	241.78	23.71	14.34
Maize-Bean Inter-Crop							
4	7.2	0.40	730.15	120.89	230.59	17.84	13.58
24	7.1	0.45	765.70	119.24	217.03	19.02	14.03
3	6.9	0.40	725.03	96.41	220.57	17.76	13.17
2	6.7	0.40	736.14	88.63	201.18	18.15	11.62
11	6.6	0.47	864.85	113.78	237.99	19.19	13.28
18	6.6	0.47	804.85	103.31	216.64	18.62	12.11
7	6.6	0.47	859.91	130.75	240.73	19.60	14.48
5	6.5	0.47	832.12	121.24	234.93	19.66	13.63
19	6.5	0.43	734.78	87.07	205.47	18.30	11.64
21	6.3	0.40	743.58	111.24	223.86	18.98	12.63
Minimum	5.8	0.37	686.64	81.51	189.88	21.26	11.51
Maximum	4.5	0.50	898.35	136.69	258.47	17.24	14.48
Mean	7.2	0.44	779.13	111.43	224.30	18.86	12.87
%Relative Reduction(RR)	-6.5%	-11.4	-11.3	-0.5	5.4	-11.7	0.9

GY= Grain Yield (tonha⁻¹), LAI=Leaf Area Index (ratio), LA= Leaf Area (cm²); EH= Ear Height (cm); PH= Plant Height (cm); SD= Stalk Diameter (mm); NL= Number of Leaves (no.)



Ent=Entries (2, 3, 4, 18 and 21); Mean= Trial mean; See the remaining traits under Table1.

Fig.1. Relative reductions in GY and secondary traits due to intercropping for five genotypes and the trials means
The genetic variance (GV) for Grain Yield (GY) was 0.31 of which Line while the Tester variance (TV)

contributed 13% and the SCA contributed 7% as opposed to the GCA contributed 30% and the additive genetic variance (AV=1.24) while the dominance variance (DV=0.26) . The GV for SD was 35.72 of which, LV contributed the highest (72%) followed by TV=18% while SCA contributed 5% as compared GCA (53%) at the same time the AV was 2.11 while the DV was 0.19. The GV's for LA/LAI were 84071/0.04 while their LV/TV was 1274/0.0005 and 95.07/0.0001 while their GCA variances were 867/676 out of which 3470/ 2706 were due to AV/DV. The GV's for PH/EH were 7180/6258 while their LV were 154/158, their TV (11.27/ 10.32) were not significantly different from Environmental Variance (EnV). Their GCA/SCA variances were 107.4/104 and 14.6/0.0001 while their AV/DV was 430/414 and 58.32/0.0001, respectively. On the other hand GV for NL was 19.2

whereas LV/TV was 0.41/0.07 and GCA of (0.29) AV of (1.18) was observed. Higher broad (H^2) and narrow senses heritability (h^2) were observed for all the studied traits ranging from 91% (LAI) to 98% (EH and PH) and 49% to 98% of the same traits respectively (Table 2). The result showed that sufficient genetic variation observed among the maize genotypes. For all of the studied traits the AV were higher than the DV which indicated that these traits suited well to be improved through selections (Griffing, 1956). High narrow and broad sense heritabilities indicated that selecting inbred lines with desirable GCA and AV were effective to pass its genetic characteristics to the next generations which might be hybrids or synthetics to be used for production under complex cropping systems such as maize-bean intercropping (Griffing, 1956; Berhanu et al., 2017).

Table2. Genetic variances and Heritability of GY and secondary traits across locations and management combined

Variances	Secondary Traits						
	GY	SD	LA	LAI	PH	NL	EH
GV	0.31	35.72	84071	0.0403	7180	19.20	6258
LV	0.17	0.71	1274	0.0005	154	0.41	158
TV	0.13	0.18	95.07	0.0001	19.14	0.07	0.11
SCA_V	0.07	0.05	676	0.0003	14.6	0.02	0.0001
GCA_V	0.30	0.53	868	0.0004	107.4	0.29	104
AV	1.24	2.11	3470	0.0015	430	1.18	414
DV	0.26	0.19	2706	0.0013	58.32	0.08	0.0001
EnV	0.07	0.20	468	0.0003	11.27	0.07	10.32
H^2	96	92	93	91	98	95	98
h^2	79	84	52	49	86	89	98

DS=Stalk Diameter (mm); LA=Leaf Area (cm²); LAI =Leaf Area Index (ratio); PH= Plant Height (cm); EH=Ear Height (cm); G= Genotype; L=Line; T=Tester; A= Additive; D=Dominance; Er= Error; V= Variances; H²/h²= Broad/Narrow Sense Heritability

Genotype x Environment x Management Effects on Secondary traits

Analysis of Variance (ANOVA) for Environment (E), Management (M) and Genotype (G) showed significant mean squares for most of the studied traits except LAI and EH for E and M, respectively (Table 3). Highly significant mean squares for Hybrids (Hb) and Checks (Ch) Vs Hybrids (ChvsHb) were observed for all the studied traits as compared to the checks (Ch) which showed highly significant mean square for PH and EH. The mean squares for M x G were highly significant for all traits except PH and NL. Significant E x M mean squares were observed for EH, SD and NL as well as significant G x E x M mean squares observed for EH and PH (Table 3). The observed variations were mainly due to M followed by E and G for most of the traits. The contribution as a result of G ranged from 1% (SD) to 48% (EH) while E contributed from 1% (LAI) to 74% (NL) and M contributed from 0% (EH) to 96% (LAI). Significant G, E, and M mean squares depicted sufficient genetic variability among the genotypes for maize-bean intercrop

compatibility while each E and M were different in classifying the genotypes as per their adaptation. Similarly significant GxE, GxM, ExM and GxExM mean squares implied that substantial rank changes in G performance as E and M changed. Different scientists reported significant G, E, M, GxE, GxM, ExM and GxExM effects for traits like GY, PH, LAI and NL in maize and sorghum crops evaluated under different cropping systems with beans (Davis and Garcia, 1983; Feyera et al., 2014; Solomon et al., 2019). Most of the variations observed were contributed by M followed by E and G for most of the traits (Table 3) which indicated that the observed difference were more due to M and E than the genetic variability. Apparently, Solomon et al., (2019) reported the highest proportions of variations were due to E followed by M and G for the traits they studied showing shift between E and M as opposed to our results which might be due to the difference in number of locations and crop management systems used for this study.

Table3. Combined ANOVA for GY and Secondary traits of maize genotypes across Location and management combined

Source	DF	GY	LAI	LA	EH	PH	SD	NL
E	1	13.64**	0.002	18028**	1524**	3541**	37.2**	17.06**
M	1	23.84**	0.29**	682850**	0.23	12916**	440.7**	2.06*
G	41	3.0**	0.01**	18799**	1405**	1628**	8.43**	4.03**
Hb	39	2.98**	0.01**	17471**	1365**	1529**	8.68**	3.89**
Ch	1	1.69**	0.001	0.12	594.1**	2197**	0.06	1.27
ChvsHb	1	4.39**	0.02**	84923**	3988**	6298**	4.85**	13.64**
E x G	41	0.56**	0.001	1974	66.7	64.07	1.23	0.38
E x M	1	0.50ns	0.001	1494	477.6**	153.09	13.6**	38.75**
M x G	41	1.01**	0.003**	4501**	104.5**	121.41	1.38*	0.41
G x E x M	41	0.52**	0.001	2420	77.25*	131.7*	1.26	0.45
Error	160	0.19	0.001	1523	48.62	86.98	0.88	0.39
CV		7.11	7.09	4.73	6.25	4.28	4.72	4.88
Mean		6.14	0.47	824.8	111.6	218.1	19.94	12.79
H ²		96	93	91	98	98	92	95
h ²		79	52	49	98	86	84	89
% Contribution E		33.7	1	3	52	20	8	74
% Contribution M		58.89	96	95	0	71	91	9
% Contribution G		7.41	3	2	48	9	1	17

GY=Grain Yield (tonha⁻¹)E=Environment or Location; M= management; G=Genotype; Hb= hybrids; Ch=Checks, CV= Coefficient of Variation (%); Contrib= proportion of Contribution inflicted by G, E and M on the studied traits (%); LAI=Leaf Area Index (ratio), LA= Leaf Area (cm²); EH= Ear Height (cm); PH= Plant Height (cm); SD= Stalk Diameter (mm); NL= Number of Leaves (no.); H²= Broad Sense Heritability (%); h²= Narrow Sense Heritability (%)

Line x Tester ANOVA for Combining Abilities of maize inbredlines of Secondary traits

Significant Environment (E) and Management (M) mean squares observed for most of the studied traits except Number of Leaves (NL) for E and Ear Height (EH)/ Leaf number (NL) for M (Table 4). The GCA for the Line (L) and Tester (T) were significant for most of the studied traits except LA, LAI and EH for T. The LxT mean squares were significant only for GY, LAI and LA. Apparently, the mean squares of ExM interaction was significant for EH, SD and NL; the MxL interaction was significant for GY, LAI and LA. In addition the MxT interaction was found significant for all traits except GY and NL while the MxLxT

interaction was significant for GY, LAI and LA (Table 4).

The genotypic variation due to additive gene effect was much important than the non-additive component for all of the traits contributing from 74% in LAI to 97% in EH. The maximum contribution of GCA (L) was 96% in EH and the minimum was 64% in LAI whereas GCA (T) contributed from 1% in EH to 10% in LAI. On the contrary, the SCA (LxT) contributed the highest 26% in LAI and 20% LA (Table 4). The result depicted that additive genetic variance played very important roles in the inheritance of all traits while the non-additive component was relatively higher in LAI and LA. The result revealed that, the materials can be improved through recurrent

selection to generate improved varieties adapted to the intended E and M as it was suggested by (Griffing, 1956). Significant mean squares of MxL for GY, LAI and LA, MxT for LAI, LA, EH, PH and SD, MxLxT for GY, LAI and LA, ExMxLxT for GY depicted the combining abilities of the inbredlines were more affected due to variations in management than

environment. Similarly, fsignificant L, T, LxT, LxE, TxT for GY, PH and EH were reported from different sets of experiments conducted under contrasting environments of striga infestation, drought, low-N and their optimum counterparts (Mosisa et al., 2008; Badu-Apraku *et al.*, 2015).

Table4. ANOVA for GY and secondary traits for Lines and Testers across locations and managements combined

Source	DF	GY	LAI	LA	EH	PH	SD	NL
E	1	14.7**	0.002**	20870*	1392*	3236**	38.38*	16.89
M	1	22.13**	0.26**	627799**	2.47	12743**	425.1**	2.30
ExM	1	0.29ns	0.001	1321.4	1143**	158.34	29.42**	71.80**
L	19	3.93**	0.01**	27445**	2721**	2762**	14.76**	6.74**
T	1	19.69**	0.03	30996	131.5	3217**	27.0**	12.74*
L x T	19	1.07*	0.004*	7258*	81.93	228.7	1.55	0.54
E x L	19	0.47**	0.002	2304	55.67	70.92	1.56	0.59
M x L	19	1.59**	0.003**	5038**	96.27	166.5	1.29	0.46
E x M x L	19	0.62**	0.001	1873	79.57	82.97	1.25	0.41
E x T	1	0.48ns	0.0001	783.1	8.34	25.24	0.20	1.37
M x T	1	0.31ns	0.01**	25270**	634.7**	329.8*	2.71*	0.58
E x M x T	1	0.05ns	0.001	182.3	52.71	176.7	0.08	1.62
E x L x T	19	0.66**	0.001	1542	70.45	49.88	0.93	0.15
M x L x T	19	0.50**	0.003**	3162*	90.33	77.55	1.44	0.37
E x M x L x T	19	0.40*	0.001	3005	69.32	159.3	0.96	0.31
Error	160	0.2	0.001	1443	50.00	84.64	0.87	0.44
CV		7.21	6.94	4.59	6.29	4.20	4.66	5.17
Minimum		4.7	0.43	769.64	87.35	195.57	18.58	11.86
Maximum		7.3	0.52	922.04	134.3	244.29	22.01	14.20
%Contribution L_GCA		65.1	64	76	96	87	83	85
% Contribution T_GCA		17.2	10	4	1	5	8	8
% Contribution LXT_SCA		17.8	26	20	2	8	9	7

E=Environment or Location; M= management; G=Genotype; CV= Coefficient of Variation (%); Hb= (hybrids or Crosses) L= GCA due to Lines; T= GCA due to Tester; LxT= SCA; LAI=Leaf Area Index (ratio), LA= Leaf Area (cm²); EH= Ear Height (cm); PH= Plant Height (cm); SD= Stalk Diameter (mm); NL= Number of Leaves (no.)

General Combining ability effects of maize inbredlines for Secondary traits

Inbredlines depicted wide range of variability for their GCA effects, ranging from significantly low to high values (Table 5 and 6). For instance; L2, L3, L4, L18 and L19 showed desirable positive GCA effects for GY.

Three inbredlines (L2, L4 and L6) showed significant desirable negative GCA effects for LAI and LA while four inbredlines (L9, L11, L17 and L18) showed significant and positive GCA values for the same traits. Seven lines (L1, L2, L13, L14, L18, L19 and L20) had significant and negative GCA effects for PH and EH while

three lines (L7, L8 and L9) expressed significant positive GCA effects for SD. Similarly, six lines (L2, L12, L14, L17, L18 and L19) showed desirable negative and significant GCA Effects for NL (Tables 5 and 6). The Tester showed significant GCA effects for all traits except for EH. Tester2 (T2) showed significant and desirable GCA effects for most of the studied traits while Tester1 (T1) depicted the opposite. In general, five inbredlines (L2, L3, L4, L18 and L19) showed desirable GCA effects constantly for the studied traits across the two managements (Tables 5 and 6). Significant GCA effects of L showed the genetic variability among the used inbredlines in these experiments. For e.g., from our study 3-7 lines depicted desirable GCA effect for each trait. Positive and significant GCA values are required to select inbredlines for improving traits with the highest economic significance such as GY; PH, EH and LA however inbredlines with significant negative GCA values for PH, EH and LA are required for their compatibility to maize-bean intercropping system. Compatibility is basically reflected as positive Land

Equivalent Ratio (LER) which is a function of good productivity of each component crops (Francis, 1985; Mahajan et al., 1990). For example minimized LA, LAI, PH and NL in maize varieties are desirable since they allow light penetration and air circulations enhancing photosynthesis in the component crop ultimately enhancing the productivity of the system as a whole (Francis, 1985; Mahajan et al., 1990). Maize genotypes with increased SD resist lodging, on the contrary increased LA, LAI, PH and NL in maize contributed to lodging and ultimately yield loss (Davis and Garcia, 1983; Francis, 1985; Mahajan et al., 1990) which suggested that negative GCA effects are more desirable for all traits except GY and SD. Despite lack of report on combining abilities of maize inbredlines under sole maize and maize-bean intercrop interactions, findings from (Mosisa et al., 2008; Badu-Apraku et al., 2015; Berhanu et al., 2017) showed that inbredlines depicted variability in their performance under contrasting environments.

Table 5. GCA Effect for GY and secondary traits of adaptation for Lines and Testers across managements

						Sole Maize					
Line	GY	LA	PH	SD	NL	Line	GY	LA	PH	SD	NL
1	0.54*	-3.14	-2.29*	0.1	-0.45	14	-0.7**	-18.51	-18.03**	-1.68**	-0.75*
2	1.27**	-58.72*	-14.86**	-0.91	-0.95**	15	-1.1**	-70.55**	12.82**	-1.03	0.36
3	0.57*	10.87	3.17**	-0.22	0.51	16	0.3	16.61	17.44**	0.82	0.62
4	0.19	-50.04*	-2.75*	0.03	0.2	17	0.2	47.41*	3.89**	-0.19	-0.73*
5	-0.25	-21.29	3.19**	0.54	0.14	18	1.15**	24.8	-4.61**	-0.68	-0.48
6	-0.59*	-72.89**	-6.14**	0.26	-0.001	19	0.63*	29.59	-25.9**	-0.72	-0.83*
7	-0.8**	45.98*	11.19**	1.81**	0.7*	20	1.08**	7.64	-2.22*	-0.38	-0.49
8	-0.57*	-34.65	24.1**	2.18**	0.79*	T1	0.24**	19.3**	4.06*	-0.39*	-0.26*
9	0.05	67.65**	21.49**	2.05**	1.44**	T2	-0.24**	-19.3**	-4.06*	0.39*	0.26*
10	-0.43	16.39	1.06	0.88	0.45	SE_L	0.25	21.73	4.8	0.54	0.34
11	-1.06**	94.31**	-1.36	-0.36	0.25	SE_T	0.08	6.87	1.52	0.17	0.11
12	-0.35	-16.05	-2.28*	-1.52**	-0.35	SE(Dif)L	0.35	30.73	6.78	0.77	0.48
13	-0.13	-15.42	-17.91**	-0.99	-0.42	SE(Dif)T	0.11	0.59	0.28	0.09	0.07
Maize-Bean Inter-crop											
1	0.21	-28.7	-4.5	-0.08	-0.47	14	-0.47*	-11.7	-13.3**	-1.12**	-0.37
2	0.54**	-50.7**	-21.7**	-0.36	-0.96**	15	-0.49*	10.2	6.9	-1.19**	0.24
3	0.31	-49.5**	-6.6	-1.1**	0.43	16	-0.06	22	19.1**	0.61	0.31
4	1.2**	-35.7*	-1.5	-0.44	0.88**	17	-0.09	60.3**	6.5	-0.08	-0.69*
5	0.01	16.7	2.7	0.76*	0.52	18	0.45*	38.8*	-5.8	-0.06	-0.71*
6	0.01	-42.9*	-8.8	-0.31	-0.11	19	0.4*	-36.3*	-21.7**	-0.57	-1.03**
7	-0.38*	56.6**	14.8**	0.96**	1.23**	20	-0.37*	-43.9*	-18.4**	0.14	-0.34
8	-0.16	-21.7	21.9**	1.75**	0.32	T1	0.28**	1.9	2.41*	-0.19*	-0.16*
9	-0.6**	80.7**	28.3**	2.05**	1.28**	T2	-0.28**	-1.9	-2.41*	0.19*	0.16*
10	-0.71**	-28.6	-0.9	-0.43	0.05	SE_L	0.18	16.99	4.49	0.34	0.28
11	0.12	97.9**	10.9*	0.44	0.5	SE_T	0.06	5.37	1.42	0.11	0.09
12	-0.05	-35*	1.1	-0.49	-0.85**	SE(Dif)L	0.57	24.03	6.35	0.48	0.39
13	0.12	1.3	-8.8	-0.5	-0.22	SE(Dif)T	0.08	7.6	2.01	0.15	0.12

L= GCA due to Lines; T= GCA due to Tester; LXT= SCA; LAI=Leaf Area Index (ratio), LA= Leaf Area (cm²); EH= Ear Height (cm);

PH= Plant Height (cm); SD= Stalk Diameter (mm); NL= Number of Leaves (no.), SE= Standard Error; SE (Dif) = Standard Error difference

Table 6. GCA Effect for secondary traits of adaptation for multiple cropping systems across location and managements

Line	Traits						
	GY	LAI	LA	EH	PH	SD	NL
1	0.36	-0.01	-15.08	-7.3*	-3.3	0.004	-0.48
2	0.89**	-0.03*	-54.07**	-11.6**	-18.1**	-0.71	-0.99**
3	0.48*	-0.02	-18.12	-3.2	-2.1	-0.61	0.42
4	0.68**	-0.02	-41.55*	7.6*	-2	-0.21	0.57*
5	-0.11	-0.001	1.11	6.4	3.8	0.8*	0.36
6	-0.31*	-0.04*	-57**	-0.7	-7.5	-0.05	-0.03
7	-0.54*	0.03*	50.14*	20.6**	12.6*	1.46**	0.96**
8	-0.32	-0.01	-29.23	16.8**	22.6**	1.97**	0.51
9	-0.3	0.05**	73.81**	15.9**	25.1**	2**	1.35**
10	-0.58*	-0.01	-4.58	7.9*	0.6	0.29	0.24
11	-0.5*	0.04*	95.4**	3.4	4.9	0.002	0.38
12	-0.19	-0.01	-27.3	-5.9	-0.6	-1.01*	-0.58*
13	-0.07	-0.01	-5.89	-8*	-12.9**	-0.82*	-0.29
14	-0.58*	1E-04	-14.11	-15.7**	-15.8**	-1.42**	-0.58*
15	-0.77**	-0.02	-30.97	0.5	9.2	-1.09*	0.31
16	0.13	-0.001	16.58	21.9**	18.1**	0.69	0.49
17	0.07	0.05**	56.62**	5.4	5.6	-0.05	-0.71*
18	0.83**	0.03*	30.36*	-10.1**	-5.7	-0.34	-0.6*
19	0.52*	-0.01	-3.24	-25.1**	-23.6**	-0.67	-0.95**
20	0.32	-0.02	-22.86	-18.5**	-10.9*	-0.25	-0.37
T1	0.26**	0.01	10.2	-0.7	3.28**	-0.3*	-0.21*
T2	-0.26**	-0.01	-10.2	0.7	-3.28**	0.3*	0.21*
SE_L	0.22	0.02	19.51	3.5	4.7	0.47	0.31
SE_T	0.07	0.01	6.17	1.1	1.47	0.15	0.1
SE(Dif)L	0.31	0.023	27.593	4.93	6.595	0.665	0.442
SE(Dif)T	0.10	0.01	8.73	1.56	2.09	0.21	0.14

Note: Parameters are illustrated under Table5.

Conclusion and Recommendation

Even though the year, management and locations involved in this experiment is very limited, the significant interaction effect between G, M and E for those traits showed the need to start breeding for specific than wider adaptation. However breeding for specific adaptation is only effective if the market size for such varieties are large enough and the seed sector is well established. The existing breeding strategy in Ethiopia is to develop varieties adapted to the multiple biotic and abiotic stresses and suitable to mono cropping system which

completely ignores small scale farmers producing maize under different cropping system. Therefore farmers were left with no choice but to use either their own land races, old varieties or those varieties released for mono cropping which usually resulted in poor production or productivity of the maize based cropping system. The result from this research showed that it is possible to develop high yielding varieties across different maize based cropping systems which gives alternative modern varieties for small scale farmers practicing multiple cropping system so that they can improve the low maize based cropping system production and productivity without compromising the production

and productivity of those farmers growing maize as a mono crop. Therefore we recommend four maize hybrids (Entry 2, 3, 4 and 18) varieties that performed well under sole maize and showed resilience under maize-bean intercropping conditions for possible release. These varieties were not only the top performers consistently across the two cropping systems but also were significantly high yielder than the recently released hybrid check and the recommended check for maize-bean intercropping compatibility in the central rift valley areas of Ethiopia.

Despite lack of any lines to be used as checks for comparing the performance of the lines used in this experiment, five inbredlines (L2, L3, L4, L18 and L19) depicted desirable genetic variations across the two cropping systems consistently. Therefore we recommend these inbredlines to start crossing program to develop hybrids and synthetics that are suitable for both mono crop and maize based diverse cropping systems within the drought stress affected maize growing agro-ecology of Ethiopia.

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Optimizing Sowing Depth and Seeding Rate of Pelleted Seed for Reducing Lodging and Improving Yield of Tef

¹Bizuwork Tafes, ¹Gebrekidan Feleke, ¹Almaz Meseret Gezahegn, ¹Sisay Eshetu,

¹Solomon Chanyalew, ¹Worku Kebede, ²Zerihun Tadele, and ³Dominik Klauser

¹Ethiopian Institute of Agricultural Research, Debre Zeit Agricultural Research Center, P.O. Box 32, Debre Zeit, Ethiopia; ²University of Bern, Institute of Plant Sciences, Altenbergrain 21, CH-3013 Bern, Switzerland; ³Syngenta Foundation for Sustainable Agriculture, Basel, Switzerland

Abstract

The low productivity of tef is associated with problems inherent to tef botany and lodging. The small seed size of tef poses a major inheritance problem during sowing operations. Techniques such as pelleting seed with organic matter are effective to make them uniform in size and shape. A field study was conducted to determine optimum sowing depth and seed rate of pelleted tef for reducing lodging, and improving productivity of tef under Vertisol conditions during two consecutive cropping seasons (2019 and 2020). A factorial combination of four sowing depths (0, 1, 2 and 3 cm) and three pelleted tef seed rates (60, 90 and 120 kg/ha~5, 7.5 and 10 kg/ha of un-pelleted tef) were used as a treatment. The experiments were laid out in RCBD with three replications. Sowing depth had a significant effect on biomass and grain yield of tef. Tef sowing at the shallowest depth (0 cm) and 1 cm gave the highest biomass yield (11889 kg/ha and 9639 kg/ha, respectively) and grain yield (2786 kg/ha and 2536 kg/ha, respectively). In contrast, the deepest sowing (3 cm) reduced biomass and grain yield of tef. Seed rate played an important role in the biomass yield of tef, the highest biomass yield (10399 kg/ha) was recorded from the 120 kg/ha seed rate of pelleted tef. Regarding lodging, the deepest sowing and lowest seed rate reduced lodging index and a number of root lodged plant. The average lodging index for the deepest sowing (3 cm) was 30.8%, while the shallowest (0 cm) was 69.3%. The result revealed that pelleted tef seed can successfully emerge from a depth of 1 cm without any apparent penalty of yield. Tef even emerged from 2 to 3 cm depth, while showing reduced lodging, but these had a yield penalty. Therefore, it can be concluded that a 1 cm sowing depth and 90 kg/ha pelleted tef are optimal for sowing pelleted tef seed for reducing lodging and improving yield.

Keywords: Lodging, Pelleted seed, Sowing depth, Seed rate, Tef

Introduction

Ethiopia is the origin and center of diversity for many economically important crops including tef [*Eragrostis tef* (Zucc.) Trotter], which belongs to the grass family and genus *Eragrostis* (Vavilov, 1951). Of the main cereal crops grown in the country, tef remains a crucial

food crop in terms of area coverage, production size, food and nutritional security as well as commercial value (Solomon *et al.*, 2019). Tef is a resilient crop that outperforms other cereals in terms of its husbandry and utilization efficiency (Minten *et al.*, 2018). Among the cereals grown in the country, tef is the first in terms of acreage, and the second

most important cereal after maize in terms of grain production (CSA, 2020). The mean countrywide productivity of tef is about 1.8 tons/hectare, which is very low as compared to other crops such as wheat 2.9 tons/ha and maize 4.5 kg/ha tone (CSA, 2020). This low tef yield is seemingly explained by the limited knowledge about possible avenues for improving tef productivity, combined with problems inherent to tef botany (Habtegebrial *et al.*, 2007; Berhe *et al.*, 2011; Fufa *et al.*, 2011).

The small size of tef seed poses problems during sowing and makes it difficult to control population density and its distribution. In addition, sowing depth and lodging of tef is a major cause in tef production (Seyfu, 1997). Tef is traditionally sown by manual seed broadcasting on wet soil and lightly covered with packed soil to prevent drying out (Ben-Zeev *et al.*, 2018). For instant, shallow sowing depth would require avoiding seed desiccation in scattered rainfall or dry period. Ethiopian tef growers believed that tef seed will not emerge from 5 to 7 cm sowing depth (Bimro, 2016). However, under hot and dry soil conditions, deeper sowing of tef is recommended to guarantee seedling establishment (Kebede *et al.*, 1986). As a general rule of thumb, seeds should not be sown deeper than five times their width (Paff and Asseng, 2018), as tef tiny seed size (0.4-0.7mm width and 1-1.4 mm length) thus maximum sowing depth is 2-3 mm. Elsewhere, the recommended sowing depth for tef is between 3 up to 15 mm (Andrea, 2008).

Plant lodging is defined as the permanent displacement of the stem from the vertical, which is caused by environmental conditions as well as morphological plant traits (Seyifu, 1983). It is the most

significant yield-reducing problem in tef, accounting for up to 35% of yield losses (Van Delden *et al.*, 2010; Berry *et al.*, 2004). Certain studies relate tef lodging to stem characteristics (stem lodging) (Würschum *et al.*, 2017), while others (Van Delden *et al.*, 2010 and Alemu and Tefera, 2019) pointed to shoot-root junction traits (root lodging) as major contributors to tef lodging. In cereal crops like wheat, deeper sowing has been shown to induce a longer, deeper root crown, thus improving plant anchorage and reducing root lodging and hence, reduced lodging could be an additional benefit of deeper sowing in tef (Pinthus, 1974; Ben-Zeev *et al.*, 2020). The impact of seed rate on lodging was studied in various cereal crops. In wheat (*Triticum aestivum* L.), lower seed rate and direct drilling increased the size of the root plate, plant anchorage, and crown root length, thus reducing the risk or severity of lodging (2004). In rice (*Oryza sativa*), lower seed rates were associated with lower mutual shading, resulting in stronger stems, higher plant biomass, shorter basal internodes, and reduced lodging (Shah *et al.*, 2019). In addition, maize (*Zea mays* L.), low plant densities led to shorter basal internodes, higher culm and root diameters, and more roots, resulting in less lodging (Xue *et al.*, 2017). Very recently (Ben Zeev *et al.*, 2020), the study demonstrated for the first time, the feasibility of tef production under irrigated Mediter-ranean conditions and the potential of a reduced sowing rate as a remedy for lodging.

In seed technology, seed pelleting is a most useful technique for increasing the size of small seeds like tef, and coating them to make bigger, rounder, smoother, and more uniformly-sized seeds. The pelleting technique that can be adopted indirect sown small-seeded crops like

sesame is seed pelleting, which modifies the microenvironment of the seed in favor of the seed (Alex *et al.*, 2017). It is a coating technique that is used for handling of small-seeded crops and increases precision planting. It is not only increases the seed size but also reduces the seed rate, makes crop and seedling establishment uniformly and maintains the seed moist by making moisture available from the soil. However, to date, there has not been enough information regarding on pelleted tef seed for tef husbandry. Thus, keeping in view the above background and considering the importance of tef in the national economy, the study was designed to determine optimum sowing depth and seed rate of pelleted tef seed concerned on seedling emergence, growth and development, lodging, and productivity of tef.

Materials and Methods

Description of experimental site

The trial was conducted at Debre Zeit Agricultural Research Center research field for two consecutive cropping seasons (2019 and 2020) under rain-fed conditions. Debre Zeit Agricultural Research Center is located in East Shewa Zone of Oromia Regional State of Ethiopia. It is found 47 km away from South East of Addis Ababa, Ethiopia. Its geographical location is 8° 44' N latitude and 38° 58' E longitude. The altitude is about 1900 meters above sea level while, the majority of trial fields are heavy soils (*Vertisol*) with few pockets of light soil (*Alfisols/Mollisols*) (WRB, 2006). The rainfall pattern was well distributed in the 2019 and 2020 cropping months (June-October) with 678 mm, and 615 mm, respectively, at DZARC (Figure 1). Generally, rainfall received in the five months between planting to physiological maturity was optimum.

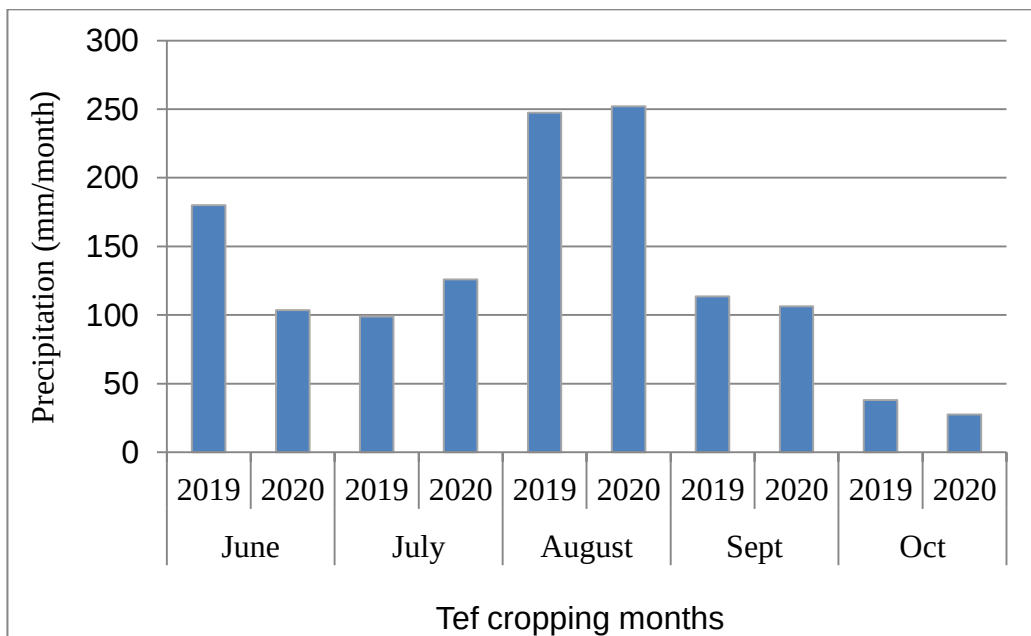


Figure 1. Rain fall distribution (mm) of during tef growing seasons (June to October) in 2019, and 2020 at DZARC.

Seed pelleting procedures

Pelleting process was done at Debre Zeit Agricultural Research Center (DZARC) in tef breeding laboratory room using a seed pelleting automatic machine (A-2000 Stockerau-Austria, Central CoATER type CCLAB). Tef variety, DZ-Cr-438 RIL91A (Dagme), which represent long maturity groups for the central highlands, was used as a test variety. The machine used in the pelleting process is composed of a convex stainless steel chamber, which has an adjustable and automated rotation speed. The pelleting technique consisted of 100 g of tef seeds, sawdust (wooden meal) 270 g, dry binder (donalim) 15 g and clay (pansil) 15 g followed by 100 g wet binder and 1140 g water were mixed in the plastic jar, intercalated with the coated materials, which were added until the pellets achieved the required diameter to be classified by a 2-2.4 mm round hole sieve. The binders, in the form of a powder, were mixed with the products along with water sprays during the pelleting process. Those seeds that did not reach a minimum required size, 2-2.4 mm, were returned to the machine to complete the pelleting process, the procedure was repeated until all the pellets reached minimum established the width of 2-2.4 mm.

Experimental design and field management

The experiment was laid out in Random Complete Block Design (RCBD) with a factorial arrangement using three seed rates (60, 90 and 120 kg/ha) of pelleted seed which are equivalent to (5, 7.5 and 10 kg/ha of un-pelleted tef seed), respectively, and four sowing depth [0 (control), 1, 2, and 3 cm]. Soil preparation included deep tilling and flattening with a heavy-duty leveler and crumble roller tool to obtain a smooth and even seedbed. A 2 m by 1.5 m plot size was used. Each treatment was replicated three times. A hole was made along in 20 cm row spacing using a hoe. To ensure an accurate sowing depth, the soil hole was measured by the ruler before planting then the seeds were sown using manually drilling and covered with a thin layer of soil.

Assessment of agronomic traits

Seedling emergence was recorded after 50% of seed emerged in each plot. Days to heading was scored as 50 % of the plant gave heading. Plant height was measured from the ground to the tip of tillers using a ruler and the mean value were determined in cm. Total tillers (both effective and non-effective) and productive tillers (effective tillers) were determined the crop reached physiological maturity by counting all the tillers from five randomly selected plants in each net plot and then calculating the mean value. Panicle length was measured in the field when the crop reached at physiological maturity. Five plants were randomly selected from each plot and measurements were made using a ruler from the bottom to the top of the panicle and calculated the average panicle length per plot. Aboveground biomass yield (AGBY): At maturity, the whole aboveground plant parts, including leaves, stems, and seeds from the net plot area in each plot were harvested, sun-dried and weighed and then expressed in kg ha⁻¹. Harvest index (HI) was calculated from the ratio of grain yield (GY) (GY at 12.5% grain moisture content to the above-ground biomass (AGB) (seed + straw) and it is expressed in percentage. Grain yield (GY): after harvesting, threshed grains were separated, cleaned the seed, and then after the grain were weighed by electronic balance. The GY was corrected to a moisture content of 12.5%, wet bases while a moisture tester was employed for measuring the moisture content.

Assessment of lodging traits

Lodging index: the degree of lodging was assessed just before the time of harvest by visual-observation based on the scales of 1-5 where, 1 (0-15°) indicates no lodging, 2 (15-30°) indicates 25% lodging, 3 (30-45°) indicates 50% lodging, 4 (45-60°) indicates 75% lodging and 5 (60-90°) indicates 100% lodging (Donald, 2004). The scales were determined by the angle of inclination of the main stem from the vertical line to the base of the stem by visual observation. Each plot was divided based on the displacement of the aerial stem into all scales by visual observation. Then each scale was multiplied by the

corresponding percentage given for each scale and the average of the scales represents a lodging percentage of that plot. Root lodging was assessed 10 days after physiological maturity. A metal frame with inner dimensions of 50 cm by 50 cm was placed across the crop in two spots per plot and the number of roots lodged plants within this frame area was counted and recorded.

Statistical analysis

Statistical analysis was conducted using SAS software and included a two-way analysis of variance. When significant treatment effects occurred, means separation were compared using LSD (0.05).

Results and Discussion

Days to seedling emergence and plant establishment

Days to seedling emergence in tef were significantly ($p \leq 0.05$) affected by the main effect of sowing depth (Table 1). Nevertheless, the main effect of the pelleted tef seed rate and the interaction of sowing depth with seed rate were nonsignificant. Days to seedling's emergence were delayed by 8.4 days from the shallowest sowing depth (0 cm) to 15.9 days at the deepest sowing (3 cm). However, there was nonsignificant difference in days required to germinate between 0 and 1 cm planting depth. Seedling emergence days were significantly delayed by 89% in the 3 cm sowing depth treatment as compared to 0 cm

planting depth, but there was no significant difference from the seed planted at 2 cm sowing depth (Table 1). The delayed seedling emergence in deeper sowing (3cm depth) might be due to lower soil temperatures and took longer shoot grew result in delayed seedling emergence. According to Sharma *et al.* (2019), the seedling emergency has a direct impact on seed-to-soil contact as well as seeds' access to adequate moisture and temperature. Days of emergency were significantly delayed at the deepest sowing compared to the other shallow depths. Similar studies by Kirby (1993); Ben-Zeev *et al.*, (2020) found that, sowing tef at 1 or 2 cm depth has no or only minor effects on seedling emergence, however, sowing at 3 cm depth had a significant delay on this variable.

The days to heading were significantly affected by sowing depth but days to maturity, plant height and panicle length were not significantly affected by sowing depth (Table1). Similarly, the main effect of pelleting tef seed rate and the interaction effects of two factors were not significantly affected the above-mentioned traits. Days to heading was ranged from 58 to 61.5 days from 0 cm sowing depth and at 3 cm, respectively, and were generally prolonged days to heading as sowing depth increased (Table 1). This might be due to delayed seedling emergence in deeper sowing. Similar results were reported by Kirby (1993) and Ben-Zeev *et al.* (2020), sowing of tef in 3 cm depth was delay days to heading as compared to shallow sowing depth (0 cm).

Table1. Effects of pelleted tef seed rate and sowing depth on the seedling emergence and plant growth at DZARC over two years

Treatments	DSE	DH	DM	PH (cm)	PL (cm)
Seed rate (kg/ha)					
60 pelleted ~ (5)	12.7	59.7	104.0	125.85	47.7
90 pelleted ~ (7.5)	11.6	59.6	103.6	128.48	47.4
120 pelleted ~ (10)	10.8	58.6	102.6	128.47	47.1
Sowing depth					
0 cm	8.4c	58.0b	101.9	130.18	48.5
1cm	10.2bc	58.8ab	102.9	128.13	47.9
2 cm	12.4ab	58.8ab	103.2	126.21	46.7
3 cm	15.9a	61.6a	105.6	125.88	46.5
CV (%)	2.1	6.2	8.3	6.5	6.6

DSE = days of seedling emergence; DH = days to heading; DM = days to maturity; PH = Plant height; PL= Panicle length; Means with the same letter in columns are not significantly different at 5% level of significance; CV (%) = coefficient of variation.

Total tillers and productive tillers

The main effects of pelleted seed rate and sowing depth had highly significantly affected the number of total tiller and productive tillers per plant. But the interaction effect of the two factors was not significant. The highest number of total tillers (9 plants) and productive tillers (6.7 plants) were obtained from the low pelleted seed rate (60 kg/ha) (Figures 1 and 2), respectively, but was not significantly different from the rate of 90 kg/ha. On the other hand, the lowest number of total tillers (7 tillers/plant) and productive tillers (5 tillers/plant) were produced at the highest pelleted seed rate (120 kg/ha) (Figure 1 and 2). The improvement in total and productive tillers at the lowest pelleted seed rate might be due to the low number of plants which were produced more number of tillers per plant. In contrast, sowing of higher seed rates of tef leads to competition among plants for nutrients, water, and sunlight, resulted in decreased tillers number per plant. More recently, studies by Alemu and Tefere (2019) and reported that tef cultivars sowing at a lower seed rate gave the highest tillers per plant.

Regarding to the sowing depth, the highest number of total tillers (9.5 tillers/plant) and productive tillers (6.9 tillers/plant) were obtained from the deepest sowing (3 cm), while the lowest number of total tillers (6.1 tillers/plant) and productive tillers (4.8 tillers/plant) were obtained in the shallowest sowing depth (0 cm) (Figure 3 and 4). The highest total tillers and productive tillers obtained from deep sowing might be due to in more deep sown had low seedling emergence, which resulted in low population density this lead that low plant population, the crop produced more tillers per plant. On the other hand, high seedling emergences were observed at a sowing depth of 0 and 1 cm it causes more population density reflected, low tillers numbers per plant. In contrast to these result, Kirby (1993) and Photiades and Hadjichris-todoulou (1984) found that a reduction in number of leaves and internode lengths, plant height and tiller number in deep sowing for wheat and barley. Similarly, Ben-Zeev *et al.* (2020) reported that sowing tef seeds at 3 cm depth significantly reduced tillers numbers.

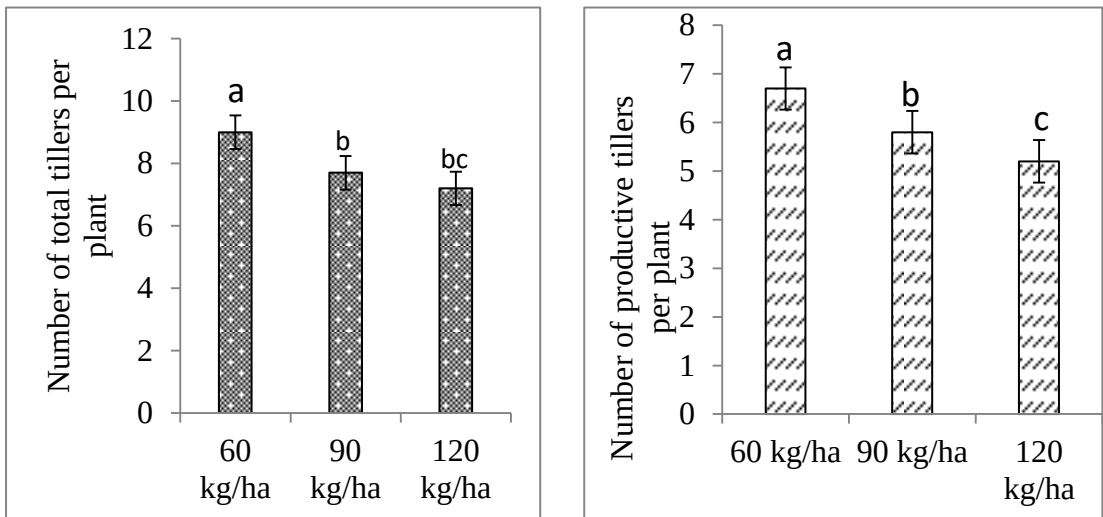


Figure 1& 2. Effects of different pelleted tef seed rate on the total tillers and productive tillers per plant on Vertsol conduction

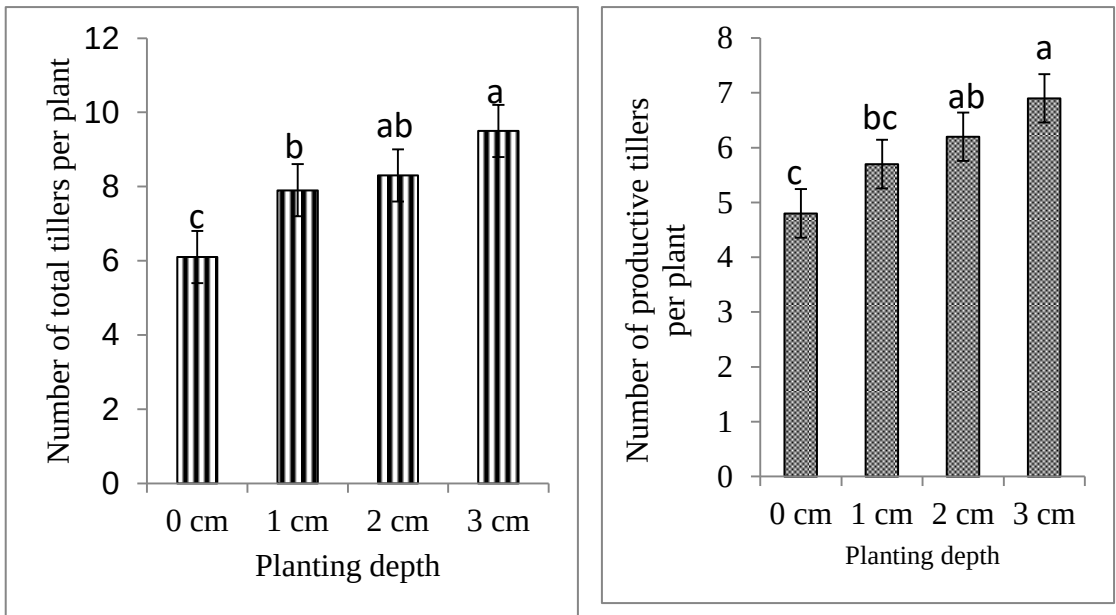


Figure 3 & 4. Effects of different sowing depth of tef seed on the total tillers and productive tillers per plant on Vertisol conduction

Biomass, grain yield and harvest index

Sowing depth had a significant effect on both biomass and grain yield while it had no significant effect on the harvest index. Interactions of sowing depth and pelleted tef seed rate were not significant (Table 2).

Sowing tef at 3cm depth significantly reduced biomass and grain yield as compared to shallow planting depth (0 cm). When compared to shallow sowing (0 cm) with a biomass yield of 11889 kg/ha and grain yield of 2785.9 kg/ha, deep sowing (3 cm) reduced biomass yields by 50% and grain yields by 39%. The negative effects of deep sowing on the biomass and grain yield were attributed to reduced plant establishment as a result reduced plants per meter square consequence reduce biomass and grain yield of tef. Similarly, plants sown at 3 cm depths grew in to shorter, developed lower plants per meter square and gave a lower grain yield than plants in the shallower sowing depth (Ben-Zeev *et al.*, 2020). Similarly, Kirby, (1993) and Photiades and Hadjichris-todo-ulou (1984) reported a reduction of biomass, and

grain yield of wheat and barley, respectively in deeper sowing.

Regarding the seed rate, biomass yield was significantly affected by the pelleted tef seed rate (Table 2). Nevertheless, grain yield and harvest index were not significantly affected by the pelleted tef seed rate (Table2), suggesting compensation for the lower plant density by a number of tillers resulted in no significant difference achieved. The highest biomass yield (10399 kg/ha) was recorded from the 120 pelleted tef seed rate treatment, which was equivalent to 10 kg/ha un-pelleted tef seed rate. On the other hand, the lowest biomass yield was attended 60 kg/ha of pelleted seed rate of tef which was equivalent to 5 kg/ha of un-pelleted tef seed rate. Increasing the pelleted seed rate indicated significantly increases biomass yield of tef. There was a consistent increase in biomass yield with increasing pelleted tef seed rate. The highest biomass yield in the highest pelleted seed rate was probably the presence of maximum plants per meter square produced. The current result was strongly supported by Ben-Zeev *et al.* (2020).

Table2 . Effects of pelted tef seed rate and sowing depth on biomass yield, grain yield, and harvest index at DZARC over the two years

Treatments	AGBY (kg/ha)	GY (kg/ha)	HI (%)
Seed rate (kg/ha)			
60 pelleted ~ (5)	8878b	2295.2	0.27
90 pelleted ~ (7.5)	9750ab	2455.0	0.26
120 pelleted ~ (10)	10399a	2493.9	0.24
Sowing depth			
0 cm	11889a	2785.9a	0.24
1cm	9639b	2535.5ab	0.27
2 cm	9254bc	2333.3b	0.27
3 cm	7921c	2004.3c	0.25
CV (%)	18.3	17.9	25.0

AGBY=Aboveground biomass yield; GY= Grain yield; HI= Harvest index; Means with the same letter in columns are not significantly different at 5% level of significance; CV (%) = coefficient of variation.

Lodging index

Lodging index and root lodging were significantly affected by pelleted tef seed rate and sowing depth. However, the interaction effect of seed rate with sowing depth was not significant. The highest pelleted seed rate (120 kg/ha) had the highest lodging index value (56%) and the lowest pelleted seed rate (60 kg/ha) had the lowest lodging index (30%), while the intermediate seed rate (90 kg/ha) had intermediate lodging index values (44%), which did not significantly deferred from the highest and lower seed rates (Figure 5). In this finding, a low seed rate led to shorter basal internodes, higher culm and root diameters, and more roots, resulting in less lodging index. In sorghum (*Sorghum bicolor* L.), lower plant densities also led to stronger and thicker culms, which decreased the risk of lodging (Teetor *et al.*, 2017).

Regarding on the sowing depth, the average lodging index in 3 cm sowing depth was much lower (30.8%) than from the shallow sowing depth (0 cm) (69.3%) (Figure 6). Moreover, sowing depth has been shown significantly reduce root lodging in tef. The deepest sowing has been shown the lower number of root lodging of tef as compared to the shallowest sowing depth (Figure 7). Sowing of pelleted tef seed at 3 cm depth significantly reduced the average lodging index and root lodging compared to 0 and 1 cm sowing depth. This was possibly due to the formation of a deeper root length (Jabesa and Abraham, 2017) which improves plant anchoring to the soil. Recent report showed that deeper sowing of tef (Ben-Zeev *et al.* 2020; Würschum, 2017; Getahun *et al.*, 2018) and other cereals (Jabesa and Abraham, 2017) have been reflected an association between deeper sowing with reduced root lodging.

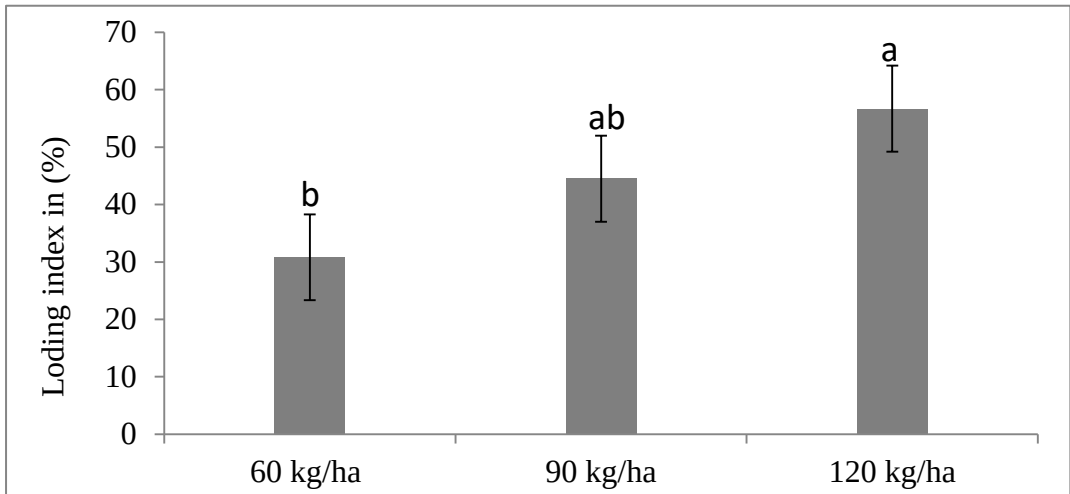


Figure 5. Effects of different pelleted tef seed rate on the lodging index of tef on Vertisol

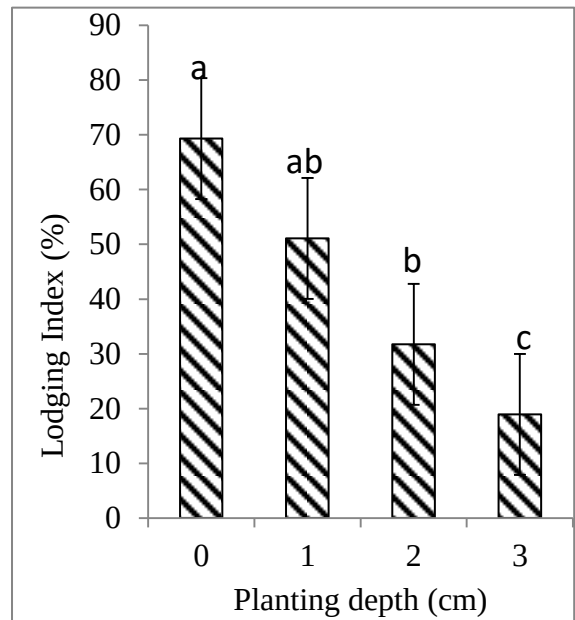
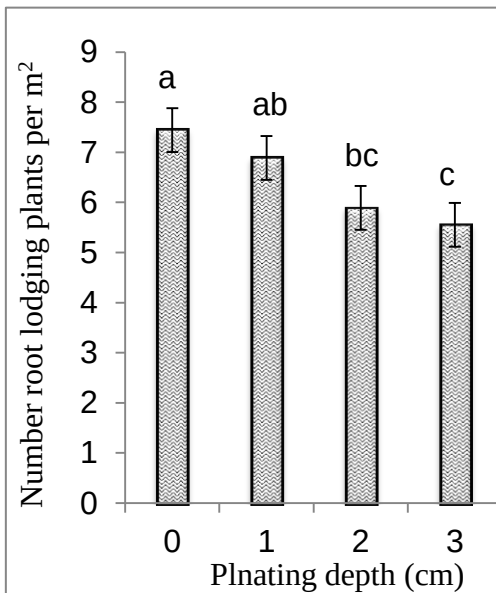


Figure 6 & 7. Effects of different sowing depth on the lodging index and number of root lodging of tef on Vertisol



Figure 8. Root lodging (left) and stem lodging (right) in tef grown in field plots. Photo credited to Bizuwork Tafes.



Figure 9. Stand establishment of pelleted tef seed grown at DZARC. Photo credited to Bizuwork Tafes.

Conclusion

Based on the result, sowing depth and pelleted tef seed rate had a significant effect on yield, yield components and lodging index of tef. Pelleted tef seed successfully emerged from a depth of 1 to 2 cm without any apparent penalty of yield. Tef even emerged from 3 cm depth and reduced lodging, while showing reduced lodging, but this had a penalty of grain yield and biomass yield. The use of tef

seed at a rate of 90 kg/ha produced better biomass, grain yield and reduced lodging index. Therefore, sowing of pelleted tef seed in 1 to 2 cm depth with 90 kg/ha seed rate should be recommended for produced highest tef grain yield. Future research should take combining different pelleted materials and sowing depth with different soil moisture levels, seed rate, soil type and lodging to increases tef productivity.

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Genetic Variability and Association of Traits in Soybean (*Glycine max* (L.) Genotypes in Ethiopia

Masreshaw Yirga¹, Yechalew Sileshi¹, Abush Tesfaye², and Mesfin Hailemariam¹

¹Ethiopian Institutes of Agricultural Research, Jimma Agricultural Research, Field crop division, P.O. Box, 192, Jimma, Ethiopia; ²International Institutes of Tropical Agriculture, PMB 5320, Oyo Road 200001, Ibadan, Nigeria; E-mail: yirgamasresha@gmail.com

Abstract

The study was conducted at Jimma and Metu, southwestern Ethiopia during 2019 main cropping season to estimate the extent of genetic variability and association among traits in 100 soybean genotypes (*Glycine Max* (L.)). The field experiment was laid down in 10 x 10 simple lattice design. The combined analysis of variance revealed the presence of significant ($P < 0.01$) and wide range of variation among the tested genotypes for most of the traits. The maximum grain yield per hectare was recorded on genotypes; T1-EL-OS-JM17-E1, T4-EL-LG-65-JM17-A11 and T4-EL-LG-65-JM17-F2 (2.50 t/ha each) while the minimum (0.85 t/ha) was obtained from T5-EL-LD-77-JM17-D4. High yielding genotypes had a yield advantage of 32.98% and 61.29% compared with the standard checks (Nyala and Clark 63k), respectively. Subsequent combined high genotypic coefficients of variation (GCV), high heritability (H^2) and high genetic advance as present of mean (GAM) were recorded for plant height (24.80%, 87.85% and 47.95%), number of pods per plant (25.34%, 69.38% and 43.55%) and hundred seed weight (20.74%, 75.29% and 37.12%), which denotes, these traits can be improved through direct selection more easily than other traits. Cluster analysis categorized 100 soybean genotypes into five clusters. The maximum inter cluster distance was found between clusters-IV and V, suggesting superior recombinants can be realized by crossing genotypes in these clusters. Principal component analysis (PCA) revealed that, the 1st four PCA with Eigen values exceeding one were responsible for about 72.62 % of the total variation. Out of the entire variations, 1st PCA and the 2nd PCA accounted for more than two third of the total variations (53.13%). Therefore, discrimination of the genotypes into different clusters was mainly due to number of pod per plant, number of seed per plant, grain yield, plant height, days to flowering, days to maturity and hundred seed weight. Grain yield exhibited significant ($P < 0.05$) and positive phenotypic and genotypic correlation coefficient to days to maturity, plant height, number of pod per plant, number of seed per plant, number of branch per plant and soybean rust. Except days to maturity and frog eye leaf spot, all other traits showed positive direct effect on grain yield. Number of pod per plant and plant height showed positive direct effect and strong positive genotypic correlation coefficient with grain yield. Therefore, these traits should be considered as important selection indices for yield improvement program. Generally, the present study revealed the existence of enormous genetic variability among soybean genotypes for various important morphological traits.

Keywords: GCV, PCV, Heritability, GA, Cluster, Correlation, Path coefficient

Introduction

Soybean (*Glycine max* L., 2n=40) belongs to the genus *Glycine* in the family *Leguminosae* (Bernard and Weiss, 1973). It is a high value and profitable crop due to its versatile uses. Soybean grain is rich in quality protein (40%) and oil (20%) content (Singh *et al.*, 2008; Fekadu *et al.*, 2009). Soybeans represented 59% of the world's vegetable oilseed production (USDA, 2022). The by-product or soy meal is also the main source of protein used for farm animal; livestock, poultry, and pig feeding (Clarke and Wiseman, 2000; Stevanovic *et al.*, 2017). Moreover, in low input farming systems, it is an ideal crop in improving and amending soil properties through nitrogen fixation and the ability to break lifecycles of pests and diseases in cereal rotation system (Graham and Vance, 2003). Therefore, soybean is the crop of great promise for most developing countries faced with extensive malnutrition and food insecurity.

The major producing and supplying countries in the world are Brazil, USA, Argentina and China, accounting for more than 90% of the world production. African producers contribute less than 1% of the world soybeans. South Africa, Nigeria and Zambia are the top soybean producers; While, Ethiopia is the sixth producer on the continent (Cornelius and Goldsmith, 2019).

In Ethiopia, FAFA food factory has been using soybean to prepare balanced food particularly for the most vulnerable subset of impoverished families like women and children (MOA, 2018). The utilization and consumption of locally prepared Soybean-based foods such as porridge; kukis, biscuit, bread, soymilk and yogurt are becoming accepted and popular in the country. According to CSA (2020) report, the estimated area coverage, total production and productivity in Ethiopia was 54,543.26 hectare, 125,623.20 ton, and 2.3 ton/ha, respectively. This means, the gap between its potential and national average productivity remains high due to several production constraints. Limited availability of adaptable improved varieties, different biophysical stresses, poor extension services, poor management practices and lack of market access for small scale farmers are the major problems.

Pre-breeding activity in any crop is an art of evaluation of genetic resources with identification their desirable traits (Merriam, 1991). The information obtained on characterization of genetic resources of crop plants is useful, both for breeding and for the purpose of germplasm conservation (Brown *et al.*, 1990). Such knowledge and visualization can be achieved through the study of morphological, structural and functional attributes of germplasm as the carrier of all hereditary characteristics of any given species (Jaramillo and Baena, 2000). The main morphological markers vital to distinguish variation based on external

observation differences in soybean germplasm are days to flowering, days to physiological maturity, plant height, number of pod per plant, number of seed per plant, number of branch per plant, hundred seed weight and grain yield. Oil and protein content are also widely used nutritional values for soybean genetic variability assessment. Therefore, soybean genetic resources with these important traits should be systematically characterized using different genetic variance components and multivariate analysis.

Introduction and local hybridization are paramount important sources of germplasm to initiate soybean variety development program in Ethiopia. Since the inception of soybean research in Ethiopia, a number of germplasm were enhanced from these two methods. So far, genetic variability study was conducted on some soybean germplasm in the country by different researchers, each reported the presence of considerable genetic variations among the tested genotypes (Abush et al., 2017; Yechalew et al., 2021; Mesfin, 2018; Masreshaw et al., 2021; Abady et al., 2013; Aditya et al., 2011). As the genetic materials are always updated from different sources in different year, the previous genetic information do not totally infer other set of genetic

resources. Considering the above facts, the present investigation was necessitated to undertake the comprehensive assessment of the genetic diversity among the introduced soybean genotypes in Ethiopia.

Materials and Methods

The field experiment was conducted at Metu and Jimma, south western Ethiopia during 2019 main cropping season. Metu has an altitude of 1558m.a.s.l. and the mean annual temperature ranges from 12.7-28.9 °C with annual rainfall of 1829 mm, while Jimma has an altitude of 1754 m.a.s.l with the average annual temperature of from 26.3-26.3°C with its mean annual rainfall of 1,572mm. The major soil type in southwest Ethiopia is Nitosols (Paulos, 2001). Metu site is characterized by strong soil acidity and low phosphorus level (1.92) with the PH of 4.82, while Jimma is characterized by moderate soil acidity and phosphorus level (4.9) with the PH of 5.46 (Abushet et al., 2017). One hundred soybean genotypes including two standard check varieties (Nyala and Clark-63K) were evaluated in this study using simple lattice design. The genotypes were introduced from external source as breeding material (table 1).

Table 1.Detailsof the100 Soybean genotypes

Geno	Designation	Description	Source of materials	Geno	Designation	Description	Source of material
1	T1-EL-OS-JM17-A13	Inbred line	USA	51	T4-EL-LG-65-JM17-C15	Inbred line	USA
2	T1-EL-OS-JM17-A15	Inbred line	USA	52	T4-EL-LG-65-JM17-C18	Inbred line	USA
3	T1-EL-OS-JM17-B11	Inbred line	USA	53	T4-EL-LG-65-JM17-C20	Inbred line	USA
4	T1-EL-OS-JM17-B14	Inbred line	USA	54	T4-EL-LG-65-JM17-E24	Inbred line	USA
5	T1-EL-OS-JM17-C2	Inbred line	USA	55	T4-EL-LG-65-JM17-F2	Inbred line	USA
6	T1-EL-OS-JM17-D4	Inbred line	USA	56	T4-EL-LG-65-JM17-G1	Inbred line	USA
7	T1-EL-OS-JM17-D6	Inbred line	USA	57	T4-EL-LG-65-JM17-G9	Inbred line	USA
8	T1-EL-OS-JM17-D14	Inbred line	USA	58	T4-EL-LG-65-JM17-G27	Inbred line	USA
9	T1-EL-OS-JM17-E1	Inbred line	USA	59	T4-EL-LG-65-JM17-I14	Inbred line	USA
10	T1-EL-OS-JM17-E2	Inbred line	USA	60	T5-EL-LD-77-JM17-A2B	Inbred line	USA
11	T1-EL-OS-JM17-E3	Inbred line	USA	61	T5-EL-LD-77-JM17-A5	Inbred line	USA
12	T1-EL-OS-JM17-E5	Inbred line	USA	62	T5-EL-LD-77-JM17-A7	Inbred line	USA
13	T1-EL-OS-JM17-E6	Inbred line	USA	63	T5-EL-LD-77-JM17-A9	Inbred line	USA
14	T1-EL-OS-JM17-E13	Inbred line	USA	64	T5-EL-LD-77-JM17-A11	Inbred line	USA
15	T1-EL-OS-JM17-E15	Inbred line	USA	65	T5-EL-LD-77-JM17-A14	Inbred line	USA
16	T1-EL-OS-JM17-E18	Inbred line	USA	66	T5-EL-LD-77-JM17-A15	Inbred line	USA
17	T1-EL-OS-JM17-E23	Inbred line	USA	67	T5-EL-LD-77-JM17-A17	Inbred line	USA
18	T1-EL-OS-JM17-E27	Inbred line	USA	68	T5-EL-LD-77-JM17-B16	Inbred line	USA
19	T1-EL-OS-JM17-E28	Inbred line	USA	69	T5-EL-LD-77-JM17-C1	Inbred line	USA
20	T1-EL-OS-JM17-G13	Inbred line	USA	70	T5-EL-LD-77-JM17-C3	Inbred line	USA
21	T1-EL-OS-JM17-H6	Inbred line	USA	71	T5-EL-LD-77-JM17-C4	Inbred line	USA
22	T1-EL-OS-JM17-H9	Inbred line	USA	72	T5-EL-LD-77-JM17-C6	Inbred line	USA
23	T1-EL-OS-JM17-H12	Inbred line	USA	73	T5-EL-LD-77-JM17-C7	Inbred line	USA
24	T2-EL-LG-90-JM17-I12	Inbred line	USA	74	T5-EL-LD-77-JM17-C25	Inbred line	USA
25	T2-EL-LG-90-JM17-I15	Inbred line	USA	75	T5-EL-LD-77-JM17-D4	Inbred line	USA
26	T2-EL-LG-90-JM17-I22	Inbred line	USA	76	T5-EL-LD-77-JM17-E10	Inbred line	USA
27	T3-EL-LG-63-JM17-A1	Inbred line	USA	77	T5-EL-LD-77-JM17-E25	Inbred line	USA
28	T3-EL-LG-63-JM17-A3	Inbred line	USA	78	T5-EL-LD-77-JM17-E27	Inbred line	USA
29	T3-EL-LG-63-JM17-A8	Inbred line	USA	79	T5-EL-LD-77-JM17-F3	Inbred line	USA
30	T3-EL-LG-63-JM17-A10	Inbred line	USA	80	T5-EL-LD-77-JM17-F4	Inbred line	USA
31	T3-EL-LG-63-JM17-A17	Inbred line	USA	81	T5-EL-LD-77-JM17-F11	Inbred line	USA
32	T3-EL-LG-63-JM17-A22	Inbred line	USA	82	T5-EL-LD-77-JM17-F15	Inbred line	USA
33	T3-EL-LG-63-JM17-A28	Inbred line	USA	83	T5-EL-LD-77-JM17-F27	Inbred line	USA
34	T3-EL-LG-63-JM17-B4	Inbred line	USA	84	T5-EL-LD-77-JM17-F28	Inbred line	USA
35	T3-EL-LG-63-JM17-B6	Inbred line	USA	85	T5-EL-LD-77-JM17-G7	Inbred line	USA
36	T3-EL-LG-63-JM17-B1	Inbred line	USA	86	T5-EL-LD-77-JM17-G18	Inbred line	USA
37	T3-EL-LG-63-JM17-C1	Inbred line	USA	87	T5-EL-LD-77-JM17-G29	Inbred line	USA
38	T3-EL-LG-63-JM17-E8	Inbred line	USA	88	T5-EL-LD-77-JM17-H1	Inbred line	USA
39	T3-EL-LG-63-JM17-E14	Inbred line	USA	89	T5-EL-LD-77-JM17-H3	Inbred line	USA
40	T3-EL-LG-63-JM17-E17	Inbred line	USA	90	T5-EL-LD-77-JM17-H30	Inbred line	USA
41	T3-EL-LG-63-JM17-E30	Inbred line	USA	91	T5-EL-LD-77-JM17-H31	Inbred line	USA
42	T3-EL-LG-63-JM17-E31	Inbred line	USA	92	T5-EL-LD-77-JM17-H43	Inbred line	USA
43	T3-EL-LG-63-JM17-F11	Inbred line	USA	93	T5-EL-LD-77-JM17-H44	Inbred line	USA
44	T3-EL-LG-63-JM17-F29	Inbred line	USA	94	T5-EL-LD-77-JM17-I3	Inbred line	USA
45	T3-EL-LG-63-JM17-I31	Inbred line	USA	95	T5-EL-LD-77-JM17-I22	Inbred line	USA
46	T3-EL-LG-63-JM17-I36	Inbred line	USA	96	T5-EL-LD-77-JM17-I24	Inbred line	USA
47	T4-EL-LG-65-JM17-A8	Inbred line	USA	97	T5-EL-LD-77-JM17-I34	Inbred line	USA
48	T4-EL-LG-65-JM17-A11	Inbred line	USA	98	T5-EL-LD-77-JM17-I35	Inbred line	USA
49	T4-EL-LG-65-JM17-A13	Inbred line	USA	99	Nyala	Check variety	-
50	T4-EL-LG-65-JM17-B8	Inbred line	USA	100	Clark 63K	Check variety	-

Each genotype was planted in a plot of two rows and four meter length with regular spacing of 5cm between plants and 60cm between rows. Planting was done with two seeds per hill and latter

Agronomic traits such as days to flowering, days to maturity, plant height (cm), number of pod per plant, number of seed per plant, number of branch per plant, crop lodging, shattering, hundred seed weight (gm) and grain yield(t ha⁻¹) were recorded. Disease for bacterial blight, soybean rust and frog eye leaf spot data was also recorded. The scoring system was 1-9 scale (1=immune, 9=susceptible, then 1-3=resistant,4-6=moderately resistant and 7-9 = susceptible. Prior to proceeding with the analysis of variance (ANOVA), homogeneity test was made for each variable using the $F_{\max}$ test and then all the data considered were subjected to combined analysis of variance (ANOVA) over environment. Analysis for simple lattice design was performed using the SAS program software. The total variability for the traits was quantified using pooled analyses of variance over two locations using the following model:

$$P_{ijklt} = \mu + l_t + r_{i(t)} + b_{j(i)(t)} + g_k + (gl)_{kt} + e_{ijklt}$$

where P_{ijklt} = phenotypic value of k^{th} genotype under i^{th} replication at t^{th} location and j^{th} incomplete block with replication i , location t ; $l_t = t^{th}$ location; $r_{i(t)}$ = the effect of replication i with location t ; $b_{j(i)(t)}$ = the effect of incomplete block j with in replication i and location t ; g_k = the effect of k^{th} genotype; μ = grand mean

thinned to one plant /hill at 2-3 weeks after emergence. All the agronomic management practices were applied for the experiment as per the recommendation.

and $(gl)_{kt}$ = the interaction effects and e_{ijklt} = random error.

Partitioning of the total variation into components due to genotype (δg^2), environment (δe^2) and genotype by environment interaction (δge^2) deviations was performed from the analyses of variance by calculating the expected mean squares and similarly the components from pooled analysis of variance across locations were calculated. The coefficients of variations at phenotypic and genotypic levels were estimated using the formula adopted by Johnson *et al* (1955) as:

$$PCV = [\sigma_p / \bar{x}] \times 100$$

$$GCV = [\sigma_g / \bar{x}] \times 100$$

Where σ_p = phenotypic standard deviation ($\sigma_g + \sigma_e$), σ_g =genotypic standard deviation, σ_e = environmental standard deviation and $\bar{x}$ = grand mean for the trait x ; PCV and GCV =phenotypic and genotypic coefficients of variation respectively.

Estimate of heritability

Broad-sense heritability (H^2) for traits was estimated for pooled analyses over two locations using the formula adopted by Allard (1960) as:

$$\sigma_p^2 = \sigma_g^2 + \sigma_{ge}^2/e + \sigma_e^2/re.$$

$$H^2 = \frac{\sigma_g^2}{\left[\sigma_g^2 + \frac{\sigma_{ge}^2}{e} + \frac{\sigma_e^2}{er} \right]} \times 100$$

Where σ_p^2 =phenotypic variance, σ_g^2 = genotypic variance, σ_{ge}^2 = variance

genotype by environment interaction, σ_e^2 = environmental variance, e = number of environment and r = number of replications.

Genetic advance in absolute unit (GA) and percent of the mean (GAM), assuming selection of the superior 5% of the genotypes, was estimated in accordance with the methods illustrated by Johnson *et al*(1955) as:

$$GA = k\sigma_p H^2$$

$$GAM = (GA/x) \times 100$$

Where k = the standardized selection differential at 5% selection Intensity ($k = 2.063$), σ_p = phenotypic standard deviation, H^2 = Heritability and x = Grand mean.

Mean data for each trait was subjected to multivariate analysis techniques. Cluster analysis was employed using SAS statistical package. Genetic divergence to estimate the genetic distance between clusters was determined using the generalized Mahalanobis's D^2 statistics (Mahalanobis, 1936). The D^2 values obtained for pairs of clusters were considered as the calculated values of Chi-square (X^2) and tested for significance both at 1% and 5% probability levels against the tabulated value of X^2 for 'P' degree of freedom, where P is the number of traits considered (Singh and Chaudhary, 1987). The principal components (PC) analysis was employed in order to minimize the traits into a new set of linearly combined measurements and to identify the traits contributing large part of the total variation among the genotypes. The analysis was performed by using SAS software. In this analysis, only PCs with Eigen values greater than one were considered as important for the total variations.

Correlation analysis was also performed using SAS statistical package to determine the level of associations among the studied traits. Path coefficient analysis was calculated using the formula suggested by (Dewey and Lu, 1959). To determine direct and indirect effect of different variables on yield as:

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

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

Result and Discussions

Combined analysis of variance

The results from the combined analysis of variance across two locations has presented in table 2. The pooled analysis of variance revealed that, the mean square due to location was significant ($P \leq 0.01$) for all the traits except number of branches per plant, indicating the distinct nature of the two test locations. Mean squares due to genotype were differed significantly ($P \leq 0.01$) with respect to all the traits except for bacterial blight, meaning genotypes were responded differently for each trait.

Mean squares due to location $\times$ genotype were significant for plant height, soybean rust, frog eye leaf spot and hundred seed weight, implying genotypes exhibited different relative performance in each location for these traits.

Table 2. Mean squares of the combined analysis of variance for yield and related traits of 100 soybean genotypes at two locations, evaluated during 2019

Source of variations	Traits											HSW (gm)	YLD (t/ha)
	DF	DTF	DTM	PH	NPP	NSP	NBP	LG	SR	BB	FLS		
Loc	1	214.6*	7992.4**	15601.3**	727.9**	7905.9**	0.44	11.90**	386.12**	9.61**	930.25**	249.96**	13.54**
Rep(Loc)	2	23.2ns	14.4 ns	499.2**	1211.2**	6233.7**	2.68**	0.09 ns	11.80**	2.89**	30.25**	0.524 ns	3.22**
Block(Loc*Rep)	36	52.4 ns	13.9	63.8**	42.5*	474.0*	0.46 ns	0.12*	1.08 ns	0.47**	2.23**	8.11**	0.27**
Geno	99	56.3*	34.3**	156.3**	76.9**	512.7**	0.76**	0.11*	2.05**	0.32 ns	0.72**	11.54**	0.34**
Loc*Geno	99	44.4 ns	10.7 ns	34.3**	29.3 ns	332.9 ns	0.39 ns	0.11*	2.22**	0.32 ns	0.72**	4.06*	0.18 ns
Error	162	44.5	9.5	11.5	27.9	287.67	0.34	0.08	1.22	0.24	0.43	3.04	0.141

Where, * = significant at ($P \leq 0.05$) and **= significant at ($P \leq .01$), loc=location, geno=genotype, DF=degree of freedom, DTF = days to 50% flowering, DTM = days to 95% pod maturity, PH = plant height, NPP = number of pod per plant, NSP= number of seed per plant, SP= NBP=number of branch per plant, LG=lodging, SH=shattering ,SR=soybean rust, CBB=common bacterial blight, FLS=frog eye leaf spot HSW=hundred seed weight, YLD= grain yield ton ha⁻¹

Performance of soybean genotypes for yield and related traits

The performance of the genotypes (table 3) ranged widely for number of seed (30.15-118.65), days to flowering (26.75-66.75), grain yield (0.85-2.5 t/ha), plant height (33.35-67.30 cm), number of pods(15.70-37.70), days to maturity (115.50-130.75), hundred seed weight (8.78-17.53gm), soybean rust (2.0-5.0), frog-eye leaf spot (1.5-4.0),number of branch (2.90-5.30),crop lodging(1.17-2.0) and bacterial blight (1.16-2.0) (table 3).More than 56% and 80% of the tested soybean genotypes had mean yield exceeding the standard check varieties (Nyala and Clark 63k), respectively. The maximum yield was recorded on genotypes T1-EL-OS-

JM17-E1, T4-EL-LG-65-JM17-A11 and T4-EL-LG-65-JM17-F2 (2.50 t/ha each) followed by T3-EL-LG-63-JM17-E14 (2.40 t/ha). The high yielding genotypes had a yield advantage of 32.98% and 61.29% compared with the standard checks (Nyala and Clark 63k), respectively.

Therefore, traits which obtained highest ranges were played important role in the total variability of soybean genotypes. Indicating, the scope for selection of these traits for further breeding works. In agreement with this result wide range of variation for number of pod, grain yield and plant height, number of seed and hundred seed weight was reported by Abushet *al* (2017) and Neelimaet *al* (2018).

Table 3. Range and Mean values of yield and other morphological traits of 100 soybean genotypes evaluated across two sites.

		Trait											
No.	Designation	DTF	DTM	PH	NPP	NSP	NBP	LG	SR	BB	FLS	HSW	yld
1	T1-EL-OS-JM17-A13	56.75	119.75	45.63	32.93	66.60	4.25	1.38	3.50	1.00	2.00	12.18	2.08
2	T1-EL-OS-JM17-A15	57.50	122.50	46.08	33.20	59.38	4.35	1.13	4.00	1.00	2.00	11.23	1.98
3	T1-EL-OS-JM17-B11	57.00	120.75	40.18	29.50	56.40	3.80	1.00	3.50	2.00	2.50	12.43	1.78
4	T1-EL-OS-JM17-B14	57.00	121.00	48.48	31.75	60.00	4.20	1.25	4.50	1.00	2.50	11.93	2.18
5	T1-EL-OS-JM17-C2	55.25	120.25	44.33	32.30	63.63	3.50	1.00	3.50	1.00	2.00	10.05	2.33
6	T1-EL-OS-JM17-D4	57.00	121.00	49.73	30.63	55.60	3.70	1.25	3.50	1.00	3.50	11.63	1.90
7	T1-EL-OS-JM17-D6	58.00	124.25	53.75	33.35	65.13	4.00	2.00	3.00	1.00	2.00	12.03	2.00
8	T1-EL-OS-JM17-D14	57.50	126.50	51.55	29.05	54.90	4.05	1.25	4.00	1.00	2.00	13.53	1.40
9	T1-EL-OS-JM17-E1	56.50	121.50	49.33	37.70	72.43	4.45	1.25	4.00	1.00	2.00	10.93	2.50
10	T1-EL-OS-JM17-E2	57.00	121.50	60.45	33.20	63.18	3.90	1.50	4.00	1.50	2.50	11.00	2.25
11	T1-EL-OS-JM17-E3	57.00	125.50	50.85	31.10	63.13	3.95	1.25	4.50	1.00	2.50	13.03	1.78
12	T1-EL-OS-JM17-E5	57.50	124.50	43.43	30.50	51.95	3.95	1.13	2.50	1.00	2.50	11.98	1.83
13	T1-EL-OS-JM17-E6	26.75	120.75	41.40	29.28	56.88	4.05	1.00	3.50	1.00	2.50	12.13	1.85
14	T1-EL-OS-JM17-E13	56.50	122.50	42.40	29.38	55.53	3.30	1.13	3.00	1.00	2.50	11.23	1.80
15	T1-EL-OS-JM17-E15	57.50	120.75	43.40	28.25	55.48	3.85	1.00	2.50	2.00	2.00	11.93	1.50
16	T1-EL-OS-JM17-E18	56.00	119.00	49.73	32.10	60.33	3.85	1.13	4.50	1.50	2.50	12.80	1.98
17	T1-EL-OS-JM17-E23	55.50	120.00	41.10	35.00	72.55	3.65	1.00	2.50	1.00	2.00	11.15	1.63
18	T1-EL-OS-JM17-E27	57.50	121.25	55.35	33.70	67.60	4.15	1.63	3.00	1.00	2.50	11.45	2.15
19	T1-EL-OS-JM17-E28	56.75	120.75	53.13	31.75	64.13	4.40	1.38	2.50	1.00	3.00	12.38	2.20
20	T1-EL-OS-JM17-G13	56.25	120.50	51.03	34.20	68.35	4.25	1.25	4.50	1.00	1.50	12.48	2.38
21	T1-EL-OS-JM17-H6	56.50	121.25	44.03	31.50	59.53	4.35	1.25	3.50	1.00	2.00	12.03	2.35
22	T1-EL-OS-JM17-H9	56.00	120.75	45.75	36.83	71.38	4.30	1.00	3.00	1.00	2.00	12.55	2.10
23	T1-EL-OS-JM17-H12	59.75	126.25	56.00	34.75	73.23	4.15	1.50	3.00	2.00	2.50	14.15	2.35
24	T2-EL-LG-90-JM17-I12	56.00	127.00	62.15	33.45	65.30	4.45	1.00	2.50	1.00	2.00	12.43	1.98
25	T2-EL-LG-90-JM17-I15	57.75	124.25	51.55	27.53	53.13	4.20	1.00	4.00	1.00	2.50	14.28	1.98
26	T2-EL-LG-90-JM17-I22	55.00	124.25	58.65	27.33	44.30	4.35	1.13	3.00	1.00	2.50	16.18	1.65
27	T3-EL-LG-63-JM17-A1	55.25	129.25	52.45	32.70	60.65	4.60	1.00	2.50	1.00	2.00	12.93	1.83
28	T3-EL-LG-63-JM17-A3	55.00	121.25	52.40	22.10	36.95	4.25	1.00	2.50	1.50	3.00	16.25	1.50
29	T3-EL-LG-63-JM17-A8	59.00	127.00	61.45	37.15	67.48	4.20	1.25	3.00	1.00	2.00	14.40	1.85
30	T3-EL-LG-63-JM17-A10	58.75	129.75	58.70	32.85	55.83	3.90	1.25	4.00	1.50	2.50	14.40	2.00
31	T3-EL-LG-63-JM17-A17	56.00	125.75	55.23	31.95	118.65	4.00	1.00	2.50	1.00	3.00	11.83	1.85
32	T3-EL-LG-63-JM17-A22	54.00	128.25	50.85	31.38	62.35	3.45	1.00	2.00	1.00	1.50	14.85	1.95
33	T3-EL-LG-63-JM17-A28	55.50	127.25	57.90	26.33	58.28	3.75	1.25	2.50	1.00	2.50	15.25	2.08
34	T3-EL-LG-63-JM17-B4	58.00	130.75	57.10	29.85	54.98	3.90	1.13	4.50	1.00	2.00	14.85	2.15
35	T3-EL-LG-63-JM17-B6	56.50	123.50	48.38	27.85	52.20	3.95	1.50	3.00	1.00	3.50	13.45	1.75
36	T3-EL-LG-63-JM17-B1	56.50	124.50	48.10	23.93	44.93	4.25	1.13	3.50	1.00	2.00	13.83	1.88

Table3. (Continued)

No.	Designation	Trait											
		DTF	DTM	PH	NPP	NSP	NBP	LG	SR	BB	FLS	HSW	YLD
37	T3-EL-LG-63-JM17-C1	56.75	124.25	49.83	28.53	53.63	4.20	1.13	3.50	1.00	2.50	14.30	1.88
38	T3-EL-LG-63-JM17-E8	59.50	127.00	55.05	28.88	49.25	4.10	1.00	3.50	1.00	2.00	14.43	1.68
39	T3-EL-LG-63-JM17-E14	55.25	119.25	40.33	24.10	47.90	2.95	1.00	3.50	1.50	2.50	13.93	2.40
40	T3-EL-LG-63-JM17-E17	55.75	121.75	44.80	25.65	47.15	3.95	1.25	2.50	1.00	3.00	16.35	1.50
41	T3-EL-LG-63-JM17-E30	54.75	124.50	46.15	25.40	45.75	3.95	1.13	2.50	1.00	2.00	17.10	1.98
42	T3-EL-LG-63-JM17-E31	56.00	120.75	47.35	27.88	57.25	4.50	1.00	5.00	1.00	2.50	13.23	2.20
43	T3-EL-LG-63-JM17-F11	53.50	120.50	52.83	32.68	57.13	3.50	1.38	3.00	1.00	2.00	16.23	1.88
44	T3-EL-LG-63-JM17-F29	58.00	125.00	55.05	32.68	58.73	4.40	1.00	2.50	1.00	2.50	16.70	2.03
45	T3-EL-LG-63-JM17-I31	57.50	122.50	49.23	28.50	50.80	4.80	1.50	3.50	1.00	3.50	11.08	1.98
46	T3-EL-LG-63-JM17-I36	56.50	119.25	41.95	29.48	53.85	4.10	1.00	3.00	1.00	2.50	15.30	1.68
47	T4-EL-LG-65-JM17-A8	56.25	124.00	52.70	35.00	74.75	4.20	1.25	4.50	1.50	3.50	13.43	2.23
48	T4-EL-LG-65-JM17-A11	56.00	122.50	54.45	32.13	63.03	4.65	1.38	4.50	1.00	2.00	15.50	2.50
49	T4-EL-LG-65-JM17-A13	56.50	121.50	47.38	31.10	60.35	4.20	1.50	4.50	1.00	2.50	13.93	2.13
50	T4-EL-LG-65-JM17-B8	56.50	121.25	49.83	31.20	58.23	4.35	1.25	4.00	1.00	2.50	14.23	1.70
51	T4-EL-LG-65-JM17-C15	56.75	124.00	51.38	27.15	52.43	3.60	1.00	3.00	1.50	2.50	14.40	1.65
52	T4-EL-LG-65-JM17-C18	58.25	125.00	58.53	28.83	51.33	3.55	1.50	4.00	1.00	2.00	17.00	2.20
53	T4-EL-LG-65-JM17-C20	59.00	123.50	57.03	29.33	58.00	3.20	1.13	3.25	1.00	2.00	15.93	2.03
54	T4-EL-LG-65-JM17-E24	55.00	119.50	37.08	26.15	46.10	3.25	1.13	3.50	1.00	3.00	11.93	1.63
55	T4-EL-LG-65-JM17-F2	57.25	122.50	65.75	29.65	57.43	4.60	1.38	2.50	1.00	3.00	15.20	2.50
56	T4-EL-LG-65-JM17-G1	55.50	120.00	50.03	25.80	52.48	4.20	1.25	4.50	1.00	3.00	12.40	1.98
57	T4-EL-LG-65-JM17-G9	55.25	120.75	49.35	26.75	47.30	3.90	1.25	4.50	1.00	2.00	14.88	2.18
58	T4-EL-LG-65-JM17-G27	55.50	120.75	45.18	31.25	64.80	3.75	1.75	4.50	1.00	2.00	12.88	2.13
59	T4-EL-LG-65-JM17-I14	56.00	121.50	46.25	25.45	47.65	3.60	1.13	2.00	1.00	2.00	14.83	1.80
60	T5-EL-LD-77-JM17-A2B	55.25	121.00	46.43	23.53	44.53	3.40	1.13	3.00	1.00	2.00	15.65	1.68
61	T5-EL-LD-77-JM17-A5	54.75	121.75	55.78	27.95	49.80	4.25	1.25	2.50	1.50	2.50	13.13	1.60
62	T5-EL-LD-77-JM17-A7	55.00	119.75	53.30	26.60	52.20	3.60	1.13	3.50	1.00	2.50	15.03	2.03
63	T5-EL-LD-77-JM17-A9	55.00	121.25	49.13	23.00	39.20	3.90	1.00	3.00	1.50	2.00	15.98	1.88
64	T5-EL-LD-77-JM17-A11	55.25	120.75	58.70	24.85	49.73	3.70	1.13	3.50	1.00	2.50	16.75	2.08
65	T5-EL-LD-77-JM17-A14	54.00	121.00	51.63	25.33	52.38	3.70	1.25	3.50	1.00	2.00	16.70	2.13
66	T5-EL-LD-77-JM17-A15	56.25	121.75	53.00	26.25	47.00	4.00	1.13	3.50	1.00	2.50	14.63	1.85
67	T5-EL-LD-77-JM17-A17	55.75	122.50	46.25	21.00	42.23	3.35	1.00	2.50	1.50	3.00	16.68	1.43
68	T5-EL-LD-77-JM17-B16	54.00	122.25	45.25	24.38	46.28	3.55	1.00	2.00	1.00	2.50	16.08	
69	T5-EL-LD-77-JM17-C1	54.50	118.75	40.55	21.45	37.25	3.90	1.00	2.00	1.00	3.00	15.85	1.33
70	T5-EL-LD-77-JM17-C3	53.75	119.00	42.90	17.55	33.00	2.90	1.00	3.00	1.50	4.00	15.13	1.35
71	T5-EL-LD-77-JM17-C4	53.75	117.00	41.40	15.70	30.15	3.30	1.38	2.50	1.00	3.50	15.73	1.33
72	T5-EL-LD-77-JM17-C6	55.00	120.50	47.65	24.30	46.15	3.70	1.13	3.50	1.00	2.50	14.88	1.93

Table3. (Continued)

No.	Designation	Trait											
		DTF	DTM	PH	NPP	NSP	NBP	LG	SR	BB	FLS	HSW	YLD
74	T5-EL-LD-77-JM17-C25	53.50	116.50	42.75	22.10	42.08	3.35	1.13	3.50	1.00	3.50	14.83	1.58
75	T5-EL-LD-77-JM17-D4	55.50	116.75	33.35	20.50	42.48	5.30	1.00	2.50	1.50	4.00	10.63	0.85
76	T5-EL-LD-77-JM17-E10	54.50	117.25	37.13	19.05	35.20	3.20	1.25	2.00	2.00	3.00	14.83	1.20
77	T5-EL-LD-77-JM17-E25	56.00	119.75	35.58	21.20	40.90	3.85	1.25	3.50	1.00	3.00	12.30	1.30
78	T5-EL-LD-77-JM17-E27	55.25	122.25	45.25	22.38	42.58	3.05	1.13	3.50	1.00	2.00	17.53	1.53
79	T5-EL-LD-77-JM17-F3	54.00	115.50	41.68	21.45	40.75	3.30	1.00	2.50	1.00	3.00	15.68	1.55
80	T5-EL-LD-77-JM17-F4	54.25	120.25	46.05	26.50	47.03	3.85	1.38	3.50	1.00	3.00	15.53	1.65
81	T5-EL-LD-77-JM17-F11	55.50	118.50	39.53	26.25	47.80	3.60	1.13	3.00	1.00	3.00	14.33	2.00
82	T5-EL-LD-77-JM17-F15	54.75	118.25	40.43	22.15	39.78	3.40	1.00	2.50	1.50	3.00	14.95	1.65
83	T5-EL-LD-77-JM17-F27	39.00	121.25	45.10	25.98	52.70	3.30	1.00	3.00	1.00	2.00	15.05	1.25
84	T5-EL-LD-77-JM17-F28	55.25	122.00	47.15	22.65	42.40	3.85	1.13	3.50	1.00	3.50	13.95	1.63
85	T5-EL-LD-77-JM17-G7	55.00	120.50	44.65	23.25	41.10	3.85	1.00	3.50	1.50	2.50	16.78	1.75
86	T5-EL-LD-77-JM17-G18	54.25	122.50	40.43	23.10	44.95	3.90	1.25	3.00	1.00	2.50	14.65	1.25
87	T5-EL-LD-77-JM17-G29	55.75	118.25	44.93	21.15	40.15	3.35	1.13	2.50	1.50	2.50	14.80	1.48
88	T5-EL-LD-77-JM17-H1	55.25	119.25	36.30	21.50	40.18	3.40	1.00	2.00	1.00	2.50	13.73	1.20
89	T5-EL-LD-77-JM17-H3	55.50	119.50	42.48	26.40	51.03	3.70	1.00	2.50	1.00	2.50	15.45	1.75
90	T5-EL-LD-77-JM17-H30	54.25	119.50	40.13	23.90	44.23	3.30	1.00	4.00	2.00	3.00	12.73	1.40
91	T5-EL-LD-77-JM17-H31	54.25	116.50	41.40	22.20	43.70	3.60	1.13	3.00	1.00	3.00	15.80	1.65
92	T5-EL-LD-77-JM17-H43	56.00	122.75	53.28	30.30	57.43	4.35	1.25	3.00	1.00	2.50	14.55	2.03
93	T5-EL-LD-77-JM17-H44	55.25	121.25	40.48	24.85	44.75	3.35	1.00	3.00	1.50	3.50	12.73	1.25
94	T5-EL-LD-77-JM17-I3	53.25	122.50	51.55	24.30	47.98	3.40	1.00	2.00	1.50	2.00	17.43	1.65
95	T5-EL-LD-77-JM17-I22	55.00	122.75	58.15	24.63	47.25	3.65	1.00	2.00	1.00	2.50	15.55	1.58
96	T5-EL-LD-77-JM17-I24	55.75	122.50	54.35	25.85	50.13	3.70	1.25	2.50	1.00	2.00	14.48	2.13
97	T5-EL-LD-77-JM17-I34	55.25	116.25	43.43	25.65	41.48	3.83	1.00	2.50	1.50	3.50	15.85	1.75
98	T5-EL-LD-77-JM17-I35	54.75	119.50	41.68	19.50	37.65	3.05	1.00	2.50	1.00	3.50	15.30	1.18
99	Nyala	59.50	126.75	50.35	28.88	53.78	3.85	1.00	2.00	1.50	2.00	15.38	1.80
100	Clark 63K	66.75	130.00	67.30	30.70	59.80	4.55	1.75	3.50	2.00	1.50	8.78	1.55
	minimum	26.75	115.50	33.35	15.70	30.15	2.90	1.00	2.00	1.00	1.50	8.78	0.85
	mean	55.61	121.93	48.53	27.62	53.00	3.88	1.17	3.20	1.16	2.53	14.06	1.82
	maximum	66.75	130.75	67.30	37.70	118.65	5.30	2.00	5.00	2.00	4.00	17.53	2.50
	R2 (%)	62.75	89.86	93.68	78.46	72.48	71.75	79.8	82.21	71.54	94.97	83.59	80.73
	CV	11.99	2.61	10.91	22.84	35.22	15.80	24.35	35.39	45.81	34.78	13.13	21.96
	LSD	9.31	4.29	5.85	7.38	23.68	0.85	0.39	1.54	0.69	0.91	2.43	0.14
	P-value	NS	**	**	*	**	**	**	**	NS	**	**	**

CV, Coefficient of variation, R2, Coefficient of determination, LSD, Least significant difference. *, ** denote significance difference at 5% and 1% probability levels, respectively; NS: non-significant.

Estimation of genotypic and phenotypic coefficients of variation

Grand means, the estimates of genotypic and phenotypic variance, genotypic (GCV) and phenotypic coefficients of variation (PCV), broad-sense heritability (H^2), genetic advance (GA) and genetic advance expressed as percent of mean (GAM) presented in table 4. The ranges for PCV and GCV were (4.68%-46.88%) and (4.08%-24.38%), respectively. The present finding illustrated that, PCV was higher than GCV for all studied traits, suggesting the observed variation in the soybean genotypes were both the combination of genotypic and environment effect. According to Deshmukhs *et al* (1986) descriptions, high phenotypic and genotypic coefficients of variation were recorded for number of seed (40.62% and 28.3%), number of pod (30.43% and 25.34%), soybean rust (46.88% and 28.47%), frog eye leaf spot (43.97% and 21.29%), plant height (26.45% and 24.80%), hundred seed weight (23.90% and 20.74%), respectively. High PCV and GCV indicated, the genotype could be reflected by the phenotype, which means selection will be effective based on the phenotypic performance for these traits.

However, the extent of the environmental influence on any character is indicated by the magnitude of the differences between PCV and GCV. Large differences reflect high environmental influence, while small differences reveal high genetic

influence (Akinwaleet *al.*, 2011). Accordingly, the difference between PCV with the corresponding GCV values was relatively higher for frog eye leaf spot, soybean rust, and number of seed and gain yield, suggesting the high influence of the environment on these traits. Though, the difference between PCV and GCV was comparatively low for plant height, hundred seed weight and number of pod, indicating the minimal influence of environment on the expression of these traits. Therefore, selection based on phenotypic performance would be effective to bring considerable improvement in these traits. The current finding is in agreement with Masreshawet *al* (2021) and Neelimaet *al* (2018) who reported high GCV and PCV for number of pod, number of seed, plant height and hundred seed weight.

Heritability and genetic advance

Gadde (2002) generally classified heritability estimates as low (<30%), moderate (30-60%) and high (>60%). Based on this classification, plant height (87.85%), days to maturity (76.25%), hundred seed weight (75.29%), number of pod (69.38%) and number of branch (60.08%) exhibited high heritability estimates. On the other hand, moderate broad sense heritability estimates were observed for number of branch (60.08%), number of seed (48.56%) and soybean rust (36.89%), while other traits were found low heritability estimates. Similar to the current finding high heritability

estimates on plant height, days to maturity, hundred seed weight and number of pod was reported by (Neelima *et al.*, 2018; Abushet *et al.*, 2017;

Aditya *et al.*, 2011; Yechalewet *et al.*, 2019; Masreshaw *et al.*, 2021).

Table 4. Estimates of variance components for 11 traits of 100 soybean genotypes

Traits	Range		mean	(σ^2g)	(σ^2p)	H(%)	GCV (%)	PCV (%)	GA	GAM(%)
	Min	Max								
DTF	26.75	66.75	55.60	11.80	45.15	26.14	6.18	12.08	3.62	6.52
DTM	115.50	130.75	121.93	24.80	32.53	76.25	4.08	4.68	8.97	7.36
PH	33.35	67.30	48.53	144.80	164.83	87.85	24.80	26.45	23.27	47.95
NPP	15.70	37.70	27.62	49.00	70.63	69.38	25.34	30.43	12.03	43.55
NSP	30.15	118.65	53.00	225.03	463.40	48.56	28.30	40.62	21.57	40.69
NBP	2.90	5.30	3.88	0.42	0.70	60.00	16.70	21.56	1.04	26.69
LG	1.00	2.00	1.17	0.03	0.11	27.27	14.80	28.35	0.19	15.95
SR	2.00	5.00	3.20	0.83	2.25	36.89	28.47	46.88	1.14	35.67
FLS	1.50	4.00	2.53	0.29	1.24	23.43	21.29	43.97	0.54	21.26
HSW	8.78	17.53	14.06	8.50	11.29	75.29	20.74	23.90	5.22	37.12
YLD	0.85	2.50	1.28	0.10	0.26	39.22	17.38	27.75	0.41	22.45

(σ^2g)=genotypic variance, (σ^2P)=phenotypic variance, H= broad sense heritability, GCV=genotypic coefficient of variance, PCV= phenotypic coefficient of variance, GA=genetic advance, GAM= genetic advance as percent of mean. DTF = days to 50% flowering, DTM = days to 95% pod maturity, PH = plant height, NPP = number of pod per plant, NSP= number of seed per plant, SP= NBP=number of branch per plant, LG=lodging, SH=shattering, SR=soybean rust, FLS=frog eye leaf spot HSW=hundred seed weight, YLD= yield per ha-1

Johnson *et al.* (1955) categorized the genetic advance as the percent of mean as low (0-10%), medium (10-20%) and high ($\geq 20\%$). Based on these category the highest GAM was observed from the present study for plant height (87.85%) followed by number of pod (43.55%), number of seed (40.69%), hundred seed weight (37.12%), soybean rust severity (35.67%), number of branch (26.69), yield (22.45) and frog eye leaf spot severity (21.26%). In contrast, the remaining traits showed low estimates of GAM. Traits which showed low GCV and low GAM were under high environmental influence; hence selection based on such traits would be less effective. High heritability estimates accompanied by the high genetic

advance is usually more helpful in predicting increase under selection than heritability estimates alone (Johnson *et al.*, 1995).

Accordingly, combined high GCV, high heritability and high GAM were recorded for plant height (24.80%, 87.85% and 47.95%), number of pod (25.34%, 69.38% and 43.55%) and hundred seed weight (20.74%, 75.29% and 37.12%). Hence, this trait can be improved through direct selection more easily than other traits. Masreshaw *et al.* (2021) reported similar result with this investigation, high heritability combined with high GAM for plant height and hundred seed weight was reported by Abushet *et al.* (2017), while Aditya *et al.* (2011) and Neelima *et al.*

(2018) were reported combined High heritability with high GAM for plant height and number of pod .

However, other traits showed low to moderate heritability along with low genetic advance, suggests that those traits are influenced by environmental effects and are most likely governed by both additive and non-additive (dominant, epistemic) type of gene action (Abate *et al.*, 2015), this would make complicated to improve these traits through simple selection, to the extent that cross breeding is the best alternative method for improvement of such kind of traits.

Cluster analysis

Cluster analysis categorized 100 soybean genotypes into five clusters (table 5). The grouping pattern showed; cluster-I contained highest number of genotypes (57%) followed by cluster-II (35%), cluster-III (5%), cluster-IV (2%) and cluster-V (1%). In cluster analysis, if the categorization is successful, individuals within (homogenous) shall be closer and different clusters (heterogeneous) shall be farther apart (Hair *et al.*, 1995). The distribution pattern of genotypes in to different cluster might be difference in

genetic background through their pedigree.

Cluster characterization using quantitative traits

Mean performance of clusters (table 6) for the 11 traits reflected that the genotypes in cluster-III exhibited the highest mean yield, days to flowering, soybean rust, number of pod and branch. Even though, the genotypes in this cluster had relatively highest soybean rust severity level, the score value lays in moderately resistant level, Genotypes in cluster I were characterized by medium mean values for all the traits except for highest in crop lodging. Genotypes in Cluster-II were characterized by shortest plant height, early maturity date, minimum number of pod, number of seed, number of branch and highest hundred seed weight. Cluster-IV possessed accessions with short days to flowering, lowest score in frog eye leaf spot disease, and lowest in crop yield. Conversely, cluster-V which comprised of only one genotype was mainly characterized late physiological maturity, tallest plant height, highest score for frog eye leaf spot, lowest for crop lodging and hundred seed weight.

Table 5. The distribution of 100soybean genotypes in to five clusters tested at Jimma and Mettu (2019).

Cluster No.	No. geno.	genotypes (%)
I	57	57 T1-EL-OS-JM17-A13, T1-EL-OS-JM17-A15, T1-EL-OS-JM17-B11, T1-EL-OS-JM17-B14, T1-EL-OS-JM17-C2, T1-EL-OS-JM17-D4, T1-EL-OS-JM17-D6, T1-EL-OS-JM17-D14, T1-EL-OS-JM17-E2, T1-EL-OS-JM17-E3, T1-EL-OS-JM17-E5, T1-EL-OS-JM17-E13, T1-EL-OS-JM17-E15, T1-EL-OS-JM17-E18, T1-EL-OS-JM17-E27, T1-EL-OS-JM17-E28, T1-EL-OS-JM17-G13, T1-EL-OS-JM17-H6, T2-EL-LG-90-JM17-I12, T2-EL-LG-90-JM17-I15, T2-EL-LG-90-JM17-I22, T3-EL-LG-63-JM17-A1, T3-EL-LG-63-JM17-A8, T3-EL-LG-63-JM17-A10, T3-EL-LG-63-JM17-A22, T3-EL-LG-63-JM17-A28, T3-EL-LG-63-JM17-B4, T3-EL-LG-63-JM17-B6, T3-EL-LG-63-JM17-C1, T3-EL-LG-63-JM17-E8, T3-EL-LG-63-JM17-E31, T3-EL-LG-63-JM17-F11, T3-EL-LG-63-JM17-F29, T3-EL-LG-63-JM17-I31, T3-EL-LG-63-JM17-I36, T4-EL-LG-65-JM17-A11, T4-EL-LG-65-JM17-A13, T4-EL-LG-65-JM17-B8, T4-EL-LG-65-JM17-C15, T4-EL-LG-65-JM17-C18, T4-EL-LG-65-JM17-C20, T4-EL-LG-65-JM17-F2, T4-EL-LG-65-JM17-G1, T4-EL-LG-65-JM17-G9, T4-EL-LG-65-JM17-G27, T5-EL-LD-77-JM17-A5, T5-EL-LD-77-JM17-A7, T5-EL-LD-77-JM17-A11, T5-EL-LD-77-JM17-A14, T5-EL-LD-77-JM17-A15, T5-EL-LD-77-JM17-H3, T5-EL-LD-77-JM17-H43, T5-EL-LD-77-JM17-I3, T5-EL-LD-77-JM17-I22, T5-EL-LD-77-JM17-I24, Nyala, Clarck 63K
II	35	35 T3-EL-LG-63-JM17-A3, T3-EL-LG-63-JM17-B1, T3-EL-LG-63-JM17-E14, T3-EL-LG-63-JM17-E17, T3-EL-LG-63-JM17-E30, T4-EL-LG-65-JM17-E24, T4-EL-LG-65-JM17-I14, T5-EL-LD-77-JM17-A2B, T5-EL-LD-77-JM17-A9, T5-EL-LD-77-JM17-A17, T5-EL-LD-77-JM17-E10, T5-EL-LD-77-JM17-C1, T5-EL-LD-77-JM17-C3, T5-EL-LD-77-JM17-C4, T5-EL-LD-77-JM17-C6, T5-EL-LD-77-JM17-C7, T5-EL-LD-77-JM17-C25, T5-EL-LD-77-JM17-D4, T5-EL-LD-77-JM17-B16, T5-EL-LD-77-JM17-E25, T5-EL-LD-77-JM17-E27, T5-EL-LD-77-JM17-F3, T5-EL-LD-77-JM17-F4, T5-EL-LD-77-JM17-F11, T5-EL-LD-77-JM17-F15, T5-EL-LD-77-JM17-G7, T5-EL-LD-77-JM17-G18, T5-EL-LD-77-JM17-G29, T5-EL-LD-77-JM17-H1, T5-EL-LD-77-JM17-F28, T5-EL-LD-77-JM17-H31, T5-EL-LD-77-JM17-H44, T5-EL-LD-77-JM17-I34, T5-EL-LD-77-JM17-I35, T5-EL-LD-77-JM17-H30
III	5	5 T1-EL-OS-JM17-E1, T1-EL-OS-JM17-E23, T1-EL-OS-JM17-H9, T4-EL-LG-65-JM17-A8, T1-EL-OS-JM17-H12
IV	2	2 T1-EL-OS-JM17-E6, T5-EL-LD-77-JM17-F27
V	1	1 T3-EL-LG-63-JM17-A17

Table 6. Cluster mean values for 11 traits of 100 soybean genotypes tested at Jimma and Mettu (2019).

Cluster	Traits										
	DTF	DTM	PH	NPP	NSP	NBP	LG	SR	FLP	HSW	YLD
I	56.69	123.11	51.98	29.80	56.66	4.01	1.23**	3.37	2.33	13.75	1.96
II	54.96	119.86*	42.96*	22.76*	42.22*	3.62*	1.10	2.90	2.86	14.90**	1.58
III	56.80**	122.50	48.98	35.86**	72.87	4.15**	1.20	3.40**	2.40	12.44	2.16**
IV	32.88*	121.00	43.25	27.63	54.79	3.68	1.01	3.25	2.25*	13.59	1.55*
V	56.00	125.75**	55.23**	31.95	118.65**	4.00	1.00*	2.50*	3.00**	11.83*	1.85

**, * represents maximum and minimum values respectively, DTF = days to 50% flowering, DTM = days to 95% pod maturity, PH = plant height, NPP = number of pod per plant, NSP= number of seed per plant, SP= NBP=number of branch per plant, LG=lodging, SH=shattering, SR=soybean rust, FLS=frog eye leaf spot ,HSW=hundred seed weight, YLD= yield ton per ha-1

Genetic divergence (D²)

Multivariate analysis by means of Mahalanobis' D² statistics is a useful tool in quantifying the degree of genotypic divergence among biological populations and to assess the relative contribution of different components to the total divergence at intra and inter-cluster levels (Das and Gupta, 1984). The values of pair wise average intra and inter-cluster divergence (D²) among 100 soybean genotypes in five clusters based on 11 quantitative traits are presented in table 7. Thus, the inter-cluster distances in all the cases were greater than the intra-cluster distances suggesting wider diversity among the genotypes of the distant clusters. The intra-cluster degree of diversity was maximum in cluster-IV (7.82), indicating that the genotypes in cluster IV were a little bit heterogeneous as compared to those in other clusters. Generally, the range of intra-cluster values indicated homogeneous nature of the genotypes within the clusters.

The chi-square test revealed the existence of highly significant differences among the paired inter

cluster distance except cluster I with II and III. The maximum inter-cluster distance was found between cluster-IV and V (760.20) followed by cluster-II and V (605.30), cluster-I and V (538.10), and cluster-III and V (427.70). The highest value of inter-cluster distance indicated that the genotypes belonging to these cluster were far diverged. The lowest inter-cluster distance was recorded between clusters-I and II (10.68) followed by cluster-I and III (13.83), which means a close relationship between the genotypes. Cluster-V was found divergent from other clusters chiefly due to days to maturity, plant height number of pods per plant and frog eye leaf spot, indicating maximum contribution of these traits towards the divergence. Similarly, cluster-III was found diverged from cluster I, II and IV due to the highest in grain yield, days to flowering, soybean rust, and number of pod and branch. On the other hand cluster I and II were diverged from cluster IV due to their highest crop lodging and hundred seed weight, respectively.

Table 7 .Pair wise average intra (bold) and inter cluster divergence values (D²) among 100 soybean genotypes in five clusters based on 11 traits tested at Jimma and Metu (2019).

Cluster	I	II	III	IV	V
I	(1.12)	10.68	13.83	243.50**	538.10**
II		(2.10)	39.66*	245.50**	605.30**
III			(5.99)	267.60**	427.70**
IV				(7.82)	760.20**
V					(0.00)

*, **= significant, (p<0.01) $\chi^2=24.72$, and (p<0.05) $\chi^2=19.67$, respectively

Jgadevet *al.* (1991) stated that the traits contributing maximum towards the

divergence should be given greater emphasis for deciding the type of

cluster for the purpose of further selection and choice of the parents for hybridization. In this perspective, intra cluster mean performance for days to physiological maturity, plant height, and frog eye leaf spot in cluster-V was maximum and greater than the mean of other clusters, suggesting that the role of those traits towards the divergence between cluster-V with other clusters. Generally, maximum genetic segregation and recombination will be expected from cross that involve parents from the significant inter cluster distance. In the present investigation, superior hybrids or recombinants can be exploited by crossing genotypes from cluster-V with other clusters. Moreover, the heterosis could also be exploited by crossing between genotypes with moderate diversity like cluster-III and V followed by cluster- II and IV, I and VI, and II and III. The current result is in support the previous findings (Tadesse and Sentayehu, 2015; Abush *et al.*, 2017)

Principal component analysis (PCA)

Principal component analysis was done using 11 quantitative traits with the intention of minimizing the dimensionality of large number of interrelated traits in a given data set and retaining maximum information about the genetic variation (table 8). Accordingly, the first four principal components with Eigen values exceeding one were responsible for about 72.62 % of the total variation among the genotypes. Maximum

variation was accounted from the first principal component (39.31%) followed by the second (13.82%) principal components, which means, out of the entire variations, the first and the second principal components accounted for more than two third of the total variations (53.13%).

The first principal component that accounted maximum variation (39.31%) was due to the principal contribution of positive discriminatory traits like number of pod per plant, number of seed per plant, grain yield, plant height and days to maturity. The considerable variation observed in the second principal component (13.82%) was attributed to hundred seed weight, days to maturity and plant height. Traits which had substantial contribution to the third principal component (10.26%) were days to flowering, crop lodging and frog eye leaf spot. On the other hand, hundred seed weight, grain yield and soybean rust predominantly influenced the variation in the fourth principal component. Consistent with this finding earlier investigators also found comparable result from different soybean genotypes (Tadesse and Sentayehu, 2015; Abush *et al.*, 2017; Yechalewet *et al.*, 2019).

Chahal and Goal (2002) inferred that characters with the largest absolute values closer to unit within the first principal component influence the clustering more than those with lower absolute values closer to zero. Therefore, in the current investigation

discrimination of the accessions in to different cluster was mainly due to number of pod per plant, number of

seed per plant, grain yield, plant height, days to flowering, days to maturity and hundred seed weight.

Table 8. Eigenvectors and Eigen values of the first four principal components for 11 traits of 100 soybean genotypes tested at Jimma and Metu (2019).

Traits	Principal component			
	Prin1	Prin2	Prin3	Prin4
DTF	0.19	0.14	0.64	-0.14
DTM	0.31	0.43	0.03	-0.24
PH	0.34	0.40	0.18	0.07
NPP	0.43	-0.10	-0.23	-0.12
NSP	0.38	-0.13	-0.28	-0.23
NBP	0.29	-0.18	0.17	-0.27
LG	0.24	-0.15	0.48	0.28
SR	0.21	-0.35	0.03	0.58
FLP	-0.26	-0.34	0.39	-0.13
HSW	-0.21	0.56	0.02	0.40
YLD	0.36	-0.03	-0.15	0.43
Eigen values	4.32	1.52	1.13	1.02
Total variance (%)	39.31	13.82	10.26	9.25
Cumulative variance (%)	39.31	53.13	63.39	72.62

DTF = days to 50% flowering, DTM = days to 95% pod maturity, PH = plant height, NPP = number of pod per plant, NSP = number of seed per plant, SP = NBP = number of branch per plant, LG = lodging, SH = shattering, SR = soybean rust, FLS = frog eye leaf spot HSW = hundred seed weight, YLD = yield per ha-1

Association among Quantitative Traits

Phenotypic (r_{ph}) and genotypic (r_g) correlation of yield and component traits

The result revealed that, genotypic correlation coefficients were generally higher in magnitude than phenotypic correlation coefficients values (table 9) for most of the paired traits, indicating the strong inherent association among these traits. Accordingly, grain yield exhibited significant and positive phenotypic and genotypic association with days to maturity ($r_{ph}=0.38$; $r_g=0.26$), plant height ($r_{ph}=0.50$;

$r_g=0.50$), number of pod per plant ($r_{ph}=0.49$; $r_g=0.65$), number of seed per plant ($r_{ph}=0.20$; $r_g=0.54$), and number of branch per plant ($r_{ph}=0.19$; $r_g=0.33$), indicating genotypes characterized by lately matured, tallest plant height, maximum number of pod, seed and branch per plant were high yielder. Alternatively, days to flowering showed positive and significant phenotypic and genotypic correlations with days to maturity ($r_{ph}=0.16$; $r_g=0.31$), plant height ($r_{ph}=0.19$; $r_g=0.33$) and number of pod per plant ($r_{ph}=0.12$; $r_g=0.22$), hence, indirect selection in favor of these traits can improve gain yield in soybean.

Table 9. Genotypic (above diagonal) and Phenotypic (below diagonal) correlation coefficients among 11 traits of 100 soybean genotypes tested at Jimma and Metu (2019).

Trait	DTF	DTM	PH	NPP	NSP	NBP	LG	SR	FLS	HSW	YLD
DTF		0.31**	0.33**	0.22*	0.15ns	0.21*	0.29**	0.08ns	-0.10ns	-0.13ns	0.18ns
DTM	0.16**		0.68**	0.48**	0.42**	0.31**	0.17ns	0.07ns	-0.46**	-0.06ns	0.26*
PH	0.19**	0.71**		0.50**	0.43**	0.37**	0.37**	0.14ns	-0.37**	0.06ns	0.50**
NPP	0.12*	0.38*	0.47**		0.83**	0.50**	0.34**	0.33**	-0.48**	-0.48**	0.65**
NSP	0.05ns	0.04ns	0.14**	0.64**		0.39**	0.26*	0.23**	-0.34**	-0.47**	0.54**
NBP	0.09ns	0.17**	0.28**	0.44**	0.34**		0.26**	0.25*	-0.11ns	-0.37**	0.33**
LG	0.16**	0.39**	0.4**	0.21**	0.01ns	0.16**		0.31**	-0.11ns	-0.26**	0.34**
SR	0.07ns	0.41**	0.37**	0.28**	-0.03ns	0.15**	0.29**		-0.13ns	-0.28**	0.46**
fls	-0.11*	-0.66**	-0.52**	-0.23**	0.13*	-0.05ns	-0.37**	-0.52**		0.01ns	-
HSW	0.01ns	0.25**	0.28**	-0.0ns	-0.21**	-0.09ns	0.06ns	0.11*	-0.30**		0.41**
YLD	0.09ns	0.38**	0.50**	0.49**	0.20**	0.19**	0.32**	0.36**	-0.40**	0.17**	-
											0.14ns

*, ** = significant at probability level of ($p < 0.01$) and ($p < 0.05$), respectively. DTF = days to 50% flowering, DTM = days to 95% pod maturity, PH = plant height, NPP = number of pod per plant, NSP = number of seed per plant, SP = NBP = number of branch per plant, LG = crop lodging, SH = shattering, SR = soybean rust, FLS = frog eye leaf spot, HSW = hundred seed weight, YLD = yield per ha⁻¹

On the other hand, grain yield also showed significant positive phenotypic and genotypic correlation with soybean rust reaction ($r_{ph}=0.36$; $r_g=0.46$) and lodging ($r_{ph}=0.32$; $r_g=0.34$), suggesting that high crop load aggravates soybean rust severity and crop lodging, which pose a challenge for breeders to improve these traits simultaneously. While, grain yield found negative phenotypic and genotypic correlation with frog eye leaf spot reaction ($r_{ph}=-0.40$; $r_g=-0.41$), which has important implication in the improvement of this trait during disease resistant soybean variety development. In the same manner, yield displayed positive phenotypic and negative genotypic correlation with hundred seed weight ($r_{ph}=0.17$; $r_g=-0.14$). The other yield related traits also had either positive or negative phenotypic and genotypic linear relationship with each other as indicated in the table 9 above.

The current phenotypic and genotypic correlations of traits were in agreement with the previous report for most of the traits. Similar to these result, Mesfin (2018) found that days to maturity, plant height and number of seed per plant showed significant positive genotypic and phenotypic correlation with grain yield. Positive and strong phenotypic and genotypic correlation of pod with grain yield was also confirmed by Chamundeswarriet al (2003) and Aditya *et al.* (2011).

Generally, the association could be either genetic or environment or else the contribution of both factors. Therefore, positive correlation among

paired traits might allow improving both traits simultaneously, whereas for a negative correlation, selection for improving one trait will likely cause decreases the other trait (Rangaswamny, 1995). Kearsey and Pooni1 (1996) also suggested that the positive and significant association of traits due to the effect of genes can be the existence of strong coupling linkage between genes or the traits might be the result of pleiotropic genes that could control the traits in the same direction, while the negative correlation might be because of different genes or pleiotropic genes that have dominance on the traits which would control in different direction.

Path coefficient analysis

Correlation coefficient among paired traits may not give a complete picture for a parameter like yield which is either directly or indirectly controlled by several other traits. In these circumstances, path analysis provides a means of partitioning the correlation coefficients into the measures of direct and indirect effects of independent variables on the dependent variable. Path analysis also effectively measure the relative importance of causal factors (Ali and Shakor, 2012), which helps to build an effective selection program. In the current research, path-coefficient analysis was carried out at genotypic level using grain yield as dependent variable and other traits as independent variables (Table10).

The path coefficient analysis revealed that number of pods per plant (0.295)

observed the maximum positive direct effect on grain yield followed by plant height (0.294). High and positive direct effect on yield was also found from soybean rust, which means high crop load makes a crop susceptible to soybean rust. Moderate positive direct effects were recorded from hundred seed weight (0.195) and number of seed per plant (0.133), while Number of branches per plant (0.015), days to flowering (0.038) and crop lodging (0.0028) had low degree of positive direct effects on grain yield.

Conversely, negative direct effects on grain yield was exhibited from physiological maturity (-0.304) and frog-eye leaf spot disease (-0.134). Comparable to this finding, Mesfin (2018) reported as number of pods per plant, number of seeds and hundred seed weight showed positive direct effect on grain yield. Moreover, according to Malik *et al* (2006), days to physiological maturity had negative direct effect on grain yield.

Table 10. Estimate of direct (bold diagonal) and indirect effects (off diagonal) at genotypic level of 11 traits on yield in 100 soybean genotypes

Trait	DTF	DTM	PH	NPP	NSP	NBP	LG	SR	FLS	HSW	rg _(xy)
DTF	0.038	-0.094	0.098	0.098	0.020	0.003	0.008	0.023	0.014	-0.025	0.184
DTM	0.012	-0.304	0.199	0.217	0.056	0.005	0.005	0.019	0.062	-0.011	0.257
PH	0.013	-0.205	0.294	0.223	0.057	0.005	0.010	0.039	0.050	0.012	0.499
NPP	0.008	-0.146	0.146	0.449	0.111	0.007	0.010	0.093	0.064	-0.093	0.650
NSP	0.006	-0.127	0.126	0.375	0.133	0.006	0.007	0.065	0.046	-0.092	0.545
NBP	0.008	-0.093	0.108	0.224	0.052	0.015	0.007	0.069	0.014	-0.072	0.333
LG	0.011	-0.052	0.108	0.152	0.034	0.004	0.028	0.086	0.014	-0.051	0.335
SR	0.003	-0.020	0.041	0.149	0.031	0.004	0.009	0.282	0.017	-0.054	0.460
FLS	-0.004	0.141	-0.110	-0.215	-0.045	-0.002	-0.003	-0.035	-0.134	0.003	-0.405
HSW	-0.005	0.018	0.018	-0.214	-0.063	-0.005	-0.007	-0.078	-0.002	0.195	-0.144

Residual effects (U) = 0.42

DTF = days to 50% flowering, DTM = days to 95% pod maturity, PH = plant height, NPP = number of pod per plant, NSP= number of seed per plant, SP= NBP=number of branch per plant, LG=crop lodging, SH=shattering, SR=soybean rust, FLS=frog eye leaf spot HSW=hundred seed weight, YLD= yield per ha-1, rg(xy)= genotypic correlation coefficient between yield per tree and other traits.

Traits which showed positive direct effect on yield had less magnitude of path coefficient values than their correlation values, implying less indirect influence of these traits by means of other component traits. The correlation coefficient of hundred seed weight with yield was negative, but the direct effect was positive, indicating the importance of indirect effect of this trait via other traits.

Generally, number of pod per plant and plant height not only found high and positive direct effect ($p=0.449$ and 0.294) but also showed strong and positive genotypic correlation coefficient ($r_g=0.65$ and 0.499) with grain yield, respectively. Therefore, these traits should be considered as important selection indices for yield improvement program. Residual effect in path analysis determines how best the component (independent) variables account for the variability of the dependent variable, yield (Singh and Chaudhary, 1985). To this end, the residual effect in the present study was 0.42 (table 10), showing that 58% of the variability in grain yield was explained by the component factors. Therefore the remaining unexplained variability will either due to non-studied traits or the influence of environment on the traits.

Conclusions

Presence of genetic variability is one of the pre-request to perform selection in any breeding program. From the current investigation the tested soybean

genotypes were found genetically diverse in terms of different morphological traits. Combined high genotypic coefficients of variation (GCV), high heritability (H^2) and high genetic advance as present of mean (GAM) were recorded for plant height (24.80%, 87.85% and 47.95%), number of pod per plant (25.34%, 69.38% and 43.55%) and hundred seed weight (20.74%, 75.29% 37.12%). Hence, this trait can be improved through direct selection more easily than other traits. A total 100 soybean genotypes were grouped into five clusters. The maximum inter cluster distance was found between clusters-IV and V, suggesting superior hybrids or recombinants can be realized by crossing genotypes in these clusters. Principal component analysis (PCA) revealed that, the 1st four PCA with Eigen values exceeding one were responsible for about 72.62 % of the total variation. Out of the entire variations, 1stPCA and the 2ndPCA accounted for more than two third of the total variations (53.13%). On other hand, number of pod per plant and plant height were found maximum positive direct effect on grain yield, also showed strong and positive genotypic correlation coefficient with grain yield, thus, selection pressure could profitably be applied on these traits. Finally this research will enhance the utilization of variation present with in soybean genotypes for selection program. In the future, such a study should include other quality parameters with biochemical and molecular marker assisted techniques.

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Yield Stability Analysis of Large-Seeded Common Bean Varieties in Major Bean Growing Areas of Ethiopia

Girum Kifle Ejigu¹, Hussein Mohammed .² and Berhanu Amsalu Fenta¹

¹ Ethiopian Institute of Agricultural Research (EIAR), Melkassa Agricultural Research Center, Ethiopia,

²Hawassa University, Hawassa, Ethiopia; E-mail: girumkifle@gmail.com

Abstract

Twenty large seeded common bean varieties released over two decades were evaluated at five locations in 2017 main cropping seasons in Ethiopia. The objective of the study was to determine the magnitude and pattern of $G \times E$ interaction and yield stability. The study was conducted using a randomized complete block design with three replications. $G \times E$ interaction and yield stability were estimated using AMMI and GGE stability methods. Pooled analysis of variance for grain yield showed significant differences at $p \leq 0.01$ among the main effects of genotypes and environments and at ($p \leq 0.01$) for $G \times E$ interaction effects. This indicated that either the genotypes differentially responded to the changes in the test environments or the test environments discriminated the genotypes or both. Environment effect accounted for 43.05% of the total yield variation; whereas, genotype and $G \times E$ interaction effects accounted for 26.27% and 30.67%, respectively. Environmental variation contributes a high percent to the total variability which indicates that differences among environments were the major reason for a different performance on grain yield. GEI variance was a little higher than a genetic variance. The first two principal components accounted for cumulative 71.67% interaction effects, which, indicated the majority of interaction effects were within two principal components. The AMM and GGE models identified genotypes G10, G1, G3, and G18 that display higher grain yield and stability. The five testing locations were grouped into two mega environments, namely; Arsi Negele, Haramaya, and Sirinka as one group with 'G13' and 'G14' as the best genotypes, and Alem Tena and Melkassa as the second group with G19 (DAB-107) as the best genotype. Hence, it can be recommended that a rigorous breeding effort is aimed at the development of enhanced populations and the release of stable and high yielding genotypes.

Keywords: *Phaseolus vulgaris* L., Grain yield, Stability, AMMI, GGE

Introduction

Common bean (*Phaseolus vulgaris* L.) is considered the main grain legume for human consumption and represents an essential source of proteins, carbohydrates, fibers, and trace

minerals in several countries worldwide (Myers and Kmiecik, 2017). Common bean is one of the major pulses in Ethiopia. It is a basic food used daily in the Ethiopian diet and export crop. To meet this demand, common beans are grown throughout

the year under different cultivation systems. It holds the second-largest share of the area (306,186.59 ha) under pulse crops preceded by Faba bean in main season production. It also ranks second (520,979.3 tons) after Faba beans (9, 217, 61.5 tons) in total production in the 2017/18 cropping season (CSA, 2017). The average yield for the 2016/17 crop is approximately 1.4 t/ha and total production is 520,979.3 tons (CSA, 2017), which is low as compared to some top producing countries in Africa like Tanzania (1,140,444 tons), Uganda (1,024,742 tons), and Kenya (846,000 tons).

The crop is well adapted to areas that receive average annual rainfall ranges from 500 – 1500 mm with an optimum temperature range of 16 – 24 °C, and with a frost-free period of 105 to 120 days. It performs best on deep, friable, and well-aerated soils with an optimum pH range of 6.0 to 6.8 (Kay, 1979). Areas within altitude ranges of 1200 – 2200 m.a.s.l are optimum altitude for common bean production (Acland, 1971; Cobley, 1976).

Although common bean is one of the most important crops in the country, productivity has been regarded as very low. This was due to the current farming systems being a result of the interaction of abiotic, biotic, and social factors, each of which causes a significant reduction of yield (Wortmann et al., 1998).

In Ethiopia, the common bean breeding program was initiated in 1972, at Melkassa Agricultural

Research Centre (MARC) of the Ethiopian Institute of Agriculture Research (EIAR) with the objectives of improving grain yield, resistance to important common bean diseases, and development of improved crop management practices. The national bean improvement program has released fifty-eight improved common bean varieties until the year 2017 (MoA, 2017) that can meet local consumption and export market. Though improved common bean varieties have been released for general production under different recommendation areas or a wide range of environments. However, crop genotypes grown in different environments would frequently encounter significant fluctuations in yield performance and stability.

The concept of genotype by environment interaction for yield stability has been a concern for plant breeders. Common bean is cultivated in diverse environments. Studies on adaptability and yield stability of cultivars and lines have indicated the importance of the interaction between genotypes and environments (GEI). Robertson (1959); and Yang and Baker (1991) agreed that the genotype by environment interactions is usually perceived as uneven variations among genotypes from one environment to another. They also explained as the expression of different sets of genes from different environments and the response variation of the same set of genes to variable environments could be the factors accountable for the inconsistency issue. In addition,

significant differences among the test genotypes/ varieties, locations, and genotypes /variety by location interaction in grain yield have been extensively reviewed by different authorities (Barili et al. 2016, Singh et al., 2007, Ghaderi et al. 1984, Wondimu et al., 2011, and Keneni et al., 2011).

Stability analysis is used to identify greater stability and high yielding genotypes. There is an extensive set of techniques widely applied in stability analysis to provide further information on the real multivariate response of genotypes to environments. But the universal method that has been approved by everyone has not been yet introduced (Kaya et al., 2006). Among the multivariate analysis techniques, the additive main effects and multiplicative interaction (AMMI) model is the powerful method in assessing GEI and stability of genotypes from multi-environment trials and the genotype main effects and genotype by environment interaction effects (GGE) model. The results can be graphed in a useful biplot that shows both main and interaction effects for genotypes and environments. AMMI and GGE models are used frequently for statistical analyses in agricultural research (Gauch, 2006).

The Additive Main Effects and Multiplicative Interaction Model (AMMI) was found suitable to handle both the main effects and GEI in multilocal yield trials. The

AMMI model combines regular analysis of variance for additive effects with principal component analysis for multiplicative structure within the interaction. AMMI biplot is considered to be an effective tool to diagnose GEI patterns graphically. The biplot displays the PCA scores plotted against each other provides visual inspection and interpretation of the GEI components. Integrating biplot display and genotypic stability statistics enables genotypes to be grouped based on the similarity of performance across diverse environments. AMMI analysis is commonly being used in GE interaction data analysis in many crops to identify superior genotypes for specific or wide adaptation. In common bean crops (Carbonell et al. 2004; Ferreira et al., 2006) were used AMMI analysis to identify superior genotypes for specific or wide adaptation.

The GGE model (GGE biplot) was proposed by Yan et al. (2000), allowing visual examination of the relationships among the test environments, genotypes, and the genotype-by-environment interactions (GxE interaction). The GGE biplot displays the genotype main effect (G) and the genotype by environment interaction (GE) in two-way data. It is an effective tool for mega environment analysis (“which-won-where” pattern), whereby specific genotypes can be recommended to specific mega-environments, to identify the mean

performance and stability of genotype, and environmental evaluation.

Based on seed size, yield stability and performance of released varieties of common beans were not studied, and hence evaluation of high-yielding and well-adapted common bean varieties is required to use materials for further breeding purposes and revalidate the production domain. Therefore, the objective of this study was attempted to study the magnitude and pattern of genotype by environment interaction effects and performance stability of

grain yield in 20 large seeded common bean varieties released in the period 1970 to 2017.

Material and Methods

Experimental Design

Cultivars were evaluated at the experimental stations of Melkassa, Arisi Negele, Alem Tena, Haramaya, and Sirinka during the main season of 2017. Soil physiochemical analyses and other characteristics related to the assessment sites are shown in Table 1.

Table 1. Description of locations used for the study

Location	Soil type	Altitude (m.a.s.l)	Latitude	Longitude	Annual average		Rainfall (mm)	Sowing date
					Min (°C)	Max (°C)		
Alem Tena	Andosols	1610	8°18'N	38°57'E	12.9	29.8	728	19 th July 2017
Aris Negele	Nitosols	1890	7°35'N	38°65'E	11.1	25.2	876	14 th July 2017
Haramaya	Fluvisol	1980	9°26'N	42°03'E	12.3	24.3	790	24 th July, 2017
Melkassa	Andosols	1550	8°30'N	39°21'E	16	28.8	763	13 th July, 2017
Sirinka	Eutricvertiol	1880	11°08'N	39°28'E	15.3	28.3	806	1 st August 2017

Where, m.a.s.l = meters above sea level

Source: Melkassa Agricultural Research Centers and National Meteorology Agency

Plant Material

Twenty Ethiopian large seeded common bean varieties released from 1970 to 2017 were evaluated (Table 2). These varieties represent a large part of the genetic variability that exists among large seeded common bean cultivars grown during the approximately 20 years of history of large seeded common bean breeding in Ethiopia. Seed samples were obtained from MARC, Haramaya universities, and South Agricultural Research Institute (SARI). Information about the cultivars is available in supplementary Table 2. The

experiments were arranged in a randomized complete block design with three replications. The experimental plots consisted of four 4-m rows, spaced 0.4 m apart, with 10cm between seeds. Fertilizer was applied to each plot at the rate of 18 kg N and 46 kg P₂O₅ ha⁻¹ in the form of Di-ammonium phosphate (DAP) at planting. Hand weeding was used to control weeds during the growing period. No pesticide or fungicide was used for the control of insects or diseases. The trials were conducted under rain-fed conditions. The central two rows were used for data

collection. For data analysis, grain yield measured from a net plot size of 3.2 m² was converted into kg ha⁻¹ at

12.5 % standard grain moisture content.

Table 2. Description of large-seeded common bean varieties used in the study.

S.N	Official/local Name	Variety Name	Year of release	Breeder/Maintainer
G1	ICS-15541	Gobe Rasha-1	1998/99	MARC/EIAR
G2	AFR-772	Ibado	2003	ARARC/SRARI
G3	RAB-484	Melkadima	2006	MARC/EIAR
G4	Cranscope	Cranscope	2007	MARC/EIAR
G5	ACOS Red	Montcalm	2007	MARC/EIAR
G6	Batu	Batu	2008	MARC/EIAR
G7	SUG131	Deme	2008	MARC/EIAR
G8	AFR-716	Loko	2009	BARC/OARI
G9	GLP-2	GLP-2	2011	MARC/EIAR
G10	ECAB 0247	Babile	2012	HU
G11	ECAB0060	Fedis	2012	HU
G12	ECAB0203	Hirma	2012	HU
G13	K-132	Hundane	2012	HU
G14	ECAB-0056	Morka	2012	MARC/EIAR
G15	RXR-10	Tininke	2012	HU
G16	AFR-702-1	Ramada	2013	HwRC/SARI
G17	SAB 736	Ado	2015	MARC/EIAR
G18	SAB 632	Tafach	2015	MARC/EIAR
G19		DAB-107	2017	MARC/EIAR
G20	Bifort large seeded-5	Gorossa	2017	MARC/EIAR

Where BARC = Bako Agricultural Research Centre, HU = Haramaya University, EIAR = Ethiopian Institute of Agricultural Research, MARC = Melkassa Agricultural Research Centre, SRARI = South Regional Agricultural Research Institute,

Data Analysis

The grain yield data was used to analyses of variance using SAS (statistical analysis system) version 9.2 (SAS, 2009) and analysis of variance for each location, combined analysis of variance over locations. AMMI and GGE biplot analyses were computed using the GenStat 18th edition software program 2016. Simple inspection of the residual plot was used to examine if there is an issue on the heterogeneity of variances or homogeneity of error variances of the locations was tested using Bartlett test (Bartlett, 1947 in Steel and Torrie, 1980). The combined

analyses of the trials (across locations) were done to determine differences between genotypes across locations and also to determine whether there was a significant difference among environments and GEI. The combined analysis was performed using a mixed model, for each character across location (Location, block, as random, was genotype considered fixed variable (McIntosh, 1983). Mean separation was carried out using Tukey at a 5% probability level of significance.

Stability analysis

Additive Main effects and Multiplicative Interaction (AMMI) model

AMMI analysis: - Following testing of the significance of the GxE mean square means over three replications for grain yield of genotype i at location j was subjected to Additive Main Effects and Multiplicative Interaction (AMMI) stability analysis using SAS (Hussien et al., 2000). The AMMI model is

$$Y_{ij} = \mu + g_i + e_j + \sum_{k=1}^n \lambda_k \gamma_{ik} \delta_{jk} + \varepsilon_i$$

Where: Y_{ij} = is the yield of i th genotype in the j th environment

μ = the grand mean

g_i and e_j = are the genotype and environment deviations from the grand mean, respectively;

λ_k = the singular value of the principal component (PC) axis k ; these are usually known as Interaction Principal Component Axes (IPCA). There are (Min (G, E))-1 PC axes. If number of environments is less than number of genotypes then we have a total E-1 PC axis.

γ_{ik} and δ_{jk} = are the genotype and environment principal components scores for axis k ;

n = is the number of statistically significant principal components in the AMMI model

ε_i = is the residual term consisting statistically non-significant PC axes. If we have E IPCA, then ε_i has E- n components.

The degrees of freedom (df) for the IPCA were calculated based on the following Method (Zobel et al., 1988).
df = G + E - 1 - 2n

Where: G = the number of genotypes.
E = the number of environments. n = the n th axis of IPCA

Identification of stable and high yielding Genotypes

The identification of stable and high yielding common bean genotypes was done based on AMMI Stability Value (ASV) and Genotype Selection Index (GSI).

AMMIs Stability Value (ASV)

After testing the significance of the GEI mean square for yield and AMMI stability analysis AMMI stability value (ASV) for each genotype was calculated using the following formula.

$$ASV = \sqrt{\left[\frac{SS_{IPCA1}}{SS_{IPCA2}} \times IPCA1 \text{ Score} \right]^2 + (IPCA2 \text{ score})^2} \quad (\text{Purchase et al. 2000})$$

Where, ASV= AMMI stability value; SS= sum of square; IPCA1 and IPCA2= the first and the second interaction principal component axes, respectively. Genotypes with lower values of ASV were considered to be stable.

Genotype Selection Index (GSI)

Mohammadi and Amri, (2008) suggested that the most stable genotypes would not necessarily have the best yield performance, hence there is a need for approaches that incorporate both mean yield and stability in a single index. For the simultaneous selection of yield and stability, a new approach known as genotype selection index (GSI) was recommended by Farshadfar (2008). GSI was calculated by the following formula:

$$\text{GSI} = \frac{\text{RASV} + \text{RY}}{\text{RASV} + \text{RY}}$$

Where RASV is the rank of a genotype by its AMMI stability value and RY is the rank of a genotype by mean grain yield. The lowest ASV is given rank of 1 and the highest mean grain yield is given rank of 1. GSI incorporate both mean yield and stability in a single criterion. Low value of this parameter shows desirable genotypes with high mean yield and high stability.

GGE model

In order to have a clear insight into the interaction and the general pattern of adaptation of varieties, GGE biplot of varieties and environments was performed. The GGE model (GGE biplot) was proposed by Yan et al., (2000), allowing genotype by

environment interaction (GEI) of multiple environmental trial data to be visually examined.

The model for a GGE biplot (Yan, 2002) based on singular value decomposition (SVD) of the first two principal components is:

$$P = G + GEI + E \text{ or } P - E = G + GEI$$

The observed phenotypic value (P) consists of variances of the environment (E), the genotype (G) and the genotype and environment interaction (GEI).

The above formula was in terms of variance components, when presented as effects which have the unit of originally measured values, they become.

$$y_{ij} = \mu + \alpha_i + \beta_j + \phi_{ij}$$

$$y_{ij} - \mu - \beta_j = \alpha_i + \phi_{ij}$$

Where; y_{ij} = the expected yield of genotype i in environment j

μ = the grand mean of all observation

α_i = the main effect of genotype i

β_j = the main effect of genotype j

ϕ_{ij} = the interaction between genotype i and environment j

Instead of trying to separate G and GEI, GGE biplot keeps G and GEI together and partition this mixture GGE into two multiplicative terms.

$$y_{ij} - \mu - \beta_j = g_{i1}e_{i1} + g_{i2}e_{2i}\alpha_j + \phi_{ij} + \varepsilon_{ij}$$

Where g_{i1} and e_{i1} are called the primary scores of genotype i and environment j , respectively; g_{i2} and e_{2j} are the secondary scores for genotype i and environment j , ϕ_{ij} is the residue not explained by the primary and secondary effect. Actually, a GGE biplot is constructed by plotting g_{i1} against g_{i2} and e_{i1} against e_{2j} in a single scatter plot. The most common way to implement the above formula is by subjecting the GGE data to singular value decomposition (SVD) as shown below;

$$y_{ij} - \mu - \beta_j = \lambda_1 \xi_{i1} \eta_{j1} + \lambda_2 \xi_{i2} \eta_{j2} + \xi_{ij}$$

Where λ_1 and λ_2 are the singular values of the first and second largest principal components, PC1 and PC2,

respectively; ξ_1 and ξ_2 are the eigenvectors of genotype i for PC1 and PC2, respectively, and η_1 and η_2 are the eigenvectors of environment j for PC1 and PC2.

Result and Discussion

Results of single location analysis of variance for grain yield traits for large-seeded common bean genotypes tested at five locations in the 2017 cropping season are presented in Table 3. ANOVA of data at individual locations revealed a significant difference ($P < 0.01$) among the genotypes in grain yield traits at all locations. There was a large genotypic variance in the 20 large-seeded genotypes included in this study.

Table 3. Single location analysis of variance for grain yield in large-seeded common bean genotypes measures in five locations in 2017 cropping season

Source of variation	DF	Mean Square				
		Alem Tena	Arsi Negele	Haramaya	Melkassa	Sirinka
Rep	2	5167712***	9288613***	2124632***	1019339.5**	1165126.7**
Genotype	19	386141.5***	866159.6***	507687.8***	654257.4***	358619.3**
Error	38	88676.54	167356.8	135956.9	139605	145901.4
CV		14.41	12.93	15.19	15.97	14.89

*, **, *** = Significant at $p < 0.05$; $p < 0.01$; $p < 0.001$ respectively; Degrees of freedom (DF); replication (Rep); Coefficient of variance (CV)

Combined analysis of variance revealed significant differences ($P < 0.01$) among environments, genotype, and genotype x environment interaction for grain yield (Table 4). The results showed that the genotypes have different performance in the testing environments and the

environment have a different impact on the genotype yield performances. A significant GEI is common in experiments of this nature and it refers to the modification of genetic factors by environmental factors and the role of genetic factors in determining the performance of genotypes in different

environments. The current result was in agreement with the finding of Kebere *et al.*, (2006), and Barili *et al.*, (2016) reported the presence of the

significant effect of genotype, environments, and their interaction on common bean grain yield.

Table 4. Combined analysis of variances of yield for 20 large-seeded genotypes grown at five locations during the 2017 cropping seasons

Source of variation	DF	MS
Gen	19	1279164.3**
Env	4	9956847**
Rep(Env)	10	3753084.4**
GEI	76	373425.31**
Residue	190	135499.3
CV%		14.6

** = Significant at 1% probability, DF = degrees of freedom, CV % = coefficient of variance and MS = mean square

Mean performance of genotypes across locations for grain yield

Grain yields at Alem Tena ranged from 1326 kg ha⁻¹ for Deme released in 2008 to 2737.8 kg ha⁻¹ for DAB-107 released in 2017. At Arsi Negele, this range was from 2038 kg ha⁻¹ for Montcalm released in 2007 to 3991.6 kg ha⁻¹ for Babile released in 2012. The mean yield ranges from 3205 kg ha⁻¹ for Ado released in 2015 to 3205 kg ha⁻¹ for Hirna released in 2012 at Haramaya. Similarly, the mean grain yield attained at Melkassa, ranged from 1311.3 for Tinike released in 2012 to 3014.4 kg ha⁻¹ DAB-107 released in 2017. At Sirinka, this range was from 1579.2 kg ha⁻¹ for Montcalm released in 2007 to 3113.7 kg ha⁻¹ for Babile released in 2012.

In grain yield, frequent changes in rank orders were observed among the performances of the genotypes across the environments. For instance, genotype DAB-107 exhibited the

highest grain yield of 3113.7 kg ha⁻¹ at Sirinka, 3014.4 kg ha⁻¹ at Melkassa, and 2737.8 kg ha⁻¹ at Alem Tena while at Aris Negele and Haramaya it ranked 13th and 10th, respectively. These results showed differences in grain yield performance among the tested genotypes in different environments. Likewise, Kassaye (2006), Yayis, *et al.*, (2011) indicated differential responses in yield among different common bean genotypes.

The average grain yield of genotypes released after 2012 that showed maximum values includes 2737.8 (DAB-107), 3991.6 (Babile), 3205 (Hirina), 3014.4 (DAB-107), and 3113.7 (DAB-107), at Alem Tena, Aris Negele, Haramaya, Melkassa, and Sirinka respectively. The minimum grain yield of 1326 (Deme) released in 2008, 2038 (Montcalm) released in 2007, 1623.7 (Ado) released in 2015, 1311.3 (Tinike) released in 2012 and 1579.2 (Montcalm) released in 2007 was achieved at Alem Tena, Aris Negele, Haramaya, Melkassa, and

Sirinka accordingly. Generally, the mean of individual genotypes in each location showed that there was a gradual increase in grain yield however; the increment was not in association with a year of release or age of the genotypes.

The mean average grain yield of the genotypes across the environments ranged from the lowest to the highest grain yield (1875 – 2875 kg ha⁻¹). The highest means grain yield value is obtained 2872 kg ha⁻¹ on the recently released (2017) large-seeded genotype DAB-107 followed by Hirina released in 2012 with mean 2802 kg ha⁻¹, whereas the lowest mean grain yield value of 1875 kg ha⁻¹ was obtained on Montcalm genotype released in 2007 (Table 5). The difference between the highest yielder 'DAB-107' genotype and the lowest yielder Montcalm genotype was 997 kg ha⁻¹ in grain yield.

The average environmental grain yield across genotypes ranged from the lowest of 2066.8 kg ha⁻¹ at Alem Tena to the highest of 3164.6 kg ha⁻¹ at, Aris Negele with a grand mean of 2512.89 kg ha⁻¹ (Table 5). The overall yield performance of Alem Tena and Melkassa was lower than that of Aris Negele, Haramaya, and Sirinka. Mainly due to higher temperature and lower total rainfall that might shorten the growth period at Melkassa and Alem Tena, gave rise to lower yields (Table 5 and Table 1). The present study indicated that genotypes responded differently to the different

environments in terms of grain yield. Different authors support this finding. *Perreira et al.*, (2010), *Fikre et al.*, (2011), and *Faria et al.*, (2013) indicated that bean genotypes can have a different response and relate highly to environmental change.

Stability analysis based on Additive Main effects and Multiplicative Interaction (AMMI) model

AMMI analysis of variance for grain yield of tested large-seeded genotypes across environments showed that genotypes, environment, and the GEI were highly significant (Table 6). According to Table 6, the main effects of genotype and environment accounted for 26.27 % and 43.05%, respectively and GEI accounted for 30.67% of the total sum of squares for grain yield. This indicated that the environments were diverse and caused the greatest variation in grain yield.

The major component of environmental variability was rainfall, with annual rainfall ranging between 728 mm (Alem Tena) and 876 mm (Aris Negele) (Table 5) and it is common in Ethiopia; the higher the altitude the higher the rainfall. This study clearly showed that the environments were distinct, and the genotypes responded differently to the different environments in terms of grain yield. The GEI sum of squares was larger than that of genotypes, which complicates the selection of superior and adaptable genotypes. Similar results were reported in common beans by *Asfaw* (2011), *Correa, et al.*, (2016).

Table 5. Mean grain yield in kg ha⁻¹ of 20 large-seeded common bean genotypes tested at five locations during the 2017 cropping season

Genotypes	Yield					Mean
	AT	AN	HU	MK	SK	
Gobe Rasha-1	2406.1 ^{ab}	3302.3 ^{abcd}	2321.3 ^{abc}	2652.5 ^{ab}	2928.4 ^a	2722
Ibado	2250.6 ^{abc}	3625.3 ^{ab}	2308.5 ^{abc}	2973.1 ^a	2586.3 ^{ab}	2749
Melka Dima	2388.6 ^{ab}	3351.6 ^{abc}	2457.4 ^{abc}	2109.3 ^{abc}	2410.5 ^{ab}	2544
Cranscope	2527.3 ^{ab}	3256.8 ^{abcd}	1901.3 ^{bc}	1716.3 ^{bc}	2405.6 ^{ab}	2361
Montcalm	2076.5 ^{abcd}	2038 ^d	1723.2 ^{bc}	1955.8 ^{abc}	1579.2 ^b	1875
Deme	1326 ^d	3217 ^{abcd}	2104.2 ^{abc}	1913.8 ^{abc}	2601.8 ^{ab}	2233
Batu	1680.8 ^{bcd}	2656.9 ^{bcd}	2679.3 ^{abc}	1704 ^{bc}	2595.3 ^{ab}	2263
Loko	2419.8 ^{ab}	3625.3 ^{ab}	2781.2 ^{ab}	2152.3 ^{abc}	2526.2 ^{ab}	2701
GLP-2	2086.9 ^{abcd}	2874.9 ^{abcd}	3070.4 ^a	2681.5 ^{ab}	2540.5 ^{ab}	2651
Morka	1984.3 ^{abcd}	3190 ^{abcd}	2649.5 ^{abc}	2855.3 ^{ab}	2720.7 ^{ab}	2680
Tininke	1963.7 ^{abcd}	2238.1 ^{cd}	2237.8 ^{abc}	1311.3 ^c	2467.6 ^{ab}	2044
Fedis	1760.9 ^{bcd}	3662.9 ^{ab}	2334.2 ^{abc}	2500.5 ^{ab}	2893.3 ^a	2630
Babile	1995.4 ^{abcd}	3991.6 ^a	2617.3 ^{abc}	2518.6 ^{ab}	2844.9 ^a	2794
Hirna	1840.8 ^{abcd}	3701.8 ^{ab}	3205 ^a	2228 ^{abc}	3032.7 ^a	2802
Ramada	1449.5 ^{bcd}	3562.4 ^{ab}	2613.5 ^{abc}	2179.5 ^{abc}	2533.8 ^{ab}	2468
Ado	1811 ^{bcd}	2239.2 ^{cd}	1623.7 ^c	2466.7 ^{abc}	1959.5 ^{ab}	2020
Tafach	2183.1 ^{abcd}	2863.1 ^{abcd}	2084.9 ^{abc}	2479.1 ^{ab}	2522.4 ^{ab}	2427
Hundane	2098.9 ^{abcd}	3324.7 ^{abc}	2833.8 ^{ab}	2405.7 ^{abc}	2555.2 ^{ab}	2644
DAB-107	2737.8 ^a	3015.8 ^{abcd}	2477.5 ^{abc}	3014.4 ^a	3113.7 ^a	2872
Gorossa	2348.9 ^{abc}	3554.2 ^{ab}	2526.2 ^{abc}	2974.9 ^a	2500.4 ^{ab}	2781
Mean	2066.8	3164.6	2427.5	2339.6	2565.9	2512.9
CV%	14.4	12.9	15.2	16.0	14.9	14.6

AT: Alem Tena; AN Aris Negele; HU: Haramaya; Mk: Melkassa; SK: Sirinka; CV: coefficient of variation; Means in a column followed by similar letters are not significantly different at the 0.05 probability level based on Tukey HDS; bold values are highest yields in each test environment.

Table 6. Additive Main effect and Multiplicative Interaction (AMMI) analysis of variance for grain yield (kg/ha) of large-seeded genotypes across environments

Source of variation	DF	SS	MS	TSS Explained %
ENV	4	39827388	9956847.00***	43.05113
GEN	19	24304122	1279164.33***	26.27137
GEI	76	28380323	373425.30***	30.67751
PC1	22	12852083	584185.59***	45.28519
PC2	20	7487645	374382.25***	26.38323
PC3	18	5361280	297848.89***	18.89084
PC4	16	2679315	167457.19***	9.44075
Residuals	190	25744870	135499	

*, **, and *** implies significance at $p < 0.05$, $p < 0.01$ and $p < 0.001$, respectively; DF = degree of freedom; SS = sum square; MS= mean square; TSS= total sum square; ENV= environment; GEN= genotype; GEI =genotype by environment interaction and PC = principal component

AMMI stability value (ASV) and Genotype selection index (GSI)

Table 7 indicates the different stability parameters that can determine the

stability of a given genotype across the tested environment. Accordingly, the AMMI stability value and Genotype selection index should be simultaneously seen before deciding on the stability of a genotype.

Purchase *et al.* (2000) proposed a new method for a quantitative stability measure named AMMI stability value (ASV). The ASV, which is the distance from the coordinate point to the origin in a two-dimensional scatter gram of PC1 scores against PC2 score, should also be seen to decide the stability of a genotype. In the ASV method, the genotype with the least ASV score is the most stable whereas those with the highest ASV are considered unstable. ASV discriminated genotypes Melka Dima, Morka, GLP-2, and Hundane respectively the most stable, and Montcalm, Hirna and SAB 736 were unstable (Table 16). However, Mohammadi and Amri, (2008) suggested that the most stable genotypes would not necessarily give the best yield performance, hence there is a need for approaches that incorporate both mean yield and stability in a single index.

For a simultaneous selection of yield and stability, Farshadfar (2008) recommended a new approach known as the genotype selection index (GSI). GSI was calculated by adding the rank of AMMI stability value (RASV) and the rank of mean grain yield of genotypes (RY) across environments. This parameter's least value is considered the most stable with a high grain yield genotype. Based on the genotype selection index, the most

desirable genotype for selection of both stability and high grain yield was Morka (G10) followed by GLP-2 (G9), Gobe Rasha-1(G1), Gorossa (G18), and Melka Dima (G3). While, genotypes Montcalm (G5), SAB 736 (G16), and Tininke (G11) were unstable among tested genotypes, in addition, this study found out that Morka, GLP-2, and Gobe Rasha-1, Gorossa, and Melka Dima genotypes have the highest mean performance and stable (used for wide adaptation). However, Montcalm, SAB 736, and Tininke had the lowest mean performance and were unstable. These results are similar to the results, observed in the AMMI2 biplot in this study. Hagos and Fetien (2011) and Ezatollah *et al.* (2011) studied the effect of GEI using AMMI in corn genotypes, using different stability parameters. As result, they presented GSI as the best approach, due to identified genotypes that have both high mean yield and stable yield performance across different environments. Genotypes G19, G14, and G13 had high mean grain yield among tested genotypes but were placed far from the biplot origin suggesting that they were not stable (Table 7). However, G14 and G13 genotypes appeared to be specifically adapted to the environment Arsi Negele, Haramaya, and Sirinka. G19 specifically adapted to Alem Tena and Melkassa (Figure 2).

Table 7. Mean grain yield, ASV, GSI values, and ranks of large-seeded size common bean genotypes in five environments 2017.

Genotypes Code	Genotypes Name	Mean yield	RYi	IPCA1	IPCA2	ASVi	RASVi	GSli	RGSli
G1	Gobe Rasha-1	2722	6	5.315	-2.771	9.534	6	12	2
G2	Ibado	2749	5	3.77	-14.611	15.98	10	15	8
G3	Melka Dima	2543	12	0.355	4.393	4.435	1	13	5
G4	Cranscope	2361	15	3.747	6.173	8.915	5	20	11
G5	Montcalm	1875	20	18.831	4.909	32.693	20	40	20
G6	Deme	2233	17	-12.485	-4.674	21.934	14	31	17
G7	Batu	2263	16	-7.142	15.067	19.424	12	28	15
G8	Loko	2701	7	-4.879	5.601	10.074	7	14	6
G9	GLP-2	2651	9	2.345	5.582	6.882	3	12	2
G10	Morka	2680	8	1.221	-5.83	6.195	2	10	1
G11	Tininke	2044	18	1.702	22.502	22.691	15	33	18
G12	Fedis	2630	11	-9.145	-10.403	18.831	11	22	13
G13	Babile	2794	3	-11.581	-8.712	21.703	13	16	9
G14	Hirna	2802	2	-17.975	5.618	31.361	19	21	12
G15	Ramada	2468	13	-15.875	-5.499	27.797	17	30	16
G16	SAB 736	2020	19	-16.912	-7.339	29.942	18	37	19
G17	SAB 632	2427	14	9.15	-2.292	15.871	9	23	14
G18	Hundane	2644	10	-3.771	2.468	6.928	4	14	6
G19	DAB-107	2872	1	14.798	0.499	25.404	16	17	10
G20	Gorossa	2781	4	4.709	-10.682	13.395	8	12	2

RYi=rank in yield, IPCA1, 2= interaction principal component axis 1 and 2, ASVi= AMMI stability value, RASVi= rank of AMMI stability value, GSli= genotype selection index, RGSli=Rank genotype selection index

AMMI Biplots

Analysis of the AMMI model Table 7 showed that the first principal component (PC1) accounted for 45.29% and the second principal component (PC2) accounted for 26.38% interaction sum of squares. The other interaction effects were explained by the remaining principal components. The first two principal components accounted for cumulative 71.67% interaction effects, which, indicated the majority of interaction effects were within two principal components. In agreement with this, Tadesse *et al.* (2017) reported the first two axes (71.2%) explained a high percentage of the sum square of the GEI and the highest part of the pattern of the GEI will be captured. Furthermore, Zobel *et al.* (1988)

showed that AMMI with PCA1 and PCA2 is usually selected and more appropriate to clarify the GEI and relationship of genotypes and environments.

AMMI2 biplot was generated using genotypic and environmental scores of the first two AMMI multiplicative components to cross-validate the interaction pattern of the 20 large-seeded common bean genotypes within five environments (Figure 1). In the AMMI2 biplot, environments with low IPCA1 and IPCA2 scores that are placed close to the origin have a high contribution to the stability of genotypes and low contribution to GE interaction. Furthermore, when IPCA1 was plotted against IPCA2, Purchase (1997) pointed out that the closer the

genotypes score to the center of the biplot (fig. 1), the more stable they are. In this study, AMMI2 biplots indicated genotypes G10 (Morka), G1 (Gobe Rasha-1), G3 (Melka Dima), G9 (GLP-2), and G18 (Hundana) were demonstrated low interactive action over environments. This revealed that these genotypes demonstrated lower

fluctuations to the changes in the growing environment. Whereas G11(Tininke), G5(Montcalm)), G14 (Hirna), and G16 (SAB 736) were located far away from the origin indicating their large contribution to the total GEI variance are considered as unstable genotypes.

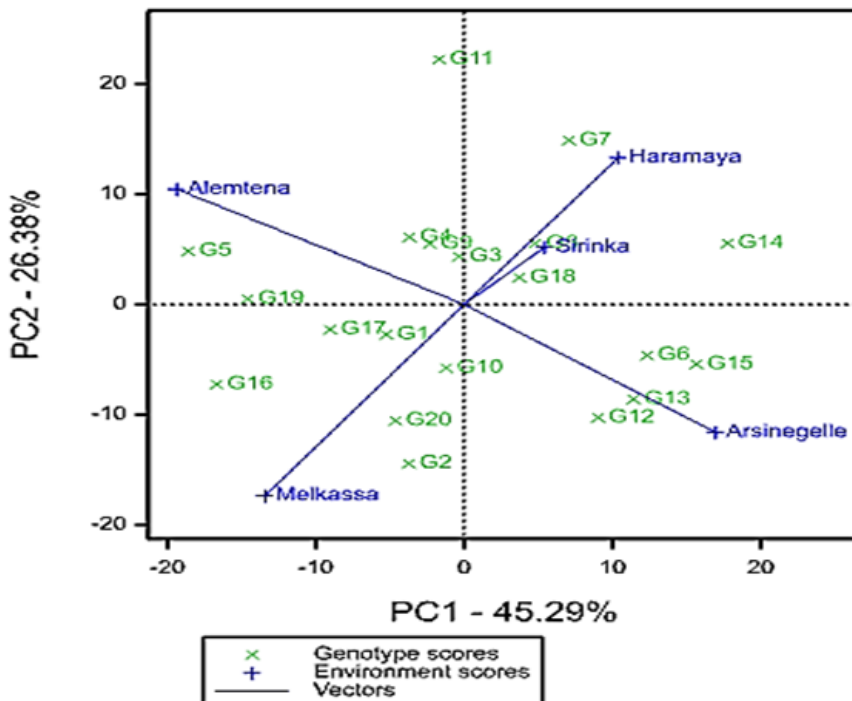


Figure 1. AMMI biplot with the first two components from data on 20 large seeded genotypes across five environments in Ethiopia. The shortening (codes) of genotypes is as given in Table 7.

Genotype and genotype by environment interaction effects (GGE) model

In this study, the GGE biplot will be interpreted using two principal components that explained 74.44% of yield variations. In agreement with Sousa *et al.* (2015) who evaluated twenty-seven early-cycle soybean genotypes; the GGE biplot model were presented greater

efficiency by retaining most of the variation in the first two main components (61.46%).

Determining the best genotype in an environment (Which-won-where)

Which-won-where graph is constructed first by joining the farthest genotypes forming a polygon.

Subsequently, perpendicular lines are drawn from the origin of the biplot to each side of the polygon, separating the biplot into several sectors with one genotype at the vertex of the polygon. These lines are referred to as equality lines (Yan 2001). Genotypes at the vertices of the polygon are either the best or poorest in one or more environments.

In the current study, at the vertices of the polygon there are seven divisions with genotypes 'G19' (DAB-107), 'G13'(Babile), 'G14' (Hirna), 'G7' (Batu), 'G11' (Tininke)', 'G5' (Montcalm) and 'G16' (SAB 736) as the corner or vertex genotypes (fig 2). Based on this analysis, the testing

locations were partitioned into two mega-environments. mega-environment one was represented by Alem Tena and Melkassa with G19 (DAB-107) the winning genotype and mega-environment two consisted of Arsi Negele, Haramaya, and Sirinka with 'G13' (Babile) and 'G14'(Hirna) as the winning genotypes. While, G5', 'G7', 'G11,' and 'G16' (released in 2007, 2008, 2012, and 2013 respectively) were not the best in any of the environments since no environments fell into sectors with these cultivars. Correa et al. (2016) used this model when evaluating the common bean genotypes that exhibit high grain yield and stability across multiple environments.

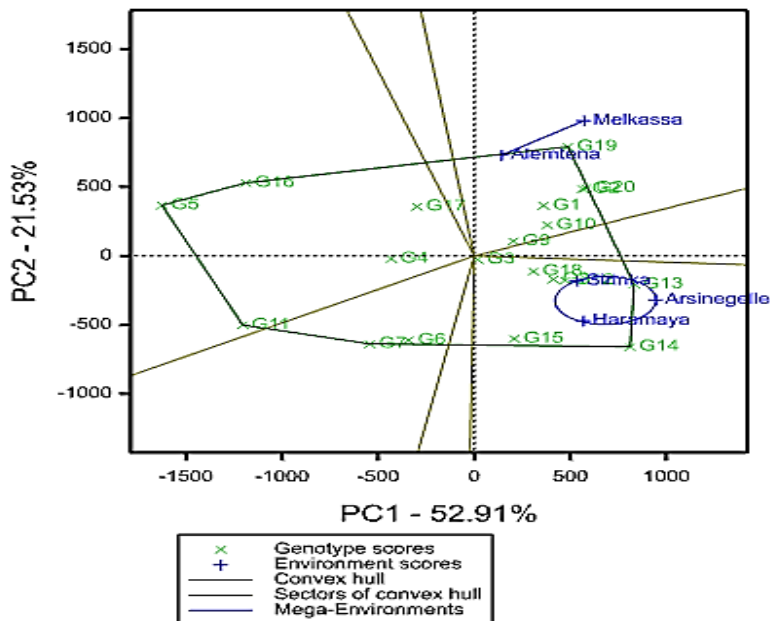


Figure 2. The which-won-where view of the GGE biplot for 20 large seeded genotypes data growing in 5 environments. The shortening (codes) of genotypes is as given in Table 7

Comparison of the Genotypes with the Ideal Genotype

The ideal genotype is defined as one that has the highest performance in all environments and is stable. Genotype-focused scaling generates a ranking of the cultivars in terms of both mean performance and stability. GGE biplot based on genotype-focused scaling for comparison the genotypes with the ideal genotype is presented in Fig 3. Yan and Rajcan, (2002) suggested that an ideal genotype should have the

highest mean performance and be consistently stable in all environments and it is graphically defined by having the longest vector length without GEI and represented by an arrow in the center of the concentric circles. Hence, genotypes located closer to the ideal genotypes are more desirable than others are. In line with this, Morka (G10) was more stable than others were and G1, G3, and G18 were greater than the other genotypes (Figure 3).

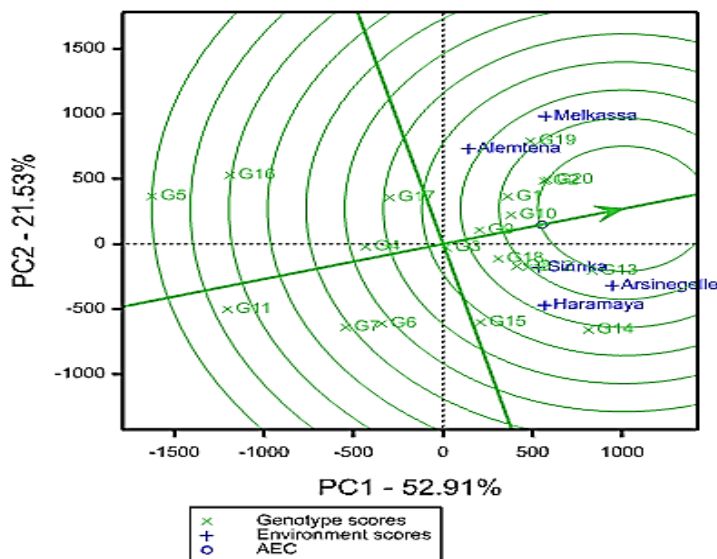


Figure 3. GGE-biplot based on genotype-focused scaling for comparison the genotypes with the ideal genotype for 20 large seeded common beans. The shortening (codes) of genotypes is as given in Table 7.

Comparison of the Environment with the Ideal Environment

Rank environments with reference to the ideal environment. The ideal environment is defined as the most discriminating and representative. It

generates a ranking of the test environments in terms of both criteria. An ideal environment should have a greater power of discrimination in terms of genotype main effects with high PC1 score and the most representative of all of the other

environments, which is zero PC2, scores (Yang *et al.*, 2009). In the same way as the ideal genotype, the ideal environment is only an estimate and serves as a reference for the choice of site for multi-environment testing. Figure 4 defines an ideal test environment, which is the center of the concentric circles. This is a point on the AEA in the positive direction (most representative), with a distance to the biplot origin equal to the longest vector of all environments (most informative).

In the current study, Aris Negele is closest to this point, therefore, the greatest capacity for discriminating between genotypes, and favored the selection of superior genotypes, whereas Alem Tena was poorest for selecting cultivars adapted to the whole region. Recently, GGE biplots have been used in common bean (Asfaw *et al.* 2008), (Zelege *et al.* 2016), (Correa *et al.* 2016) used to investigate the adaptability and phenotypic stability of different genotypes from different locations.

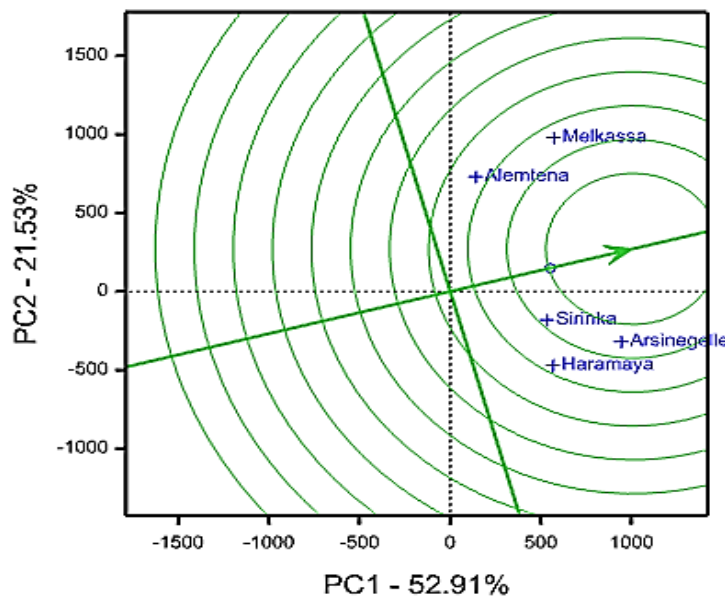


Figure 4. GGE-biplot based on environment-focused scaling for comparison the environments with the ideal environment for 20 large seeded genotypes data growing in 5 environments.

Conclusion and Recommendation

This study determined genotype by environment interaction effect,

stability of genotypes, and representativeness and discriminating ability of environments of grain yield in large seeded common bean released varieties grown in Ethiopia. Whenever varieties are released for small-scale

and commercial production, information on genotype by environment interaction and stability indicates their general and/or specific adaptations need- to be available to the users. The study has clearly and with ease confirmed that large seeded common bean grain yield was highly affected by environmental variation followed by genotype by environment interaction and genotypic effect contributing the least.

In this study, AMMI and GGE models were used to identify the most stable and high yielding genotypes among the released large-seeded genotypes in Ethiopia. As a result, both models identified genotypes G10, G1, G3, and G18 display higher grain yield and stability among tested genotypes in this study. Except for G10, the remaining best performed and stable genotype genotypes were released for specific adaptations however this has a look discovered that G1, G3, and G18 genotypes may be directed as wide adaptation genotypes in the county. Genotypes 'G13' and 'G14' were exhibited average stability in location Arsi Negele, Haramaya, and Sirinka however these genotypes were released for east and west Hararghe. On the other hand, high yielding genotype G19 (DAB-107) specific adaptations on Alem Tena and Melkassa.

In addition, the environment Aris Negele preferred for the selection of superior genotypes for large-seeded common bean genotypes than the other testing locations. GGE biplot

reveals that the five testing locations were grouped into two mega environments. Even though, the result is from one-year data at five locations. As a result, to conduct the over location trials effectively with limited resources, discriminative locations encompassing representative locations may be included, rather than extending the trials extensively over related locations.

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BLUP and Stability Analysis of Multi-Environment Trials in Lentil (*Lens culinaris* Medic) Genotypes under Rainfed Condition of Ethiopia

Assefa Funga¹, Nigusie Girma¹, Lijalem Korbu¹, Dagnachew Bekele¹, Ridwan Mohammad¹, Fasil Hailu¹, Genet Mengistu¹, Amin Fedlu¹, Abebe Hailu², Nigusie Kefelegn³, Tadele Tadesse⁴, Yasin Goa⁵, and Asnake Fikre^{1*}

¹Ethiopian Institute of Agricultural Research (EIAR), Debre Zeit Agricultural Research Center (DZARC), Debre Zeit, Ethiopia; ²Gondar Agricultural Research Center, Gondar, Ethiopia

³Debre Birhan Agricultural Research Center, Debre Birhan, Ethiopia; ⁴Sinana Agricultural Research Center, Sinana, Ethiopia; ⁵Areka Agricultural Research Center, Areka, Ethiopia.

E-mail: assefalem2@gmail.com

Abstract

Twenty-five lentil genotypes including the check varieties were evaluated each over three seasons (2016 – 2018) at 8 locations (Akaki, Chefe Donsa, Dabat, Debre Zeit, Enewari, Hosanna, Kokate, Sinana) resulting in 11 environments in randomized completely block design with row column information. A factor analytic model was fitted to the pattern of genotype by environment (G×E) interaction using R ASReml package and predicted yield (t/ha) values for all genotypes under evaluation were obtained. The model adequately explained 90.6% of the G×E variance at an FA-2 of yield data. Environment and genotype evaluation based on GGE biplots has revealed a number of discriminative and representative environments while identifying ideal and high performing genotypes. Environment Db18LN was most discriminating followed by EN17LN, SN18LN and DZ16LP, whereas CD16LP and DZ16LP were found to be representative test site. Genotypes 6(DZ-2012-Ln-0218) was identified as high yielder and stable than other test genotypes and proposed for verification in the year 2020 for release as new variety and in the year 2021 it then registered with variety name “Furi” on the national catalogue of Ministry of Agriculture of the country.

Keywords: ASReml package, BLUP, Lentil yield stability, GGE Biplots, Factor Analytic

Introduction

Lentil (*Lens culinaris* Medic) is the important pulse crops in Ethiopia that is dominantly produced in the crop-livestock based farming systems of the central, north and northwest highlands

of Ethiopia where vertisols are dominating. The crop can also grow in the lowland parts of the country provided that early maturing, resistant/tolerant to rust and low moisture stress varieties are developed.

Lentil has multiple uses in the country. The crop is good sources of dietary protein. It is also a rich source of essential vitamins, minerals, and important amino acids like lysine. The crop is also endowed with unique property in maintaining and improving soil fertility through symbiotic biological nitrogen fixation. Thus, it leaves substantial amount of residual nitrogen for subsequent crops and adds plenty of organic matter to maintain and improve soil health and fertility (Gaur *et al.*, 2010). Hence, Ethiopian farmers usually grow the crop in rotation with cereals.

Besides being key components in the diets, lentil also attracts higher market prices than other staple crops, making them an important source of income for farmers. Despite the versatile uses of lentil in Ethiopia as stated above, the national average productivity of the crop in 2018/19 cropping season was 1.42 ton/ha (FOSTAT 2018; CSA 2019) as compared to its potential yield about 2.5 t/ha. Similarly, area under lentil production was 99,754 ha in 2018/19, but it was reduced to 87,444 ha in 2019/20 season, showing a 12.34% reduction in area coverage within a year (CSA 2020). Production and productivity follow the same trend of reduction as well. There are several factors accountable for this reduction and, for the significant yield gap between the achieved and the potential yield in the country. Even though, major diseases like rust and the newly emerged viral disease are recently causing major yield loss, however, the

continuous varietal (genetic) and environmental variability are playing significant role in the stability of a given genotype/cultivar.

Regarding environmental variability, testing genotypes of annual crops for grain yield on a multi-locational or multi-year basis frequently shows GE interaction that complicates the selection or recommendation of materials. According to Annicchiarico (1997), it is possible to cope with genotype by year or genotype by location by year interaction effects only through selection for yield stability across environments defined as location by year combinations.

Kanouni, et al (2015) stated that GE analysis is important tool that help to identify superior varieties and their adaptation to and stability in diverse agro ecologies. In line to this fact, Padi, (2007) also observed that differential performance of chickpea under diverse environmental conditions decreases yield stability. Inefficiency in the GE analysis of variance may also result in wrong selection of genotypes for yield. There are many models for conducting GE whose applicability depends on the experimental data, the number of environments, and the accuracy of collected data and environmental information.

Earlier research work done in advancing GE by authors such as Gauch 1992; Imrie and Hacker 1993; Kang and Gauch 1996; Cooper and

Hammer 1996 have contributed significantly to the understanding and make use of the Biplot analysis as a tool. However, the way GE is measured and addressed between different users of different sectors varies. In this regard, Yan and Tinker (2006) stated that, biometricians and quantitative geneticists concentrate primarily on quantification of GE, while breeders and other practitioners are often concerned primarily with matching genotypes with environments.

The primary aim of a plant breeding in multi environment trials (MET) is selection either of potential new varieties or potential parents (Yan and Tinker, 2006). Selection requires definition of the trait(s) of interest and formation of an appropriate index based on these traits. Although it has been argued that environments (that is trials) can be regarded as traits in METs it is clear that this assumption may not be generally applicable, particularly for those METs which span several years of testing. Trial locations are usually chosen to represent a target “environment”. The target environment could be an agro-ecological zone of commercial significance, or an environment classified by disease pressure or other biotic or abiotic factors. The trait of interest would therefore be the yield performance for the set of trials that align with the target environment (Yan and Tinker, 2006). In this study, we used average of grain yield ton per

hectare of genotypes determined for individual environments using BLUPs fitted by factor analytic model in ASReml package, and biplot analysis implemented by GGE biplot with the aim to understand genotype by environment interaction in lentil, identification of best wide adaptable genotype across locations in the potential growing area of Ethiopia

Materials and Methods

Description of eco-location and genotypes

A study was undertaken by using germplasm of different genetic background to determine their level of GE in their biological yield responses. Twenty-five lentils advanced breeding genotypes including check varieties were evaluated each over three seasons between 2016 and 2018 at 8 locations resulting in 11 environments. The test genotypes were derived from series of trials called Preliminary Variety Trial (PVT) and National Variety Trial (NVT) tested at potential environments. Randomized complete block design with three 3 and 4 replications for PVT and NVT was used respectively. Each genotype was planted on four rows of 4m long in 20cm by 2cm inter and intra row spacing. Production was all under rain fed condition. The geographic information of testing sites is presented in Table 1.

Table 1. List of Test Environments, number of genotypes used, and their respective Geographic information

Test Site	Environment	No Genotypes	No Replication	Altitude (m.a.s.l)	Latitude (°N)	Longitude (°E)
Akaki	AK16LP	25	3	2207	8.87	38.85
Akaki	AK17LN	14	3	2207	8.87	38.85
Chefe Donsa	CD16LP	25	3	2450	8.96	39.1
Chefe Donsa	CD17LN	14	3	2450	8.96	39.1
Dabat	Db18LN	14	4	2557	12.97	37.77
Debre Zeit	DZ16LP	25	3	1910	8.73	39
Debre Zeit	DZ18LN	14	4	1910	8.73	39
Enewari	EN17LN	14	3	2667	9.88	39.15
Hosanna	HS18LN	14	4	2295	7.55	37.86
Kokate	KK18LN	14	4	2140	6.87	37.82
Sinana	SN18LN	14	4	2439	7.11	40.22

NB: PVT = Preliminary variety Trial, NVT = National Variety Trial, AK16LP=Lentil PVT at Akaki in 2016, AK17LN=Lentil NVT at Akaki in 2017, CD16LP=Lentil PVT at Chefe Donsa in 2016, CD17LN=Lentil NVT at Chefe Donsa in 2017, Db18LN=Lentil NVT at Dabat in 2018, DZ16LP=Lentil PVT at Debre Zeit in 2016, DZ18LN=Lentil NVT at Debre Zeit in 2018, EN17LN=Lentil NVT at Enewari in 2017, HS18LN=Lentil NVT at Hosanna in 2018, KK18LN=Lentil NVT at Kokate in 2018, SN18LN=Lentil NVT at Sinan in 2018

Table 2. List of genotypes over test years of 2016, 2017 and 2018 respectively

Code	Genotypes	Source	Remark
1	DENBI	MSI	Released variety
2	DERASH	MSI	Released variety
3	DZ-2012-Ln-0020	Introduction	Advanced line
4	DZ-2012-Ln-0050	Introduction	Advanced line
5	DZ-2012-Ln-0054	Introduction	Advanced line
6	DZ-2012-Ln-0218	Introduction	Advanced line
7	DZ-2012-Ln-0219	Introduction	Advanced line
8	DZ-2012-Ln-0228	Introduction	Advanced line
9	DZ-2012-Ln-0231	Introduction	Advanced line
10	DZ-2012-Ln-0232	Introduction	Advanced line
11	DZ-2012-Ln-0233	Introduction	Advanced line
12	DZ-2012-Ln-0234	Introduction	Advanced line
13	DZ-2012-Ln-0235	Introduction	Advanced line
14	DZ-2012-Ln-0236	Introduction	Advanced line
15	DZ-2012-Ln-0237	Introduction	Advanced line
16	DZ-2012-Ln-0238	Introduction	Advanced line
17	DZ-2012-Ln-0239	Introduction	Advanced line
18	DZ-2012-Ln-0240	Introduction	Advanced line
19	DZ-2012-Ln-0241	Introduction	Advanced line
20	DZ-2012-Ln-0242	Introduction	Advanced line
21	DZ-2012-Ln-0243	Introduction	Advanced line
22	DZ-2012-Ln-0244	Introduction	Advanced line
23	DZ-2012-Ln-0245	Introduction	Advanced line
24	DZ-2012-Ln-0255	Introduction	Advanced line
25	Check	Own gene pool	Local check

NB: MSI = Micro seed increase

Observations and data collection crop phenology traits

Days from sowing to the stages when 50% of the plants have started flowering was recorded from each plot as days to 50% flowering (DTF). Similarly, days from sowing to the stages when 90% of the pods mature was recorded from each plot as days to 90% maturity (DTM) and measurement of plant height in centimeter (PLH) was taken from five randomly selected plants from the ground to the tip using a ruler at maturity.

Grain Yield and Yield Component Traits

Hundred seed weight (HSW) of randomly selected hundred seeds weighed on a sensitive balance in gram was taken. Biomass yield (BMY) weight of all above ground plant part per plot was taken in gram and then converted to ton per hectare. Weight of seeds harvested from central two rows per plot in gram was taken and then converted to ton per hectare as grain yield (YLD). Grain harvest index (GHI) was also calculated as the ratio of grain yield to biological yield.

Statistical analysis

The genetic merit of each genotype for all traits was evaluated being combined over environments by best linear unbiased prediction (BLUP) using restricted maximum likelihood (REML) for variance component

estimation in R. Pearson correlation was used to evaluate the association among traits. Factor analytic model was fitted using ASReml-R package and the predicted yield (tha^{-1}) values for all genotypes under evaluation were obtained base on procedures demonstrated by Kelly et.al. (2017). GGE biplot analysis was performed using R GGEBiplotGUI package of version 1.0.9 (Frutos et al 2014) using the BLUPs mean produced from factor analytic output. The GGE biplot methodology was used to analyse genotype performance for each environment, genotype stability, representative environment, and discriminating power of each environment.

Results and Discussion

Significant differences were observed among test genotypes for all of the characters under study indicated presence of considerable amount of variability in the tested genotypes. This variation could be exploited to improve yield (Table 3). High heritability was observed for all traits ranging over 85% for biomass yield t/ha to 98% for days to 50% flowering. Genotype DZ-2012-Ln-0245 get flowered early within 53 days, while genotype DZ-2012-Ln-0236 flowered lately within 68 days. The most early maturing genotype DZ-2012-Ln-0218 matured within 107 days, while late maturing genotype DZ-2012-Ln-0020 matured in 125 days. Variety Denbi was the tallest (36.24 cm) followed by genotype DZ-2012-Ln-0238 (36.27

cm). On the other hand, genotype DZ-2012-Ln-0243 (28.71 cm) was the shortest among all. Genotype DZ-2012-Ln-0228 had large seed size (3.7 cm) followed by DZ-2012-Ln-0243, and DZ-2012-Ln-0244 (3.6 cm). Local check on the other hand, had small seed size (2.1 cm). The highest grain harvest index (37%) was obtained from genotype DZ-2012-Ln-0218 which is now known by the variety name “Furi”. Conversely, genotype

DZ-2012-Ln-0235 had the smallest grain harvest index (16%). Variety Derash had the maximum biological yield (6.44 t/ha), while local check scored the minimum biological yield (3.99 t/ha). Genotype DZ-2012-Ln-0218 was found to be high performing in grain yield (2.33 t/ha), while genotype DZ-2012-Ln-0237 performed poorly in grain yield (0.86 t/ha).

Table 3. Mean values, and variance components viz of traits for different lentil genotypes across test Environments

Genotype	DTF	DTM	PLH	HSW	GHI	BMV	YLD
DENBI	57	111	36.42	2.4	0.33	5.76	2.13
DERASH	56	109	35.35	2.8	0.32	6.44	2.09
DZ-2012-Ln-0020	64	125	32.50	3.2	0.21	4.57	1.01
DZ-2012-Ln-0050	55	109	34.81	2.9	0.35	5.95	2.07
DZ-2012-Ln-0054	57	111	33.13	3.0	0.33	5.26	1.82
DZ-2012-Ln-0218	55	107	35.47	2.9	0.37	6.30	2.33
DZ-2012-Ln-0219	58	118	30.13	2.8	0.29	4.36	1.17
DZ-2012-Ln-0228	61	123	32.22	3.7	0.20	4.98	1.10
DZ-2012-Ln-0231	57	118	32.99	3.3	0.24	4.79	1.15
DZ-2012-Ln-0232	62	121	32.73	3.3	0.22	4.66	1.05
DZ-2012-Ln-0233	61	117	31.48	3.2	0.29	5.38	1.65
DZ-2012-Ln-0234	63	122	32.99	3.5	0.18	5.11	0.97
DZ-2012-Ln-0235	66	123	32.90	3.3	0.16	5.00	0.88
DZ-2012-Ln-0236	68	125	30.86	2.7	0.22	4.31	0.86
DZ-2012-Ln-0237	68	124	30.18	3.3	0.19	4.49	0.86
DZ-2012-Ln-0238	58	114	36.27	3.0	0.31	5.58	1.79
DZ-2012-Ln-0239	54	109	30.81	3.3	0.28	4.92	1.53
DZ-2012-Ln-0240	55	109	31.64	2.6	0.29	4.89	1.48
DZ-2012-Ln-0241	55	110	28.90	3.2	0.31	4.39	1.48
DZ-2012-Ln-0242	55	112	30.79	3.1	0.33	4.51	1.58
DZ-2012-Ln-0243	54	108	28.71	3.6	0.31	4.63	1.50
DZ-2012-Ln-0244	60	116	35.32	3.6	0.28	5.70	1.76
DZ-2012-Ln-0245	53	111	30.13	2.7	0.29	4.31	1.22
DZ-2012-Ln-0255	55	109	29.72	3.1	0.34	4.25	1.48
LOCAL CHECK	55	107	30.14	2.1	0.28	3.99	1.22
Grand mean	58	115	32.264	3.1	0.28	4.98	1.45
Heritability	98%	97%	89%	97%	92%	85%	96%
Genotype Variance	20.64	40.89	6.30	0.16	0.00	0.59	0.21
Residual Variance	5.40	10.47	9.52	0.10	0.00	1.15	0.12
LSD	2.83**	4.24**	2.73**	0.32**	0.07**	1.11**	0.41**
CV	3.97	2.82	9.57	10.37	22.74	21.57	23.76
No of Environments	11	9	6	11	9	10	11

NB: DTF= days to 50% flowering, DTM = days to 90% maturity, HSW = hundred seed weight in gram, PLH = plant = height in cm, BMV= biomass yield ton per hectare, GHI = Grain harvest index, YLD: grain yield ton per hectare.

The estimates of correlation coefficients among the yield and its attributing traits are given in Table 4. Days to 50% flowering displayed positive and significant correlation between days to 90% maturity and hundred seed weight while days to 90% maturity was found positively and significantly correlated with days to 50% flowering and hundred seed weight. Plant height showed positive and significant correlation with biomass yield, grain harvest index, and grain yield. Hundred seed weight showed also positive and significant correlation with days to 50% flowering and days to 90% maturity. Biomass yield showed positive and significant correlation with plant

height, grain harvest index, and grain yield. Grain harvest index showed positive and significant correlation with plant height, biomass yield, and grain yield (Table 4). In the current study, grain yield was positively and significantly correlated with plant height, biomass yield and grain harvest index. This indicates that these traits were positively associated to grain yield because of linkages of genes governing the characters at coupling phase and direct selection based on these traits may ultimately improve the seed yield. These results were in agreement with the findings of Hussan et al. (2018), Chowdhury et al. (2019) and Kishor et al. (2020).

Table 4. Phenotypic correlation coefficients among different yield and yield component traits in lentil genotypes

	DTF	DTM	PLH	HSW	BMV	GHI	YLD
DTF	1						
DTM	0.691**	1					
PLH	-0.086ns	-0.094ns	1				
HSW	0.389**	0.404**	0.044ns	1			
BMV	-0.138ns	-0.259*	0.697**	0.041ns	1		
GHI	-0.717**	-0.556**	0.342**	-0.439**	0.393**	1	
YLD	-0.490**	-0.487**	0.642**	-0.233*	0.831**	0.820**	1

NB: ** = significant at 1% and * = significant at 5% probability level, ns=non-significant

DTF= days to 50% flowering, DTM = days to 90% maturity, HSW = hundred seed weight in gram, PLH = plant = height in cm, BMV= biomass yield ton per hectare, GHI = Grain harvest index, YLD: grain yield ton per hectare

A Multi-Environment Trial (MET) analysis was undertaken across the set of 11 environments using the raw data. FA models were found useful not only for adequately estimating/predicting genotype by environment (GxE) effects for balanced and unbalanced experiments, but also for estimating the covariance structure of GxE effects and conducting biplot analysis. Moreover, the correlated environments

can be established based on the estimated GxE covariance structure, and help breeders choose genotypes based on BLUPs averaged across correlated environments. Accordingly, factor analytic model was fitted using ASReml-R package and the predicted yield (t/ha) values for all genotypes under evaluation were obtained base on procedures demonstrated by Kelly et.al. (2017).

A factor analytic model adequately explained 90.58% of the GxE variance at an FA-2 for yield. Table 5 presents a summary of the REML estimates of the total variance accounted for the effects for yield. These results demonstrate the complex nature of cross-over GxE interaction present for these data. The FA-2

model provides a satisfactory fit for most environments except KK18LNPE and EN17LNPE suggesting that these sites were generally not as well correlated with the other sites (environments). In addition, these sites had lower genotype variance than residual variance.

Table 5. Percent of Variations Explained by the Model in the Experiment

Environment	fac_1	fac_2	all	Genotype Variance	Residual Variance	Heritability	Mean yield t/ha
AK16LPPE	88.04	0.41	88.5	0.295	0.055	94%	1.06
AK17LNPE	83.44	16.6	100	0.110	0.342	49%	2.95
CD16LPPE	82.87	17.1	100	0.204	0.095	87%	1.78
CD17LNPE	73.66	23.8	97.5	0.158	0.126	79%	1.94
Db18LNPE	89.31	4.72	94	0.636	0.228	92%	1.95
DZ16LPPE	82.79	3.19	86	0.395	0.053	96%	1.34
DZ18LNPE	86.38	13.6	100	0.159	0.038	94%	0.90
EN17LNPE	66.48	33.5	100	0.043	0.131	50%	3.08
HS18LNPE	82.76	0.56	83.3	0.020	0.009	89%	0.72
KK18LNPE	59.8	40.2	100	0.006	0.016	61%	0.82
SN18LNPE	94.65	5.35	100	0.080	0.329	49%	1.75
Cumulative			90.58%				

NB: AK16LPPE=Lentil PVT at Akaki in 2016, AK17LN=Lentil NVT at Akaki in 2017, CD16LPPE=Lentil PVT at Chefe Donsa in 2016, CD17LNPE=Lentil NVT at Chefe Donsa in 2017, Db18LNPE=Lentil NVT at Dabat in 2018, DZ16LPPE=Lentil PVT at Debre Zeit in 2016, DZ18LNPE=Lentil NVT at Debre Zeit in 2018, EN17LNPE=Lentil NVT at Enewari in 2017, HS18LNPE=Lentil NVT at Hosanna in 2018, KK18LNPE=Lentil NVT at Kokate in 2018, SN18LNPE=Lentil NVT at Sinan in 2018, PVT = Preliminary variety Trial, NVT = National Variety Trial

Figure 1A presents the dendrogram using the REML estimate between environments correlation matrix as the similarity measure using the total effect. Two clusters were formed at a cut-off about 0.2 for the fitted value of yield data. The heatmap plot to provide further evidence that the clusters suggested from the dendrogram appear to describe the pattern of cross-over GxE (figure 1B).

A dendrogram classified the sites/Environments into two groups. The first group consisted of 6

environments (AK16LPPE, HS18LNPE, Db18LNPE, DZ18LNPE, KK18LNPE and DZ16LPPE). These environments had showed yield performance of low to medium magnitude. The second group of environments consisted of 5 environments such as AK17LNPE, CD16LPPE, CD17LNPE, EN17LNPE and SN18LNPE. Yield performance of genotypes in the second group was relatively higher indicating the suitability of these testing sites. Hence, they are the most representative of the overall lentil growing areas in the

country, which means breeders could have the opportunity to select a genotype with wider adaptability using those fewer testing sites. In addition, this has an important implication in reducing costs of conducting multi-location trials.

Furthermore, the heatmap graph

illustrated in Fig. 2 classified the test environments into two major clusters in a similar manner with the dendrogram result. Accordingly, there was a strong and positive correlation among environments except for environment KK18LNPE, which showed weak and positive correlation with few other environments.

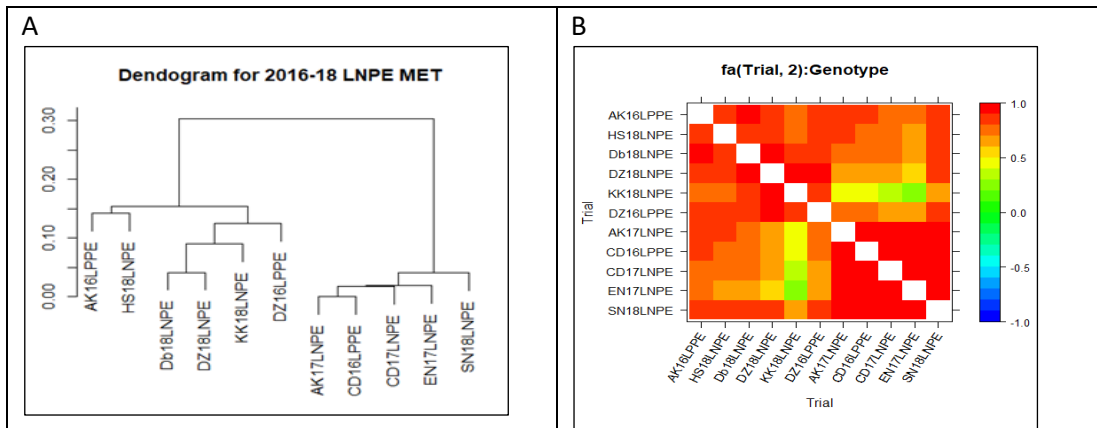


Figure 1. Dendrogram of the dissimilarity matrix of the additive effects for yield data (A). Heat map of mean grain yield of 25 lentil genotypes (t/ha) (B).

NB: AK16LPPE=Lentil PVT at Akaki in 2016, AK17LN=Lentil NVT at Akaki in 2017, CD16LPPE=Lentil PVT at Chefe Donsa in 2016, CD17LNPE=Lentil NVT at Chefe Donsa in 2017, Db18LNPE=Lentil NVT at Dabat in 2018, DZ16LPPE=Lentil PVT at Debre Zeit in 2016, DZ18LNPE=Lentil NVT at Debre Zeit in 2018, EN17LNPE=Lentil NVT at Enewari in 2017, HS18LNPE=Lentil NVT at Hosanna in 2018, KK18LNPE=Lentil NVT at Kokate in 2018, SN18LNPE=Lentil NVT at Sinan in 2018, PVT = Preliminary variety Trial, NVT = National Variety Trial

An interactive biplot implementation in R for modeling genotype-by-environment interaction in measuring the performance of trials (environments) in which 25 lentil genotypes were tested based on the suggestion given by Yan and Tinker (2006) and Frutos et al, (2014) are illustrated as follows using yield data of table 3.

Environment evaluation based on GGE Biplots

In evaluating relationships among test environments, the environment-vector

view of the GGE biplot for the data in Table 6 was used. It is based on an environment-centered (centering = 2) GE table without any scaling (scaling = 0), and it is environment-metric preserving (SVP = 2) and its axes are drawn to scale (default feature of GGEbiplotGUI) (Frutos, et al, 2014). This biplot explained 96% of total variation of the environment-centered GE table. Assuming that it adequately approximates the environment centered two-way table in Figure 2.

Table 6. Mean yield (ton ha⁻¹) of 25 lentil genotypes tested at eleven environments in years between 2016 and 2018.

GID	Genotype	Environments										
		AK16LP	AK17LN	CD16LP	CD17LN	Db18LN	DZ16LP	DZ18LN	EN17LN	HS18LN	KK18LN	SN18LN
1	DENBI	2.19	3.33	2.07	2.46	2.76	2.38	1.44	3.88	0.90	0.95	1.81
2	DERASH	2.00	3.32	2.55	2.28	2.93	2.32	1.47	3.44	0.85	0.93	1.97
3	DZ-2012-Ln-0020	0.53	2.41	1.37	1.41	0.66	0.77	0.23	3.09	0.49	0.70	1.43
4	DZ-2012-Ln-0050	1.80	3.36	2.36	2.00	2.89	2.10	1.33	3.19	0.97	0.93	2.02
5	DZ-2012-Ln-0054	1.43	3.09	2.08	1.99	2.37	1.66	1.11	3.05	0.77	0.85	1.91
6	DZ-2012-Ln-0218	2.05	3.54	2.61	2.71	3.29	2.97	1.63	3.23	0.85	0.92	2.13
7	DZ-2012-Ln-0219	0.64	2.55	1.28	1.51	1.05	1.41	0.40	2.95	0.54	0.72	1.57
8	DZ-2012-Ln-0228	0.69	2.47	1.60	1.51	0.79	0.63	0.32	3.23	0.52	0.72	1.43
9	DZ-2012-Ln-0231	0.89	2.54	1.33	1.62	0.93	1.02	0.42	3.42	0.56	0.75	1.42
10	DZ-2012-Ln-0232	0.63	2.44	1.45	1.47	0.72	0.72	0.28	3.19	0.51	0.71	1.42
11	DZ-2012-Ln-0233	1.16	2.83	2.05	2.33	1.49	1.48	0.64	3.37	0.73	0.77	1.59
12	DZ-2012-Ln-0234	0.52	2.38	1.34	1.40	0.58	0.68	0.20	3.15	0.48	0.70	1.39
13	DZ-2012-Ln-0235	0.39	2.31	1.27	1.32	0.42	0.57	0.11	3.09	0.45	0.68	1.36
14	DZ-2012-Ln-0236	0.43	2.30	1.27	1.33	0.38	0.48	0.10	3.18	0.45	0.68	1.33
15	DZ-2012-Ln-0237	0.33	2.29	1.16	1.29	0.41	0.70	0.09	3.01	0.44	0.67	1.38
16	DZ-2012-Ln-0238	1.41	3.10	1.98	2.05	2.50	1.63	1.27	2.92	0.88	0.86	1.99
17	DZ-2012-Ln-0239	1.10	2.78	2.07	1.87	1.45	1.16	0.57	3.31	0.63	0.79	1.59
18	DZ-2012-Ln-0240	1.05	2.83	1.82	1.66	1.69	1.43	0.76	3.04	0.61	0.77	1.73
19	DZ-2012-Ln-0241	0.87	2.74	1.86	1.68	1.48	1.27	0.58	2.93	0.60	0.76	1.70
20	DZ-2012-Ln-0242	0.85	2.82	1.92	1.57	1.68	1.29	0.68	2.75	0.58	0.73	1.80
21	DZ-2012-Ln-0243	1.06	2.84	1.86	1.56	1.84	1.64	1.01	2.93	0.66	0.84	1.80
22	DZ-2012-Ln-0244	1.43	2.93	2.35	2.28	1.68	1.33	0.75	3.63	0.73	0.83	1.58
23	DZ-2012-Ln-0245	0.85	2.59	1.39	1.62	1.09	1.24	0.47	3.24	0.57	0.75	1.51
24	DZ-2012-Ln-0255	1.00	2.66	1.74	1.78	1.35	1.36	0.50	3.24	0.60	0.77	1.58
25	LOCAL CHECK	1.23	2.38	1.65	1.45	0.49	1.43	0.43	4.29	0.54	0.79	1.08

NB: AK16LP=Lentil PVT at Akaki in 2016, AK17LN=Lentil NVT at Akaki in 2017, CD16LP=Lentil PVT at Chefe Donsa in 2016, CD17LN=Lentil NVT at Chefe Donsa in 2017, Db18LN=Lentil NVT at Dabat in 2018, DZ16LP=Lentil PVT at Debre Zeit in 2016, DZ18LN=Lentil NVT at Debre Zeit in 2018, EN17LN=Lentil NVT at Enewari in 2017, HS18LN=Lentil NVT at Hosanna in 2018, KK18LN=Lentil NVT at Kokate in 2018, SN18LN=Lentil NVT at Sinan in 2018, PVT = Preliminary variety Trial, NVT = National Variety Trial

The lines that connect the test environments to the biplot origin are called environment vectors. According to Equation given by Kroonenberg, (1995) the cosine of the angle between the vectors of two environments approximates the correlation between them. The genotypes were represented on the biplots as the points derived from their scores for the first two components, and the environments as the vectors from the biplot origin to their points. The cosine of angle between a pair of environment vectors approximates correlation between them (Yan and Kang, 2003). An acute angle ($<90^\circ$) indicates a strong positive correlation; an angle close to 90° indicates the environments are not correlated, whereas an obtuse angle close to 180° represents a strong negative relationship (Kroonenberg, 1995). These graphic analyses were done using R GGEBiplotGUI package of version 1.0.9 as presented by Frutos et al (2014).

Accordingly, all the tested environments were displayed on the second and third quadrants of the GGE Biplot (Fig. 2). The largest angle

formed between environments EN17LN and Db18LN; EN17LN and SN18LN were slightly larger than 90° , implying that the GE is moderately large. The remaining environments had angle less than 90° implying strong positive correlation among themselves. The presence of close associations among test environments suggests that the same information about the genotypes could be obtained from fewer test environments, and hence the potential to reduce testing cost. If two test environments are closely correlated consistently across years, one of them can be dropped without loss of much information about the genotypes (Yan and Tinker, 2006). Thus, some of the test environments such as Akaki (AK16LP, AK17LN), Chefe Donsa (CD16LP, CD17LN), Debre Zeit (DZ16LP, DZ18LN) and Dabat (Db18LN) can be dropped as they generate the same information about the genotype. On the other hand, the angles formed between EN17LN and KK18LN and also between EN17LN and DZ18LN close to 90° and hence have no correlation.

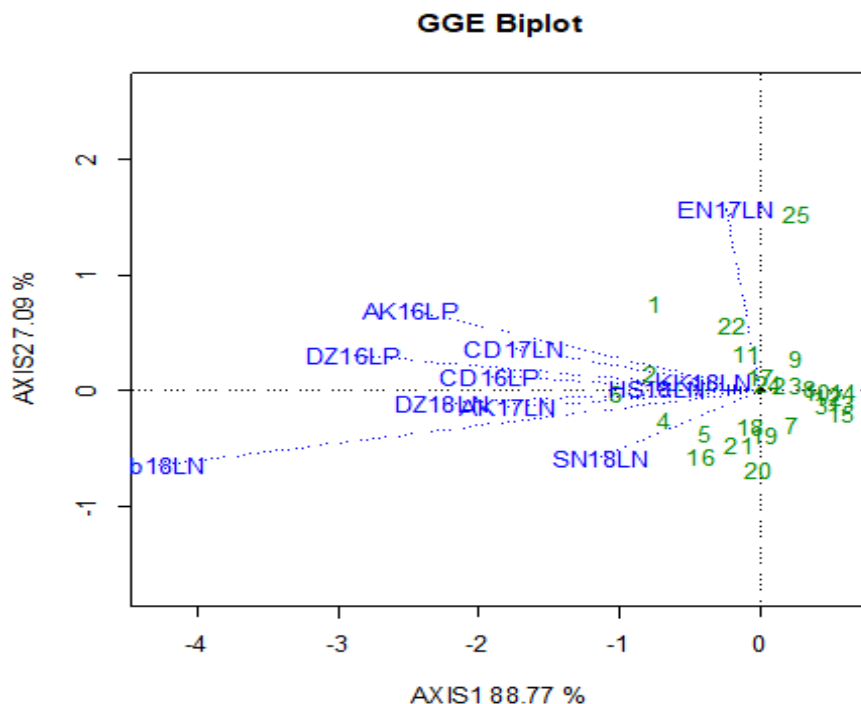


Figure 2. The environment-vector view of the GGE biplot to show similarities among test environments

The discriminating ability of test environments is shown in figure 3. The concentric circles on the biplot help to visualize the length of the environment vectors, which is proportional to the standard deviation within the respective environments and is a measure of the discriminating ability of the environments. Therefore, among the eleven environments, Db18LN was most discriminating (informative) followed by DZ16LP and AK16LP. KK18LN was least discriminating followed by HS18LN as these environments are located around the origin of the graph (Figure 3).

Regarding representativeness the test environments Yan and Tinker (2006)

stated that the average environment represented by the small circle at the end of the arrow has the average coordinates of all test environments. The Average Environment Axis (AEA) is the line that passes through the average environment and the biplot origin. Accordingly, a test environment that has a smaller angle with the AEA is more representative of other test environments. Thus, CD16LP and DZ16LP are most representative whereas EN17LN and SN18LN least representative. Test environments that are both discriminating and representative like DZ16LP is good test environments for selecting generally adapted genotypes. Discriminating but non-representative test environments such as Db18LN are

useful for selecting specifically environments can be divided into adapted genotypes if the target mega-environments.

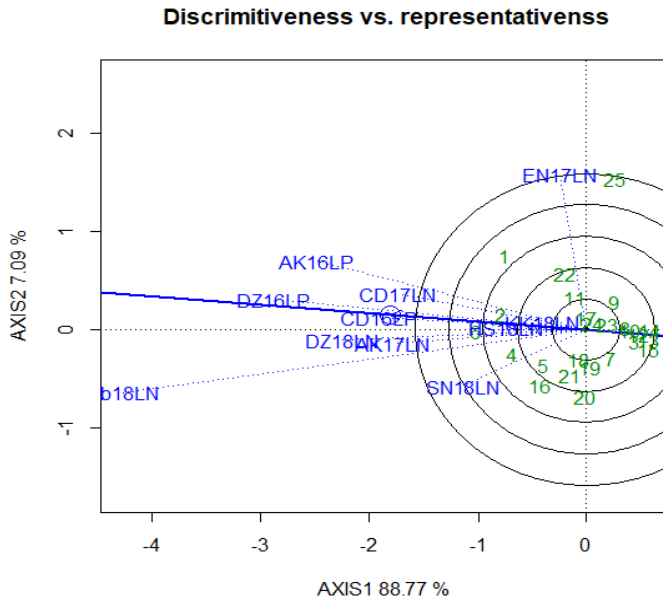


Figure 3. The discrimination and representativeness view of the GGE biplot

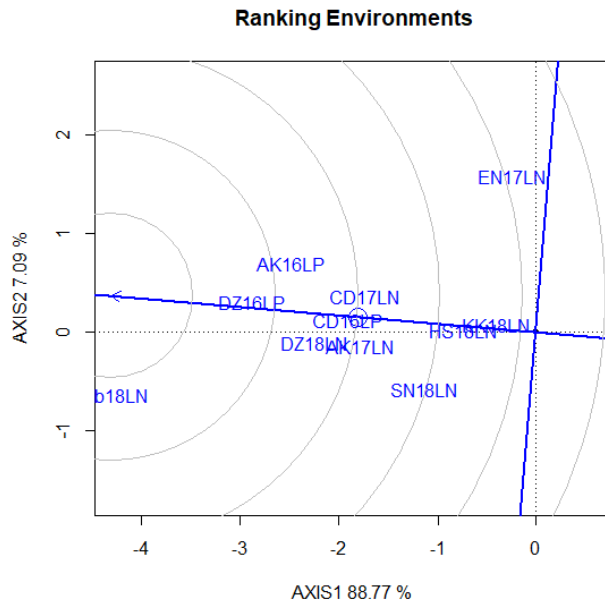


Figure 4. The discrimination and representativeness view of the GGE biplot to rank test environments relative to an ideal test environment.

Within a single mega-environment, the ideal test environment should be most discriminating (informative) and at the same time most representative of the target environment. Figure 4 defines an “ideal test environment”, which is the center of the concentric circles. It is a point on the AEA with a distance to the biplot origin equal to the longest vector of all environments (“most informative”). DZ16LP is closest to this point and is, therefore, best, whereas KK18LN was the poorest for selecting cultivars adapted to the whole region.

Genotype evaluation based on GGE Biplots

To evaluate the mean performance and stability of the genotypes within a single mega-environment, the data should be genotype-metric preserving ($SVP = 1$) for appropriate genotype evaluations (Yan and Tinker, 2006). Accordingly, the single-arrowed line called Average Environment Coordinate (AEC) abscissa (or AEA) points to higher mean yield across environments. Thus, genotype 6 was found to be the highest with the potential grain yield of $3.54 \text{ (t/ha}^{-1}\text{)}$ at AK17LN, followed by 1 and 2 whereas genotype 14 had the lowest mean yield. The AEC ordinate points to greater variability (poorer stability) in either

direction. Thus, genotype 25 was highly unstable whereas 17 were highly stable. Genotype 25 was highly unstable because it had lower than expected yield in environments DZ18LNPE and AK16LPPE but higher than expected yield in AK17LNPE, and EN17LNPE environments (Figure 5).

Ranking genotypes relative to the Ideal Genotype

A genotype is said to be an ideal if it had both high mean yield performance and high stability across environments. Figure 6 defines an “ideal” genotype (the center of the concentric circles) to be a point on the AEA (“absolutely stable”) in the direction towards the pointing of the arrow and has a vector length equal to the longest vectors of the genotypes on AEA (“highest mean performance”). Therefore, genotypes located closer to the ‘ideal genotype’ are more desirable than others. Thus, genotype 1, 6 and 2 were more desirable than the other genotypes. However, genotypes 1 and 2 are released varieties and thus no need of discussing about them. On the other hand, genotype 14 was the poorest genotype because it consistently performed poorly across environments.

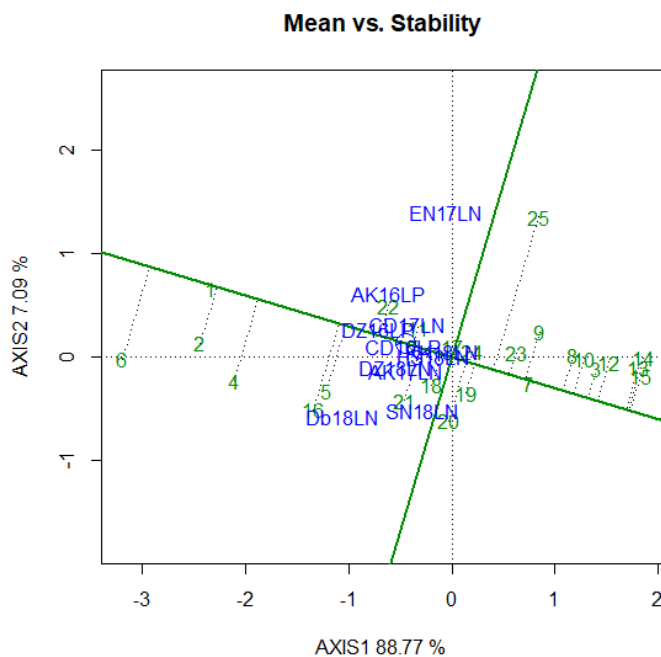


Figure 5. The average-environment coordination (AEC) views to show the mean performance and stability of the genotypes.

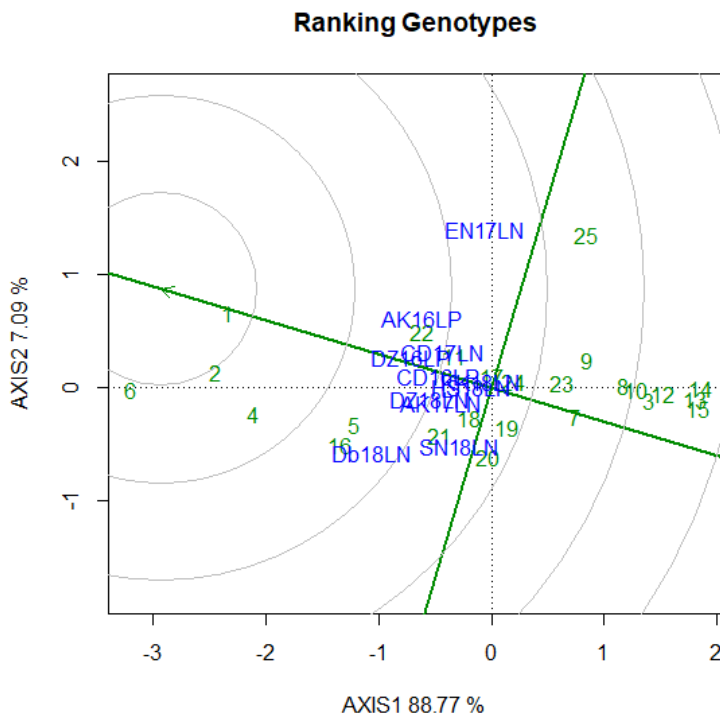


Figure 6. Ranking cultivars based on both mean performance and stability for experimental set A

Which-won-where?

One of the most attractive features of a GGE biplot is its ability to show the which-won-where pattern of a genotype by environment data set (Yan and Tinker, 2006). The polygon formed by connecting the markers of the genotypes that are farthest away from the biplot origin, such that all other genotypes are contained in the polygon. Figure 7 also contains a set of lines perpendicular to each side of the polygon. These perpendicular lines divide the biplot into several sectors. The winning genotype for each sector is the one located at the respective vertex. Genotypes located at the vertices of the polygon reveal the best or the poorest in one or other environment (Yan and Tinker 2006; Fructos *et al*, 2014).

Seven sectors were created with genotype's code number 6, 1, 25, 14, 20 and 16 as the vertex genotype. Environments EN17LN fell in the sector in which genotype 25 was the vertex cultivar, meaning that genotype 25 was the best cultivar for EN17LN site. The other ten environments fell in the sector in which genotype 6 was the vertex cultivar, which mean that genotype 6 was the best cultivar for these ten environments. No environments fell into sectors with genotype 14 and 20 as the vertices, indicating that these cultivars were not the paramount in any of the environments. In general, this result further verified the results depicted in the dendrogram (Fig. 1A).

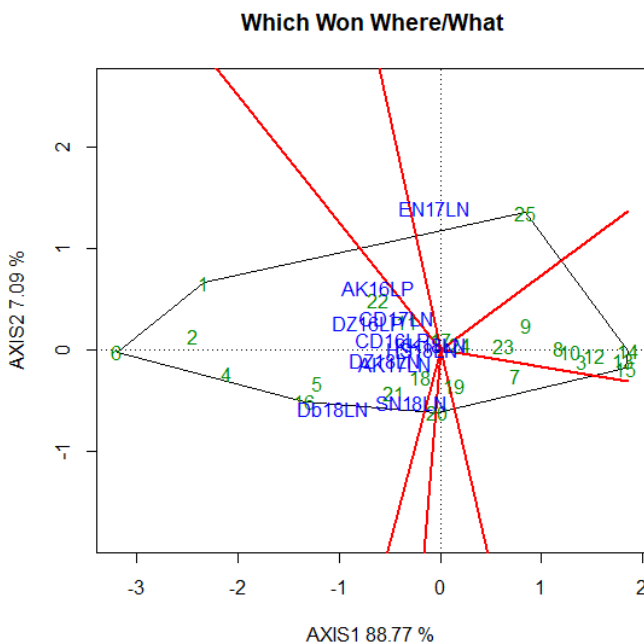


Figure 7. The which-won-where view of the GGE biplot.

Conclusions

A multi-environment trial (MET) analysis was undertaken across the sets of 11 environments for estimating the GxE effects with BLUPs by using factor analytic (FA) models, and thereby conducting GGE biplot analysis based on BLUPs of FA models. As a result, both informative and representative test environments were identified and also superior genotypes of high and stable performance were known within target environment. So, plant breeders can therefore, have such a more robust platform for evaluation of crop cultivars with greater confidence in selecting superior cultivars across a range of environments without minding about the limited amounts of seeds of test genotypes and size of experimental plots as unbalanced structure of test genotypes can easily be analyzed and BLUPs determined with FA model.

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Genetic Variability, Heritability, and Genetic Advance in Mung Bean [*Vigna radiata* (L.) Wilczek] Genotypes

Tekle Yoseph^{*1}, Firew Mekbib², Berhanu Amsalu Fenta³, and Zerihun Tadele⁴

¹Southern Agricultural Research Institute, Jinka Agricultural Research Center, P.O. Box 96, Jinka, Ethiopia; Email Address: tekleyoseph486@gmail.com; ²Haramaya University, School of Plant Sciences, P.O. Box 138,

Dire Dawa, Ethiopia; Ethiopian Institute of Agricultural Research (EIAR), Ethiopia;

⁴University of Bern, Institute of Plant Sciences, Altenbergrain 21, 3013 Bern, Switzerland.

Abstract

Assessment of genetic variability in crop species is one of the major activities to meet the diversified goals in plant breeding programs. However, there is a lack of sufficient information on the genetic variability study of mung bean. Therefore, field experiment was conducted on sixty mung bean genotypes with the objectives to assess the genetic variability, heritability, and genetic advance for desirable traits that have a vital role in determining and designing breeding strategies. The experiment was conducted at Jinka Agricultural Research Center laid out in a 6×10 alpha lattice design with two replications during the 2018 cropping season. The analysis of variance revealed highly significant ($P \leq 0.001$) differences for most of the traits indicating the existence of high genetic diversity among the genotypes. High estimates of genotypic coefficient of variance (GCV) and phenotypic coefficient of variance (PCV) was observed for harvest index (48.77% and 59.73%). The lowest GCV and PCV estimates were obtained for days to flowering (3.26% and 6.82%), days to maturity (2.08% and 4.20%), seed yield per hectare (0.34% and 0.45%), and biomass yield per hectare (0.08% and 0.13%). Terminal leaf length, terminal leaf width, peduncle length, plant height, number of primary branches per plant, seeds per pod, seed yield per plant, hundred seed weight, seed yield per hectare, biomass yield, and harvest index exhibited high heritability values. High heritability coupled with high GAM estimates was recorded for plant height, the number of primary branches per plant, hundred seed weight, and harvest index. In general, the observed variability could help to develop breeding schemes for mung bean.

Keywords: Diversity, Heritability, Phenotypic variation, Quantitative traits, Selection

Introduction

Mung bean [*Vigna radiata* (L.) Wilczek] is an important legume crop. It is a self-pollinated crop with a diploid chromosome number of $2n = 2x = 22$ and a genome size of 579 Mb

(Parida *et al.*, 1990). Mung bean seed is rich in easily digestible protein which makes it an important component of a balanced diet. Seeds are also a very good source of the minerals calcium, iron, zinc, potassium, phosphorus, and vitamins

such as vitamin K and dietary fibers (Keatinge *et al.*, 2011). It can restore soil fertility through nitrogen fixation. Mung bean is one of the most important grain legumes extensively cultivated in arid, semi-arid, and subtropics of the world. It is one of the most important pulse crops and becoming the most important cash crop in Ethiopia after the common bean.

Assessment of genetic diversity in mung bean genotypes would facilitate the development of elite cultivars. Omima *et al.* (2018) suggested that having information on the magnitude of genetic variability is the number one criterion for successful breeding. Genetic variability is a key for the success of a plant breeding program since it provides an opportunity to breeders to make the selection for desirable superior individuals from a genetically diverse base population (Partap *et al.*, 2019). Understanding the level of genetic variability might support plant breeders' decision on the selection of parental genotypes with a broad genetic base for further genetic improvement and amenities in the development of the breeding strategy (Souza and Sorrells, 1991; Singh, 2002; Denton and Nwangburuka, 2011; Prasanthi *et al.*, 2012; Omima *et al.*, 2018). The lack of adequate variability has been considered as one of the major bottlenecks in mung bean improvement and the success of its improvement needs the use of wide genetic variability in respect of

important economic characters present in the population (Bhanu *et al.*, 2016).

Estimates of genetic parameters indicate the relative importance of the various types of gene effects affecting the total variation of a plant character. Heritability plays a significant role in plant breeding and serves as an extrapolative guide to realize the breeding value. The estimation of heritability along with genetic advance is more applicable than the heritability value alone (Johnson *et al.*, 1955; Shukla *et al.*, 2006). There is a direct relationship between heritability and response to selection, which is referred to as genetic advance (Nwangburuka and Denton, 2012; Ogunniyan and Olakojo, 2015; Omima *et al.*, 2018). Genetic advance used as a measure to predict the expected progress and to find the actual gain expected under selection (Larik *et al.*, 2000; Nwangburuka and Denton, 2012; Ogunniyan and Olakojo, 2015). If the value of genetic advance is large in the succeeding generation, there will be good progress over the population mean. Genotypic and phenotypic coefficients of variation along with heritability plus genetic advance are very essential to improve traits of interest (Denton and Nwangburuka, 2011; Gbaguidi *et al.*, 2013).

Since many characters of economic importance are highly influenced by environmental conditions; the improvement of a crop mainly depends upon the amount, nature, and magnitude of genotypic variability

present in the population. Yimram *et al.* (2009) suggested that the quantitative nature of agromorphological traits like the genotypic variance, phenotypic variance, heritability, and the genetic advance are the most important traits for phenotypic selection of crops. However, proper evaluation of the extent of genetic variation available for yield components, their heritability values, and genetic advance could be of great significance for the breeders to choose the best genotypes for improvement (Itefa *et al.*, 2014).

Mung bean is a highly self-pollinated crop lacks natural variability for seed yield and yield-related traits is very narrow in mung bean which makes the selection ineffective. Saeed *et al.* (2007) observed low genetic variability in mung bean genotypes due to the narrow genetic backgrounds of local collections. Genetic diversity studies on black gram genotypes have been reported by different authors (Sharma *et al.*, 2006; Konda *et al.*, 2009; Senapati and Mishra, 2010; Reddy *et al.*, 2011; Meshram *et al.*, 2013; Deepshikha *et al.*, 2014; Ramya *et al.*, 2014; Kumar *et al.*, 2015; Patel *et al.*, 2015; Gowsalya *et al.*, 2016; Patidar *et al.*, 2018). Though, information on the genetic diversity, heritability, and genetic advance of mung genotypes in Ethiopia is limited. Therefore, the present study was

conducted to assess the genetic variability, heritability, and genetic advance of mung bean genotypes.

Materials and Methods

Descriptions of the Study Area

The field experiment was conducted at Jinka Agricultural Research Center (JARC) during the main cropping season from March to June 2018. Jinka Agricultural Research Center is located 729 km southwest of Addis Ababa at 36° 33' 02.7" E, 05° 46' 52.0" N, and at an altitude of 1420 meters above sea level. The maximum, minimum, and average temperatures of the center are 27.68°C, 16.61°C, and 22.14°C, respectively with the mean annual rainfall of 1381 mm. The soil type of the center is Cambisols (Mesfin *et al.*, 2017).

Experimental Materials

The experimental materials consisting of sixty mung bean genotypes were used for this study, forty four genotypes were obtained from Melkassa Agricultural Research Center (MARC) and 16 genotypes were collected from Southern Nations, Nationalities, and People's (SNNP) (Table 1).

Table 1. List of genotypes used for diversity study in 2018

Genotype	Code	Genotype	Code	Genotype	Code	Genotype	Code
VC6489-9-1	G38	N-26	G43	NLLP-MGC-04	G4	Acc003	G47
NLLP-MGC-10	G10	NLLP-MGC-16	G16	NVL-1	G44	Acc004	G48
NLLP-MGC-06	G6	VC2778A(KPS2)	G29	NLLP-MGC-15	G15	Acc005	G49
NLLP-MGC-20	G20	VC6469-12-34A	G37	HARSHA	G39	Acc006	G50
NLLP-MGC-14	G14	NLLP-MGC-09	G9	NLLP-MGC-08	G8	Acc007	G51
NLLP-MGC-19	G19	VC6368(46-40-4)	G34	NLLP-MGC-05	G5	Acc008	G52
NLLP-MGC-21	G21	NLLP-MGC-01	G1	NM92(VC6370-92)	G31	Acc009	G53
NLLP-MGC-11	G11	NLLP-MGC-24	G24	NLLP-MGC-23	G23	Acc0010	G54
NLLP-MGC-12	G12	VC6492-59A	G35	V2709 BG	G42	Acc0011	G55
VC1973A	G28	VC6370(30-65)	G33	NLLP-MGC-27	G27	Acc0012	G56
VC6510-151-1	G36	NLLP-MGC-07	G7	VC3890A	G30	Acc0013	G57
CN9-5	G41	NLLP-MGC-26	G26	NLLP-MGC-25	G25	Acc0014	G58
NLLP-MGC-02	G2	NLLP-MGC-17	G17	NLLP-MGC-22	G22	Acc0015	G59
NM94(VC6371-94)	G32	NLLP-MGC-18	G18	Acc001	G45	Acc0016	G60
BARI-MUNG 2	G40	NLLP-MGC-03	G3	Acc002	G46	NLLP-MGC-13	G13

Genotypes with initial "Acc" were obtained from Southern Nations, Nationalities, and People's Region (SNNPR), and other genotypes were obtained from Melkassa Agricultural Research Center (MARC); G: Genotype.

Experimental Design and Procedures

The experiment was laid out using a 6 × 10 alpha lattice design. The plot size was 3 m long, 0.3 m between rows, and 0.05 m between plants. It consists of five rows accommodating 60 plants per row. The distance between plots, intra blocks, and replications was 1, 1.5, and 2 m, respectively.

Data Collection

The descriptor of mung bean developed by the International Board for Plant Genetic Resources (IBPGR, 1980) was followed for data collection. A plot basis data collected for days to flowering, days to maturity, and hundred seed weight (g), The data were collected from the central three rows for the determination of seed yield includes seed yield per plot (g), biomass yield (g), and harvest index (%). While, plant basis data collected for plant height (cm), number of primary branches per plant, number of pods per plant, number of seeds per pod, pod length (cm), peduncle length (cm), number of pods per cluster, terminal leaflet length (cm) and terminal leaflet width (cm).

Data Analyses

The analysis of variance (ANOVA) was carried out by using the SAS computer software version 9.0 (SAS, 2007) as per the following linear model for alpha lattice design. The means were separated by using the Duncan procedure at 5%, 1%, and 0.1% levels of significance. The linear

model for the alpha lattice design is as follows:

$$Y_{ijk} = \mu + R_i + B_{ij} + T_k + e_{ijk}$$

Where μ =the grand mean of trait Y; R_i = the effect of Replicate i; B_{ij} = effect of Block j within Replicate I; T_k =Effect of treatment k., e_{ijk} =error

Estimation of phenotypic and genotypic variance components

The phenotypic and genotypic variance components and coefficient of phenotypic and genotypic variability were estimated based on the method suggested by Burton and De vane (1953) as follows:

$$\text{Genotypic variance } (\sigma^2_g) = \frac{MS_g - MS_e}{r}$$

Environmental variance (σ^2_e) mean square = MS_e

$$\text{Phenotypic variance } (\sigma^2_p) = \sigma^2_g + \sigma^2_e$$

Where: MS_g = mean square due to genotypes

MS_e = Environmental variance (error mean square)

r = Number of replications

The phenotypic coefficient of variance (PCV) and genotypic coefficient of variance (GCV) was estimated following the procedure of Kumar *et al.* (1985) as:

Phenotypic coefficient of variation (PCV) = $(\sqrt{\sigma^2_p} / \text{grand mean}) \times 100$

Genotypic coefficient of variation (GCV) = $(\sqrt{\sigma^2_g} / \text{grand mean}) \times 100$

Estimation of broad-sense heritability and genetic advance

Broad sense heritability (H) expressed as a percentage of the ratio of the genotypic variance (σ^2_g) to the phenotypic variance (σ^2_p) and was estimated on genotype mean base as described by Allard, (1999) as:

$$\text{Heritability } (h^2_b) = (\sigma^2_g / \sigma^2_p) \times 100$$

Genetic advance in the absolute unit (GA) and percent of the mean (GAM), assuming selection of superior 5% of the genotypes were estimated following the methods illustrated by Johnson *et al.* (1955) as; $GA = K * \sigma_p * h^2_b$

Where: K = the standardized selection differential at 5% selection intensity ($k=2.063$), σ_p = phenotypic standard deviation on mean basis, h^2_b = heritability in broad sense

Genetic advance as percent of the mean was calculated to compare the extent of the predicted advance of different traits under selection, using the formula described by Comstock and Robinson (1952).

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

GAM=genetic advance as percent mean, GA=genetic advance under selection, $\bar{X}$ = Mean of the population in which selection employed.

Results and Discussion

Analysis of Variance

The analysis of variance results showed significant differences among

mung bean genotypes for all the studied traits (Table 2). The observed genotypic and phenotypic variations among the genotypes indicated the presence of genetic variability for yield improvement by selection. Similarly, the presence of variability among mung bean genotypes reported from different studies (Hemavathy *et al.*, 2015; Shiv *et al.*, 2017; Himabindu and Roopa Lavanya, 2017; Muthuswamy *et al.*, 2019; Dhunde *et al.*, 2021). Likewise, Garg *et al.* (2017) observed significant differences amongst 30 mung bean genotypes for days to flowering, days to maturity, plant height, number of branches per plant, number of pods per plant, number of seeds per pod, pod length, 100-seed weight, seed yield, biological yield, and harvest index. Similar results were reported by several authors (Rao *et al.*, 2006; Singh *et al.*, 2009; Reddy *et al.*, 2011; Dhoot *et al.*, 2017), who observed significant differences among the mung bean genotypes for the number of seeds per pod, hundred seed weight, seed yield per hectare, biomass yield and harvest index. Similar results were recorded (Balachandran *et al.*, 2010; Kumar *et al.*, 2015; Priyanka *et al.*, 2016; Nagmi and Lal, 2017; Rolaniya *et al.*, 2017; Partap *et al.*, 2019) on black gram genotypes, indicating that the presence of considerable genetic variability among the genotypes.

Simple Measure of Variability

The estimates of means, range, genotypic, and phenotypic variances and their coefficients of variation,

heritability in a broad sense, genetic advance, genetic advance as a percentage of means, and standard errors of the studied traits for sixty mung bean genotypes were presented in (Table 3). High variability was recorded for peduncle length, seeds per pod, seed yield per plant, hundred seed weight, seed yield per hectare, biomass yield, and harvest index for the tested genotypes (Table 3). Therefore, the present finding showed that the presence of inherent genetic variability among the mung bean genotypes, suggesting a good opportunity for the selection of genotypes with desirable traits for further improvement. The existence of variability suggesting that the presence of additive gene effects is important for improving those traits through direct phenotypic selection. Similar study results were reported by Reddy *et al.* (2003) on 36 mung bean genotypes, Khairnar *et al.* (2003) on 22 mung bean genotypes, Rao *et al.* (2006) on 60 mung bean genotypes, and Makeen *et al.* (2007) on 646 mung bean genotypes.

The variance due to days to flowering showed that the genotypes differed significantly (Table 2) and the mean values ranged from 30 to 47 days with an overall mean of 41.68 (Table 3). Early flowering was recorded on most of the studied genotypes except in a few genotypes. The variance due to days to maturity depicted that the genotypes differed significantly (Table 2) and the mean values ranged from 75 to 97 days with an overall mean of

90.98 (Table 3). The present study showed that most of the genotypes attained their maturity early, suggesting a good opportunity to obtain drought escaping materials from the tested genotypes in the drought-prone areas of the country through simple phenotypic selection. This result is in line with the report of Mak and Yap (1980), who suggested that early maturity may provide an opportunity for selection for drought-stressed environmental conditions.

The analysis of variance results depicted that there were significant variations observed among the genotypes for the terminal leaf width (Table 2). As indicated in Table 3, the mean values for terminal leaf length ranged from 3.2 to 9.8 (cm) with a mean of 5.88 (cm), while the mean values for terminal leaf width ranged from 6.2 to 15.0 (cm) with the overall mean of 10.28 (cm). The analysis of variance results revealed that there were significant differences observed among the genotypes for plant height (Table 2). The mean for plant height (cm) ranged from 18.4 to 78.2 with an overall mean of 37.42 (Table 3). The values for peduncle length (cm) ranged from 4.6 to 13.0 with an overall mean of 8.35 (Table 3). The analysis of variance results for pod length showed that there were significant variations observed among the genotypes for pod length (Table 2). The mean for pod length (cm) ranged from 5.0 to 13.6 with an overall mean of 9.88 (Table 3). The analysis of variance results for pods per plant

showed that there were significant variations observed among the genotypes for the number of pods per plant (Table 2) and ranged from 9.0 to 46.0 with an overall mean of 19.52 (Table 3). The analysis of variance results depicted that there were significant differences observed among the genotypes for the number of seeds per pod (Table 2) and ranged from 4.0 to 13.0 with the mean value of 9.53 (Table 3). This finding is in agreement with the report of Ahmad *et al.* (2012), who observed a sufficient amount of variability for seeds per pod

with the mean value for seeds per pod ranged from 5.18 to 10.85 on mung bean genotypes. As shown in (Table 2), the analysis of variance results depicted that there were significant differences observed among the genotypes for seed yield per hectare. As indicated in Table 3, the values for seed yield per hectare ranged from 0.81 to 1.81 ($t\ ha^{-1}$) with a mean of 1.24 ($t\ ha^{-1}$). From these results, it was suggested that there was a wide range of variability among mung bean genotypes for seed yield and yield-related traits.

Table 2. Analysis of variance for 17 quantitative traits studied on mung bean at Jinka, in 2018.

Traits	Mean Square of Replication (DF=1)	Mean Square of Genotype (DF=59)	Mean Square of Blocks Within Rep (DF=10)	Mean Square of Error (DF=49)	LSD (5%)	CV (%)
DTF	67.500**	9.915*	24.296***	6.217	5.007	5.98
DTM	25.208ns	18.194*	69.042***	11.058	6.679	3.66
PTL	0.012ns	2.867*	1.777ns	1.671	2.596	15.48
TLL	8.154*	2.961*	3.411*	1.568	2.515	21.30
TLW	1.666ns	3.367**	2.128ns	1.564	2.512	12.17
PDCL	0.200ns	3.814***	1.366ns	0.891	2.347	11.30
PHT	11.163ns	127.264***	44.957ns	32.373	11.428	15.21
BRN	0.033ns	0.745***	2.015***	0.276	1.056	17.34
PODL	2.760ns	4.727*	2.650ns	1.580	3.269	12.72
PPC	7.500*	1.632*	1.200ns	0.389	2.200	15.03
PPP	163.33ns	60.237*	41.37ns	38.167	12.40	31.65
SPP	1.220ns	4.621***	2.045ns	1.719	2.634	13.76
SYPP	0.0029ns	0.3050**	6.0788***	0.1400	0.7515	9.42
HSW	5.663***	1.661***	7.017***	0.424	1.308	12.17
SYLD	572683***	49792***	260218***	14178	239.159	9.60
BM	12580601***	458227***	3111440***	184920	863.727	9.89
HI	0.0037***	0.00057***	0.00258***	0.0002	0.0289	4.88

LSD=least significance difference, CV = coefficient of variation (%), DF= degree of freedom, DTF=days to flowering, DM= days to maturity, PTL = petiole length (cm), TLL = terminal leaf length (cm), TLW = terminal leaf width (cm), PDL = peduncle length (cm), PHT= plant height (cm), BRN=number of primary branches per plant, PODL = pod length (cm), PPC=number of pods per cluster, PPP=number of pods per plant, SPP= number of seeds per pod, SYPP= seed yield per plant (g), HSW= hundred seed weight (g), SYLD= seed yield ($kg\ ha^{-1}$), BM= biomass yield ($kg\ ha^{-1}$), HI=harvest index.

Estimations of Genetic Parameters

Estimates of variance components

Genetic parameters such as genotypic variance, phenotypic variance, genotypic and phenotypic coefficients of variation (GCV and PCV %), heritability, and genetic advance are presented in Table 3. The GCV and PCV values for days to flowering (3.26% and 6.82%), days to maturity (2.08% and 4.20%), petiole length (9.28% and 18.04%), terminal leaf length (14.2% and 25.57%), terminal leaf width (9.23% and 15.29%), peduncle length (13.2% and 19.27%), plant height (18.41% and 23.88%), the number of primary branches per plant (15.83% and 23.57%), pod length (10.32% and 19.44%), the number of pods per cluster (11.3% and 28.71%), number of pods per plant (17.02% and 35.93%), the number of seeds per pod (12.64% and 18.68), seed yield per plant (10.08% and 13.56%), 100-seed weight (14.72% and 19.06%), and harvest index (48.77% and 59.73%). Similar results were reported by Garg *et al.* (2017) for the number of pods per plant, biological yield, harvest index, and seed yield per plant; by Rao *et al.* (2006) for pods per plant, seed yield per plant, and biological yield; by Pandey *et al.* (2007) for harvest index and seed yield per plant; by Kumhar and Chaudhary (2007) for seed yield per plant; and Makeen *et al.* (2007) and Anand *et al.* (2016) for the number of pods per plant and seed yield; by Mehendi *et al.* (2013) for the number of clusters per plant and plant height; Hozayn *et al.* (2013) for plant height and 100-seed weight; Jyothsna

and Anuradha (2013) for pod length; Swathi (2013) for the number of clusters per plant; Garg *et al.* (2017) for plant height, the number of branches per plant and 100-seed weight, thus offering the moderate scope for further improvement of these traits through simple selection. Therefore, the study of GCV and PCV in mung bean genotypes showed variability for almost all the studied traits (Table 4), indicating the existence of wider genetic variation among the genotypes, and these results were strongly supported by the previous works on snake gourd (Rana and Pandit, 2011; Deepa and Mariappan, 2013; Ahsan *et al.*, 2014; Khan *et al.*, 2016).

The PCV and GCV values were considered as low (0 to 10%), moderate (10 to 20%), and high with the value greater than 20% (Sivasubramanian and Madhavamenon, 1973; Deshmukh *et al.*, 1986). In this study, the result of variance components, genotypic coefficient of variation (GCV), and phenotypic coefficient of variation (PCV) of the traits exhibited that the magnitude of GCV and PCV was maximum for harvest index (48.77% and 59.73%), while moderate estimates of GCV and PCV were observed for traits such as hundred seed weight (14.7% and 19.0%), the number of seeds per pod (12.6% and 18.6%), pod length (10.3% and 19.4%), seed yield per plant (10.08% and 13.5%) and peduncle length (13.23% and 19.2%). This finding is

in agreement with the work of Sharma *et al.* (2018) reported moderate estimates GCV and PCV for most of the studied traits on mung bean genotypes. In the present study, moderate GCV and highest PCV values of (14.23%, 25.5%), (18.41%, 23.8%), (15.83%, 23.5%), (11.30%, 28.7%) and (17.02%, 35.9%) were noted for terminal leaf length, plant height, the number of primary branches per plant, the number of pods per cluster and the number of pods per plant, respectively (Table 3).

However, low GCV and moderate PCV estimates were observed for petiole length (9.28% and 18.0%) and terminal leaf width (9.23% and 15.2%), indicating that the presence of a narrow spectrum of variability for these traits and the existence of a high environment influence leading to the limited scope for improvement by simple phenotypic selection alone. In this line Shiv *et al.* (2017) reported low to moderate GCV and PCV values for plant height, primary branches per plant, and hundred seed weight. The result also depicted that the lowest GCV and PCV estimates (3.26% and 6.82%), (2.08% and 4.20%), (0.34% and 0.45%), and (0.08% and 0.13%), were recorded for days to flowering, days to maturity, seed yield per hectare and biomass yield per hectare, respectively (Table 3). Sharma *et al.* (2018) similarly observed low estimates of GCV and PCV for the number of seeds per pod (7.87% and 9.05%), days to maturity (6.11% and 6.20%), days to 50% flowering (6.03%

and 6.11%), pod length (3.52% and 6.83%). Likewise; Mehandi *et al.* (2013) reported low estimates of GCV and PCV for days to 50% flowering, days to maturity, and pod length; Garg *et al.* (2017) for days to 50% flowering and days to maturity; Jyothsna and Anuradha (2013) also reported low estimates of GCV and PCV for days to flowering, and Swathi (2013) for relative water content. Also, Makeen *et al.* (2007), Nan and Anuradha (2013), and Kumhar and Choudhary (2007) reported low GCV and PCV values for most of the studied traits on mung bean. Therefore, offering little scope for further improvement of these traits through simple selection, but it rather indicated that there is considerable possibility of further improvement through crossing followed by appropriate selection for these characters.

In the present investigation, the PCV values of all traits were higher than GCV values, indicating that the greater influence of the environment on these traits. This finding is in harmony with the previous reports on mung bean genotypes (Sadiq *et al.*, 2005; Siddique *et al.*, 2006; Makeen *et al.*, 2007; Tabasum *et al.*, 2010; Sheetal *et al.*, 2014; Jangra and Yadav, 2015; Abbas *et al.*, 2018; Sandhiya and Saravanan, 2018). Likewise, Jagdhane *et al.* (2017) reported that the magnitude of PCV was higher than GCV for the number of clusters per plant (32.51%, 31.33%) followed by the number of primary branches per plant (32.95%, 30.58%), the number

of pods per plant (24.07%, 20.07%), plant height (12.10%, 12.74%), harvest index (11.89%, 13.09), seed yield per plant (10.16%, 11.49%), and seeds per pod (8.33%, 12.44%) on 20 mung bean genotypes.

The estimates for GCV ranged from 0.08% for biomass yield per hectare to 48.77% for harvest index. The values for PCV ranged from 0.13% for biomass yield per hectare to 59.73% for harvest index (Table 3). This finding is in line with the report of Jangra and Yadav (2015) who observed wide differences between phenotypic (PCV) and genotypic (GCV) coefficient of variance in traits like days to maturity and the number of branches per plant, signifying that their susceptibility to environmental fluctuations than other characters with narrow differences. Generally, high genetic variability was observed among the mung bean genotypes for all the studied traits. The observed variability was the sum of variation arising due to the genotypic and environmental effects. As a result, knowledge of the nature and magnitude of genetic variations contributing to the genetic gain under selection is essential.

The maximum values for the difference between GCV and PCV were recorded for pods per plant (17.02 to 35.94%) followed by pods per cluster (11.30 to 28.7%), indicating that the expressions of these traits were relatively more influenced by the environments. However, the

minimum differences between GCV and PCV estimates were noted for harvest index (48.77 to 59.7%) followed by biomass yield per hectare (0.08 to 0.13%), indicating that these traits had low environmental influence and had a reasonable effect on genotypic factors or fixable genes on the expression of these traits. This result agreed with the previous reports by Pandiyan *et al.*, (2006), Prakash (2006), Rao *et al.* (2006), Singh *et al.* (2009), Kumar *et al.* (2010), Suresh *et al.* (2010), Tabasum *et al.* (2010), Reddy *et al.* (2011), Prakash and Shekhawat (2012), Gadakh *et al.* (2013), Prasanna *et al.* (2013), Ahmad *et al.* (2014), Javed *et al.* (2014), Ahmad *et al.* (2015), Das and Barua (2015), Muralidhara *et al.* (2015), Vir and Singh (2016), and Shiv *et al.* (2017) who reported that a narrow gap between GCV and PCV, indicating a narrow range of environmental influence on the studied traits. Generally, the existence of narrow gaps between the genotypic coefficients of variation and that of the phenotypic variation for some of the studied traits indicated that phenotypic variability was largely due to genetic differences and less environmental influence. In general, phenotypic and genotypic coefficients of variations suggested that there are good opportunities for the improvement of mung bean through direct selection. Therefore, selection based on the phenotype alone can be effective for the improvement of these traits.

Estimates of heritability and genetic advance

The results of broad-sense heritability (H^2) and genetic advance for various traits of mung bean genotypes are presented in Table 3. Estimates of heritability ranged from (15.49%) for the number of pods per cluster to (66.67%) for harvest index (Table 3). Heritability values are used to predict the expected progress to be achieved through the process of selection. As reported by Dabholkar (1992), heritability is generally classified as low (<10%), moderate (10-30%), and high (>30%). Higher magnitudes of heritability were observed for harvest index (66.67%), hundred seed weight (59.62%), plant height (59.45), seed yield per hectare (55.94%), seed yield per plant (55.17%), peduncle length (47.1%), for the number of seeds per pod (45.74%), for the number of primary branches per plant (45.1%), and biomass yield per hectare (42.49%). Abbas *et al.* (2018) correspondingly reported higher magnitudes of heritability were observed for the hundred seed weight (97%), plant height (94%), biological yield (89%), pods per plant (83%), harvest index (85%), and seed yield (84%) on mung bean genotypes and which agrees with the earlier reports of (Rohman and Hussain, 2003; Siddique *et al.*, 2006; Idrees *et al.*, 2006) on mung bean.

In the present study, heritability estimates of greater than 30% were recorded for terminal leaf width, peduncle length, plant height, number

of primary branches per plant, seeds per pod, seed yield per plant, hundred seed weight, seed yield per hectare, biomass yield and harvest index. Therefore, these highly heritable traits are expected to remain stable under different environments, as the environment is less influential and could easily be improved through selection pressure. High heritability estimates indicated the variability observed was mainly under genetic control with less environmental influence on the traits. A similar result reported by Singh *et al.* (2014), indicated that there were high heritability values observed for the studied traits, indicating that the variation arises due to additive genetic effect. This is inline with the previous studies on mung bean (Kapoor *et al.*, 2005; Sadiq *et al.*, 2005; Gul *et al.*, 2007; Ahmad *et al.*, 2012; Perera *et al.*, 2017), on black gram (Veerasmani *et al.*, 2005), on chickpea (Arshad *et al.*, 2002; Khan *et al.*, 2005), and on lentil (Neha *et al.*, 2005; Hakim *et al.*, 2006). In general, traits having high heritability estimates were mainly controlled by additive types of genes while those traits with low heritability indicate those characters are highly influenced by environmental effects and governed by the non-additive types of genes.

Though the estimates of high heritability alone will not ensure the amount of gain through selection, rather a heritability estimate with GAM considered together can help to conclude the nature of gene action

governing particular traits. Johnson *et al.* (1955) indicated that the estimates of heritability alone fail to indicate the response to selection. As suggested by Johnson *et al.* (1955), GMA percent was considered as low (<10%), moderate (10-20%), and high (>20%). The estimate of genetic advance as percent of the mean (GMA) at 5% selection intensity ranged from 0.11% (biomass yield per hectare) to 82.14% (harvest index). Heritability alone does not provide a true indication of the genetic potentiality of the genotypes due to interaction between genotype and environment. The selection of traits based on heritability and genetic advance as percent of mean is of great importance to the breeder for making criteria for improvement in a complex character. High genetic advance coupled with high heritability was observed for plant height (29.28% and 59.45%), the number of primary branches per plant (21.93% and 45.1%), hundred seed weight (23.44% and 59.6%), and harvest index (82.14% and 66.67%). Dhunde *et al.* (2021) similarly observed high heritability estimates (52.9%) coupled with high genetic advance as percent of the mean (20.074%) for the trait plant height on thirty-five mung bean genotypes, indicating the impact of additive gene expression and which coincides with the earlier reports by (Jagdhane *et al.*, 2017; Shiv *et al.*, 2017; Ramakrishnan *et al.*, 2018) for the number of primary branches per plant and pods per plant on mung bean. Similarly, Garg *et al.* (2017) observed high heritability and high

genetic advance for plant height, number of branches per plant, pod length, number of seeds per pod, hundred seed weight, and number of pods per plant, biological yield, seed yield, harvest index. Similar results reported by Hemavathy *et al.*, (2015), Pandey *et al.* (2007), Itafa *et al.* (2014), Rao *et al.* (2007), Hari *et al.* (2017) Godakh *et al.* (2013) and Jagdhane *et al.* (2017) for different traits for plant height, seed yield per plant, number of pods per plant, seed yield per plant and harvest index, and biological yield per plant. Also, Jagdhane *et al.* (2017) reported that high heritability (99.00%) coupled with high genetic advance was observed in the biological yield of 20 mung bean genotypes.

High heritability values coupled with high genetic advance as a percent of mean were reported by Ahmad *et al.* (2012) for hundred seed weight, pod length, and pods per plant; by Yusufzai *et al.* (2017) for the number of pods per plant, which coincides with the report by Itafa *et al.* (2014) for seed yield per hectare and pods per plant on mung bean genotypes. Similar results were obtained on black gram genotypes (Sharma *et al.*, 2006; Konda *et al.*, 2009; Balachandran *et al.*, 2010). Likewise, various authors (Nehru *et al.*, 2009; Idahosa *et al.*, 2010; Manggoel *et al.*, 2012; Ajayi *et al.*, 2014) reported high heritability coupled with high GAM for hundred seed weight on cowpea genotypes, indicating that the possibility of direct selection. Similarly, high heritability

with a high genetic advance in percent of mean was observed on soybean genotypes (Jain and Ramgiry, 2000; Mehetre *et al.*, 2000; Agarwal *et al.*, 2001). Likewise, Ansari *et al.* (2004) reported that a high heritability estimate observed on bread wheat genotypes reflects the large heritable variance which may offer the possibility of improvement through direct selection.

In the present study, high heritability along with high genetic advance as percent of mean was observed for some of the traits, indicating the preponderance of additive gene action with low environmental influence for the determination of these traits, and hence simple selection would be more effective for the improvement of these characters. This result is in line with various reports that high heritability estimates along with high genetic advance as a percent of the mean for some of the studied traits on mung bean genotypes (Jain and Ramgiry, 2000; Mehetre *et al.*, 2000; Agarwal *et al.*, 2001; Sultana, 2015), indicating that the traits were controlled by additive genes and direct selection of these characters would be effective. Singh and Rai (1981) suggested that high heritability coupled with high genetic advance is an indicator of a greater proportion of the additive genetic variance and consequently a high genetic gain is expected from the selection. Therefore, the selection of these traits would offer the opportunity for the improvement of seed yield in mung bean. On the contrary, low

heritability coupled with low genetic advances as a percent of mean for days to maturity was noted on mung bean genotypes (Sultana, 2015), which coincides with the work of Nehru *et al.* (1999) who observed low heritability coupled with low genetic advance as a percent of the mean. Low heritability for seed yield was reported by Tickoo and Jain (1988) on mung bean.

High heritability and moderate genetic advance as a percent of mean have been observed for terminal leaf length, terminal leaf width, and peduncle length, the number of seeds per pod, and seed yield per plant indicating equal importance of additive and non-additive gene actions. Therefore, this signifying that selection for the traits could be effective for mung bean improvements since the expression of the trait is governed by additive genes and is less influenced by environmental factors. There is an influence of fixable additive gene effects on the inheritance of these traits, and therefore, selection for these traits might lead to fast-track genetic improvement. This finding is in agreement with the work of Singh *et al.* (2009) in green gram genotypes, who reported that high heritability and moderate genetic advance as a percent of mean for days to 50% flowering and days to maturity on mung bean. Similar observations were reported (Idahosa *et al.*, 2010; Ajayi *et al.*, 2014) on cowpea and Nehru *et al.* (1999) on soybean genotypes.

Moderate heritability coupled with moderate GAM was observed for the number of pods per plant, indicating that traits might be governed by nonadditive gene action and such traits could not be improved through simple or direct selection. Moderate heritability coupled with low GAM was observed for days to flowering, days to maturity, petiole length, and pods per cluster, signifying that the type of gene action that governs the expression of these traits is non-additive gene action, and also the environment had negatively influenced the expression of the traits. This finding is in line with Dhunde *et al.*

(2021) reported moderate heritability coupled with low genetic advance as percent mean for some of the studied traits on thirty-five mung bean genotypes. Similar results were reported in mung bean (Tabasum *et al.*, 2010; Himabindu and RoopaLavanya, 2017; Shiv *et al.*, 2017). In this study high heritability and low GAM estimates were observed for seed yield per hectare and biomass yield per hectare. This finding is in agreement with the report of (Rao *et al.*, 2006; Makeen *et al.*, 2007) on mung bean.

Table 3. Estimates of mean, range, variance components, coefficients of variability, heritability, and genetic advance of the 17 quantitative traits of mung bean at Jinka, in 2018.

Traits	Mean $\pm$ SE	Range	σ^2_n	σ^2_a	σ^2_{nh}	GCV	PCV	H ² b	GA	GAM
DTF	41.68 $\pm$ 0.28	30-47	1.85	6.22	8.07	3.26	6.82	22.92	1.34	3.22
DTM	90.98 $\pm$ 0.39	75-97	3.57	11.06	14.63	2.08	4.20	24.40	1.93	2.12
PTL	8.35 $\pm$ 0.14	4.6-13	0.60	1.67	2.27	9.28	18.04	26.43	0.82	9.84
TLL	5.88 $\pm$ 0.15	3.2-9.8	0.70	1.57	2.26	14.23	25.57	30.97	0.96	16.34
TLW	10.28 $\pm$ 0.14	6.2-15.0	0.90	1.56	2.47	9.23	15.29	36.44	1.18	11.49
PDL	8.35 $\pm$ 0.14	4.6-13.0	1.22	1.37	2.59	13.23	19.27	47.10	1.56	18.73
PHT	37.42 $\pm$ 0.81	18.4-78.2	47.45	32.37	79.82	18.41	23.88	59.45	10.96	29.28
BRN	3.03 $\pm$ 0.0691	2.0-3.0	0.23	0.28	0.51	15.83	23.57	45.10	0.66	21.93
PODL	9.88 $\pm$ 0.17	5.0-13.6	1.04	2.65	3.69	10.32	19.44	28.18	1.12	11.30
PPC	4.15 $\pm$ 0.101	2.0-5.0	0.22	1.20	1.42	11.30	28.71	15.49	0.38	9.18
PPP	19.52 $\pm$ 0.651	9.0-46.0	11.04	38.17	49.20	17.02	35.93	22.44	3.25	16.63
SPP	9.53 $\pm$ 0.161	4.0-13.0	1.45	1.72	3.17	12.64	18.68	45.74	1.68	17.63
SYPP	3.97 $\pm$ 0.06	2.42-5.42	0.16	0.13	0.29	10.08	13.56	55.17	0.61	15.44
HSW	5.25 $\pm$ 0.11	4.14-6.42	0.62	0.42	1.04	14.72	10.06	50.62	1.25	22.44
SYLD	1.24 $\pm$ 0.026	0.81- 1.81	17.81	14.17	31.84	0.34	0.45	55.94	6.51	0.52
BM	0.25 $\pm$ 0.022	0.50- 5.66	12.66	10.40	23.06	0.60	0.42	40.40	1.07	0.14
HI	0.29 $\pm$ 0.005	0.14-0.31	0.02	0.01	0.03	48.77	59.73	66.67	0.24	82.14

DTF=days to flowering, DM= days to maturity, PTL = petiole length (cm), TLL = terminal leaf length (cm), TLW = terminal leaf width (cm), PDL = peduncle length (cm), PHT= plant height (cm), BRN=number of primary branches per plant, PODL = pod length (cm), PPC=number of pods per cluster, PPP=number of pods per plant, SPP= number of seeds per pod, SYPP= seed yield per plant (g), HSW= hundred seed weight (g), SYLD= seed yield (t ha⁻¹), BM= biomass yield (t ha⁻¹), HI=harvest index.

Conclusions

There were significant variations observed among the mung bean genotypes for most of the studied traits. Harvest index was found to be with high estimates of GCV and PCV which indicated the presence of enough variation among the genotypes for this trait. The estimates of variances due to genotypic, phenotypic, and environmental effects for the seventeen characters of mung bean showed wide variation among different traits. A wide range of phenotypic variability was observed among all the traits studied. Maximum genotypic and phenotypic variances (GCV and PCV) was recorded for harvest index (48.77% and 59.73%), whereas lowest for biomass yield per hectare (0.08% and 0.13%) followed by seed yield per hectare (0.34% and 0.45%). Therefore, there is a chance for selection for the majority of the traits in the genotypes. The phenotypic coefficients of variability had higher values as compared to their corresponding genotypic coefficients for all traits, indicating that the environment had a significant role in the expression of traits, which makes the selection for such traits based on the phenotypic variance alone is often misleading.

High estimates of heritability coupled with high genetic advance as a percent of mean were recorded for plant height, the number of primary branches per plant, a hundred seed

weight, and harvest index. Therefore, the presence of high heritability values coupled with high genetic advance as a percent of the mean for these traits suggested that the preponderance of additive gene action with low environmental influence and the improvement of these characters and could be effective through direct phenotypic selection. Thus, this is an opportunity for the improvement of mung bean genotypes. Terminal leaf length, terminal leaf width, peduncle length, plant height, number of primary branches per plant, seed yield per plant, hundred seed weight, seed yield per hectare, biomass yield per hectare, and harvest index showed high heritability values which are believed to be governed by additive gene actions and selection for their improvement could be effective. High heritability coupled with high genetic advance as percent of the mean are attributed to additive gene effect was observed for plant height, hundred seed weight, and harvest index. Hence, high heritability coupled with moderate genetic advance estimates for terminal leaf length, terminal leaf width, peduncle length, the number of seeds per pod, and seed yield per plant and seed yield per hectare.

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Quantitative Traits Diversity in Anchote (*Coccinia abyssinica* (Lam.) Cogn.)) Accessions from Ethiopia

Desta Fekadu Mijena^{1,2}, Sentayehu Alamerew²,
Kibebew Assefa¹, and Mandefro Nigusse³

¹Ethiopian Institute of Agricultural Research, Debre Zeit Center, P.O.Box, 32, Bishoftu, Ethiopia.

²Jimma University, School of Plant Sciences and Horticulture, Department of Plant Breeding and Genetics, P.O.Box 378, Jimma, Ethiopia; ³Ethiopian Institute of Agricultural Research, P.O.Box 2003, Addis Ababa,

Ethiopia; desdar2008@gmail.com

Abstract

Anchote (*Coccinia abyssinica* (Lam.) Cogn.) is an indigenous root crop that used as food and nutritional security and socioeconomically important crop in Ethiopia. Although, the crop has a great potential, lower attention was given by the research and development programs in the country. Even though very few studies have been done regarding the genetic diversity of anchote on a few numbers of accessions, the present study included more accessions from vast production areas of the crop. The present study was conducted to assess the genetic diversity within and among 400 accessions of anchote from Ethiopia using quantitative traits. The field trials were laid out in randomized triple lattice design with three replications. Data on 22 quantitative traits were collected and subjected to analysis of variance and multivariate analysis. Results of the analysis of variance indicated except number of locules per fruit and 6 locules per fruit, all traits showed significant variation ($p \leq 0.01$) among the accessions. Wide ranges have been exhibited among the accessions for all root traits; root number per plant (1-13), root weight per plant (0.02-3.52 kg), total root yield (1.67-293.33 t/ha), root length (6.4-30.08 cm), root width (6.09-33.16 cm) and root dry weight (12.9-55g/100g). Similarly, fruit and seed traits also exhibited wide ranges. Highest positive and significant correlation was resulted between root traits; total root yield ($r=0.37^{**}$, root diameter ($r=0.34^{**}$). Root yield was negatively correlated with seed yield (-0.001) but fruit length was positively correlated with all root traits. The cluster analysis showed the existence of five divergent groups in which they were diverse and varied irrespective of their collection areas. The results of principal component analysis (PCA) indicated that the accessions were grouped into seven components based the evaluated traits, significant (eigen value > 1) and explained 55.08 % of the total variability. The variation exhibited in this experiment could be attributed to environmental and genetic factors. The variability exhibited among anchote germplasm of Ethiopia will be an excellent approach in the screening and selection of promising and contrasting genotypes of anchote in future works.

Keywords: Anchote, Ethiopia, quantitative traits, indigenous, root crop

Introduction

Anchote [(*Coccinia abyssinica* (Lam.) Cogn.] an indigenous, perennial underutilized vine crop in Ethiopia. It is a multi-species crop that belongs to the genus *Coccinia* and family *Cucurbitaceae*. The genus *Coccinia* comprises 27 species, all of which are confined to sub-Saharan Africa where it is diversified into various habitat types (Demissie et al., 1996). A total of eight species of *Coccinia* are found in Ethiopia (Abera et al. 1995). Among these species, *C. abyssinica* is the only species cultivated for its edible tuberous roots and the young shoots used as leaf vegetables (Abera et al. 1995).

The name ‘anchote’ is derived from native language of Oromo, Afan Oromo in Ethiopia, and refers to the edible tuber of the cultivated races of *Coccinia abyssinica*.

It is also known by different vernacular names at different places and tribe such as anchote in Wollega, Jimma, Iluababor, Buno Bedelle, and Benishangul Gumuz, ‘*Yeamora misa*’ in Gonder, Gojam, Wollo, and central Ethiopia, ‘Ushushe’ in Walaita, ‘Shushe/ Ashushe’ in Dawero, ‘Ajo’ in Kaffa, ‘Wechecho’ in Tigray (Amsalu et al., 2008; Desta, 2011; Abera, 1995; Amare, 1974b; Habtamu and Kelbessa, 1997; Demel et al., 2010).

However, its cultivation as a root crop is common in Wollega, Iluababor, Jimma, Kaffa, and Sidama (Amare, 1973 and Desta et al., 2021), it is not

well known by other parts of Ethiopia and the world. It is mainly grown for its storage root yield even though its young leaf and immature fruit also used as a side dish in western Ethiopia. Anchote is a very important crop due to its economic, food, feed, income, medicinal and socio-cultural values (Abdisa, 2000; Abera, 1995). It is a good source of vitamins, minerals, protein, carbohydrate, and calcium compared to other root crops and can be used as a strategic crop to alleviate protein deficiency in areas of nutrition with low protein sources (Amsalu et al., 2008). Tubers of anchote are boiled and prepared with local butter and served with ‘*injera*’ during special ceremonies like wedding, betrothals, circumcision, birthdays, the Finding of the True Cross ‘*Meskel*’ and New Year holidays. Tubers of wild anchote are not edible although widely used for animal fattening in West Wollega areas (Abera, 1995; Desta et al.; 2021). Ethiopian traditional medicinal practitioners use anchote to treat different type of diseases such as diabetes, gonorrhea, tuberculosis, asthma, cancer, and cholesterol lowering (Amare, 1985).

In spite of its importance as food and nutritional security crop, the genetic diversity based on morphological, biochemical and molecular level on anchote germplasm collected from all producing areas of Ethiopia were not studied.

Study on the patterns of genetic variability among and within

populations is a valuable tool that may help to develop conservation strategy and future breeding programs. Genetic diversity assessment has potential uses in evolution, breeding and conservation of genetic resources. Genetic diversity based on morphological characters is therefore the backbone of classification, conservation and genetic improvement of the crop for both present and future use.

According to Din *et al.* (2010) scientific classification of the plant still relies on quantitative traits, this technique is much easier, cost effective, simple to score, requires less time and no need of any technical knowledge (Tewodros, 2016). Besides, it is also powerful taxonomic tool and has been utilized for the preliminary grouping of landraces prior to their characterization using more precise marker technologies.

Therefore, the aim of this study is to investigate the extent and pattern of diversity within and among 400 accessions of anchote using agro-morphological quantitative traits.

Materials and Methods

Plant material

Four-hundred anchote seed accessions were collected from western and south western and north western Ethiopia, ten administrative zones (East Wollega, West Wollega, Kelem Wollega, Horro Guduru Wollega, Buno Bedelle, Iluababor, Jimma, Bench Maji, West Shewa and Hulet Ej Enese; 40 woredas and 127 kebeles from the altitude range of 1412 to 3025 m above sea level (Figure 1 and Appendix Table 1). The seeds were collected from women farmers across the collection areas, as they are the sole responsible for the seed maintenance.

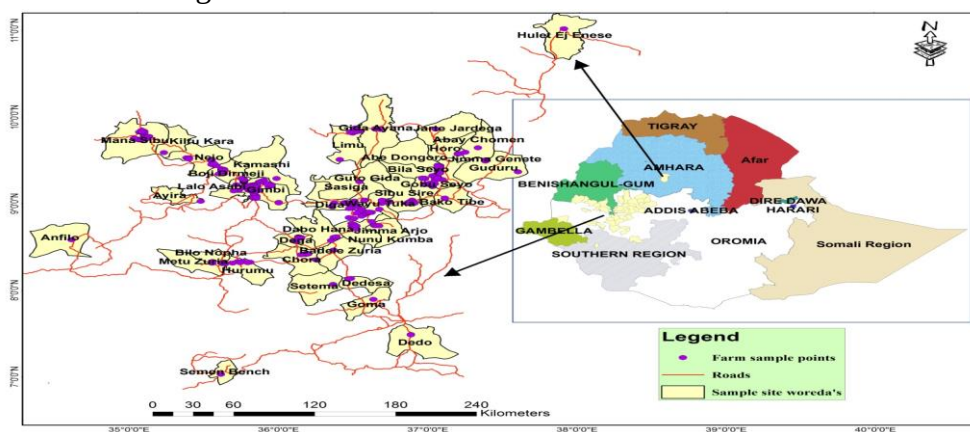


Figure 1. Anchote accessions collection areas from different producing areas of Ethiopia

Study site

The study was conducted at the research site of Debre Zeit Agriculture

Research Centre (DZARC), Bishoftu during the off-seasons of 2017 and 2018 by using irrigation. DZARC is located at latitude 08°44' N and

longitude of 38°58' E, with an altitude of 1860 meters above sea level (*m.a.s.l.*). The area receives mean annual rainfall of 851 mm with mean minimum and maximum temperature of 8.9°C and 24.3°C, respectively and the soil at the site is the vertisols, heavy black (DZARC, 2008 and Desta *et al.*, 2011).

Experimental design

The field trials were laid out in randomized triple lattice design with three replications (Patterson and Williams, 1976), four ridges per plot with spacing of 0.6 m between rows and 0.2 m between plants, and ten plants per ridge. Anchote accessions were randomly distributed in twenty blocks in each replication. Planting was carried out at off season, in March and harvested in July, using seeds in a single row on the ridge. All the recommended cultivation practices for anchote such as weeding, watering and fertilizer application rates were followed.

Data collection and analysis

Morphological quantitative traits of all the 400 accessions were scored using CIP-standard descriptors of sweet potato (Hijmans, 1991), report of a Working Group on Cucurbits (ECPGR, 2010), minimum descriptors for *Cucurbita* spp., cucumber, melon and watermelon (ECPGR, 2008), descriptors for melon (IPGRI. 2003), and morphological and agronomic descriptors for the of cassava (Fukuda *et al.*, 1998).

A total of 22 quantitative; 16 aerial and 6 storage root characters were evaluated for each accession (Table 2). Data recorded for aerial parts were average expressions of characters of 10 sample plants for each trait. Storage root descriptors were recorded considering the most representative expression of the character shown in medium-to large sized storage roots of ten plants. Data analysis was made with SAS 9.3.1 software (SAS Institute, 2000).

Table 2. Morphological quantitative traits measured in 400 anchote accessions

Trait	Code	Description
Number of root per plant	RNPP	The clustered number of roots per plant were counted for 10 plants
Root weight per plant (kg)	RWPP	10 sampled roots was measured using a sensitive balance (BP 16000-S) and the average was recorded
Total root yield (t/ha)	RYLD	Total weight from 24 plants from the middle three rows
Root length(cm)	RL	10 sampled roots measured using ruler
Root diameter(cm)	RD	10 sampled roots measured using caliper
Root dry matter (%)	RDWT	The dry weight of 100g fresh root after oven dried at 105 °C for 24 hours
Fruit length(cm)	FL	Length of the fruit measured for 10 samples from top to bottom using ruler
Fruit diameter (cm)	FD	Width of the 10 sampled fruit is measured using a caliper
Number of strip lines on fruit surface	NST	The strip lines on the surface were counted from 10 sampled fruits
Number of locules per fruit	NLF	10 sampled fruits were cut longitudinally and the locules extracted and counted
Number of seeds per fruit	NSPF	After cutting the fruit longitudinally the seeds were extracted, washed and counted
Number of seeds per plant	NSPL	Number of seeds were counted from all the fruits of 10 sampled plants
Fruit weight (g)	FW	10 sampled fruits were weighed using a sensitive balance
Thousand seed weight (g)	THSW	1000 seeds counted and weighed using a sensitive balance
Vine length(cm)	VL	Vines of 10 sampled plants measured using ruler
Seed yield(kg)	SYD	Seed yield per plant(kg)
Flower length and width(cm)	FLOL, FLOW	Flower size measured for 10 sample flowers using ruler
Number of sepal and petal	NSE, NPE	Counted from the flowers
Petiole length(cm)	PL	Petiole length measured for 10 sample leaves using ruler
Days to maturity	DM	Days to maturity recorded when > 90% of the leaves turned yellow

Results and Discussion

Significant variability within and among the 400 anchote accessions have been observed. The comparison of range, standard deviation, and mean showed variations among accessions for all traits except the number of locules per fruit which is the same, 6 per fruit, for all accessions. The storage root traits with sufficient discriminative power to differentiate the accessions were identified based on their significant p-value ($P < 0.001$). Wider ranges among traits have been exhibited for all root traits

(root number per plant, root weight per plant, root yield, root length, root diameter, root dry weight), fruit and seed traits (number of seeds per locule, number of seeds per fruit, fruit weight, thousand seed weight, seed yield per plant), and vine length. The average root yield of anchote was 60.11 tones per hectare (Table 3). As the yield and yield related traits are controlled by a set of genes, besides being influenced by environmental factors, which justifies their high amplitude, confirms the degree of difference among anchote accessions of Ethiopia which may implicate the potential for selection and other improvement

methods. Similar findings were reported on 202 anchote accessions collected from western and south western Ethiopia by Bekele *et al.*

(2017), and Desta *et al.*, (2011) on 36 anchote accessions.

Table 3. Variance analysis of 22 quantitative traits of 400 anchote accessions

Traits	CV (%)	Mean + SE	Range	Traits	CV (%)	Mean + SE	Range
RNPP	48.82	3.00(1.60)	1.00-13.00	NSPF	31.88	103.04(34.22)	26.60-1094.00
RWPP	41.71	0.72(0.34)	0.02-3.52	FW	21.70	330.33(73.26)	107.18-678.20
RYLD	41.71	60.11(28.39)	1.67-293.33	THSW	19.39	43.53(11.00)	10.80-71.20
RL	18.08	11.11(2.22)	6.40-30.08	SYD	51.77	441.07(264.35)	18.50-1520.00
RW	18.46	11.12(2.26)	6.09-33.16	VL	29.09	2.61(0.77)	0.50-5.20
RDWT	10.61	32.78(8.48)	12.90-55.00	FLOL	20.35	2.05(0.44)	1.00-5.33
FL	25.00	5.33(0.89)	2.80-9.40	FLOW	26.84	2.18(0.62)	1.00-9.17
FW	16.14	4.09(0.45)	2.80-7.00	NSE	5.13	4.98(0.26)	3.67-6.00
NST	6.48	8.88(0.59)	6.40-10.80	NPE	3.54	5.01(0.18)	3.33-6.00
NLF	0.00	6.00(0.00)	6.00-6.00	PL	17.60	3.00(0.55)	1.00-5.40
NSPL	19.97	18.27(3.69)	6.40-73.60	DM	10.51	129.34(15.68)	95.00-155.00

Key: RNPP- Root number per plant, RWPP- Root weight per plant(kg), RYLD- Total Root yield(t/ha), RL- Root length(cm), RD- Root diameter(cm), RDWT -Root dry weight(g), FRL- Fruit length(cm), FRD- Fruit diameter(cm),NST- Number of strips on fruit surface, NLF- Number of locules per fruit, NSPL- Number of seeds per locule, NSPF- Number of seed per fruit, FW- Fruit weight(g), THSW- Thousand seed weight(g), SYD- Seed yield per plant(g), VL- Vine length(m), FLOL- Flower length(mm), FLOW- Flower width(mm), NSE- Number of sepals, NPE- Number of petals, PL- Petiole length, DM- Days to maturity

The correlation coefficient between quantitative characters of accessions of anchote is presented in table 4. Correlation coefficients show strong relationships between some quantitative traits, while some traits have no relationship at all or are negatively related with one another. The highest positive and significant correlation is shown by correlation between root weight per plant and root yield ($r = 0.99^{**}$) and root length with root diameter (0.74^{**}) followed by root number per plant with root weight per plant (0.44^{**}), root yield (0.44^{**}), root length (0.38^{**}), and root diameter (0.43^{**}). The root yield was

negatively correlated with the seed yield (-0.001) but positively with root length (0.45^{**}) and root diameter (0.58^{**}), may be due to the competition for accumulation of assimilates between the roots and the seeds. The fruit length was positively correlated with most root traits; root number per plant (0.21^{**}), root weight per plant (0.37^{**}), total root yield (0.37^{**}), root length (0.19^{**}), and root diameter (0.34^{**}). Similar findings were reported by Desta *et al.*, 2011; Bekele *et al.*, 2017, Hassen *et al.*, 2013 on anchote accessions.

Table 4 . Correlation coefficients

	RN PP	RWPP	YLD	RL	RD	FRL	FRD	DWT	NST	NSPL	NSPF	FW	THSW	SYD	VL	FLOL	FLOW	NSE	NPE	PL	DM
RNPP		0.44**	0.44**	0.38**	0.43**	0.21**	0.01	0.02	0.03	-0.02	-0.00	0.02	0.22	0.04	0.01	0.01	0.01	0.01	0.02	-0.03	-0.02
RWPP			0.99**	0.45**	0.57**	0.37**	0.001	0.01	0.02	0.02	0.02	0.01	0.01	0.002	-0.03	0.02	0.03	0.01	0.02	0.02	-0.02
YLD				0.45**	0.58**	0.37**	-0.001	0.01	0.01	0.01	0.02	0.01	0.01	-0.001	0.03	0.02	0.02	0.01	0.02	0.02	-0.02
RL					0.74**	0.19**	0.01	0.01	-0.01	-0.01	-0.03	-0.04	0.01	-0.02	0.04	0.02	-0.002	0.01	0.02	0.01	-0.04*
RD						0.34**	0.02	0.001	-0.002	0.01	-0.01	-0.01	0.01	-0.03	0.03	0.02	0.002	0.004	0.01	0.01	0.03
FRL							0.004	0.01	-0.001	0.01	0.01	0.01	0.002	-0.02	-0.01	0.01	0.001	-0.03	-0.01	0.01	0.03
FRD								0.37**	0.28**	0.25**	0.31**	0.31**	-0.03	0.04*	0.01	0.001	-0.02	0.02	-0.04	0.003	-0.02
DWT									0.21**	0.21**	0.35**	0.35**	0.04	0.08*	0.03	0.06**	0.03	0.02	-0.02	-0.02	-0.04
NST										0.15**	0.11**	0.16**	0.01	0.03	0.03	0.01	0.04	-0.05	-0.01	0.02	-0.02
NSPL											0.24**	0.26**	0.01	0.03	0.03	0.03*	0.03	0.03	-0.02*	-0.02	0.01
NSPF												0.18**	0.01	0.002	-0.002	0.01	0.02	0.04	-0.02	-0.01	0.01
FW													0.003	0.04	0.002	0.05*	0.02	0.01	0.001	-0.03	-0.03
THSW														0.17**	-0.014	-0.001	-0.02	0.01	0.04	-0.06**	-0.01
SYD															-0.015	0.01	0.04	0.02	-0.01	-0.07**	0.04
VL																0.07**	0.02	0.07**	0.04*	-0.01	0.06*
FLOL																	0.47**	-0.06	-0.03	0.03*	-0.04*
FLOW																		-0.06*	-0.06*	0.01	-0.08**
NSE																			0.04*	-0.01	0.03
NSP																				0.01	0.03
PL																					-0.06**
DM																					

Key: RNPP- Root number per plant, RWPP- Root weight per plant(kg), RYLD- Total Root yield(t/ha), RL- Root length(cm), RD- Root diameter(cm), RDWT -Root dry weight(g), FRL- Fruit length(cm), FRD- Fruit diameter(cm),NST- Number of strips on fruit surface, NLF- Number of locules per fruit, NSPL- Number of seeds per locule, NSPF- Number of seed per fruit, FW- Fruit weight(g), THSW- Thousand seed weight(g), SYD- Seed yield per plant(g), VL- Vine length(m), FLOL- Flowerlength(mm), FLOW- Flower width(mm), NSE- Number of sepals, NPE- Number of petals, PL- Petiole length, DM- Days to maturity

The number of clusters determined based on the pseudo-F and t^2 values, such that the pseudo-F reaches its pick and at the same time, it is larger than values before and after it in the list, while the pseudo t^2 is being at its minimum then followed by large numbers. Thus, cluster analysis grouped the 400 anchote accessions based on their similarity in to five different groups with different sizes based on 22 quantitative traits (Figure 2). The number of accessions grouped

into each cluster was diverse and varied irrespective of their collection areas from 152 in cluster I to 16 in cluster V. This result agrees with Bekele *et al.* 2017 for 202 anchote accessions collected from mostly western Ethiopia and planted at Holeta. Cluster I was the largest and consisted 152 (38%) of the total accessions and cluster IV and III were consisted 114 (28.5%) and 90(22.5%) respectively (Table 5).

Table 5. Distribution of 400 anchote accessions into 5 clusters based on quantitative traits.

Clusters	No. of accessions in each cluster	Accession numbers	Contribution in %
I	152	1,2,3,11,19,21,26,27,28,30,41,45,46,47,49,50,51,54,57,58,65,67,68,73,74,79,81,83,85,89,92,93,100,101,102,103,104,109,110,112,113,114,119,120,121,123,124,125,127,130,132,133,134,136,137,140,141,146,147,153,154,155,159,160,162,163,166,168,169,170,172,173,176,177,178,180,182,184,188,193,194,195,199,201,205,206,207,209,210,211,213,214,215,216,224,227,231,236,237,246,250,251,257,258,260,261,262,265,270,271,273,274,276,279,280,283,287,291,293,297,298,299,304,305,314,316,318,319,321,323,324,325,329,335,339,345,348,349,350,351,353,364,371,375,380,381,385,386,394,395,397,399	38.00
II	28	94,150,151,158,233,242,249,253,254,255,272,284,296,346,354,356,358,360,365,366,367,370,372,373,388,390,392,393	7.00
III	90	36,38,40,42,43,48,52,66,84,86,87,88,90,91,92,95,96,97,98,99,116,128,129,131,139,142,143,144,145,148,149,152,156,157,165,167,179,185,191,196,198,200,217,229,230,234,235,238,239,240,241,244,245,247,248,252,256,259,263,264,266,267,268,269,275,281,282,289,290,300,302,336,337,338,342,344,347,352,355,357,359,363,368,369,382,383,384,387,391,396,400	22.50
IV	114	4,5,6,7,8,9,10,12,13,14,15,16,17,18,20,22,24,25,29,31,32,33,34,35,37,44,53,56,59,61,62,63,64,69,70,71,72,75,76,77,78,80,82,105,106,107,108,111,115,117,118,122,126,135,161,164,171,174,175,181,183,187,189,190,192,197,202,203,204,208,212,218,219,220,221,222,223,225,226,277,278,285,286,288,294,295,301,303,306,307,308,309,310,311,312,313,315,317,320,322,326,327,328,330,332,333,334,340,343,374,376,377,378,379	28.50
V	16	341,401,402,403,404,405,406,407,408,409,410,411,412,413,415,416	4.00

Table 6. Membership of ten administrative zones of anchote accessions' origin in five clusters

Administrative zones	Clusters					Sub Total
	I	II	III	IV	V	
Buno Bedelle	12	5	6	5	1	29
East Wollega	53	6	29	56	11	155
Horro Guduru Wollega	2	3	6	5	4	20
Iluababor	2	9	9	-	-	20
Kelem Wollega	2	-	-	-	-	2
West Wollega	78	7	34	46	-	165
Jimma	-	1	2	2	-	5
Kaffa	-	-	1	-	-	1
West Shewa	-	-	2	-	-	2
Gojam	-	-	1	-	-	1
Total						400

Regarding the share of the collection sites with administrative zones, East Wollega and West Wollega contributed 39 % and 41.25% respectively as both administrative zones were the major producing areas than the remaining collection areas (Table 6).

The cluster means of 22 quantitative characters based on the five clusters showed that cluster I had the highest value in most of the characters that considered in this study; root number and weight per plant, total root yield,

root length, fruit length, number of seeds per locule, thousand seed weight and petiole length. Cluster II showed high performance in number of seeds per fruit, vine length, and flower sizes while cluster III was good in fruit diameter and number of strip lines on the fruit surface and the early days to maturing. Cluster IV was better only in root diameter while cluster VI showed highest fruit diameter, root dry weight, number of seeds per fruit, fruit weight, seed yield per plant, sepal and petal number, and days to maturity (Table 7).

Table 7: Cluster mean and standard deviation for morphological quantitative traits of 400 anchote accessions grown at DZARC

Clusters		Variables																					
		rnpp	rwpp	tyld	rl	rd	frl	frd	dwt	nst	nlf	nspl	nspl	fw	thsw	syd	vl	fjol	flow	nse	nse	pl	dm
I	Mean	2.97	0.72	59.19	11.14	10.79	32.51	5.41	4.07	8.76	6.02	18.30	101.19	326.30	46.17	448.58	2.70	1.93	2.07	5.01	5.01	3.0	134.40
	Stdev.	1.76	0.44	35.97	4.71	1.69	8.45	1.47	0.46	0.72	0.00	5.60	20.59	79.05	28.78	272.39	0.83	0.34	0.55	0.43	0.20	0.62	14.11
II	Mean	2.96	0.70	58.45	10.31	10.42	29.94	5.46	4.05	8.89	6.00	18.14	103.21	326.19	43.86	516.65	2.85	1.98	2.15	5.04	5.05	2.94	134.11
	Stdev.	1.35	0.37	30.94	2.04	2.17	10.93	0.81	0.45	0.52	0.00	2.56	19.28	71.30	9.90	280.71	0.69	0.40	0.51	0.33	0.15	0.93	15.99
III	Mean	2.95	0.65	53.87	11.05	11.08	30.76	5.55	4.12	8.91	6.00	17.76	102.35	328.87	45.50	498.89	2.82	1.94	1.99	5.04	5.04	2.96	130.55
	Stdev.	1.47	0.26	21.47	2.70	2.90	8.34	1.09	0.59	0.55	0.00	2.97	21.61	75.10	10.60	258.44	0.72	0.34	0.50	0.32	0.28	0.43	15.08
IV	Mean	2.69	0.67	56.16	11.12	11.24	30.66	5.28	4.05	8.76	6.00	18.04	99.81	317.21	41.02	356.85	2.73	1.91	2.07	5.00	5.04	2.92	135.72
	Stdev.	1.51	0.31	26.12	2.76	2.93	7.90	0.82	0.45	0.71	0.00	3.47	20.88	63.02	11.01	222.23	0.80	0.33	0.50	0.28	0.24	0.56	15.38
V	Mean	2.88	0.61	50.42	10.53	10.56	33.14	5.58	4.13	8.88	6.00	17.29	109.70	372.99	41.36	585.28	2.38	1.76	2.12	5.10	5.06	2.53	140.94
	Stdev.	1.78	0.18	15.05	1.33	1.44	9.89	1.25	0.41	0.57	0.00	3.36	19.57	92.90	9.37	319.20	0.77	0.28	0.57	0.38	0.25	0.72	11.58

Key: RNPP- Root number per plant, RWPP- Root weight per plant(kg), RYLD- Total Root yield(t/ha), RL- Root length(cm), RD- Root diameter(cm), RDWT- Root dry weight(g), FRL- Fruit length(cm), FRD- Fruit diameter(cm), NST- Number of strips on fruit surface, NLF- Number of locules per fruit, NSPL- Number of seeds per locule, NSPF- Number of seed per fruit, FW- Fruit weight(g), THSW- Thousand seed weight(g), SYD- Seed yield per plant(g), VL- Vine length(m), FJOL- Flower length(mm), FLOW- Flower width(mm), NSE- Number of sepals, NPE- Number of petals, PL- Petiole length, DM- Days to maturity

Cluster II showed high performance in number of seeds per fruit, vine length, and flower sizes while cluster III was good in fruit diameter and number of strip lines on the fruit surface and the early days to maturing. Cluster IV was better only in root diameter.

Cluster VI showed highest fruit diameter, root dry weight, number of seeds per fruit, fruit weight, seed yield per plant, sepal and petal number, and days to maturity.

The results of principal component analysis (PC) in this study reduced the observed characters to seven principal components with eigen value that were greater than 1.0 and explained the diversity among 22 traits of 400 anchote accessions tested for 55.08% (Table 8). On the loading plots the traits' relationships (Figure 3) the first PC resulted mainly from variations in root number per plant, seed yield, fruit diameter, root diameter, root length, thousand seed weight, root weight per plant and number of sepals, while the second PC was based on variations in number of seeds per fruit, flower length, fruit length, flower width, and number of strips on the fruit. The present result agrees with similar works on anchote germplasm by Bekele *et al.*, 2017 and Desta *et al.*, 2011. The principal components, PC1 to PC7 accounted for 16.52%, 10.44%, 7.18%, 5.85%, 5.38%, 4.93% and 4.77% of total variation respectively. Root traits; root number per plant, root weight per plant and

total root yield contributed positively across all the principal components. The quantitative traits that contributed more positively to PC1 were root number per plant, root weight per plant, fruit diameter, number of locules per fruit, thousand seed weight, vine length, flower length, and days to maturity, while the remaining 13 traits were negatively associated with PC1. All root traits except root diameter, root dry weight, fruit weight, number of sepals, number of petals and petiole length have positive contribution to PC2, whereas the rest of traits were negatively associated. PC3 exhibited positive association with all root traits, fruit length, number of strips per fruit, number of seeds per fruit and plant, thousand seed weight, flower width, number of sepals and number of petals while the remaining traits were negatively associated. All root traits except the root yield exhibited positive contribution to PC4. Root number and weight per plant, root length and diameter, fruit length, number of strips on fruit surface, number of seeds per fruit and plant, thousand seed weight, sepal and petal number, and petiole length traits were positively associated to PC5. All root traits except root length, fruit length and diameter, root dry weight, number of locules, seed yield per plant, and vine length contributed positively to PC6 and all the traits except total root yield, seed yield per plant and flower length in PC7 had positive contribution.

Table 8. Variant component scores of 22 traits of the first seven principal components for 400 anchote accessions

Variables	PC1	PC2	PC3	PC4	PC5	PC6	PC7
Root no./plant	0.3342	0.4758	0.4768	0.3835	0.442	0.2988	0.0163
Root weight/plant	0.4543	0.4645	0.3308	0.3889	0.3125	0.4346	0.0962
Root yield(t/ha)	-0.1118	0.6586	0.6699	-0.1902	-0.1309	0.0822	-0.1731
Root length(cm)	-0.1176	0.5795	0.6006	0.1541	0.1273	-0.4014	0.2002
Root diameter(cm)	-0.2584	-0.2258	0.6182	0.1523	0.4462	0.2681	0.3866
Fruit length(cm)	-0.1969	-0.2364	0.2092	0.2135	0.5488	0.4126	-0.4785
Fruit diameter(cm)	0.4448	-0.2084	-0.3531	0.3017	-0.5688	0.202	0.3352
Root dry weight(g)	-0.2345	0.2176	0.3917	-0.2382	-0.2459	0.4714	0.3556
Number of strips on fruit surface	-0.1648	-0.1704	0.3149	0.2241	0.2079	-0.5035	0.6268
Number of locules per fruit	0.2222	-0.1959	-0.1945	-0.2734	-0.4986	0.2398	0.5238
Number of seed per locule	-0.2564	-0.2561	0.4499	0.2928	0.3117	-0.3209	0.3217
Number of seed per fruit	-0.6494	-0.1831	0.3736	0.1916	0.2143	-0.3022	0.2237
Fruit weight(g)	-0.2388	0.2179	-0.2729	0.491	-0.5635	-0.2202	0.2918
Thousand seed weight(g)	0.2555	-0.1408	0.3205	-0.7219	0.4791	-0.1286	0.1287
Seed yield per plant	-0.3099	-0.2465	-0.2471	0.6596	-0.2145	0.2035	-0.2323
Vine length(cm)	0.4878	-0.2772	-0.2699	0.3527	-0.3573	0.2323	0.4649
Flower length(cm)	0.5991	-0.2266	-0.1787	-0.1787	0.4434	-0.2538	-0.4506
Flower width(cm)	-0.1396	-0.1277	0.5962	-0.6457	-0.1221	-0.2416	0.2169
Number of sepals	-0.0727	0.0526	0.0687	0.0792	0.0685	-0.6868	0.6924
Number of petals	0.0585	0.0459	0.6262	-0.7609	0.1431	-0.0249	0.02915
Petiole length(cm)	0.0025	0.7054	-0.7087	-0.0053	0.0075	-0.0021	0.0032
Days to maturity	1	0	0	0	0	0	0
Eigenvalue	3.4691	2.1929	1.5072	1.2288	1.1304	1.0353	1.0019
Prportion (%)	16.52	10.44	7.18	5.85	5.38	4.93	4.77
Cumulative (%)	16.52	26.96	34.14	39.99	45.37	50.3	55.08

The first two PCs were plotted to observe the relationship between 400 accessions of anchote based on 22 traits (Fig. 3) as similarly reported by Bekele *et al.*, 2017 and Wondimu *et al.*, (2014) in anchote accessions and Tairo *et al.* (2008); Afuape *et al.* (2011) and Ravishanker *et al.*, (2013) in sweet potato genotypes.

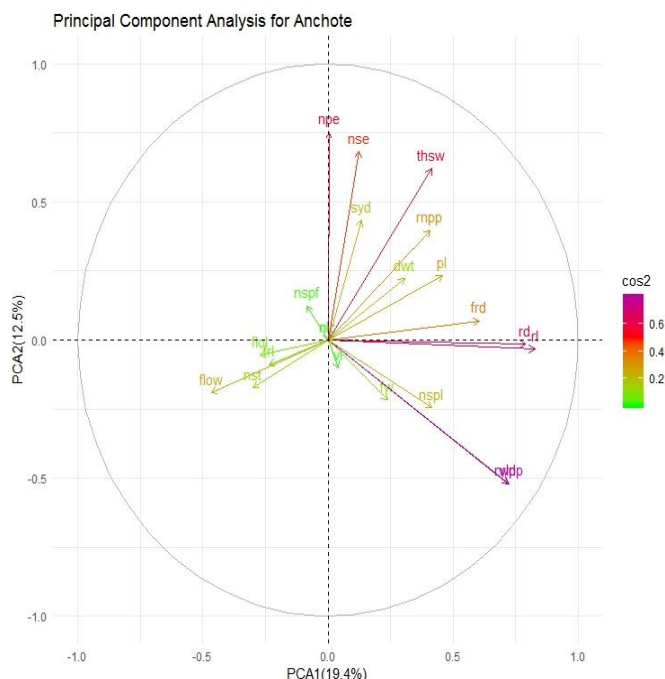


Figure 3. Scattered diagram of first two principal components based on mean values of 22 quantitative traits and anchote accessions

The projection of component traits on PC 1 and PC 2 revealed that the number of tubers per plant, root dry weight (g), root diameter (cm), root length(cm), fruit diameter(cm), fruit weight(g), seed yield per plant(g), root weight per plant(kg) and thousand seed weight(g) are positively associated with total root yield. In contrast flower length and width, number of strips of the fruit surface, and fruit length were associated negatively and not important to be considered in morphological diversity studies. The dissimilarity coefficient of genotypes ranged from 1.49 to 155.64, showed a wider considerable variability among the anchote accessions. Depending on the above facts and figures, the evaluated anchote accessions have showed wider genetic base. From all the characters,

root weight per plant, root length, fruit diameter, number of seeds per fruit, vine length, and flower length were found to be the most discriminative parameters differentiating accessions collected from different parts of Ethiopia. Thus, the given technique of analysis could be helpful to select diverse parents and helps to widen the gene-pool of anchote in future breeding programs.

Conclusion and Recommendation

Identifying the quantitative diversity among the accessions of anchote helps to promote research and development of the crop. The result of analysis of variance indicated significant variations among the 400 anchote

accessions for all the root, fruit and seed traits, and vine length from the 22 quantitative parameters.

136 accessions from the 400 tested in this study were the most yielders with more than the average root yield; 60.11 tones/hectare of which accessions; 117, 147, 161, 175, 262, 267, 301, 310, 326, 349, 367, 368, 370, 374, 375, 377, 388, 393 and 407, were the top 20. In contrary, accessions 285, 150, 280, 261, 31, 49, 155, 7, 25, and 11 were the top lowest yields.

The yielding potential variability showed a high genetic diversity of anchote germplasm in Ethiopia and this work proved to be an excellent approach in the screening and selection of promising and contrasting genotypes of anchote. Genetic resources of anchote revealed in this study represent a valuable asset for the breeding programs of the crop. The variations among the tested 400 anchote accessions could be due to genotype, geographical sources and agronomic practices.

The highest correlation coefficient has been exhibited between root weight per plant and root yield ($r = 0.99^{**}$) and root length with root diameter (0.74^{**}) and the root yield was negatively correlated with the seed yield (-0.001) but positively with root length (0.45^{**}) and root diameter (0.58^{**}). The fruit length was positively correlated with most root traits; root number per plant, root weight per plant, total root yield, root length, and root diameter. The cluster analysis of

quantitative traits revealed the existence of five divergent groups with, 89% of the accessions represented by clusters I, III and IV, regardless of the geographical locations where the accessions were collected.

All the variables were grouped in seven principal components of which root and fruit traits were significant (Eigen value > 1) explaining 55.08% of the total variability. The variation is attributed to genetic and environmental factors. The results obtained from this study confirmed the existence of variability among the accessions which indicates huge potentials for selection and crossing of superior anchote genotypes for yield and yield related traits. What are your future directions.

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Appendix

Table 1. List of 400 anchote accessions with their areas of collection

Accession no.	Zone	Woreda	Kebele	Longitude	Latitude	Altitude
001/09	E.W	Sibu Sire	Sire 01	9°02'29.46"N	36°52'15.02"E	1834
002/09	E.W	Sibu Sire	Burka Talo	9°01'49.00"N	36°50'52.04"E	1791
003/09	E.W	Wayu Tuka	Wara Babbo Migna	9°03'52.98"N	36°52'05.77"E	1889
004/09	E.W	Wayu Tuka	Wara Babbo Migna	9°03'37.54"N	36°52'34.88"E	1840
005/09	E.W	Wayu Tuka	Wara Babbo Migna	9°03'47.65"N	36°52'56.35"E	1877
006/09	E.W	Wayu Tuka	Kura Migna	9°02'29.71"N	36°51'00.51"E	1825
007/09	E.W	Wayu Tuka	Kura Migna	9°01'52.93"N	36°51'01.64"E	1799
008/09	E.W	Wayu Tuka	Kura Migna	9°02'15.02"N	36°51'10.74"E	1830
009/09	E.W	Chingi	MajaAle	9°02'43.31"N	36°43'10.25"E	1823
010/09	E.W	Wayu Tuka	Gute	9°02'04.84"N	36°40'22.64"E	1884
011/09	E.W	Chingi	Gobu	9°02'55.33"N	36°43'18.10"E	1843
012/09	E.W	Chingi	Gordommo/Gaba Sanbata	9°02'33.16"N	36°43'13.09"E	1797
013/09	E.W	Chingi	Ale Gordomo	9°02'27.23"N	36°42'23.13"E	1735
014/09	E.W	Chingi	Gordommo	9°03'06.28"N	36°42'10.24"E	1935
015/09	E.W	Chingi	Ebicha	9°01'54.27"N	36°40'49.14"E	1863
016/09	E.W	Chingi	Jarte/Birbo Gibbi	9°01'55.46"N	36°40'40.97"E	1857
017/09	E.W	Ukke	Adu Bukke	9°30'39.23"N	36°33'28.60"E	1439
018/09	E.W	Ukke	Chari	9°30'18.64"N	36°33'27.18"E	1412
019/09	E.W	Leka Dullecha	Ale Qawusa	9°16'36.62"N	36°31'31.19"E	1435
020/09	E.W	Leka Dullecha	Ale Qawusa	9°02'25.94"N	36°29'12.92"E	2222

021/09	E.W	Digga	Demeksa	9°01'20.43"N	36°27'10.81"E	2178
022/09	E.W	Digga	Demeksa	9°01'19.32"N	36°26'59.71"E	2192
023/09	E.W	Digga	Geracho	9°02'03.81"N	36°26'53.86"E	2203
024/09	E.W	Leka Dullecha	Horda Qawusa	9°01'47.65"N	36°25'39.68"E	2110
025/09	E.W	Leka Dullecha	Horda Qawusa	9°01'58.86"N	36°25'38.05"E	2090
026/09	E.W	Leka Dullecha	Horda Qawusa	9°01'59.79"N	36°25'21.80"E	2064
027/09	E.W	Leka Dullecha	Gatama 01	8°53'54.90"N	36°29'07.96"E	2170
028/09	E.W	Leka Dullecha	Horda Qawusa	9°01'28.09"N	36°25'29.94"E	2114
029/09	E.W	Leka Dullecha	Horda Qawusa	9°01'46.27"N	36°25'06.82"E	2103
030/09	E.W	Leka Dullecha	Horda Qawusa	9°01'59.35"N	36°25'20.75"E	2065
031/09	E.W	Leka Dullecha	Horda Qawusa	9°01'56.76"N	36°25'10.01"E	2078
032/09	E.W	Leka Dullecha	Horda Qawusa	9°02'01.91"N	36°25'20.10"E	2056
033/09	E.W	Leka Dullecha	Horda Qawusa	9°01'57.79"N	36°25'05.08"E	2079
034/09	E.W	Leka Dullecha	Geracho	9°01'40.61"N	36°26'04.45"E	2153
035/09	E.W	Leka Dullecha	Horda Qawusa	9°00'05.95"N	36°29'13.56"E	2244
036/09	E.W	Leka Dullecha	Horda Qawusa	9°00'19.37"N	36°29'13.28"E	2225
037/09	E.W	Leka Dullecha	Horda Qawusa	9°00'30.41"N	36°29'13.32"E	2225
038/09	E.W	Leka Dullecha	Horda Qawusa	8°59'59.66"N	36°28'49.76"E	2240
039/09	E.W	Leka Dullecha	Horda Qawusa	8°59'22.32"N	36°29'40.70"E	2264
040/09	E.W	Leka Dullecha	Horda Qawusa	8°59'55.44"N	36°30'31.60"E	2209
041/09	E.W	Leka Dullecha	Horda Qawusa	8°59'21.87"N	36°30'25.81"E	2227
042/09	W.W	Gimbi	Jogir	9°10'12.00"N	35°46'58.28"E	1776
043/09	W.W	Gimbi	Jogir	9°10'10.87"N	35°46'31.44"E	1727
044/09	W.W	Gimbi	Aba Sena	9°01'39.43"N	35°58'50.01"E	1650
045/09	W.W	Gimbi	chuta Goch	9°12'18.85"N	35°44'27.29"E	1857
046/09	E.W	Digga	Demeksa	9°01'26.43"N	36°26'11.65"E	2129
047/09	W.W	Gimbi	Inango Dambali	9°10'05.05"N	35°42'31.00"E	1843
048/09	W.W	Gimbi	Chuta Goch	9°12'15.88"N	35°44'16.34"E	1867
049/09	W.W	Gimbi	Chuta Goch	9°12'06.03"N	35°44'03.15"E	1870
050/09	W.W	Gimbi	Inango Dambali	9°10'08.88"N	35°41'45.15"E	1888
051/09	E.W	Digga	Demeksa	9°02'26.20"N	36°27'17.84"E	2199
052/09	W.W	Gimbi	Inango Dambali	9°09'49.25"N	35°40'39.86"E	1820
053/09	W.W	Gimbi	Aba Sena	9°02'00.08"N	35°58'42.00"E	1637
054/09	W.W	Gimbi	Bikiltu Tokkumma	9°11'30.45"N	35°47'16.52"E	1837
055/09	W.W	Gimbi	Gimbo 03/Gimbi Town	9°10'38.30"N	35°50'10.18"E	1930
056/09	W.W	Gimbi	Choli	9°12'55.57"N	35°49'27.30"E	1864
057/09	W.W	Gimbi	Walo Anchabi	9°14'00.50"N	35°41'56.80"E	1888
058/09	W.W	Gimbi	Lalisa Yesus	9°24'43.28"N	35°35'50.16"E	1892
059/09	W.W	Gimbi	Lalisa Yesus	9°24'47.14"N	35°36'09.86"E	1943
060/09	W.W	Gimbi	Lalisa Yesus	9°25'10.49"N	35°35'43.05"E	1917
061/09	W.W	Lalo Asabi	Garjo Siban	9°27'29.22"N	35°32'47.00"E	1732
062/09	W.W	Lalo Asabi	Haroggi Harowwa	9°27'57.57"N	35°32'26.10"E	1798
063/09	W.W	Lalo Asabi	Haroggi Harowwa	9°28'04.40"N	35°31'26.28"E	1851

064/09	W.W	Boji Dirmaji	Lata Bobine	9°21'41.84"N	35°36'22.79"E	1959
065/09	W.W	Mana Sibū Mandi	Gombo Kiltu Jale	9°50'50.05"N	35°04'29.09"E	1753
066/09	W.W	Mana Sibū Mandi	Gombo Kiltu Jale	9°50'45.38"N	35°03'35.58"E	1651
067/09	W.W	Mana Sibū Mandi	Gombo Kiltu Jale	9°50'16.38"N	35°02'38.49"E	1616
068/09	W.W	Mana Sibū Mandi	Gombo Kiltu Jale	9°51'33.05"N	35°03'03.65"E	1583
069/09	E.W	Gobbu Sayyo	Tibbe Hara	8°59'18.78"N	36°20'56.98"E	1619
070/09	E.W	Gobbu Sayyo	Tibbe Hara	9°01'47.42"N	36°21'58.99"E	1897
071/09	E.W	Leka Dullecha	Fododdo/Gatama	8°53'35.16"N	36°33'09.89"E	2013
072/09	E.W	Arjo	Kumba	8°45'25.03"N	36°29'25.67"E	2427
073/09	E.W	Leka Dullecha	Fododdo/Gatama	8°53'32.25"N	36°33'52.30"E	2028
074/09	E.W	Leka Dullecha	Fododdo/Gatama	8°52'32.89"N	36°32'50.56"E	1973
075/09	E.W	Gobbu Sayyo	Tibbe Hara	9°05'11.09"N	36°21'50.67"E	1441
076/09	E.W	Arjo	Kumba	8°46'06.66"N	36°29'07.73"E	2430
077/09	E.W	Leka Dullecha	Shakko	8°51'35.58"N	36°27'24.85"E	2474
078/09	E.W	Leka Dullecha	Bollo	8°51'05.11"N	36°29'44.01"E	2190
079/09	E.W	Leka Dullecha	Fododdo/Gatama	8°54'21.85"N	36°34'02.04"E	1902
080/09	E.W	Leka Dullecha	Shakko	8°57'26.16"N	36°32'30.67"E	1986
081/09	E.W	Nunnu Kumba	Nunnu	8°46'10.08"N	36°37'51.14"E	2313
082/09	E.W	Nunnu Kumba	Nunnu	8°46'04.84"N	36°38'26.40"E	2338
083/09	E.W	Leka Dullecha	Kawusa	8°56'09.70"N	36°31'12.17"E	2182
084/09	E.W	Leka Dullecha	Kawusa	8°54'40.67"N	36°30'02.87"E	2133
085/09	E.W	Leka Dullecha	Haro Shakko	8°58'06.93"N	36°28'29.72"E	2249
086/09	E.W	Nunu Kumba	Amuru Botoro	8°46'01.74"N	36°39'15.28"E	2253
087/09	E.W	Leka Dullecha	Badh'o	8°57'53.82"N	36°27'57.20"E	2248
088/09	E.W	Arjo	Qumba	8°48'54.34"N	36°36'26.70"E	2248
089/09	E.W	Sibu Sire	Home Baro	9°02'12.41"N	36°53'05.23"E	1842
090/09	E.W	Sibu Sire	Burka Talo	9°01'52.57"N	36°51'01.05"E	1800
091/09	E.W	Bonaya Boshe	Ejersa Gute	8°57'33.64"N	36°39'52.77"E	1759
092/09	E.W	GudeyaBila	Gonka Ija	9°14'53.50"N	36°57'56.26"E	1943
093/09	E.W	GudeyaBila	Gonka Ija	9°14'55.42"N	36°57'40.82"E	1934
094/09	E.W	GudeyaBila	Gonka Ija	9°14'48.15"N	36°57'27.68"E	1949
095/09	E.W	GudeyaBila	Kalala	9°15'49.79"N	36°59'41.92"E	1989
096/09	E.W	GudeyaBila	Gonka Ija	9°14'41.02"N	37°00'26.13"E	1910
097/09	E.W	GudeyaBila	Gonka Ija	9°15'01.93"N	37°00'31.92"E	1943
098/09	E.W	Gobbu Sayyo	Adare Tiksa	9°19'03.77"N	36°57'04.14"E	1924
099/09	E.W	Gobbu Sayyo	Adare Tiksa	9°19'02.66"N	36°57'03.43"E	1921
100/09	E.W	Gobbu Sayyo	Adare Tiksa	9°18'54.99"N	36°56'50.76"E	1941
101/09	E.W	Gobbu Sayyo	Adare Tiksa	9°18'49.47"N	36°57'03.27"E	1965
102/09	E.W	Gobbu Sayyo	Adare Tiksa	9°19'09.47"N	36°57'15.54"E	1953
103/09	E.W	Gobbu Sayyo	Adare Tiksa	9°19'20.05"N	36°56'54.49"E	1957
104/09	E.W	Gobbu Sayyo	Adare Tiksa	9°18'32.61"N	36°57'38.33"E	1965
105/09	W.W	Gimbi	Kombo Mikael	9°05'40.07"N	35°49'37.35"E	1885
106/09	W.W	Gimbi	Kombo Mikael	9°05'54.10"N	35°49'55.34"E	2006
107/09	W.W	Gimbi	Kombo Mikael	9°05'53.27"N	35°49'19.04"E	1860

108/09	W.W	Gimbi	Kombo Mikael	9°06'25.19"N	35°49'56.17"E	2008
109/09	W.W	Gimbi	Kombo Mikael	9°06'22.67"N	35°49'07.07"E	2009
110/09	W.W	Gimbi	Kombo Mikael	9°06'27.21"N	35°48'42.00"E	1919
111/09	W.W	Gimbi	Kombo Mikael	9°05'49.93"N	35°48'44.90"E	1916
112/09	W.W	Gimbi	Kombo Mikael	9°05'36.96"N	35°48'32.01"E	1938
113/09	W.W	Gimbi	Kombo Mikael	9°05'20.43"N	35°48'38.52"E	1911
114/09	W.W	Gimbi	Kombo Mikael	9°06'10.49"N	35°48'21.41"E	1995
115/09	W.W	Gimbi	Kombo Mikael	9°06'25.75"N	35°48'21.28"E	1986
116/09	W.W	Gimbi	Kombo Mikael	9°04'57.80"N	35°48'43.66"E	1860
117/09	W.W	Gimbi	Kombo Mikael	9°04'48.21"N	35°48'31.84"E	1875
118/09	W.W	Gimbi	Kombo Mikael	9°05'05.80"N	35°48'53.27"E	1868
119/09	W.W	Gimbi	Kombo Mikael	9°04'41.37"N	35°49'06.57"E	1917
120/09	W.W	Gimbi	Kombo Mikael	9°07'52.61"N	35°48'27.40"E	2028
121/09	W.W	Gimbi	Kombo Mikael	9°08'13.31"N	35°48'29.14"E	2015
122/09	W.W	Gimbi	Kombo Mikael	9°09'27.31"N	35°48'35.53"E	1888
123/09	W.W	Gimbi	Kombo Mikael	9°09'26.10"N	35°49'01.32"E	1892
124/09	W.W	Gimbi	Kombo Mikael	9°05'05.24"N	35°49'11.10"E	1848
125/09	W.W	Gimbi	Garjo Bikilal	9°13'46.15"N	35°54'47.05"E	1753
126/09	W.W	Gimbi	Garjo Bikilal	9°14'02.64"N	35°55'19.48"E	1729
127/09	W.W	Gimbi	Garjo Bikilal	9°14'12.69"N	35°55'22.72"E	1726
128/09	W.W	Gimbi	Garjo Bikilal	9°14'17.42"N	35°55'07.21"E	1734
129/09	W.W	Gimbi	Garjo Bikilal	9°14'17.49"N	35°54'33.69"E	1739
130/09	W.W	Gimbi	Garjo Bikilal	9°14'20.22"N	35°54'13.16"E	1750
131/09	W.W	Gimbi	Garjo Bikilal	9°14'34.03"N	35°54'11.09"E	1704
132/09	W.W	Gimbi	Garjo Bikilal	9°14'57.66"N	35°54'30.61"E	1661
133/09	W.W	Gimbi	Garjo Bikilal	9°14'54.55"N	35°53'54.15"E	1650
134/09	W.W	Gimbi	Garjo Bikilal	9°12'46.20"N	35°54'39.48"E	1842
135/09	W.W	Gimbi	Garjo Bikilal	9°13'31.18"N	35°55'02.51"E	1762
136/09	W.W	Gimbi	Garjo Bikilal	9°13'39.76"N	35°55'39.86"E	1771
137/09	W.W	Gimbi	Garjo Bikilal	9°13'43.95"N	35°55'39.17"E	1770
138/09	W.W	Gimbi	Garjo Bikilal	9°15'01.84"N	35°53'17.62"E	1780
139/09	W.W	Gimbi	Garjo Bikilal	9°17'24.34"N	35°52'47.19"E	2140
140/09	W.W	Gimbi	Garjo Bikilal	9°16'40.84"N	35°51'39.96"E	2052
141/09	W.W	Gimbi	Garjo Bikilal	9°16'00.38"N	35°50'54.60"E	1973
142/09	W.W	Gimbi	Garjo Bikilal	9°16'02.38"N	35°50'35.87"E	1942
143/09	W.W	Gimbi	Garjo Bikilal	9°15'59.99"N	35°50'20.79"E	1889
144/09	W.W	Gimbi	Garjo Bikilal	9°15'28.22"N	35°50'26.16"E	1891
145/09	W.W	Gimbi	Lalo Choli	9°13'26.57"N	35°49'14.83"E	1831
146/09	W.W	Gimbi	Lalo Choli	9°13'51.03"N	35°49'11.40"E	1806
147/09	W.W	Gimbi	Lalo Choli	9°14'20.70"N	35°49'45.08"E	1730
148/09	W.W	Gimbi	Lalo Choli	9°14'13.95"N	35°48'38.07"E	1793
149/09	W.W	Gimbi	Lalo Choli	9°14'03.40"N	35°48'26.41"E	1790
150/09	W.W	Gimbi	Lalo Choli	9°13'56.66"N	35°47'55.64"E	1824
151/09	W.W	Gimbi	Lalo Choli	9°13'41.94"N	35°48'02.11"E	1838
152/09	W.W	Gimbi	Lalo Choli	9°13'07.44"N	35°48'03.32"E	1847
153/09	W.W	Gimbi	Lalo Choli	9°13'02.91"N	35°48'13.15"E	1827
154/09	W.W	Gimbi	Lalo Choli	9°12'49.36"N	35°47'56.95"E	1824
155/09	W.W	Gimbi	Lalo Choli	9°13'02.03"N	35°47'55.28"E	1814
156/09	W.W	Gimbi	Lalo Choli	9°13'29.23"N	35°47'57.03"E	1845
157/09	W.W	Gimbi	Lalo Choli	9°13'16.14"N	35°48'16.95"E	1846
158/09	W.W	Gimbi	Lalo Choli	9°13'40.52"N	35°48'15.06"E	1826
159/09	W.W	Gimbi	Lalo Choli	9°13'35.80"N	35°48'25.60"E	1793
160/09	W.W	Gimbi	Lalo Choli	9°13'40.75"N	35°46'07.29"E	1839
161/09	W.W	Gimbi	Lalo Choli	9°12'59.74"N	35°47'27.49"E	1811

162/09	W.W	Gimbi	Lalo Choli	9°12'50.07"N	35°45'07.71"E	1814
163/09	W.W	Gimbi	Lalo Choli	9°12'42.65"N	35°47'28.12"E	1819
164/09	W.W	Gimbi	Lalo Choli	9°12'33.55"N	35°47'32.15"E	1809
165/09	W.W	Gimbi	Didisa Bikilal	9°16'04.73"N	35°44'32.94"E	1835
166/09	W.W	Gimbi	Didisa Bikilal	9°16'00.39"N	35°44'16.65"E	1854
167/09	W.W	Gimbi	Didisa Bikilal	9°15'55.18"N	35°44'07.13"E	1846
168/09	W.W	Gimbi	Didisa Bikilal	9°16'00.01"N	35°44'16.75"E	1853
169/09	W.W	Gimbi	Didisa Bikilal	9°16'07.72"N	35°44'03.88"E	1839
170/09	W.W	Gimbi	Didisa Bikilal	9°16'19.41"N	35°44'34.50"E	1864
171/09	W.W	Gimbi	Didisa Bikilal	9°16'30.82"N	35°44'20.96"E	1832
172/09	W.W	Gimbi	Didisa Bikilal	9°16'30.91"N	35°44'38.31"E	1875
173/09	W.W	Gimbi	Didisa Bikilal	9°16'33.28"N	35°44'54.60"E	1886
174/09	W.W	Gimbi	Didisa Bikilal	9°16'42.27"N	35°44'58.50"E	1885
175/09	W.W	Gimbi	Didisa Bikilal	9°16'56.56"N	35°44'33.78"E	1849
176/09	W.W	Gimbi	Didisa Bikilal	9°17'03.59"N	35°44'52.60"E	1870
177/09	W.W	Gimbi	Didisa Bikilal	9°17'08.52"N	35°44'34.16"E	1845
178/09	W.W	Gimbi	Didisa Bikilal	9°17'08.70"N	35°44'12.03"E	1841
179/09	W.W	Gimbi	Didisa Bikilal	9°17'17.24"N	35°44'45.32"E	1831
180/09	W.W	Gimbi	Didisa Bikilal	9°17'35.46"N	35°44'40.77"E	1802
181/09	W.W	Gimbi	Didisa Bikilal	9°17'24.18"N	35°44'13.73"E	1830
182/09	W.W	Gimbi	Didisa Bikilal	9°17'37.21"N	35°44'23.71"E	1780
183/09	W.W	Gimbi	Didisa Bikilal	9°17'48.43"N	35°44'29.76"E	1766
184/09	W.W	Gimbi	Didisa Bikilal	9°18'26.52"N	35°43'56.80"E	1846
185/09	W.W	Mana Siblu Mandi	Guyo Sachi	9°45'13.68"N	35°01'35.14"E	1574
186/09	W.W	Mana Siblu Mandi	Guyo Sachi	9°45'13.64"N	35°01'35.19"E	1619
187/09	W.W	Mana Siblu Mandi	Guyo Sachi	9°45'29.26"N	35°01'17.20"E	1575
188/09	W.W	Mana Siblu Mandi	Wajitu Mandi	9°47'10.51"N	35°05'37.63"E	1689
189/09	W.W	Mana Siblu Mandi	Wajitu Mandi	9°47'10.42"N	35°05'22.03"E	1677
190/09	W.W	Mana Siblu Mandi	Wajitu Mandi	9°46'58.16"N	35°04'58.74"E	1637
191/09	W.W	Mana Siblu Mandi	Wajitu Mandi 01	9°47'14.30"N	35°06'00.61"E	1688
192/09	W.W	Mana Siblu Mandi	Wajitu Mandi	9°46'58.65"N	35°04'46.44"E	1629
193/09	W.W	Mana Siblu Mandi	Wajitu Kiltu Lubo	9°44'43.66"N	35°02'22.39"E	1597
194/09	W.W	Mana Siblu Mandi	Wajitu Kiltu Lubo	9°44'56.57"N	35°02'50.72"E	1555
195/09	W.W	Mana Siblu Mandi	Wajitu Mandi	9°46'18.84"N	35°04'37.03"E	1608
196/09	W.W	Mana Siblu Mandi	Wajitu Mandi	9°46'28.09"N	35°04'29.06"E	1611
197/09	W.W	Mana Siblu Mandi	Wajitu Mandi 01	9°46'24.42"N	35°04'13.55"E	1607
198/09	W.W	Mana Siblu Mandi	Wajitu Kiltu Lubo	9°45'01.32"N	35°03'14.45"E	1572
199/09	W.W	Mana Siblu Mandi	Wajitu Mandi	9°46'32.96"N	35°04'01.11"E	1603
200/09	W.W	Mana Siblu Mandi	Wajitu Kiltu Lubo	9°45'13.20"N	35°03'34.14"E	1585
201/09	W.W	Mana Siblu Mandi	Wajitu Mandi 01	9°46'58.27"N	35°04'18.97"E	1622
202/09	W.W	Mana Siblu Mandi	Wajitu Mandi	9°47'44.78"N	35°04'44.43"E	1590
203/09	W.W	Mana Siblu Mandi	Wajitu Mandi 01	9°47'48.34"N	35°04'29.22"E	1589
204/09	W.W	Mana Siblu Mandi	Wajitu Kiltu Lubo	9°44'56.88"N	35°03'46.19"E	1574
205/09	W.W	Mana Siblu Mandi	Wajitu Kiltu Lubo	9°45'29.51"N	35°03'53.50"E	1587
206/09	W.W	Mana Siblu Mandi	Wajitu Mandi	9°48'07.68"N	35°04'40.67"E	1610
207/09	W.W	Mana Siblu Mandi	Wajitu Kiltu Lubo	9°45'30.49"N	35°04'13.43"E	1567
208/09	W.W	Mana Siblu Mandi	Wajitu Kiltu Lubo	9°45'14.14"N	35°04'36.22"E	1595
209/09	W.W	Mana Siblu Mandi	Wajitu Mandi 01	9°48'22.76"N	35°04'32.51"E	1610
210/09	W.W	Mana Siblu Mandi	Wajitu Kiltu Lubo	9°45'14.21"N	35°04'51.49"E	1596
211/09	W.W	Mana Siblu Mandi	Wajitu Kiltu Lubo	9°45'36.34"N	35°05'34.92"E	1622
212/09	W.W	Mana Siblu Mandi	Wajitu Mandi	9°46'54.39"N	35°05'55.53"E	1627
213/09	W.W	Mana Siblu Mandi	Wajitu Kiltu Lubo	9°46'13.01"N	35°05'53.05"E	1652
214/09	W.W	Mana Siblu Mandi	Wajitu Kiltu Lubo	9°45'56.74"N	35°00'29.85"E	1543
215/09	W.W	Mana Siblu Mandi	Wajitu Kiltu Lubo	9°45'46.48"N	35°00'37.54"E	1536

216/09	W.W	Mana Sibumandi	Wajitu Kiltu Lubo	9°45'46.71"N	35°00'47.09"E	1558
217/09	W.W	Mana Sibumandi	Wajitu Mandi 01	9°47'06.51"N	35°06'15.89"E	1688
218/09	W.W	Boji Dirmaji	Gumbo Boji	9°23'14.75"N	35°36'03.09"E	2004
219/09	W.W	Boji Dirmaji	Lata Bobine	9°23'23.60"N	35°35'57.02"E	2000
220/09	W.W	Boji Dirmaji	Lata Bobine	9°23'28.25"N	35°36'12.30"E	1965
221/09	W.W	Boji Dirmaji	Gumbo Boji	9°21'34.11"N	35°34'51.96"E	1944
222/09	H.G.W	Horro	Doyyo Bariso	9°36'09.82"N	37°11'33.91"E	2399
223/09	H.G.W	Horro	Doyyo Bariso	9°36'12.85"N	37°11'33.27"E	2392
224/09	H.G.W	Horro	Doyyo Bariso	9°36'19.70"N	37°11'42.36"E	2381
225/09	H.G.W	Horro	Doyyo Bariso	9°36'15.30"N	37°11'54.53"E	2390
226/09	H.G.W	Horro	Doyyo Bariso	9°36'05.22"N	37°12'00.61"E	2385
227/09	W.W	Boji Dirmaji	Lata Bobine	9°23'47.77"N	35°35'42.86"E	1964
228/09	H.G.W	Horro	Doyyo Bariso	9°36'22.08"N	37°12'14.99"E	2371
229/09	H.G.W	Horro	Didibbe Kistana	9°37'20.12"N	37°14'26.98"E	2369
230/09	H.G.W	Guduru	Walkitumma	9°40'30.30"N	37°19'43.49"E	2426
231/09	H.G.W	Guduru	Walkitumma	9°40'28.33"N	37°19'11.57"E	2432
232/09	H.G.W	Abay Chomen	Fincha/forest	9°31'57.98"N	37°23'22.20"E	2245
233/09	Iluababor	Ale	Ale	8°26'16.33"N	36°11'31.46"E	1974
234/09	E.W	Gute	Kichi	9°01'34.40"N	36°40'00.42"E	1840
235/09	Iluababor	Ale	Ale	8°25'50.73"N	36°10'59.04"E	1965
236/09	B.B	Bedelle	Ale	8°29'01.27"N	36°21'35.78"E	2030
237/09	W.W	Gimbi	Gimbi 03	9°11'13.38"N	35°49'42.19"E	1890
238/09	Jimma	manna	Koche	7°54'50.64"N	36°37'33.99"E	1615
239/09	E.Gojjam	hulet eju	Mota zuria	11°03'27.14"N	37°53'11.56"E	2441
240/09	W.W	Gimbi	Choli	9°12'14.19"N	35°49'22.29"E	1885
241/09	E.W	Sibu Sire	Tuqa	9°01'46.96"N	36°53'17.77"E	1815
242/09	Jimma	Dedo	Dedo zuria	7°30'27.26"N	36°52'03.20"E	2212
243/09	H.G.W	Abay Chomen	Nashe	9°32'00.54"N	37°22'18.84"E	2281
244/09	Bench Madji	Andracha	Kufe	7°02'19.25"N	35°36'46.57"E	1457
245/09	H.G.W	Abay Chomen	Mazoria	9°31'09.43"N	37°22'37.92"E	2269
246/09	Q.W	Dembi Dolo	Gida Gebo	8°35'11.84"N	34°35'02.99"E	1498
247/09	Iluababor	Ale	Sotelo	8°26'37.00"N	36°10'50.29"E	1970
248/09	E.W	Jimma Arjo	Guddanne	8°45'41.04"N	36°28'44.67"E	2297
249/09	W.W	Gimbi	Aba Sena	9°01'50.27"N	35°58'33.26"E	1630
250/09	Q.W	Dembi Dolo	Gida Gebo	8°35'09.69"N	34°35'40.21"E	1541
251/09	E.W	Guto wayu	Gute	9°03'21.83"N	36°41'16.00"E	1971
252/09	Iluababor	Ale	Sotelo	8°26'32.00"N	36°11'01.82"E	1952
253/09	E.W	Guto wayu	Gute	9°03'42.50"N	36°40'20.09"E	2133
254/09	E.W	Digga	Digga Lega	9°03'07.28"N	36°29'09.13"E	2187
255/09	W.W	Gimbi	Gimbi Adventist	9°10'14.94"N	35°50'23.85"E	1945
256/09	Jimma	Dedo	Dedo Zuria	7°30'11.60"N	36°52'12.49"E	2294
257/09	E.W	Guto wayu	Gute	9°03'26.70"N	36°40'36.65"E	2066
258/09	E.W	Digga	Digga Lega	9°01'54.52"N	36°27'26.24"E	2207
259/09	W.Sh	Bako Tibbe	Tibbe	9°05'06.06"N	37°06'20.86"E	1658
260/09	E.W	Digga	Digga Zuria	9°01'47.10"N	36°26'03.21"E	2174
261/09	E.W	Jimma Arjo	Guddanne	8°44'54.98"N	36°29'27.24"E	2450
262/09	E.W	Digga	Digga zuria	9°02'25.58"N	36°29'03.58"E	2214
263/09	W.sh	Bako Tibbe	Bacha Oda Gibe	9°05'27.02"N	37°06'02.52"E	1695
264/09	E.W	Gudeya Bila	Haro Gudisa	9°13'51.21"N	37°01'23.90"E	1877
265/09	E.W	Gudeya Bila	Haro Gudisa	9°13'25.52"N	37°01'54.19"E	1888
266/09	E.W	Gudeya Bila	Haro Gudisa	9°13'33.28"N	37°01'56.71"E	1886
267/09	E.W	Gudeya Bila	Haro Gudisa	9°13'51.97"N	37°01'28.74"E	1877
268/09	E.W	Gudeya Bila	Haro Gudisa	9°14'04.49"N	37°01'47.56"E	1877

269/09	E.W	Gudeya Bila	Haro Gudisa	9°14'15.32"N	37°01'49.49"E	1879
270/09	E.W	Gudeya Bila	Haro Gudisa	9°14'18.65"N	37°01'35.30"E	1890
271/09	E.W	Gudeya Bila	Hena Jawaja	9°14'09.72"N	37°01'31.09"E	1883
272/09	E.W	Gudeya Bila	Hena Jawaja	9°13'50.59"N	37°01'19.67"E	1877
273/09	E.W	Gudeya Bila	Hena Jawaja	9°14'17.30"N	37°01'13.26"E	1923
274/09	E.W	Gudeya Bila	Hena Jawaja	9°14'27.02"N	37°01'01.46"E	1964
275/09	H.G.W	Horro	Burkitu Oborra	9°27'53.61"N	37°04'06.99"E	3014
276/09	H.G.W	Horro	Burkitu Oborra	9°27'49.76"N	37°04'06.83"E	2806
277/09	H.G.W	Horro	Burkitu Oborra	9°27'24.62"N	37°04'00.75"E	2903
278/09	W.W	Mana Sibiu Mandi	Guyo Sachi	9°44'44.99"N	35°03'33.58"E	1590
279/09	W.W	Kiltu Kara	Dandi Gudi	9°31'52.40"N	35°22'19.50"E	1799
280/09	W.W	Kiltu Kara	Dandi Gudi	9°32'04.39"N	35°22'30.93"E	1817
281/09	W.W	Kiltu Kara	Dandi Gudi	9°32'09.40"N	35°22'09.30"E	1793
282/09	W.W	Kiltu Kara	Dandi Gudi	9°32'32.55"N	35°22'27.27"E	1747
283/09	W.W	Kiltu Kara	Dandi Gudi	9°32'33.33"N	35°21'50.32"E	1694
284/09	W.W	Kiltu Kara	Dandi Gudi	9°32'40.79"N	35°22'13.50"E	1717
285/09	W.W	Boji Dirmaji	Lata Bobine	9°24'12.07"N	35°35'26.52"E	1896
286/09	W.W	Boji Dirmaji	Lata Bobine	9°24'20.62"N	35°36'18.70"E	1918
287/09	W.W	Boji Dirmaji	Lata Bobine	9°23'50.10"N	35°35'44.46"E	1976
288/09	W.W	Nejo	Humna Wakayyo	9°30'32.40"N	35°31'10.33"E	1901
289/09	W.W	Kiltu Kara	Chara Gudi	9°31'45.47"N	35°22'30.00"E	1839
290/09	W.W	Boji Dirmaji	Lata Bobine	9°27'13.65"N	35°33'15.48"E	1853
291/09	W.W	Boji Dirmaji	Gumbo Boji	9°28'42.70"N	35°32'21.80"E	1805
292/09	W.W	Nejo	Humna Wakayyo	9°31'20.80"N	35°31'32.35"E	1914
293/09	W.W	Mana Sibiu Mandi	Guyo Sachi	9°49'56.69"N	35°03'56.82"E	1694
294/09	W.W	Mana Sibiu Mandi	Lafto Salga	9°49'46.33"N	35°04'36.46"E	1759
295/09	W.W	Mana Sibiu Mandi	Lafto Salga	9°50'05.95"N	35°04'48.14"E	1718
296/09	W.W	Nejo	Humna Wakayyo	9°31'09.60"N	35°31'28.18"E	1913
297/09	W.W	Nejo	Humna Wakayyo	9°31'36.07"N	35°31'31.17"E	1890
298/09	W.W	Mana Sibiu Mandi	Guyo Sachi	9°50'09.75"N	35°03'36.54"E	1650
299/09	W.W	Mana Sibiu Mandi	Guyo Sachi	9°50'17.03"N	35°03'53.42"E	1661
300/09	W.W	Mana Sibiu Mandi	Guyo Sachi	9°50'29.80"N	35°03'50.10"E	1655
301/09	E.W	Limmu	Bolale	9°50'21.70"N	36°28'48.42"E	2149
302/09	E.W	Limmu	Sakata Kiltu Babbo	9°51'04.95"N	36°29'27.52"E	2181
303/09	E.W	Limmu	Muka Arba Dima	9°51'13.49"N	36°28'22.20"E	2134
304/09	E.W	Limmu	Sapera	9°51'49.78"N	36°31'30.58"E	2192
305/09	E.W	Limmu	Degem Silassie	9°51'46.82"N	36°30'46.08"E	2133
306/09	E.W	Limmu	Bolale	9°51'03.51"N	36°29'03.25"E	2170
307/09	E.W	Limmu	Degem Silassie	9°51'25.62"N	36°30'09.88"E	2151
308/09	E.W	Limmu	Sapera	9°51'34.09"N	36°29'36.91"E	2115
309/09	E.W	Limmu	Muka Arba Dima	9°51'29.62"N	36°29'03.18"E	2149
310/09	E.W	Limmu	Sakata Kiltu Babbo	9°51'05.03"N	36°27'02.75"E	2122
311/09	E.W	Gida Ayana	Gute Gudina	9°53'33.86"N	36°37'03.19"E	1970
312/09	E.W	Gida Ayana	Gaba Jimata	9°53'15.79"N	36°39'41.04"E	2085
313/09	E.W	Gida Ayana	Gute Gudina	9°53'13.79"N	36°37'13.93"E	2060
314/09	E.W	Gida Ayana	Gaba Jimata	9°53'33.86"N	36°37'03.19"E	2049
315/09	E.W	Gudeya Bila	Chali Jima	9°53'00.99"N	36°39'39.42"E	2629
316/09	E.W	Gida Ayana	Gaba Jimata	9°53'07.17"N	36°39'51.96"E	2098
317/09	E.W	Gudeya Bila	Alito	9°19'22.55"N	37°02'22.78"E	2194
318/09	E.W	Gudeya Bila	Chali Jima	9°19'37.40"N	37°02'24.96"E	2192
319/09	E.W	Gudeya Bila	Chali Jima	9°19'26.06"N	37°02'06.92"E	2315
320/09	E.W	Gudeya Bila	Alito	9°19'34.34"N	37°02'02.38"E	2339
321/09	E.W	Leka Dullecha	Badh'o	8°55'13.31"N	36°34'48.24"E	1892
322/09	E.W	Leka Dullecha	Badh'o	8°55'15.97"N	36°34'57.55"E	1887

323/09	E.W	Leka Dullecha	Badh'o	8°55'10.07"N	36°35'12.47"E	1863
324/09	E.W	Leka Dullecha	Badh'o	8°55'04.73"N	36°35'24.52"E	1847
325/09	E.W	Leka Dullecha	Ale Qawusa	8°55'02.77"N	36°34'25.45"E	1899
326/09	E.W	Leka Dullecha	Badh'o	8°55'18.16"N	36°35'32.22"E	1871
327/09	E.W	Leka Dullecha	Badh'o	8°55'17.25"N	36°36'11.20"E	1825
328/09	E.W	Leka Dullecha	Badh'o	8°55'28.47"N	36°35'39.29"E	1855
329/09	E.W	Leka Dullecha	Badh'o	8°55'29.25"N	36°35'38.82"E	1854
330/09	E.W	Jimma Arjo	Hara Kekko	8°47'34.62"N	36°28'33.67"E	2478
331/09	E.W	Jimma Arjo	Wayu Warke	8°46'52.62"N	36°29'22.35"E	2355
332/09	E.W	Jimma Arjo	Wayu Qiltu	8°45'46.77"N	36°29'19.93"E	2455
333/09	E.W	Jimma Arjo	Abayyi	8°45'52.41"N	36°30'49.37"E	2313
334/09	E.W	Jimma Arjo	Hara Gabato	8°45'37.63"N	36°29'16.52"E	2424
335/09	E.W	Jimma Arjo	Hara Gabato	8°44'18.16"N	36°29'45.85"E	2349
336/09	E.W	Jimma Arjo	Hara Gabato	8°44'03.37"N	36°29'25.09"E	2294
337/09	E.W	Jimma Arjo	Hara Gabato	8°44'18.73"N	36°29'05.08"E	2308
338/09	E.W	Jimma Arjo	Tibbe Chafe	8°43'37.06"N	36°30'48.99"E	2456
339/09	B.B	Makko	Dambali Sophe	8°37'46.55"N	36°07'42.97"E	2081
340/09	B.B	Makko	Dambali Sophe	8°37'42.79"N	36°08'02.82"E	2061
341/09	B.B	Makko	Dambali Sophe	8°37'34.06"N	36°07'57.73"E	2037
342/09	B.B	Makko	Dambali Sophe	8°37'37.15"N	36°07'47.12"E	2088
343/09	B.B	Makko	Dambali Sophe	8°37'29.41"N	36°07'48.25"E	2072
344/09	B.B	Makko	Dambali Sophe	8°37'57.74"N	36°07'45.24"E	2044
345/09	B.B	Makko	Dambali Sophe	8°38'05.50"N	36°07'20.15"E	2082
346/09	B.B	Makko	Dambali Sophe	8°37'51.48"N	36°07'12.78"E	2078
347/09	B.B	Makko	Dambali Sophe	8°37'46.43"N	36°07'17.95"E	2055
348/09	B.B	Makko	Dambali Sophe	8°37'33.12"N	36°07'22.82"E	2087
349/09	B.B	Makko	Dambali Sophe	8°37'24.84"N	36°07'27.57"E	2079
350/09	B.B	Makko	Dambali Sophe	8°37'20.96"N	36°07'44.91"E	2072
351/09	B.B	Makko	Dambali Sophe	8°37'02.04"N	36°08'10.31"E	2101
352/09	B.B	Makko	Makko 01	8°34'43.13"N	36°06'54.51"E	2266
353/09	B.B	Chora	Umbe	8°35'37.51"N	36°06'50.21"E	2218
354/09	B.B	Chora	Bero Sariti	8°25'38.96"N	36°08'28.38"E	1944
355/09	Iluababor	Hurumu	Mettu Mechi	8°20'40.18"N	35°42'54.96"E	1803
356/09	Iluababor	Hurumu	Mettu Mechi	8°20'07.06"N	35°43'29.91"E	1822
357/09	Iluababor	Hurumu	Mettu Mechi	8°21'00.88"N	35°44'14.66"E	1636
358/09	Iluababor	Hurumu	Yobidola	8°21'00.18"N	35°44'24.56"E	1695
359/09	Iluababor	Hurumu	Mettu Mechi	8°19'54.58"N	35°43'55.64"E	1789
360/09	Iluababor	Hurumu	Mettu Mechi	8°20'19.89"N	35°47'56.08"E	1535
361/09	Buno Bedelle	Chora	Abdella	8°22'14.47"N	36°14'58.79"E	1947
362/09	Iluababor	Mettu	Tulubbe	8°19'28.43"N	35°32'25.43"E	1694
363/09	Iluababor	Mettu	Tulubbe	8°19'49.75"N	35°32'17.86"E	1699
364/09	Iluababor	Mettu	Adale Bishe	8°19'28.26"N	35°36'39.14"E	1670
365/09	Iluababor	Mettu	Adale Gumar	8°19'51.57"N	35°36'37.08"E	1710
366/09	Iluababor	Mettu	Adale Bishe	8°19'10.18"N	35°36'21.29"E	1668
367/09	Iluababor	Mettu	Mettu Mechi	8°19'15.42"N	35°37'52.79"E	1760
368/09	Iluababor	Mettu	Adale Gumar	8°19'03.01"N	35°37'06.00"E	1686
369/09	Iluababor	Mettu	Tulubbe	8°20'42.11"N	35°32'36.68"E	1702
370/09	Iluababor	Mettu	Mettu Mechi	8°19'39.85"N	35°40'06.85"E	1770
371/09	Iluababor	Mettu	Adale Gumar	8°19'56.80"N	35°46'07.38"E	1429
372/09	B.B	Didessa	Sasso	8°35'39.43"N	36°20'25.99"E	1659

373/09	B.B	Didessa	Masara	8°38'15.24"N	36°22'43.41"E	1671
374/09	B.B	Didessa	Yembero	8°38'00.28"N	36°22'26.22"E	1427
375/09	B.B	Didessa	Yembero	8°37'54.75"N	36°22'20.67"E	1432
376/09	B.B	Didessa	Sasso	8°37'45.79"N	36°22'04.73"E	1459
377/09	B.B	Didessa	Sasso	8°37'46.82"N	36°22'02.86"E	1463
378/09	Jimma	Gumay	Naga Agayo	8°09'17.74"N	36°28'21.92"E	2096
379/09	Jimma	Gumay	Naga Agayo	8°08'50.42"N	36°27'56.25"E	2244
380/09	B.B	Didessa	Sasso	8°37'48.74"N	36°21'58.97"E	1470
381/09	B.B	Didessa	Yembero	8°37'51.56"N	36°21'28.53"E	1427
382/09	B.B	Didessa	Sasso	8°37'58.10"N	36°22'24.76"E	1427
383/09	B.B	Didessa	Yembero	8°38'07.58"N	36°22'16.42"E	1450
384/09	H.G.W	Jimma Geneti	Bikila Nagaro	9°25'53.75"N	37°04'00.90"E	3016
384/10	H.G.W	Jimma Geneti	Bikila Nagaro	9°25'53.98"N	37°04'20.75"E	2945
386/09	H.G.W	Jimma Geneti	Gidami Dabsho	9°24'30.06"N	37°03'54.72"E	2929
387/09	H.G.W	Jimma Geneti	Gidami Dabsho	9°24'16.42"N	37°03'53.10"E	2911
388/09	H.G.W	Jimma Geneti	Gidami Dabsho	9°24'25.81"N	37°04'13.78"E	2703
389/09	H.G.W	Jimma Geneti	Gidami Dabsho	9°24'10.84"N	37°04'13.18"E	2706
390/09	H.G.W	Jimma Geneti	Gidami Dabsho	9°23'45.36"N	37°04'03.17"E	2843
391/09	E.W	Gudeya Bila	Lanfaji	9°17'55.86"N	37°02'26.65"E	2042
392/09	E.W	Gudeya Bila	Lanfaji	9°18'03.82"N	37°02'24.11"E	2051
393/09	E.W	Gudeya Bila	Lanfaji	9°18'10.48"N	37°02'19.92"E	2063
394/09	E.W	Gudeya Bila	Lanfaji	9°18'02.31"N	37°02'51.32"E	2060
395/09	E.W	Gudeya Bila	Lanfaji	9°17'55.39"N	37°02'50.81"E	2049
396/09	E.W	Gudeya Bila	Walane Lemu	9°21'03.48"N	37°02'08.19"E	2251
397/09	E.W	Gudeya Bila	Walane Lemu	9°20'53.47"N	37°02'16.31"E	2289
398/09	E.W	Gudeya Bila	Walane Lemu	9°20'40.41"N	37°02'35.54"E	2277
399/09	E.W	Gudeya Bila	Walane Lemu	9°20'33.35"N	37°02'46.15"E	2329
400/09	E.W	Gudeya Bila	Walane Lemu	9°20'14.80"N	37°02'55.30"E	2238
401/09	E.W	Gudeya Bila	Walane Lemu	9°20'09.92"N	37°02'47.05"E	2192
402/09	E.W	Gudeya Bila	Walane Lemu	9°20'10.43"N	37°02'11.83"E	2252
403/09	E.W	Gudeya Bila	Walane Lemu	9°20'25.56"N	37°02'18.44"E	2230
404/09	E.W	Gudeya Bila	Walane Lemu	9°20'44.94"N	37°01'50.14"E	2332
405/09	E.W	Gudeya Bila	Walane Lemu	9°21'00.44"N	37°01'54.05"E	2338
406/09	E.W	Gudeya Bila	Walane Lemu	9°19'55.93"N	37°02'15.88"E	2216
407/09	H.G.W	Jimma Geneti	Gamo Nagaro	9°22'45.81"N	37°04'18.96"E	2509
408/09	E.W	Gudeya bila	Bilo	9°18'26.50"N	37°03'11.15"E	2117
409/09	E.W	Gudeya bila	Ejere	9°15'21.32"N	37°02'41.72"E	1974
410/09	E.W	Gudeya bila	Chali	9°18'09.28"N	37°05'55.89"E	2803
411/09	E.W	Gudeya bila	Chali	9°18'17.31"N	37°05'41.32"E	2873
412/09	E.W	Gudeya bila	Gute Chacho	9°19'26.04"N	37°03'17.75"E	2257
413/09	E.W	Gudeya bila	Gute Chacho	9°19'11.72"N	37°03'24.73"E	2237
414/09	H.G.W	Horro	Burkitu Oborra	9°28'13.59"N	37°03'45.56"E	2699
415/09	H.G.W	Horro	Burkitu Oborra	9°28'05.24"N	37°03'17.31"E	2676
416/09	H.G.W	Horro	Burkitu Oborra	9°27'08.97"N	37°03'43.07"E	3025
	10	40	127			1412-3025

Key: E.W-East Wollega, W.W-West Wollega, Q.W-Qellem Wollega, W.Sh-West Shewa, H.G.W-Horro Guduru Wollega, B.B- Buno Bedelle

Genotype-By-Environment Interaction Effect on Storage Root Yield and Yield Components of Cassava (*Manihotesculenta* crantz) Genotypes in Different Agroecologies of Southwest Ethiopia

Tewodros Mulualem*, Neim Seman, and Getachew Etana

Jimma Agricultural Research Center, P.O. Box 192, Jimma, Ethiopia

*Corresponding author Email: tewodrosmulualem@gmail.com

Abstracts

The storage root yield of cassava is highly affected by genotype by environment (GEI) interactions. The objectives of this study were to assess the nature and magnitude of GxE interactions of cassava genotypes based on environment evaluation trials and to identify mega-environments for future breeding strategies. The study was conducted across six environments in southwest Ethiopia. Ten cassava genotypes and one local check were evaluated by using a randomized complete block design with three replications. Data from total storage root yield, root dry weight and root diameter were collected and analyzed using the additive main effect and multiplicative interaction and genotype main effect plus genotype by environment interaction bi-plot analyses. The combined analysis of variance showed significant variation for genotypes, locations, and crop year and their interactions for root dry weight and root diameter. Genotypes 8 (AAGT 191) and 6 (AAGT 108) had broad adaptability for total storage root yield, whereas, genotypes 7 (AAGT 189), 11 (local), 10 (AAGT 200) and 4 (45/72NW) were superior for root dry weight. For high total storage root yield and root dry weight, environments 2 and 4 were epitome and highly close to the ideal environment. Overall, environment 4 was the most suitable environment for discriminating among genotypes and for being a representative test environment. Three mega-environments (MGE) were identified from this study for cassava breeding; where environments 2, 5 and 6 combined into MGE-1, environments 3 and 4 fell into a separate MGE-2 and MGE-3, respectively.

Keywords: Adaptability, Bi-plot, Cassava, Genotype, Mega- Environment , Root yield, Stability.

Introduction

Cassava (*Manihotesculenta* Crantz) is an important staple crop in tropical and sub-tropical areas of the world

(Joseph *et al.*, 2020a; Bright *et al.*, 2020). It is the sixth most important food crop globally, in terms of annual production (Aina *et al.*, 2009; Joseph *et al.*, 2020b). The crop is mainly grown

for staple food of an estimated 800 million people worldwide (Tewodros *et al.*, 2020; Bright *et al.*, 2020) and has the ability to give better and appreciable yields than most staple crops in areas where drought and poor soils prevails (El-Sharkawy, 1993). Cassava plays several important roles in Africa serving as a rural staple food, famine-reserve and cash crop for households and as a raw material for industrial manufacturing (Felix and Dunstan, 1995; Séri *et al.*, 2013; Edwige *et al.*, 2021).

Although reliable statistical information on the distribution and production of cassava in Ethiopia is lacking, the crop has been cultivated in diverse environmental conditions in South, South West, and Western parts to overcome hunger and make a significant contribution in the diets of the people (Tewodros and Zelalem, 2015; Bright *et al.*, 2020). Furthermore, the crop is gaining fast popularity as an important industrial raw material in Ethiopia, leading to its widespread cultivation in different areas of the country (Séri *et al.*, 2013; Mehari *et al.*, 2015). To satisfy the growing demand of producers and consumers, cassava production needs to be extended to different parts of the country (João *et al.*, 2013). Cassava genotypes evaluated for yield in multi-location trials, wide differences are frequently observed in yield performances of the genotypes over the growing environments. This wide agro-ecological variability is the major

challenge for cassava due to high genotype x environment interaction (GEI) effect (Adetoro *et al.*, 2021). In this regard, there is few efforts so far done on evaluation of cassava genotypes for yield and yield related traits in diverse environments of Ethiopia (Tesfaye *et al.*, 2017). Further, Tewodros *et al.*, (2020) reported appraisal of better type cassava genotypes for yield and quality traits in different agroecologies of southwest Ethiopia. Identification of yield contributing traits and knowledge of GEI along with root yield stability have tremendous impact for breeding of new varieties with good adaptation in the target environments (Aina *et al.*, 2009; Edwige *et al.*, 2021). The study of GEI also support cassava breeders to develop strategies for testing and selecting genotypes most adapted to the target environments under which the genotypes will be grown (Adjebeng *et al.*, 2017).

There are two dominant statistical models in G×E study, which are the additive main effect and multiplicative interaction (AMMI) and genotype plus genotype × environment (GGE) bi-plot methods (Yan *et al.*, 2000). The models can provide valuable insights in assessing the extent of G×E interactions in multi-environmental trials of cassava in Ethiopia. The current study was, therefore, designed to assess the nature and magnitude of G×E interactions and advance insights into mega-environments for cassava in southwest Ethiopia.

Materials and Methods

Description of study areas

The field experiment was conducted at three locations, namely: Jimma, Metu and Tepi Agricultural Research Centers which are considered as the representative cassava growing areas of south-west Ethiopia. The experiment was conducted for two cropping seasons (2015-2018) in all the three locations. This made a total of six environments considering one location and one cropping season as one environment. Jimma Agricultural Research Center is located at 1753 m.a.s.l., 7° 40.00' N latitude and 36° 47'.00' E longitude. The area receives mean annual rainfall of 1432 mm with mean maximum and minimum temperatures of 29.2 °C and 8.90 °C, respectively. The soil of experimental plot is sandy loam. Metu Agricultural Research Sub-center is situated at a distance of about 625 km to the southwest of Addis Ababa. The site is located at 8°18' .00' N latitude, 35°35' .00' E longitude and at an altitude of 1550 meters above sea level. The area receives mean annual rain fall ranging from 1200 to 1520 mm. The average temperature of the area is 20°C. The soil of Metu sub-center is sandy loam. Tepi Agricultural Research Center is located at a distance of about 220 km to the west of Jimma. The site is located at 7° 40.00' N latitude, 36° 47'.00' E longitude and an altitude of 1200 meters above sea level.

Plant materials, experimental design and management

A total of 11 cassava genotypes collected from major growing areas of southwest Ethiopia were used for this study. The list of genotypes and areas of collection were presented in Table 1. The experiment was laid out in randomized complete block design with three replications in each environment. Each cassava genotype was assigned to one plot in each replication. The gross plot size for each treatment was 6m x 4m, using inter-row spacing of 1m and intra-rows spacing of 1m. Cuttings of the same size and age were used as planting material. Planting was done mid April during the main growing season of 2015-2018 following the the start of rain and sufficient soil moisture . One month after planting, seedlings were earthed up followed by frequent weeding. All other recommended agronomic practices were applied. Local materials were collected from respected tested locations of Jimma, Metu and Tepi areas.

Data collection

Data were collected from eight plants from each plot and the average values were used for data analysis. The characters that used for data collection were: total root yield (TRY) (t/ha), root dry weight (RDW) (t/ha), and root diameter (RDi) (cm).

Table 1. List of 11 cassava genotypes and their areas of collection

No	Genotypes	Zone	District	Latitude	Longitude	Altitude
1	44/72NR	Jimma	Manna	7° 40.00' N	36° 47'.00' E	1753
2	44/72NW	Jimma	Manna	7° 40.00' N	36° 47'.00' E	1753
3	45/72NR	Jimma	Manna	7° 40.00' N	36° 47'.00' E	1753
4	45/72NW	Jimma	Manna	7° 40.00' N	36° 47'.00' E	1753
5	AAGT 028	Jimma	Dedo	07°31'28N	036°53'63E	1683
6	AAGT 108	Bench maji	Sheko	07°02'91N	035°29'76E	1668
7	AAGT 189	Sheka	Yeki	07°11'22N	035°26'25E	1192
8	AAGT 191	Sheka	Yeki	07°11'22N	035°26'25E	1192
9	AAGT 192	Sheka	Yeki	07°11'30N	035°26'22E	1171
10	AAGT 200	Bench maji	Sheko	07°04'13N	035°37'74E	1320
11	*Local					

*Local materials were collected from respective testing locations around Jimma, Bench-maji and Sheka zones of southwest Ethiopia

Data analysis

The collected data were subjected to analysis of variance (ANOVA) for each location and combined over environments following the standard procedure using SAS software suggested by Fekadu *et al.* (2017) and Genstat software as prescribed by Malhotra *et al.*, (2007). The mean trait value across six environments was used in this analysis. Comparison of treatment means was done using the Fisher's protected least significant difference (LSD) test at 1% and 5% probability. A second ANOVA was conducted to determine the main and interaction effects of genotype, environment, and crop-year.

The total root yield (TRY), RDW and RDI were subjected to the combined analysis of variance and AMMI analysis, which is a combination of analysis of variance and multiplicative effect analysis. The analysis of

variance was used to partition variances into three components: genotype deviations from the grand mean, environment deviations from the grand mean, and G×E deviations from the grand mean. Subsequently, the multiplicative effect analysis was used to partition G×E deviations into different interaction principal component axes (IPCA), which were tested for statistical significance through ANOVA. To determine the G × E interaction for yield parameters, AMMI and GGE bi-plot analyses were performed. The following AMMI model was used (Gauch, 2013). Genotypic stability for each genotype will be computed using GenStat software, as prescribed by Malhotra *et al.*. (2007). The additive main effects and multiplicative interactions (AMMI) statistical model reported by Gauch and Zobel, (1996) was used to analyze yield data to obtain (AMMI)

analysis of variance and (AMMI) mean estimates as follows:

$$Y_{ger} = \mu + \alpha_g + \beta_e + \sum \lambda_n y_{gn} \delta_{en} + \rho_{ge} + E_{ger}$$

Where, Y_{ger} = yield of genotype g in environment e for replicate r , μ = grand mean, α_g = genotype mean deviation (genotype means minus grand mean), β_e = environment mean deviation, n = number of principal component analysis (PCA) axes retained in the model, λ_n singular value for PCA axis n , y_{gn} = genotype eigenvector values for PCA axis n , δ_{en} = environment eigenvector values for PCA axis n , ρ_{ge} = residuals, E_{ger} = error term.

The AMMI stability value (ASV) proposed by Purchase *et al.*, (2000)

used to quantify and rank genotypes based on yield stability. The ASV has been defined as the distance from the coordinate point to the origin in a two dimensional scatter plot of first interaction principal component axis (IPCA1) scores against the second interaction principal component axis (IPCA2) (Adjebeng *et al.*, 2017; Atung and Jeffrey, 2018). Since IPCA1 accounts for most of the GE variation, the IPCA1 scores are weighted by the ratio of IPCA1 SS (from AMMI ANOVA) to IPCA2 SS in the ASV were calculated by using the formula (Purchase *et al.*, 2000).

$$ASV = \sqrt{\left[\frac{SS_{IPCA1}}{SS_{IPCA2}} (IPCA1 \text{ score}) \right]^2 + (IPCA2 \text{ score})^2}$$

Where, Where: $\frac{SS_{IPCA1}}{SS_{IPCA2}}$ Sum of squares/ IPCA2 Sum of squares is the weight given to the IPCA1-value by dividing the IPCA1 sum of squares (from the AMMI analysis of variance table) by the IPCA2 sum of squares. The larger the IPCA score is, either negative or positive, the more adapted a genotype is to a certain environment. Smaller ASV scores indicate a more stable genotype across environments

Yan *et al.*, (2007) reported that genotype and genotype-by-environment effects must be considered simultaneously to make a meaningful decision in selection. Significant genotype by environment interaction was also analyzed by a

GGE bi-plot which was also useful in ranking genotypes based on their average performance and stability for farmer preferred traits in cassava. The GGE bi-plot model was also used to determine the influence of GEI on total root yield, root dry weight and root diameter across test environments. The model for the GGE bi-plot based on singular value decomposition (SVD) of first two principal components were calculated by using the model (Yan *et al.*, 2007):

$$Y_{ij} - \mu - \beta_j = \lambda_1 \xi_{i1} \eta_{j1} + \lambda_2 \xi_{i2} \eta_{j2} + \varepsilon_{ij}$$

Where: Y_{ij} = measured mean of genotype i in environment j , μ = grand

mean, β_j = main effects of environment j , $\mu + \beta_j$ = the mean yield across all genotypes in environment j , λ_1 and λ_2 = are the singular values (SV) for the first and second principle components (PCA 1 and PCA 2) respectively. ξ_{i1} and ξ_{i2} = are eigenvectors of genotype i for PCA 1 and PCA 2, respectively, η_{j1} and η_{j2} = eigenvectors for environment j for PCA 1 and PCA 2, respectively. ε_{ij} = residual associated with genotype i in environment j .

Results and Discussion

Analysis of variance

The combined analysis of variance (ANOVA) was performed to determine the effects of year (Y), location (L) and genotype (G) as presented in Table 2. Variance due to locations (L) were highly significant ($p \leq 0.01$) for all the traits studied. Similarly, genotype (G) was highly significant ($p \leq 0.01$) for RDW, conversely, RD_i was significant only at $p \leq 0.05$. Likewise, year (Y) was highly significant ($p < 0.01$) for all the traits, except for TRY that was significant only at $p \leq 0.05$. The Y x L interactions were highly significant ($p < 0.01$) for all the traits considered in this study. Equally, the G x Y were highly significant ($p \leq 0.01$) for RDW, and RD_i that was significant only at $p \leq 0.05$. The triple interaction effect, G x Y x L, was highly significant

($p \leq 0.01$) for RDW and RD_i and non-significant for TRY (Table 2). The non-significant interaction between genotype, location, and year (environment) (G x Y x L) for TRY of cassava support no need for multi-locational testing to identify good performers for specific locations. The significance of the year effects however indicates to the unpredictability of the cassava growing seasons in southwest Ethiopia and suggests the need to evaluate for more than two year for reliable inferences to be made on performance (Semakula and Dixon, 2007) within the overall focus of the development of stable genotypes in terms of yield and yield related traits of cassava. The significant morphological traits for the environments (as derived from location, year, and their interaction) showed significant variation that can be stimulated from the genotypes. The additional significant genotypic effect points to indicated genotypic differences for the traits and the possibility of selection for adaptation to specific environments. These observations are consistent with those of Tesfaye *et al.*, (2017) had observed similar results when seven cassava genotypes were evaluated across four locations in Ethiopia. This consistency further prompts the need for further recombination of genes to select higher performing genotypes (Adetoro *et al.*, 2021).

Table 2. Combined analysis of variance and significant tests for cassava yield and related traits of 11 genotypes tested during 2015-2018

Sources of variation	DF	TRY	RDW	RD _i
Location (L)	2	8774.4**	17537.9**	11628.9**
Genotype (G)	10	367.04	743.47**	53.9*
Year (Y)	1	904.06*	68689.5**	9854.5**
Y*L	2	3787.53**	43095.45**	10692.61**
G*L	20	328.91	490.58**	45.83*
G*Y	10	297.98	540.07**	47.30*
G*Y*L	20	244.28	3220.63**	710.23**
Error	130	272.06	233.30	30.13

*, **significant at 0.05 and 0.01% of probability level; TRY= Total root yield; RDW= Root dry weight, RD_i= Root diameter, Y = Year, L = Location, G = Genotype, Rep= Replication

The results further indicated the importance of testing genotypes in more locations as is currently practiced in order to preserve the high levels of genotype stability and wide adaptability. The environmental effect influencing TRY was reported in different cassava studies Aina *et al.* (2007); Agyeman *et al.*, 2015; Tesfaye *et al.*, (2017) reported in multi-location yield experiments, location accounted for about 92%, 85% and 69% of the total variation, whilst genotype and G×E interaction combined contribute to 4.62 and 8.27% of the total variation. In this regards, dissimilar reports obtained from Adetoro *et al.*, (2021) who reported high significant difference on genotype, location and year on TRY of cassava genotypes collected from Nigeria. This difference might be due to the fluctuation of environments in all tested areas.

Additive main effects and multiplicative interaction analysis (AMMI)

The enormous G×E interaction was examined further by using AMMI and GGE bi-plot analysis (Yan and Tinker, 2006). The AMMI analysis of variance showed highly significant effects ($p \leq 0.01$) of genotypes, environments, and GEI on cassava yield and related traits (Table 3). Genotype, environment, and GEI contributed 8.31%, 58.96% and 32.72%, respectively, to the total variation observed in TRY. Interaction principal component axes (IPCA 1 and IPCA 2), on the other hand, were non-significant ($p > 0.05$) for IPCA 2 except for IPCA 1, which was significant only at the 5% level of probability, and explaining 44.55% and 31.84% of the total GEI. The percent of variation of genotype, environment and GEI on TRY obtained from this study is comparable with the report of Atung and Jeffrey, (2018).

Table 3. AMMI analysis of variance for cassava yield and related traits of 11 genotypes tested across six environments in Southwest Ethiopia during 2015-2018

Source of variation	DF	Total root yield (TRY)				Root dry weight (RDW)				Root diameter (RDi)			
		SS	MS	Variation explained (%)	GxE Explained (%)	SS	MS	Variation explained (%)	GxE Explained (%)	SS	MS	Variation explained (%)	GxE Explained (%)
Treatments	65	44142	679.1**	67.28		224072	3447**			57295	881**	96.05**	
Genotypes	10	3670	367.0	8.31		7435	743**	3.31		539	54**	0.94*	
Environment	5	26028	5205.6**	58.96		189956	37991**	84.77		54498	10900**	95.11**	
Block	12	2698	224.8	6.11		8028	669**	3.58		682	57*	1.19**	
Interactions	50	14444	288.9	32.72		26681	534**	11.90		2259	45*	3.94**	
IPCA-1	14	6435	459.6 *		44.55	24684	1763**		92.51	2198	157**		97.30
IPCA-2	12	4600	383.4 ^{ns}		31.84	1106	92 ^{ns}		4.14	34	3 ^{ns}		0.05
Residuals	24	3409	142.0 ^{ns}		23.60	891	37 ^{ns}		3.34	26	1 ^{ns}		0.04
Error	120	32962	274.7	74.67		23085	192			3398	28	5.93	

Df. degrees of freedom, ns: non-significant ($P > 0.05$); *, ** significant at $p \leq 0.01$. SS= Sum of square, and MS= Mean square

For RDW, genotype, environment and GEI contributed 3.31%, 84.77% and 11.90% to the total variance explained, respectively. Only IPCA 1 was highly significant ($p \leq 0.01$). IPCA 1 and IPCA 2 scores explained 92.51% and 4.14% of the total GEI, respectively. Comparatively, this result was slightly lower than the report of Adetoro *et al.*, (2021) on cassava genotypes from Nigeria. For RDi, the total variation contributed by genotype, environment, and GEI was 0.94%, 95.11% and 3.94%, respectively. The two IPCAs accounted for 97.35% of the total GEI explained, each contributing to 97.30% (IPCA 1) and 0.05% (IPCA 2) (Table 3). Similarly, higher total variation was reported by Akinwale *et al.*, (2011) and Aina *et al.*, (2009) on cassava genotypes from Nigeria.

Performance of genotypes across individual locations

The mean TRY, RDW and RDi of cassava genotypes across six environments was presented in Table 4. On average, genotypes 45/72NW, AAGT 108 and respective local check had the highest mean yield across environments. Genotype 45/72NR had lowest mean total root yield of all genotypes across environments. Highest RDW was observed in the environment-4, followed by environment-2 and environment-3 (Table 4). On average, genotypes 44/72NR and AAGT 028 produced the highest and the lowest root dry weight, respectively. This finding was consistent with the result of Alex *et al.*, (2021) who reported higher mean

storage tuber yield of cassava (41.26 t/ha) genotype from Adjumani district of Uganda.

Similarly, the highest RDi was observed from genotypes 45/72NW, AAGT 189 and AAGT 108 with a value of 62.10, 57.17 and 55.20 cm, respectively (Table 4). Environment-6 and environment-2 were the best environments for the RDi with mean value of 63.92 and 62.91 cm, respectively (Table-4). In this regards, different scholars reported the highest and lowest root yield and related traits performances of cassava genotypes in different countries, for example Yan and Tinker (2006) and Adetoro *et al.*, (2021) from Nigeria; Tesfaye *et al.*, (2017) from Ethiopia. The environments contributed significantly to the differential performance of genotypes across environments resulting in either cross over or non-cross over GxE. According to Yan *et al.*, (2000) and Jandong *et al.*, (2019) who reported that the cross over effects as a significant change in performance from one environment to another, while in non-crossover interaction, a ranking of genotypes remains constant across the environment.

AMMI stability value (ASV)

The AMMI stability values revealed variations in TRY and related traits stability among the 11 genotypes (Table 5). For TRY, genotype AAGT 108 was highly stable, with an ASV value of 1.18. while, 45/72NW and 44/72NW were among the least stable genotypes; other genotypes had intermediate stability.

Table 4. Mean TRY (t/ha), TDW (t/ha) and RDl(cm) performance of 11 cassava genotypes tested across six environments.

Genotypes	TRY						Over all Mean	TDW						Over all Mean	RD <i>i</i>						Over all Mean
	Environments							Environments							Environments						
	E-1	E-2	E-3	E-4	E-5	E-6		E-1	E-2	E-3	E-4	E-5	E-6		E-1	E-2	E-3	E-4	E-5	E-6	
44/72NR	37.1	59.4	30.8	18.6	44.9	38.1	38.1	9.09	25.6	74.3	58.4	19.4	9.41	32.70	49.0	54.2	44.5	36.9	48.8	42.1	45.91
44/72NW	39.7	67.9	31.7	18.2	50.5	39.5	41.3	9.94	27.3	32.8	55.5	20.2	11.2	26.17	47.3	56.4	47.9	39.7	52.5	42.8	47.79
45/72NR	32.3	47.7	23.5	23.3	33.9	48.2	34.8	4.50	24.9	52.1	58.1	13.6	12.9	27.71	28.8	61.4	44.2	41.5	41.3	75.3	48.78
45/72NW	43.7	83.3	27.0	24.8	56.8	65.4	50.2	13.1	37.0	26.6	19.1	20.0	31.7	24.59	53.9	74.2	54.8	52.8	54.1	82.5	62.10
AAGT 028	40.6	56.6	32.3	30.6	42.9	52.0	42.5	11.4	29.8	5.63	14.8	18.3	23.2	17.21	39.9	60.9	46.5	41.9	46.8	63.6	49.96
AAGT 108	43.7	59.3	36.8	31.8	46.6	44.4	43.8	14.9	27.4	22.9	25.1	23.0	16.2	21.60	57.0	65.4	48.2	44.7	49.3	66.6	55.20
AAGT 189	38.2	69.1	25.0	22.0	47.6	53.0	42.5	11.1	31.6	4.91	87.7	19.0	22.9	29.55	62.7	67.6	46.8	45.2	46.9	73.8	57.17
AAGT 191	42.6	54.9	37.8	30.9	44.5	35.4	41.0	12.1	23.9	20.2	57.2	18.5	17.0	24.85	49.3	62.2	46.8	42.4	47.8	62.8	51.89
AAGT 192	40.4	43.6	36.8	34.9	39.9	44.9	40.1	10.7	26.2	17.2	19.8	18.0	17.7	18.28	47.0	62.8	47.1	43.0	47.6	65.2	52.13
AAGT 200	44.3	65.5	37.7	26.8	51.2	28.7	42.4	15.2	28.7	38.6	16.1	24.6	14.1	22.91	60.3	62.5	47.7	42.7	50.6	56.8	53.46
Local	40.1	74.3	25.3	23.0	50.8	58.7	45.3	12.3	34.3	18.8	16.5	19.9	26.7	21.46	52.0	64.1	45.0	42.7	44.4	71.5	53.28
Mean	40.3	61.9	31.3	25.9	46.3	46.2	42.0	11.3	28.8	28.5	38.9	19.5	18.5	24.27	49.8	62.9	47.2	43.0	48.2	63.9	52.52
LSD_(0.05)	12.9	22.9	17.4	10.4	27.5	30.6	10.9	6.8	10.3	0.02	4.8	13.4	12.7	11.7	21.8	0.81	2.94	1.05	1.5	1.36	3.85
CV_(%)	18.9	39.5	32.6	23.7	35.1	42.2	40.2	34.4	40.3	10.9	30.1	40.4	40.4	51.4	25.7	13.8	36.6	14.4	19.3	12.5	46.0

E=Environments, TRY= Total root yield; RDW= Root dry weight, RDl= Root diameter

CV=Coefficient of variation(%), LSD= Least significant difference at 5% level of probability

For RDW, genotypes 45/72NR was highly stable with ASV values of 1.46; whereas genotype AAGT 108 remained the least stable among others (ASV of 3.96). For RD_i, genotypes AAGT 191, 44/72NR and local were the most stable, with ASV values of 0.14, 0.94 and 0.95, respectively; whereas genotypes AAGT 189 and AAGT 200 were the least stable genotypes due to higher ASV values. On the other hand, data in Table 6 showed that environments ENV-1 and ENV-5 had a low ASVs score in TRY as compared to RDW and RD_i and these environments were considered highly discriminating of genotypes. Comparatively, similar ASV values were reported by Esther *et al.*, (2020) on taro genotypes from Ghana. The AMMI model does not make provision for a quantitative stability measure (Atung and Jeffrey, 2018; Jandong *et al.*, 2019). Such a measure is essential in order to quantify and rank genotypes into their TRY stability.

The ASV measure was proposed by Yan *et al.*, (2007) to cope with this problem. The ASV is the distance from zero in a two-dimensional scatter gram of IPCA1 scores against IPCA2 scores. Since the IPCA1 score contributed more to $G \times E$ sum of squares, it has to be weighted by the proportional difference between IPCA1 and IPCA2 scores to compensate for the relative contribution of IPCA1 and IPCA2 to the total $G \times E$ sum of squares. In the ASV method, a genotype with the least ASV score is the most stable. Accordingly, genotype AAGT 108 (TRY),

45/72NR (RDW) and AAGT 191 (RD_i) were the most stable. Therefore, these genotypes can be used as checks in genotype evaluations. According to Atung and Jeffrey, (2018), the larger the ASV value, either negative or positive the more specifically adapted a genotype was to certain environments. However, according to Purchase (1997), a small ASV value indicated a more stable genotype across environments (Purchase, 1997).

Additive main effect and multiplicative interaction bi-plot analysis

The AMMI 2 bi-plot analysis was conducted by plotting IPCA 1 scores against IPCA 2 scores for genotypes and environments. The AMMI 2 bi-plot analyses of TRY, RDW, and RD_i of the 11 genotypes evaluated in six environments are shown in Figure 1a-c, respectively. For TRY, the percentage of variation accounted by the IPCA 1 and IPCA 2 axes was 44.55% and 31.85%, respectively (Figure 1a). Comparatively, this result was lower than the report of Adetoro *et al.*, (2021) on the percent variation of the IPCA 1 (56.4%) and IPCA 2 axes (32.91%) for storage root yield of cassava genotypes from West Africa. Genotypes 8 (AAGT 191) and 6 (AAGT 108) had broad adaptability as they were located closer to the center of the bi-plot. Genotypes 4 (45/72NW), 11 (local), 2 (44/72NW), and 1 (44/72NR) are placed furthest from the point of origin, showing specific adaptation to the environments within their proximity on the bi-plot. Similar findings reported by Akinwale *et al.*, (2011) on 43 cassava genotypes at three different agro-ecologies of Nigeria.

Table 5. AMMI stability values (ASV) and IPCA scores TRY, RDW and RD_i of 11 genotypes tested in six environments in SW Ethiopia during 2015-2018

Genotype	TRY				RDW				RD _i			
	Mean	IPCAg1	IPCAg2	ASV	Mean	IPCAg1	IPCAg2	ASV	Mean	IPCAg1	IPCAg2	ASV
44/72NR	34.82	2.77	-1.21	3.24	20.19	1.26	1.50	2.29	11.94	-0.06	-0.93	0.94
44/72NW	37.95	2.74	-2.41	4.23	20.75	1.65	1.30	2.61	11.88	0.32	-1.08	1.29
45/72NR	34.85	-1.59	1.9	2.77	18.15	1.05	-0.23	1.46	9.20	1.67	0.52	3.73
45/72NW	50.20	-3.07	-2.37	4.56	32.44	-1.00	-2.44	2.80	14.31	-0.54	0.56	1.32
AAGT 028	42.52	-1.01	1.56	2.02	32.84	-1.79	-1.02	2.66	10.99	1.69	-0.06	3.74
AAGT 108	43.81	0.39	1.07	1.18	34.83	-2.74	1.23	3.96	14.07	-1.23	0.14	2.73
AAGT 189	42.50	-1.9	-1.08	2.64	28.81	0.87	-0.97	1.54	15.12	-2.20	0.60	4.91
AAGT 191	41.04	1.53	1.28	2.33	37.81	-1.10	0.40	1.56	12.59	0.06	-0.03	0.14
AAGT 192	39.59	0.28	3.62	3.64	31.79	-1.49	0.05	2.05	12.26	0.48	0.04	1.06
AAGT 200	42.38	2.35	-0.84	3.10	30.45	0.09	1.76	1.76	14.40	-1.87	-0.27	4.15
Local	45.37	-2.5	-1.52	3.52	30.29	-1.17	-1.54	2.23	13.13	-0.37	0.49	0.95

IPCAg = integrated principal component analysis, TRY=total root yield per hectare, RDW = root dry weight, RD_i = root diameter

Table 6. AMMI stability values (ASV) and IPCA scores TRY, RDW and RD_i of six environments tested 11 genotypes in SW Ethiopia

Genotype	TRY				RDW				RD _i			
	Mean	IPCAg1	IPCAg2	ASV	Mean	IPCAg1	IPCAg2	ASV	Mean	IPCAg1	IPCAg2	ASV
ENV-1	40.26	1.42	0.41	1.60	11.32	1.40	1.28	1.98	9.77	-1.74	0.03	2.60
ENV-2	61.99	-0.56	-4.53	4.57	28.33	2.18	-1.03	2.57	6.29	0.90	0.09	1.35
ENV-3	31.36	2.92	1.76	3.63	11.00	1.88	1.16	2.34	4.72	0.95	-0.54	1.52
ENV-4	25.93	0.99	2.89	3.08	15.40	-2.67	0.20	2.89	4.30	0.94	-0.17	1.42
ENV-5	46.08	1.00	-2.11	2.37	19.52	1.74	1.93	2.70	4.82	0.89	-0.89	1.60
ENV-6	42.59	-5.78	1.57	6.47	18.48	1.46	-3.37	3.72	6.39	1.05	1.49	2.17

IPCAg = integrated principal component analysis, total root yield per hectare (TRY), root dry weight (RDW), root diameter (RD_i)

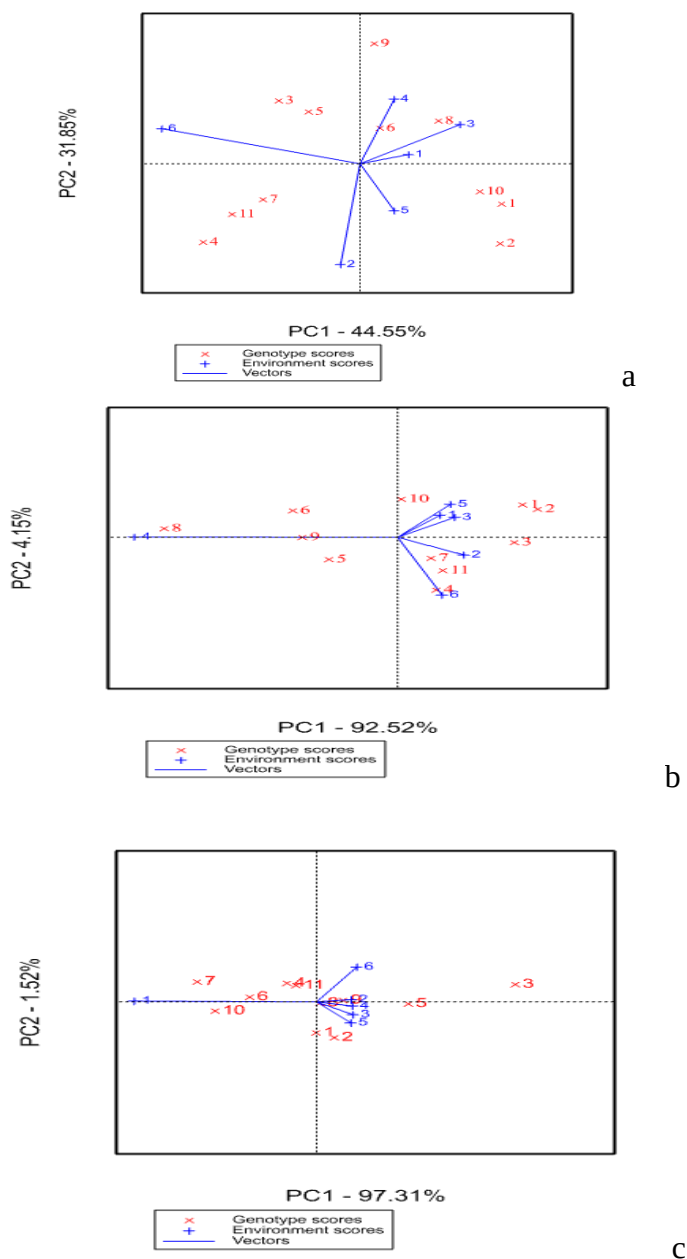


Figure 1a-c. AMMI 2 bi-plot for IPCA 1 against IPCA 2 scores for 11 cassava genotypes and six environments on (a) total root yield (TRY), (b) root dry weight (RDW) and (c) root diameter.

Moreover, genotypes 9 (AAGT 192), 8 (AAGT 191), and 6 (AAGT 108) had above-average yields and were located at the acute angle of PC1. Genotypes located on the right-hand side of the bi-plot were positively correlated with the environments on the same side. Based on this analysis, environment 6 was considered highly discriminating and had similar discriminating ability of the site since it had longer vector. Environments 1, 3 and 4, were highly positively correlated, indicating that genotypes ranked similarly with respect to TRY in these environments. This suggested that these environments might form part of the same mega-environment.

For RDW, the AMMI-2 bi-plot explained 96.67% of the total GEI (Figure.1b). The percentage of variation accounted for by IPCA-1 and IPCA-2 was 92.52% and 4.15%, respectively. According to Adetoro *et al.*, (2021), the percent variation of the IPCA 1 and IPCA 2 axes was 84.1% and 12.93%, respectively. On the other hand, Fekadu *et al.*, (2017), reported the variation of the IPCA 1 (61.63%) and IPCA 2 axes (13.99%) for root dry weight of orange fleshed sweet potato genotypes from South Ethiopia. Genotypes 7 (AAGT 189), 11 (local), 10(AAGT 200) and 4 (45/72NW) were close to the bi-plot origin; these genotypes had yields close to the overall mean yield. The following genotypes were positively correlated

with environments closer to them: 10 (5), 7 and 11 (2), 4 (6) and 8 (4). Genotypes located on the right-hand side of the bi-plot were positively correlated with the environments found on that side. To that extent, environment 4 highly discriminating in this analysis. This environment showed high discriminating ability based on longer vector. Environment 3 and 2 had longer vectors, indicating the similar discriminating ability of the site at different right angles. Environment 1 had the shortest vector, suggesting poor genotype discriminating ability.

The percentage of variation of AMMI 2 bi-plot for RDi accounted for by IPCA 1 and IPCA 2 was 97.31% and 1.52%, respectively (Figure.1c). Genotypes 1 (44/72NR), 2 (44/72NW) and 5 (AAGT 028), 8 (AAGT 191), 9 (AAGT 192) were much closer to the bi-plot center, showing broader adaptability across the environments and had positively correlated with environments located on the right-hand side of the bi-plot. Genotype 1 (44/72NR) was positively correlated with environment 5 (AAGT 028), suggesting specific adaptation to this environment. In this analysis, except environment 1, all environments had shorter vectors, which imply the low discriminating ability of the site. Most environments in this study had positive correlations. This was expected, since almost similar

environmental conditions existed between environment 1 and 2, and 3, 4 and 5 and 6 (Table 2). The positive correlation obtained between test environments also suggests that indirect selection for TRY can be applied across the sites (Otoo *et al.*, 1994). Combining these environments into a single test environment can give similar genotypic responses, thus reducing unnecessary costs and improving breeding efficiency (Gauch and Zobel, 1997). For TRY, which is the trait of economic interest, environment PC1 had both positive and negative scores. Similar results were reported by Aina *et al.* (2007) indicated the existence of cross over G×E interactions. Genotypes with large PC1 scores can be easily recognized in environments with larger PC1 scores (Yan *et al.*, 2007; Agyeman *et al.*, 2015).

Mega-environment analysis using GGE bi-plots

The polygon views of the GGE bi-plot for TRY, RDW and RDi are shown in Figure. 2a-c, respectively. In each bi-plot, different mega environments (MGEs) were grouped into sectors. Environments within the same MGE were assumed to have a similar effect

on genotype performance and were considered a homogeneous group. Similarly, genotypes within the same MGE were assumed to have a similar response to the environments located in the MGE sector. The genotype located at the vertex of the sector was considered the best-performing variety in the MGE. For TRY (Figure. 2a), principal component 1 (PC1) explained 46.19% of the total variation, while PC 2 explained 27.01%, with both axes accounting for 73.20% of the total variation. Perpendicular lines were drawn to each side of the polygon, all lines starting from the bi-plot origin.

In this analysis, three mega-environments were found, environments 2, 5 and 6 combined into MGE-1, environments 3 and 4 fell into a separate MGE-2 and MGE-3, respectively. Genotypes 4 (45/72NW), 7 (AAGT 189) and 11 (local) were the highest-yielding genotype in MGE-1. Genotype 5 (AAGT 028) won in the MGE-2. Genotype 8 (AAGT 191) was positively correlated with the environment 4 site and was the winning genotype in MGE-3.

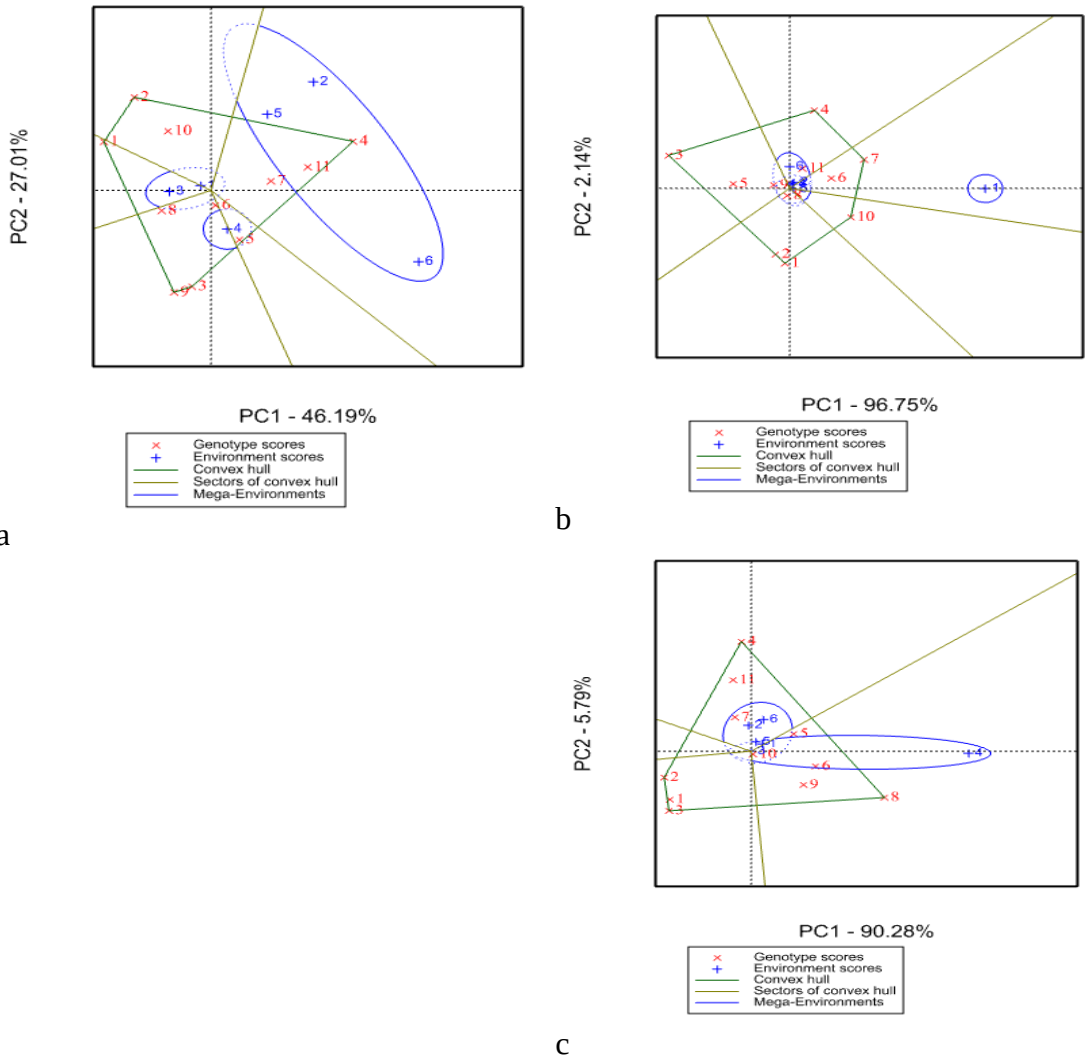


Figure 2a-c. The "which-won-where" polygon view for (a) TRY , (b) RDW and (c) RDiof of the GGE bi-plot analysis representing the performance of 11 cassava genotypes tested across six environments

For RDW, the percentage of GGE explained by PC 1 and PC 2 was 90.28% and 5.79%, respectively (Figure. 2b). The bi-plot explained 96.07% of the total variation. The bi-plot consisted of two MGEs; where environments 2, 6 and 5 are combined into MGE-1; environments 1, 3, and 4

fell to form MGE-2. Perpendicular lines were drawn to separate the respective sides of the polygon. Genotypes 7 (AAGT 189), 4 (45/72NW) and 5 (AAGT 028) were the highest yielding vertex genotype in MGE-1, whereas genotype 6 and 10 was the winner in MGE-2. Similarly,

for RD_i, the percentage variation accounted for by PC 1 and PC 2 was 96.75% and 2.14%, respectively (Figure. 2c); the total variation explained by the bi-plot was 98.89%. In this bi-plot, only two mega-environments were found; where environments 2, 3, 4, 5 and 6 combined into MGE-1 and environment 1 was fell in MGE-2. Most genotypes were the highest-yielding vertex cultivar in MGE-1, whereas, genotype 7 (AAGT 189) and 10 (AAGT 200) was the highest-yielding vertex genotype in MGE-2.

The GGE bi-plots confirm the crossover $G \times E$ interactions observed in the AMMI analysis. It is noteworthy that when crossover GEI patterns are not repeatable across years, the GE cannot be exploited (Adetoro *et al.*, 2021). Instead, it can be eluded by selecting high yielding and stable genotypes across target environments (Otoo *et al.*, 1994; Sbongeleni *et al.*, 2019). The bi-plots on RDW indicated that MGE-1 consisted of environments 2, 6 and 5; while MGE-2 had environments 1, 3, and 4. Since a mega-environment is defined as a group of locations that consistently share the best set of genotypes across years, data from multiple years are essential to decide whether or not the target province can be divided into different mega-environments (Yan *et al.*, 2007).

Genotype yield and stability using GGE bi-plots

For TRY, PC1 explained 46.19% of the variation and PC 2 explained 27.01% and a total of 73.20% of the variation (Figure.3a). This result slightly consistent with the data reported by Dumaetal *et al.*, (2019) who observed that the percentage variation of total cane yield accounted for by PC 1 and PC 2 was 45.19% and 34.93%, respectively. Genotype 4 (45/72NW) was the ideal genotype and, therefore, it was considered the most desirable genotype of all the evaluated genotypes, followed by genotypes 11 (local) and 7 (AAGT 189). The same interpretation is applicable to RDW (Figure. 3b); the percentage of PC 1 and PC 2 were 90.28% and 5.79%, respectively, (96.07% of the total variation). Genotype 5 (AAGT 028) had high RDW and was more stable than other genotypes, confirmed by its closest position to the ideal genotype.

For RD_i (Figure. 3c), the PC1 explained 96.75% and PC 2 explained 2.14% of the variation (total = 98.89%). Also lower percent of variation on RD_i were reported on different crops, Fekadu *et al.*, (2017) on sweet potato, Atung and Jeffrey, (2018) on taro Tesfaye *et al.*, (2017) on cassava genotypes from Ethiopia. Genotype 4 (45/72NW) was located closer to the ideal genotype, making the highest-yielding and most stable genotype of all genotypes tested. Yan

et al., (2007), suggested that an ideal genotype should have both high mean performance and high stability within a mega-environment. The arrow shown on the axis of the AEC abscissa compares and ranks performance of the test genotypes relative to the “ideal genotype”. Yan *et al.* (2000) defined an “ideal” genotype based on both mean performance and stability, and

the genotypes types can be ranked based on their distance from the ideal genotype. This study showed that genotype 4(45/72NW) is ideal for TRY and RD_i evaluated. This genotype is high yielding and more stable because of proximity to the ideal genotype.

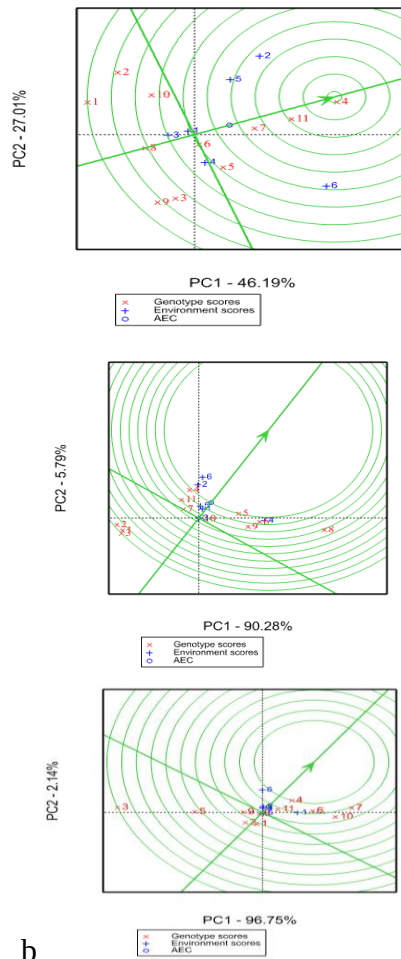


Figure 3a-c. The average environment coordination (AEC) view showing mean performance and stability of 11 cassava genotypes tested in six environments on (a) Total root yield (TRY), (b) root dry weight (RDW) and (c) diameter (RD_i).

Conclusion and Recommendation

The result of this study showed that the storage root yield of cassava was highly affected by genotype and location (environment) and the GEI contributed to the variation among the genotypes studied. This also further indicated the yields and related traits studied were varying across the six environments. Genotypes 45/72 NW, AAGT 108, and AAGT 189 were found to be widely adaptable and had yield stability across environments. Therefore, these genotypes should be recommended for release to farmers in southwest Ethiopia for production. In addition, three mega-environments were identified from the current study, further multi-environment trials (METs) need to be conducted for confirmation of the result for cassava breeding and production in the southwest Ethiopia.

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Yam Production Constraints, Farming Systems and Farmer Preferred Traits in Ethiopia: Implication for Breeding and Conservation

¹Tewodros Mulualem*, ²Firew Mekbib, ³Shimeles Hussein and ⁴Endale Gebre

¹ Jimma Agricultural Research Center, Po.Box 192, Jimma, Ethiopia

² Haramaya University, School of Plant Sciences, Po Box 138, Dire Dawa, Ethiopia

³African Centre for Crop Improvement, School of Agriculture, Earth and Environmental Sciences, University of KwaZulu-Natal, Private Bag X01, Pietermaritzburg, 3209, South Africa

⁴ Ethiopian Institute of Agricultural Research, P.O. Box 2003, Addis Ababa, Ethiopia
E-mail: tewodrosmulualem@gmail.com

Abstract

Yam production in Southwest Ethiopia is threatened by a socioeconomic, a biotic and biotic factors. The objective of this study was to document the major yam production constraints, farming systems, the number of farmers identified landraces and trait preferences from major growing areas of Southwest Ethiopia. A participatory rural appraisal study was conducted in seven yam producing districts of the region. Data were collected from 240 yam growers using a semi-structured questionnaire, focus group, key informant discussions and field observations. Yam production restraints were mainly associated with socioeconomic factors such as low attention given to the crop and dilution of the crop by improved crop technologies, which reported by 14.71 and 11.15% of respondents, respectively. Drought and wild animal attacks were the major cause of yield reduction, as reported by 14.4 and 13.93% of the respondents, respectively. A total of 38 farmers' named yam landraces was identified for their traits preferences. The major yam traits preferred by farmers were: high yield (35.42%), good market (11.05%), early maturity (8.86%), powdery after boil (10.48%) and disease resistance (3.53%). Medicinal use reported by 5.58% of respondents and white and mixture with red flesh color (5.91%) was the main farmer and market preferred traits. Yam variety development programs should therefore discourse the above constraints and farmer-preferred traits for sustainable yam production in Southwest Ethiopia.

Keywords: Farmers' landraces, participatory, preferences production, traits, yam

Introduction

Yam (*Dioscorea* spp.) is a multi-species crop that belongs to the genus *Dioscorea* and family *Dioscoreaceae* (Mignouna *et al.*, 2002; Dansi *et al.*,

2010). It is found in Africa, India, Southeast Asia, Australia and South America comprising of 600 species (Tewodros, 2013; Loko *et al.*, 2015). All species are tropical origin and cultivated for their edible starchy tubers (Paterne *et al.*, 2019). From all,

about ten yam species are cultivated for food staples serving millions of people in the tropics (Sesay *et al.*, 2013; Dansi *et al.*, 2010). West Africa is the predominant yam producing region globally (Coursey, 1967; Tamiru *et al.*, 2007). The region contributes 95% of the world's yam production with considerable varietal and genetic diversity of yams (Hamadina *et al.*, 2009; Dansi *et al.*, 2013). Although, yams are cultivated mainly in West Africa, the most important species are widely adopted in Ethiopia as cultivated and wild relatives (Terauchi *et al.*, 1992; Tamiru *et al.*, 2007; Dansi *et al.*, 2012). In Ethiopia, a large pool of yams that are widely distributed in complex cropping systems with wide genetic base in different parts of the country (Hildebrand, 2003; Wendawek *et al.*, 2013). It is the third most important root crop in Ethiopia, after cassava (*Manihot esculenta* Crantz) and sweet potato (*Ipomoea batatas* (L.) Poir) (Tamiru *et al.*, 2007). It is widely cultivated in South, Southwest and Western parts of the country and over 1.5 million people depend on it (Tewodros, 2013). In addition to the food, the storage tuber of yams contains some pharmacologically active substances (dioscorine and sapogenin) and used as medicine for ailments related to the digestive tract and reduce the blood glucose level (Jaleel *et al.*, 2007; Nashriyah *et al.*, 2012; Tewodros *et al.*, 2018). Besides, the crop is also used as female contraceptive and has higher contribution to reduce the growing

people currently facing (Scarcelli *et al.*, 2011).

The most important feature of yam is good adaptability and produce high yields in broad agro ecology (Nora *et al.*, 2006), annual cycle of food availability, diverse maturity and flexibility harvest periods without the use of large amounts of agricultural inputs (Tamiru *et al.*, 2008; Mauricio *et al.*, 2014). However, yam production in Ethiopia faces various constraints, amongst which, low yields, socioeconomic factors, lack of adapted varieties for diverse agro-ecologies and presence of biotic and abiotic stress that are threatening its production and productivity (Robert *et al.*, 2010; Happy *et al.*, 2018). Use of improved varieties with suitable agronomic practices is essential to boost yam production in the region. Further, in-depth knowledge of farmers' preferences, production challenges, and priorities are prerequisites in production and technology development (Happy *et al.*, 2018). Previous studies conducted by Tamiru *et al.*, (2011) identified drought and shortage of planting materials as the main yam production problems in Southern Ethiopia. However, the report did not fully cover the major yam growing areas of southwest Ethiopia. Thus, comprehensive assessment on production problems and farmers preferred traits present in Ethiopian yam germplasm is required to use a relatively greater number of samples from the diverse growing regions for

documentation and sustainable yam production in Southwest Ethiopia.

Participatory Rural Appraisal (PRA) is an interdisciplinary research approach useful to capture yam production constraints and farmers preferences (Happy *et al.*, 2018). For instance, participatory breeding incorporates farmers' knowledges and preferences during variety development, testing, and release (Tamiru *et al.*, 2011). This leads to increased adoption of newly developed cultivars by farmers (Dorward *et al.*, 2007). Therefore, it is important to consider farmers' needs and preferences in the yam variety development, to improve production, selection to ensure adoption of improved cultivars by farmers and to address the existed problems in an affordable and sustainable way. Hence, the objective of this study was to identify the major constraints affecting yam production and farmer-preferred yam traits in Southwest Ethiopia for future breeding programs.

Materials and Methods

Description of study areas

The study was conducted in Jimma, Sheka and Bench-maji zones, which are the major yam production areas of Ethiopia from October, 2013 to June, 2013. Accordingly, five districts namely, Manna, Dedo, Shebe-sombo, Seka-chekorsa and Kersa from Jimma zone and two districts namely Sheko and Yeki from Bench-maji and Sheka zones, respectively, were selected (Figure 1). These areas were selected for study based on strong traditions in cultivating and domesticating various yam landraces with wide genetic base (Hildebrand, 2003), high production potential and the long history of production and management system of yam with farmers' traditional knowledge (Tamiru *et al.*, 2008).

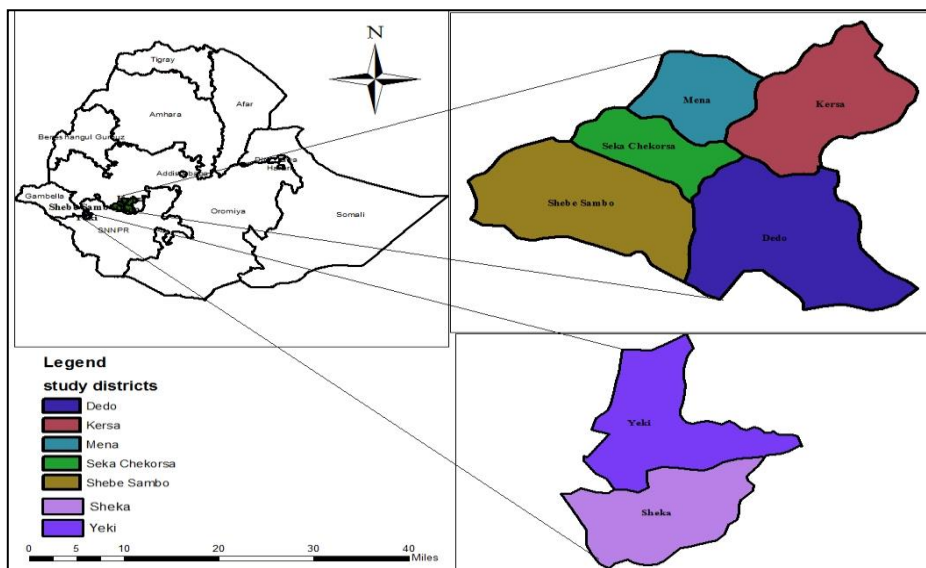


Figure 1. Administrative map of Ethiopia showing seven districts where the survey data were collected. Source Tewodros *et.al*, (2018).

Questionnaire design, sampling and data collection

For this study, stratified random sampling procedure was followed to describe the sampling units. The area was stratified first based on elevation and agroecology to wrap appropriate ecological range of yam and kebeles (small administration unit in Ethiopia) were elected and judge as main yam growing areas. A semi-structured questionnaire, transect walks and field visits (home gardens, cultivated fields) key informants and focus group discussions were used to collect information from selected farmers. Data gathered from transect walks, field visits and key informants were used to provision and confirm the information obtained from the semi-structured questionnaire. From each district on average 34 farmers, 15-20 yam producers, 10 key informants and

five development agents (DA's) were sampled from different social groups for individual interviews, group and key informants' discussions. In total, 240 farmers were interviewed using the semi-structured questionnaire and key informant discussions. Through the semi-structured questionnaire, the following data were gathered: household information, farm size, farming system used, number of landraces in each district, constraints in yam production, important crop traits preferred by farmers and market accessibility. Transect walk was also done to make direct observations on a few randomly selected fields in each village in each district. Other PRA tools used to gather information included the number of farmers' identified yam landraces grown and major production problems in all districts. In addition, farmers were asked about the type of yams, trait

preferences and utilization options were described and ranked using a 1-3 score.

Data analysis

The collected quantitative and qualitative social survey data were coded and analyzed using the IBM Statistical Package for Social Science (SPSS) software, version 21.0 as described by Jones *et al.*, (2014). Cross-tabulation tables were constructed, and descriptive statistics were generated to summarize data from the questionnaires. To make statistical inferences, descriptive statistics, frequencies and percentages were conducted to analyze relationships between variables.

Results

Description of the surveyed households:

The summary of household characteristics of the respondents was presented in Table 1. Out of 240 farmers interviewed 182 and 58 were males and females, respectively. This suggested that there was gender disparity in all tested districts. The wide gap between the number of males and females participating in the study was higher in Seka-chekorsa (27 males and 3 females) and in Shebe-sombo (23 males and 8 females). The proportion of males (22) was greater than that of females (10) in Sheko. The high percentage of male farmers suggested to their access to farm land and their position as head of the family. In this study, 103, 69 and 68 of the farmers had followed Orthodox, Muslim and Protestants, respectively. The mean age distribution of the farmers between districts revealed that the highest (55.08) and the lowest (45.62) ages was recorded in Dedo and Sheko districts, respectively (Table 1).

Table 1: Household characteristics of the surveyed districts in southwest Ethiopia

Districts	Number of farmers	Religion			Sex		Mean age of farmers	Mean family size	Mean farm size(ha)
		Ortho	Mus	Pro	Male	Female			
Dedo	38.0	20.0	8.0	10.0	28.0	10.0	55.08	8.00	1.63
Kersa	42.0	22.0	13.0	7.0	30.0	12.0	47.83	6.19	0.86
Manna	35.0	9.0	22.0	4.0	28.0	7.0	47.46	6.08	1.47
Seka-chekorsa	30.0	10.0	17.0	3.0	27.0	3.0	51.67	6.80	1.44
Shebe-sombo	31.0	19.0	7.0	5.0	23.0	8.0	52.35	6.90	1.40
Sheko	32.0	8.0	0.0	24.0	22.0	10.0	45.62	6.43	1.13
Yeki	32.0	15.0	2.0	15.0	24.0	8.0	50.11	6.80	1.51
Total	240.0	103	69.0	68.0	182.0	58.0	350.1	47.20	9.44
Mean	34.28	14.7	9.85	9.71	26.0	8.28	50.01	6.74	1.35

Ortho: Orthodox, Mus: Muslim, Pro: protestant

From the total, 202 farmers in the seven districts comprised 6-7 individuals and only 38 households embraced eight people. The number of individuals per household influenced farming operations requiring human labor. Households with more than five family members were more efficient in yam farming than families with fewer members, which predominantly outsourced their labor needs from their communities or cultivated only a small portion of their land. Most respondents (198) had more than one hectare, very few (42) farmers in Kersa had 0.86 hectare of land (Table 1).

Crop production in the study areas:

In all tested districts, farmers depended on both crops and livestock as major sources of food and income. The mean area of land being cultivated by each interviewed individual farmer ranged from 0.86-1.63 ha with a mean of 1.35 ha. (Table 1). Crops grown in the study districts included maize (*Zea mays*), coffee (*Coffea arabica*), wheat (*Triticum aestivum* L.), and taro (*Colocassia esculenta* (L.), yam (*Dioscorea spp.*), millet (*Eleusine*

coracana L. Gaertn), tomato (*Lycopersicum esculentum* L.), cassava (*Manihot esculenta* Crantz), potatoes (*Solanum tuberosum* L.) and cabbage (Table 2). From the total respondents, 24.58, 18.75 and 17.08 % of farmers' cultivated maize, coffee and yam, respectively. Some crops were grown in specific districts. For example, potato was grown in Dedo, Kersa and Manna districts, occupying 2.08% of the total respondents. Similarly, the number of farmers who cultivated cassava in Manna was almost equal to that of tomatoes in Seka-chekorsa and Shebe sombo districts (Table 2).

According to the farmers, most of the crops were grown during the rainy season, i.e. from March-June in Dedo, Kersa, Manna, Seka-chekorsa and Shebe-sombo and from October-February in Sheko and Yeki districts (Table 2). Furthermore, some socio-economic parameters related to the households surveyed such as the age of the households and family size affect the farmers' decision making in the number of crop production.

Table 2: Number of farms covered by major crops during 2015/2016 cropping season in seven tested districts of southwest Ethiopia

Crops	Districts							Total farms	Percents (%)
	Dedo	Kersa	Manna	Seka chekorsa	Shebe sombo	Sheko	Yeki		
Maize	11	12	8	7	8	5	8	59	24.58
Coffee	10	8	7	2	9	6	3	45	18.75
Wheat	6	4	5	2	3	0	0	20	8.33
Taro	1	3	1	8	3	6	6	28	11.67
Yam	8	7	3	4	2	8	9	41	17.08
Millet	1	4	5	2	2	0	4	18	7.50
Tomatoes	0	2	3	1	1	7	0	14	5.83
Cassava	0	0	1	1	1	0	2	5	2.08
Cabbage	0	0	0	3	2	0	0	5	2.08
Potato	1	2	2	0	0	0	0	5	2.08
Total	38	42	35	30	31	32	32	240	100

Yam production constraints

Yam production constraints faced by farmers in the seven districts are summarized in Table 3. The major constraints included, low attention given to the crop, drought at early stage of the crop, replaced yam farms by high value crops, wild animal attacks, stake and labor shortages, low soil fertility, shortage of farm land and low extension service. Further, during group and key informant discussion, some farmers identified drought at early stage as the main yam production constraint, followed by dilution of the crop by improved cereals technologies. Farmers' ranking production constraints across districts showed yam production was highly constrained by wild animal attacks. The main animals reported were porcupine (13.93%) and mole rat (9.29%) (Table 3). However, farmers in all districts reported, some landraces used as medicine are not preferred by porcupine and mole rats. This might be due to medicinal yams had high

poly phenols or tannin like compound and not favorite by wild animals. High porcupine attacks, reported mainly in Dedo (17 farmers), Sheko (15 farmers) and Shebesombo (13farmers) districts, respectively. Apart from the wild animal attacks, the other most yield-limiting factor in the study areas was low attention given to the crop by farmers and accounted 14.71% of the total respondents (Table 3). In all tested districts, many farmers' confirmed, young people today have less interest in yams as compared to grains. In addition, more productive maze varieties have been introduced by agricultural extension workers, who also encourage intensive cultivation practices and contend area and labor force from yam production.

Severe drought at early stage was reported by 14.4% of the respondents across all studied districts (Table 3). Most of the farmers interviewed, yam planting was done in October and November and moisture stress

happened at the emergence and subsequent months thus the plant became stunted in its growth. To alleviate drought stress problem, farmers adopted various strategies, such as inter crop yam with maize and early planting in all districts. Apart from the drought, change yam farms by cereals were also another cause of reduced yam production in the tested districts. About 11.15% of the respondents reported yam farms replaced by more economical (cereal) crops (Table 3). In Sheko and Yeki, agricultural extension workers are more knowledgeable and enthusiastic about grains, especially maize and less familiar with root and tuber crops. Furthermore, many people from northern Ethiopia had settled in all surveyed districts, often achieving majority status over the indigenous people. Having grown grains in their former region, most northerners despise yam landraces and eat them only when absolutely necessary. Thus, yam landraces have come to be regarded as low status relative to the grains sown by extension workers and new comers. Furthermore, due to the superior qualities of modern varieties (especially higher yields and higher prices), farmers increasingly replaced yam landraces by modern varieties in many fields.

Changing climatic conditions are also resulting in the loss of adaptation of some formerly high yielding landraces, forcing farmers to shift to new, better adapted landraces. Shortages of farm land (11.46%) and labor (3.56%) were also other constraints mentioned by farmers as causes of yield-limiting factor for yam in the study areas (Table 3). According to the farmers', high population pressure and city expansion in different districts are the main cause of land shortage. Further, the high rate of urban migration, especially among younger people has reduced the labor force in Sheko (13) and Dedo (5) districts. Staking is one the most agronomic practice in yam production. Similarly, 7.59% of the farmers confirmed stake shortage was considered as a yield limiting factor for yam and highly associated with the cost of the stake in the areas.

This problem is common in Manna and Dedo districts of Jimma zone (Table 3). Decline in soil fertility (0.46%), as a result of frequent cultivation of the land without furrowing was evident and some landraces have therefore been abandoned due to low productivity.

Table 3: Yam production constraints in Dedo, Kersa, Manna, Seka–chekorsa, Shebe-sombo, Sheko and Yeki districts in southwest Ethiopia

Causes	Dedo **38	Kersa **42	Manna **35	Seka chekorsa **30	Shebe sombo **31	Sheko **32	Yeki **32	Total	Percent
Low attention given to the crop	11.0	20.0	18.0	17.0	16.0	8.0	5.0	95	14.71
Drought at early season	31.0	3.0	7.0	2.0	9.0	18.0	23.0	93	14.40
Porcupine attack	17.0	7.0	5.0	25.0	13.0	15.0	8.0	90	13.93
Need more management	4.0	20.0	14.0	10.0	6.0	8.0	20.0	82	12.69
Shortage of farm land	8.0	17.0	13.0	4.0	2.0	8.0	22.0	74	11.46
Replaced by high value crop	16.0	4.0	7.0	2.0	2.0	17.0	24.0	72	11.15
Attacked by mole rat	0.0	14.0	3.0	10.0	18.0	7.0	8.0	60	9.29
Shortage of stake	11.0	0.0	13.0	10.0	12.0	1.0	2.0	49	7.59
Labor shortage	5.0	0.0	0.0	3.0	2.0	13.0	0.0	23	3.56
Low market value	0.0	2.0	2.0	0.0	0.0	0.0	0.0	4	0.62
Low soil fertility	0.0	2.0	0.0	1.0	0.0	0.0	0.0	3	0.46
Lack of extension service	0.0	0.0	1.0	0.0	0.0	0.0	0.0	1	0.15

Figures in parenthesis refer to number of farmers surveyed in each district. Source: own survey result, Sum greater than 100 is due to double counting.

** sign indicate different significance level.

Yam landraces grown in tested districts

In all tested districts, farmers identified 38 known farmers named yam landraces (Table 4). Of these four landraces, (liyan, offea, welmeka and woko) belongs to well definite species of aerial yam and are recognized based on the differences of bulbils shape, color, size and surface texture. Moreover, one species called badaye belongs to *Dioscorea alata* basically identified by early maturity and a square vine with tubers varying in shape, and white, creamy yellow or purple flesh color. Nevertheless, these characters not give the impression to provide reliable means of identification, as it tends to differ within a landrace. The other landraces are hardly identified as a species or

group of species. Furthermore, wild yams widely named as sasa and karakachi were identified in forest areas of Manna and Sheko districts by having big thorns on the surface of the vine and underground tuber. The disparity in the number of yam landraces planted per farm across the tested districts was summarized in Table 4. From all districts, a relatively large number of farms having five or more landraces were found in Kersa, Manna, Shebe-sombo and Seka-chekorsa districts of Jimma zone. Conversely, moderate number of farms having four landraces was found in Sheko and Yeki districts of Bench-maji and Sheka zone of southwest Ethiopia.

Table 4: Yam landraces recorded in the study districts of southwest Ethiopia and number of farms they were encountered

No	Name of landraces	Districts							Total
		Dedo	Kersa	Manna	Seka chekorsa	Shebe sombo	Sheko	Yeki	
1	Afra	-	2	2	-	1	3	-	8
2	Anchiro	13	18	8	8	8	-	-	55
3	Badaye	1	-	-	-	-	18	21	40
4	Badenseye	-	-	-	-	-	-	2	2
5	Baki boye	2	-	1	-	-	1	2	6
6	Bambuche	1	-	4	-	1	-	-	6
7	Banda	-	-	-	-	-	4	3	7
8	Bola boye	-	-	-	-	2	-	-	2
9	Bori boye	-	-	-	-	-	3	-	3
10	Chebesha	-	-	-	-	-	5	1	6
11	Dakuy	-	-	-	-	-	2	4	6
12	Dapo	-	-	2	-	-	-	-	2
13	Dartho	13	6	1	5	7	-	-	32
14	Doni	-	-	-	-	-	4	20	24
15	Erkabea	-	-	-	-	-	-	2	2
16	Feda	4	-	-	2	-	-	-	6
17	Geano boye	2	17	8	7	7	-	-	41
18	Gesa boye	-	-	-	-	2	-	-	2
19	Goshitea	12	7	4	6	3	-	-	32
20	Gurshume	14	6	2	-	5	-	-	27
21	Hati boye	-	10	2	1	1	-	-	14
22	Karakachi**	-	-	-	-	-	7	-	7
23	Kerta boye	6	-	-	2	1	-	-	9
24	Liyan*	-	-	-	-	-	-	9	9
25	Mecha boye	3	-	2	-	-	-	-	5
26	Offea*	-	18	4	6	4	-	-	32
27	Pada	2	-	3	2	-	-	-	7
28	Sesa**	1	-	1	-	-	-	-	2
29	Torebea	-	-	-	-	-	4	-	4
30	Tsedebeye	-	-	-	-	-	2	-	2
31	Wadela boye	-	2	2	1	3	-	-	8
32	Woko*	-	-	-	-	-	3	13	16
33	Washinea	-	-	-	-	-	-	7	7
34	Wayera	6	-	-	-	-	-	-	6
35	Welmeka*	-	3	7	-	2	-	-	12
36	Zankur	-	-	-	-	-	6	-	6
37	Zatamera	-	-	3	-	-	-	-	3
38	Zawera	4	-	-	-	-	-	-	4

* = Aerial yams, ** = wild yams,

Distribution of yam landraces

The distribution of yam landraces in conventional farms is determined by adapting to environmental stresses, drought tolerance, high market value,

seed availability, ability to adapt to different climatic conditions and farmers' objectives. The outline of yam distribution within and towards the districts follows increasing diversity. In the present study, 16

landraces had a narrow distribution and specified a single district (Table 4). The remaining 22 landraces were found in more than one district. In the whole surveyed areas, there is no common landrace had found in all districts. This confirms the real picture in regard to the abundance and distribution of yams in Southwest Ethiopia. From the total of surveyed districts, five landraces (anchiro, dartho, geano boye, goshitea and gurshume) were found in all districts of Jimma zone. However, four landraces such as banda, chebesha, doni and woko were found only in Sheko and Yeki districts of Southwest Ethiopia. Besides, there were considerable differences with regarding to the number of farms where the landrace were found. Yam landraces such as, anchiro, badaye, geano boye, goshitea, dartho and offea are the most abundant landraces as they accounted 231 in number from the total landrace of the surveyed districts. Few landraces were well represented in some districts, but almost missing from the others. For example, doni was found on 24 farms visited in Yeki. Outside of this district, it was only established in Sheko with a very low in number (4). Similarly, offea was found in most districts from the Jimma zone and its abundance is high and 18 farms in Kersa and was narrow in out of this district, for example, 4, 6 and 4 farms in Manna, Seka chekorsa and Shebe sombo, respectively. Nevertheless, the distribution of offea in Sheko and Yeki was nil. This confirmed that, the

abundance and distribution of some landraces were regional and district specific and was found in one region or district and missing in other districts and their distribution is highly associated with geographical variation.

The trends of the distribution and abundance of landraces in the districts of the Jimma zone were comparatively diverse. The landraces described in these districts were local (189 and rare (51). In most diverse districts of Dedo and Manna, the majority of the landraces were quite distributed with a relatively lower but comparable abundance. This reflected higher evenness of landrace abundance in these districts. The least diverse districts of Sheko were similar to that of Yeki. The landrace described in Sheko and Yeki were rare, unique and most of the landrace hardly exist in the districts from Jimma zone. The variation among districts with respect to the distribution and abundance landraces also evident from the number of farms surveyed and corresponding number of landraces recorded. Furthermore, variation between zones with regard to the distribution and abundance of landraces also varied. From the total surveyed study areas, 21, 5 and 3 landraces were found in Jimma, Bench-maji and Sheka zones, respectively. Besides, some landraces were found between zones of Southwest Ethiopia. For example, five landraces found in areas between Sheko and Yeki, while three landraces in areas between Jimma and Sheko.

Additionally, only two landraces were found in some districts of Jimma, Bench maji and Sheka zones in Southwest Ethiopia.

Farmer-preferred traits

The summary of farmers' preferred traits of yam in all tested districts was presented in Table 5. Based on the surveyed result, there were many selection practices were approved by farmers' based on their indigenous knowledge. Farmers in the study areas selected yam landraces for production on the basis of tuber yield, good market price, good taste, good tuber and bulbils flesh color, powdery after boil, medicinal use, maturity, ease to harvest, drought tolerance, disease and insect pest resistance (Table 5). In addition, women considered taste to be an important trait of making yam porridge. Farmers in Sheko considered yams as medicinal use to be an important trait and they usually received high market prices. Farmers

preferred early-maturing landraces, which could escape seasonal food shortage, drought and diseases. Some landraces had distinct, market-preferred traits, such as tuber color, which varied across markets. For instance, in Manna, Dedo, Shebe-sombo, Seka-chekorsa and Kersa districts, white color was preferred, whereas farmers in Sheko and Yeki preferred a red color. Large tuber size of yams, early maturing and resistance to diseases were some of the other traits preferred by farmers in the study areas. The mean farmers' preferred traits of yam in the seven districts were tuber yield 35.42%, market preference 11.05%, taste 6.71%, flesh color 5.91%, powdery after boil 10.48%, medicinal use 5.58%, maturity 8.86%, ease to harvest 7.25%, resistance to drought 5.23% and disease and pest resistance 3.53% (Table 5).

Table 5: Farmer-preferred traits (% farmers) of yam landraces in Dedo, Kersa, Manna, Seka-chekorsa, Shebe-sombo, Sheko and Yeki districts in southwest Ethiopia.

Criteria	Districts							Mean	Rank
	Dedo	Kersa	Manna	Seka chekorsa	Shebe sombo	Sheko	Yeki		
Tuber yield	34.21	35.71	34.29	33.33	32.26	34.38	43.75	35.42	1
High market price	13.16	14.29	11.43	10.00	9.68	9.38	9.38	11.05	2
Good taste	5.26	7.14	5.71	6.67	9.68	6.25	6.25	6.71	6
Good flesh color	5.26	4.76	5.71	6.67	6.45	6.25	6.25	5.91	7
Powdery after boil	10.53	9.52	11.43	13.33	12.90	15.63	0.00	10.48	3
Medicinal use	5.26	9.52	11.43	3.33	3.23	3.13	3.13	5.58	8
Maturity	7.89	7.14	8.57	10.00	9.68	9.38	9.38	8.86	4
Ease to harvest	5.26	4.76	5.71	6.67	6.45	9.38	12.50	7.25	5
Drought tolerance	5.26	0.00	5.71	6.67	6.45	6.25	6.25	5.23	9
Disease and insect pest resistance	7.89	7.14	0.00	3.33	3.23	0.00	3.13	3.53	10

Farmers' awareness on tuber yam and/or aerial yam landraces

In the present study, 50.97%, 13.78% and 35.25% of respondents familiar about storage tuber, aerial yam and both yam types preferred, respectively (Table 6). In Dedo 31.6%, Kersa 45.24%, Manna 60%, Seka-chekorsa

53.33%, Shebe-sombo 32.26%, Sheko 78.12% and Yeki 56.25% of the respondents were familiar about tuber yams. Given a chance to choose and grow among the aerial and tuber yams, 35.25% responded to growing both yams types (Table 6).

Table 6: Preference of farmers (% farmers) to grow tuber yam and/or aerial yam landraces in Dedo, Kersa, Manna, Seka-chekorsa, Shebe-sombo, Sheko and Yeki districts of southwest Ethiopia

Types of yams	Districts							Mean
	Dedo	Kersa	Manna	Seka Chekorsa	Shebe Sombo	Sheko	Yeki	
Tuber yam	31.58	45.24	60.00	53.33	32.26	78.12	56.25	50.97
Aerial yam	15.79	21.43	14.29	10.00	19.35	3.12	12.5	13.78
Both	52.63	33.33	25.71	36.67	48.39	18.75	31.25	35.25

Discussions

The results of the present study revealed that yam production practices mainly dominated by male farmers (Table 1). The lower percentage of female farmers could be due to the former land ownership system which discriminated against women in all surveyed areas. In this regard, a similar study was conducted by Tamiru *et al.*, (2011) who reported that most farming activities are a male dominated profession. In smallholder farming communities, farmers' are the major source of labor and depends on the family size (Alieu *et al.*, 2012). Hence, the larger the household size, the greater the labor force available, and, in chance, the larger the area of land cultivated. Households with only two or three members had limited labor, and therefore, they usually

cultivated areas of less than one hectare. Households of five or more members cultivated areas of more than 2 ha. Similarly, Zimmerer, (1992) and Loko *et al.*, (2015) reported that land and labor shortages are the main factor that threatens yam production in Benin. The study also showed that most active farmers were between 45 and 55 years of age in all districts (Table 1). This was due to farmers who have less than 40 years of age had other jobs in neighboring towns.

Yam grown mainly to fill food and economical gaps in all districts. Crops, such as maize, coffee, wheat, taro, yam, millet and cassava were grown specifically for food security and tomato, potatoes and cabbage were grown for cash. Farmers used yam as a source of food (yam flour mixed with wheat), roasted tuber and porridge (Scarcelli *et al.*, 2011). Most of the

farmers in tested districts preferred yam landraces that were described by high tuber yield, high market price, white and purple flesh, powdery after boil, early maturity, ease to harvest, medicinal use, drought tolerance and disease and insect pest resistance (Loko *et al.*, 2013; Loko *et al.*, 2015). According to Fekadu *et al.*, (2015) reported that farmer-preferred cultivars had large sized and orange color of sweet potato in southern Ethiopia. Further, Alieu *et al.*, (2012), reported farmer's preferences to maintain yam landraces are highly depending on their socio cultural value, foods and income source. The results from this study further showed that most of the farmers were alert of the constraints affecting their crops. Low attention given to the crop, drought, animal attacks, poor management, and shortage of farm land, dilution of the crop by improved cereal technologies, labor shortage, low soil fertility and poor extension service were reported to be the main limiting factors in yam production in all study districts (Table 3). In this regard, different researchers reported different factors that affected the production of different crops. For example, Fekadu *et al.* (2015) reported drought affects the yield of orange fleshed sweet potato grown in South Ethiopia. Further, Firew, (2012) and Happy *et al.*, (2018) who reported, floods, drought and wild animal attacks affect production of sorghum and ground nut. According to Alieu *et al.*, (2012) reported that city expansion is the main factor that affects yam production in West Africa, and Firew,

(2012) reported habitat fragmentation and over exploitation of natural resources are the cause that threaten Ethiopian crop genetic resources. Further, Loko *et al.*, (2013) reported storage insects are the major constraints that threatened yam genetic resources in Northern Benin. Farmers identify different landraces by their own descriptors with different names for management decisions (Loko *et al.*, 2015). They described their landraces in various ways and characters used to separate one from another (Scarcelli *et al.*, 2011; Tewodros, 2016). In all tested districts, a total of 38 farmers named landraces was identified by farmers for their different preferred traits.

This study designed through the participatory approach for conversation made between yam growers and yam researchers helped understand the main constraints to yam production identified by farmers in the Jimma, Bench-maji and Sheka zones of southwest Ethiopia. In this discussion, confirmed that all farmers were recognized on yams and its major production constraints. Owing to the past research neglect, farmers are often the only sources of information on yam in Southwest Ethiopia. Therefore, through the analysis of indigenous knowledge, farmers' perception in designing breeding and conservation programs are critical so as to bring practical solutions to the identified problems of the farmers in the study areas (Tamiru *et al.*, 2011) Further, in most cases, farmers' preferences are

mainly based on very specific needs and socio-cultural aspects; thus, research in collaboration with farmers becomes necessary to establish new ways of a dialogue between researchers and farmers in evaluating the characteristics of the landraces farmers' maintained in their system.

Conclusion and Recommendation

Low attention given to the crop was the major constraint for yam production followed by drought and wild animal attacks. Farmers in the study areas depended on agricultural production, such as livestock rearing and growing a range of crops, in addition to yam, for food and income generation. In all districts, 38 farmers' named landraces identified with variable distribution. Thus, farmers' indigenous knowledge of yam and local landraces must be collected, analyzed and properly documented for the research and development program in the country. In this study, high yield, good market price, powdery after the boil, early maturity and drought tolerance are the main yam traits preferred by farmers. Therefore, researchers could use farmers' identified /preferred traits as selection criteria in their breeding program to boost yam production in Southwest Ethiopia.

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Optimizing Seeding Rates and Nitrogen and Phosphorus Fertilizer Rate for High Yield and Quality of Food Oats in the Central Highlands of Ethiopia

Mebrate Tamrat^{*1}, Sakatu Hunduma¹, Tesfahun Alemu¹, and
Medemedemiyaw Neknie²

¹Crop Research Directorate, Holetta Agricultural Research Center, P.O. Box 2003, Addis Ababa, Ethiopia

²Ministry of Agriculture, Addis Ababa, P.O. Box 62347, Addis Ababa, Ethiopia; E-mail: mebtam@gmail.com

Abstract

Food oats, one of the cereal crops meant both for grain and for feed, is an important crop in marginal ecologies. It can grow on a wide range of soil types and can perform better than other small-grain cereals on acid soils. However, no sufficient agronomic research recommendations are available to improve its productivity. Hence, an experiment was conducted in 2019 and 2020 cropping seasons to determine the optimum seed and fertilizer rate for higher yield and quality of food oats. Factorial combinations of seed rate (100, 125, and 150 kg/ha), nitrogen fertilizer (21, 42, and 63 kg/ha), and phosphate fertilizer (23, 46, and 69 kg P₂O₅/ha) were laid out in a randomized complete block design with three replications. Most of the interactions and the main effect of P₂O₅ fertilizer were non-significant for grain yield and hectoliter weight. The main effects of year, location, and seed rate showed a significant effect on both grain yield, and hectoliter weight, while nitrogen showed a significant effect only on grain yield. Grain yield linearly increased as the main effects of seed and nitrogen rate increased from the lowest to the highest level. All parameters were positively and highly significantly ($P < 0.01$) correlated with or contributed to grain yield (except hectoliter weight). In general, a phosphorus fertilizer at the rate of 23 kg P₂O₅/ha together with a seed rate of 150 kg/ha and a nitrogen rate of 63 kg/ha was found to be optimum for food oat production on nitisols/red soils of the West and North Shewa zones.

Keywords: Cereal crops, North Shewa, Optimum, Quality, West Shewa

Introduction

Oat (*Avena sativa*) is a cool-season annual cereal crop abundantly grown in the central highlands, especially in the North Shewa and West Shewa Zones of Ethiopia. It also grows on a considerable scale in other parts of the country, like Arsi, Bale, and Gojam (Fekadu, 2018; Fikadu *et al.*,

2021). Oat is one of the most nutritious cereals, high in protein, and well adapted to a wide range of soil types and can perform better than other small-grain cereals on acid soils (Mosissa *et al.*, 2018). Though oats are mainly used as livestock feed, it has also been proved that the white-colored grain type can also be processed for human food. Hence, oat

as a food grain has rapidly gained increasing popularity in recent years as a result of its serum cholesterol-lowering properties, thereby preventing heart-related problems (Price *et al.*, 1987; Anderson *et al.*, 1990). In Ethiopia, even though oats have been introduced for feed production purposes, resource-poor farmers eventually used the crop as a food grain (Fekadu, 2018). Despite the relative importance of oats in the above areas, they have traditionally been considered a low-input crop and are grown on low-fertile soils without any fertilizer application, hence, it grows poorly without the addition of nutrients. Studies conducted elsewhere showed a significant increase in oat grain yield and quality. For example, the application of nitrogen up to 80 kg/ha increased grain yields in different areas (May *et al.* 2004; Hamill, 2002). Similarly, Islam *et al.* (2020) recommended the application of 90 kg N/ha for oat production in Bangladesh. Gilchrist and Jack (2003) also reported a significant ($p < 0.001$) drop in yield for each 20 kg/ha reduction in applied nitrogen from 100 kg/ha to 60 kg/ha. On the other hand, declines in test weight, kernel weight, and percent plump kernels, and increases in percent thin kernels have resulted from increasing N rates in several studies, such as May *et al.* (2004) and Mohr *et al.* (2007). Application of a P-containing seed coating often increased biomass production and grain set for oats but did not affect grain yield in Finland (Peltonen-Sainio *et al.* 2006). On the

other hand, studies in Saskatchewan consistently demonstrated substantial increases in grain yield of oat with P fertilizer application regardless of the cultivar (Mitchell *et al.* 1953). Higher oat yields have been associated with greater plant tissue P concentration in P-deficient soils (Bolland and Brennan 2005).

Seeding rate is an important crop management practice that affects grain production and can be influenced by the type and fertility of the soil, climate, establishment methods (condition of seedbed and seeding method), and the like. Accordingly, several scholars reported different results in different areas and countries. Duda *et al.* (2021) suggested a seed rate of 125 to 175 kg/ha depending on the location and the purpose for which the crop is cultivated. Marwan *et al.* (2019) reported the highest grain yields from the highest seed rate (160 kg/ha). Similarly, Byamungu and Jo (2018) reported a linear increase in grain yield as the seed rate increased from 100 to 160 kg/ha. In Ethiopia, Dawit and Teklu (2014) reported the highest seed yield (4.48 t/ha) at a seed rate of 70 kg/ha and fertilizer rates of 50 kg Urea/ha and 100 kg DAP/ha for the production of fodder oats in the highlands of Bale, suggesting that the higher fertilizer rates could result in higher lodging of oat plants and also increasing seeding rates above 70 kg/ha are more likely to reduce the size and quality of seed.

Therefore, for higher yields and quality of oats, optimizing seeding rate and nutrient management (N and P fertilizer rate) should be considered as important factors when growing food oats. However, in Ethiopia and specifically in the study areas, information on best agronomic management practices, including seeding rate and nitrogen (N) and phosphorus (P) fertilizer recommendations suitable for acid-prone areas or other soil types are scanty. Hence, some producers are using the recommendations of food barley (DAP or NPS at a rate of 150 kg/ha and a seed rate of 150 kg/ha) for food oats production (MOA 2017). Therefore, this experiment was conducted to determine the appropriate seed and NP fertilizer rate and provide information for users.

Materials and Methods

Description of the experimental site

The field experiment was conducted at West Shewa Zone, Ejere and Wolmera Zuria districts and at North Shewa Zone, Degem district during 2019 and 2020 cropping season. The test locations' geographic coordinates were 9°3' to 9°4' N latitude in the West Shewa Zone and 9°49' to 9°75' N latitude in the North Shewa Zone, 38°30' to 38°41' E longitude in the West Shewa Zone and 38°37' to 38°52' E longitude in the North Shewa Zone, and an altitudinal range of 2337 to 2391 meters above sea level in the

West Shewa Zone and 2705 to 3011 meters above sea level in the North Shewa Zone. Accordingly, the test sites in the North Shewa Zone lie at higher altitudes than those in the West Shewa Zone. The majorities of the North Shewa Zone areas have a mean annual rainfall of 800 mm to 1600 mm and mean annual minimum and maximum temperatures of 10 to 25 °C. In the West Shewa, the long-term average annual rainfall is 1100 mm while the average minimum and maximum air temperatures are 6.2 °C and 22.1 °C, respectively (Respective offices of agriculture, unpublished).

Soil characterization

A one kg composite soil sample was collected from the whole plot (from five spots) in a zigzag fashion to a depth of 0-30 cm just before sowing for determining soil pH, organic matter, total N, extractable P, exchangeable K, and cation exchange capacity (CEC). Soil pH was tested using the potentiometric method described by Tekalign (1991), organic matter was determined using the Walkley and Black method (Tekalign, 1991), total N was determined by the modified Kjeldahl method described by Tekalign (1991), extractable P was determined using the Bray II method described by Ankerman and Large (n.d.), exchangeable K was determined by the flame photometer described by FAO (2006), and CEC was determined by the flame photometer described by Hazelton and Murphy (2007). Only the first-year data is available for both localities (zones).

Treatments, experimental design, and procedures

The treatments included a complete factorial combination of three seeding rates (100, 125, and 150 kg/ha), three nitrogen levels (21, 42, and 63 kg N/ha), and three phosphate levels (23, 46, and 69 kg P₂O₅/ha). The treatments were arranged in a randomized complete block design (RCBD) with three replications. A gross plot size of 4 m² (1.6 m wide and 2.5 m long) with eight rows spaced 20 cm apart was used. Six central rows (a net plot area of 3 m²) were used for phenological, yield, and yield component data collection. The alley space between plots and replications was kept at 0.5 m and 1 m, respectively. In all plots, P₂O₅ as triple superphosphate (46%) was hand drilled in a band at planting, while urea was hand drilled in a band one-third at planting and the remainder side dressed at the tillering stage of the crop.

The improved food oat variety, namely ‘SORATAF’ was used for this experiment. According to Fikadu *et al.* (2021), this variety is known to tolerate soil acidity problems and has better nutritional quality. It contains a high percentage of protein (16.0), fat (8.4), and ash (3.6). The high lipid (8.4 %) and mineral (156.35mg/L) content of this variety make it different when compared to other small-seeded cereals. The seeds were hand drilled into 20 cm spaced rows. The seedbed was plowed three to four times before planting. Two times, hand weeding was undertaken based on the severity

of the weeds. Wheat and barley precursor crops were used in both years (2019 and 2020). Sowing was done on July 1, 2019 at the North Shewa Zone (Alidoro site), on July 24, 2019 at the West Shewa Zone (Chiree site), on June 11, 2020 at the North Shewa Zone (Degem site), and on July 24, 2020 at the West Shewa Zone (Sademo site). Harvesting by using sickles was done from the last week of December to mid-January in both years.

Crop data collection

The date of heading was recorded as the number of days from planting to a period when 50% of the spikelet produced heads. Date of physiological maturity was recorded as the number of days from planting to a period when 90% of the peduncles and spikes in a plot turn yellow. Plant height was measured from the ground level to the tip of the spike excluding the awns at physiological maturity from ten randomly selected mother plants (main shoots). The spike length was measured from the base to the top of the spike excluding awns from ten randomly selected mother plants (main shoots). Kernels per spike were taken as the average number of kernels per spike of 10 randomly chosen plants at harvest and expressed as the average number of kernels per plant. A thousand kernel weight was determined as the weight of 1000 seeds sampled from the harvested plot area using a sensitive balance. Grain yield was determined by weighing clean threshed seeds from the net plot

area. The yield was adjusted to 12.5% grain moisture, which was determined using a grain moisture tester. Hectoliter weight (HL) (kg/hl) or test weight was determined as previously described by Buerstmayr *et al.* (2007).

Statistical analysis

Data were subjected to the analysis of variance (ANOVA) following the statistical procedure for three-factor factorial experiments using the General Analysis of Variance procedure of GenStat for Windows Version 16 (VSN International, 2013). The mean comparison was performed using the Duncan Multiple Range Test (DMRT) at a 5% level of significance upon obtaining significant F-values for the main effects and interactions. Two years' data were combined upon obtaining variance homogeneity, which was tested by employing Bartlett's test. Accordingly, a combined analysis of variance over years (2019 and 2020) and locations (hereafter termed as the West Shewa Zone and the North Shewa Zone) was performed for grain yield and agronomic parameters considered.

Economic analysis

The economic analysis was performed to investigate the economic feasibility of the average main effects of seed rate and N rates following the CIMMYT (1988) procedures. The field price was obtained by a simple assessment of farm gate prices near the experimental field after harvest (January to February), which was taken as the average of the two years, and the

official prices of N and P fertilizers were used for economic analysis. Accordingly, the price of grain yield was estimated at 18.00 Ethiopian Birr (ETB) per kg. The variable costs included the cost of seed during sowing (June) and were estimated to be 20.00 ETB, while the official prices of N and P fertilizers were estimated at 33.00 and 34.00 ETB per kg, respectively. The average yield was adjusted downward to 10%, assuming a yield reduction of 10% if farmers managed the same on a larger plot. To use the marginal rate of return (MRR) as a basis for plant density and fertilizer recommendations, the minimum acceptable rate of return was set at 100% (CIMMYT, 1988). A treatment having higher total costs that vary and a lower net benefit than the immediate preceding treatment with lower total costs that vary and a higher net benefit was considered to be dominated and was eliminated from further analysis.

Results and Discussion

The experimental site's soil physicochemical properties

As indicated in Table 1, in the year 2019, the pH of both experimental fields lies in the range of 4.27 to 5.07 and was found to be strongly acidic to very strongly acidic as rated by Tekalign (1991). According to Fekadu (2018), the variety under this study ('SORATAF') showed superior performance at different locations, having an exchangeable acidity range of 0.7-2.0 Meq/100g soil. The organic

carbon of the experimental field lies in the range of 1.274 to 2.447%, which is classified as low to medium by Tekalign (1991). The total N percent in the experimental field was in the range of 0.16 to 0.21. According to Tekalign (1991), the total nitrogen content of the experimental soil lies in the moderate range. The extractable soil phosphorous lies in the range of 23.37 to 63.07 ppm, which is classified as low to very high (Ankerman and Large, n.d.), while the extractable K lies in the range of 1.64 to 1.659 [cmol (+)/kg soil], which is rated as very high (FAO, 2006). The CEC of the experimental fields lies in the range of 18.74 to 19.5 cmol (+)/kg and is classified as moderate (Hazelton and Murphy, 2007). CEC is used as a measure of soil fertility and nutrient retention capacity. Accordingly, soils high in CEC content are considered agriculturally fertile.

Phenological and growth parameters

The main effects of year, location, seed rate, and nitrogen, as well as the two-way interaction of year with location, location with seed rate, year with nitrogen, and location with nitrogen, all had a significant effect on days to 50% heading (Table 1). The earliest days to flowering were recorded in the first year (91 days) and at the West Shewa Zone (94 days) (Table 2), which is probably related to the elevation effect as the testing sites at the North Shewa Zone were at higher altitudes than those at the West Shewa Zone. In practice, crops grown

at higher altitudes require longer durations than those at relatively lower altitudes. Due to competition for resources such as water, nutrients, and sunlight, days to heading decreased linearly by 1.06% as the seed rate increased from 100 to 150 kg/ha (Table 1). In line with this result, the increment in seed rate of malt barley from 100–175 kg/ha decreased the days to 50% heading by 6% (Senait *et al.*, 2020).

As nitrogen fertilization increased from 21 kg/ha to 63 kg/ha, the days to heading decreased linearly and significantly ($P < 0.05$) from 97 to 93 days (Table 2). In contrast, while increasing levels of N fertilizer from control (0 kg N/ha) to the highest (54 kg N/ha), days to the heading of malt barley increased consistently (Terefe *et al.*, 2018), which might be attributed to the behavior of increased N fertilizer that increases vegetative growth of crops, thereby delaying heading time. Phosphorus fertilization showed a non-significant effect on the days to heading, probably related to the presence of a sufficient amount of soil phosphorus, especially in the first year.

The interaction effect of location and seed rate on days to heading was significant ($P < 0.05$) (Table 1). At West Shewa Zone, days to heading decreased linearly as the seed rate increased from 100 to 150 kg/ha, whereas there was little inconsistency at North Shewa Zone between seed rate two (125 kg/ha) and seed rate three (150 kg/ha) (Table 4). However, days to heading showed a decreasing

trend while increasing seed rates, probably due to the enhancement effect of higher seed rates on days to heading due to competition for resources.

Days to 90% physiological maturity were significantly affected by the main effects of year, location, seed rate, and nitrogen, as well as by the three-way interaction of year, location, and nitrogen (Table 1). The earliest days to 90% physiological maturity were recorded in the first year (151 days) and in the West Shewa Zone (148 days) (Table 2). The days to 90% physiological maturity decreased linearly by 0.65% as the seed rate increased from 100 to 150 kg/ha (Table 2), which might be due to plant competition for available resources. In line with this result, time to kernel maturity decreased with the increasing seeding rate of malt barley (O'Donovan *et al.*, 2012). Similarly, increasing seeding rates of malt barley from 100–175 kg/ha decreased the days to 90% physiological maturity by 5 days (Senait *et al.*, 2020). As nitrogen fertilization increased from 21 kg/ha to 63 kg/ha, there was a linear and significant ($P<0.05$) decrease in days to maturity from 155 to 154 days (Table 3). In contrast, May *et al.* (2004) reported a non-significant but increasing trend as the N rate increased from 15 to 120 kg/ha for oats. Also, Terefe *et al.* (2018) reported contrasting results in malt barley.

The main effects of year, location, and nitrogen, as well as the two-way interaction of year with location,

location with seed rate, a year with nitrogen, location with nitrogen, and the three-way interaction of year, location, and nitrogen, showed a significant effect on plant height (Table 1). Similarly, the five-way interaction of year by location by seed rate by nitrogen by phosphorus showed a significant ($P<0.05$) effect on plant height. Significantly taller plants (107 cm tall) were recorded in the first year and in the North Shewa Zone (109 cm high) (Table 2), which could be attributed to the presence of relatively higher soil total nitrogen and higher soil phosphorus availability in the first year. The tallest plants (107.4 cm high) were recorded at the highest N rate (63 kg N/ha) and the plant height increased linearly by 8.92% as nitrogen fertilization increased from 21 to 63 kg/ha (Table 2), which is probably because nitrogen promotes plant growth and increases the number of internodes and length of the internodes, which results in a progressive increase in plant height (Gasim, 2001). Similar results were obtained by Marwan *et al.* (2019), in which the tallest plants of oats were recorded at the highest nitrogen level of 80 kg/ha. Also, Islam *et al.* (2020) reported taller plants of oats for the highest rate of N applied (105 kg/ha). Seed rate and phosphorus fertilization showed a non-significant effect on plant height. However, the interaction effect of location with seed rate and location with nitrogen was significant ($P<0.05$) on plant height (Table 1). From the results, the tallest plants (111.0 cm high) were obtained at a

seed rate of 125 kg/ha at the North Shewa Zone, while no significant variation was observed between seed rates at the West Shewa Zone (Table 3). Similarly, there was a significant ($P < 0.05$) variation between nitrogen levels at both localities, and the tallest plants (99.5 and 115.2 cm high, respectively) were obtained at the highest N rate of 63 kg/ha (Table 4). In a similar experiment, the highest plant height (134.2 cm) of fodder oats was recorded at the higher fertilizer level with a seed rate of 80 and 90 kg/ha, respectively (Dawit and Teklu, 2014). Yidersal *et al.* (2020) also reported taller plants of oats from the higher N and seed rate levels (a seed rate of 100 kg/ha and an N level of 150 kg/ha).

The spike length was significantly ($P < 0.05$) affected only by the main effects of year and location and their interaction (Table 1). In contrast to the present result, Islam *et al.* (2020) reported a linear increase in spike length while increasing the N level from zero to 105 kg/ha. Significantly, the longest spikes (26.1 cm high) were recorded in the first year and the West Shewa Zone (26.3 cm high) (Table 2).

Yield and yield components

The number of seeds per spike was significantly ($P < 0.05$) affected by the main effects of year and nitrogen fertilization, as well as by the two-way interaction of year with location, a year with seed rate, and a year with phosphate fertilizer, and the three-way interaction of year by location by seed

rate (Table 1). A significantly higher number of seeds per spike (65.4 and 60.6) was recorded in the second year and at the nitrogen fertilizer level of 42 kg/ha, respectively (Table 2). In contrast, Byamungu and Jo (2018) reported a higher number of grains per spike from the highest rate of N fertilizer (90 kg/ha). As discussed by Marwan *et al.* (2019), the number of grains per panicle increased linearly as the N rate increased from 0 to 80 kg/ha.

The main effects of year, location, and nitrogen, as well as the two-way interaction of year with location and seed rate with nitrogen, showed a significant ($P < 0.05$) effect on 1000 seed weight (Table 1). The heaviest 1000 seed weights (36.98 g, 37.23 g, and 36.35 g, respectively) were found in the second year, in the North Shewa Zone, and at the lowest nitrogen level of 21 kg/ha (Table 2). In agreement with this result, May *et al.* (2004) reported a decrease in the kernel weight of oats as the N rate increased. On the contrary, Marwan *et al.* (2019) and Islam *et al.* (2020) found that higher N rates resulted in a heavier 1000 seed weight of oats. On the other hand, Byamungu and Jo (2018) reported a non-significant effect of N fertilizer on the 1000 kernel weight of oats. As depicted in Fig. 1, the highest 1000 seed weight was obtained at the combination of a seed rate of 100 kg/ha with an N rate of 21 kg/ha, followed by a combination of a seed rate of 150 kg/ha with an N rate of 21 kg/ha which might be due to the

vigorous seeds as lower intra competition in wider spacing. In contrary to this result, Byamungu and Jo (2018) reported a non-significant effect of seed rate with nitrogen interaction on 1000 seed weight of oat. Similarly, Zeki *et al.* (2005) also

reported higher 1000 seed weight at the combination of higher N rates with lower number of seeds per square meter for triticale.

Table 1. Level of significance for grain yield and some phenological-and growth parameters of food oats as affected by seed rate, nitrogen, and phosphate fertilization in the West and North Shewa Zones, combined across years and locations

Source	DTH	DTM	Plh	SPL	NSPS	TSW	GY	HL
Year (Yr)	**	**	**	**	**	**	**	**
Location (Loc)	**	**	**	**	ns	**	**	**
Replication (R)	38.759	8.65	107.53	36.78	776.30	1.11	0.101	5.867
Seed rate (Sr)	**	**	ns	ns	ns	ns	**	*
Nitrogen (N)	**	**	**	ns	**	**	**	ns
Phosphorus (P2O5)	ns	ns	ns	ns	ns	ns	ns	ns
Yr.Loc	**	**	**	**	**	**	**	**
Yr.Sr	ns	ns	ns	ns	*	ns	ns	ns
Loc.Sr	*	ns	*	ns	ns	ns	ns	ns
Yr.N	**	ns	**	ns	ns	ns	ns	ns
Loc.N	*	ns	**	ns	ns	ns	ns	ns
Sr.N	ns	ns	ns	ns	ns	*	ns	ns
Yr.P2O5	ns	ns	ns	ns	*	ns	ns	ns
Loc.P2O5	ns	ns	ns	ns	ns	ns	ns	ns
Sr.P2O5	ns	ns	ns	ns	ns	ns	ns	ns
N.P2O5	ns	ns	ns	ns	ns	ns	ns	ns
Yr.Loc.Sr	ns	ns	ns	ns	*	ns	ns	ns
Yr.Loc.N	ns	*	*	ns	ns	ns	ns	ns
Yr.Sr.N	ns	ns	ns	ns	ns	ns	ns	*
Loc.Sr.N	ns	ns	ns	ns	ns	ns	ns	*
Yr.Loc.P2O5	ns	ns	ns	ns	ns	ns	ns	ns
Yr.Sr.P2O5	ns	ns	ns	ns	ns	ns	ns	ns
Loc.Sr.P2O5	ns	ns	ns	ns	ns	ns	ns	ns
Yr.N.P2O5	ns	ns	ns	ns	ns	ns	ns	ns
Loc.N.P2O5	ns	ns	ns	ns	ns	ns	ns	ns
Sr.N.P2O5	ns	ns	ns	ns	ns	ns	ns	ns
Yr.Loc.Sr.N	ns	ns	ns	ns	ns	ns	ns	ns
Yr.Loc.Sr.P2O5	ns	ns	ns	ns	ns	ns	*	ns
Yr.Loc.N.P2O5	ns	ns	ns	ns	ns	ns	ns	ns
Yr.Sr.N.P2O5	ns	ns	ns	ns	ns	ns	ns	ns
Loc.Sr.N.P2O5	ns	ns	ns	ns	ns	ns	ns	*
Yr.Loc.Sr.N.P2O5	ns	ns	*	ns	ns	ns	ns	ns
Residual	3.165	2.047	35.090	7.017	125.6	4.698	0.220	3.163

DTH=Days to 50% heading, DTM=Days to 90% physiological maturity, Plh=Plant height, SPL=Spike length, NSPS=Number of seeds per spike, TSW=Thousand seeds weight, HL=Hectoliter weight and GY=Grain yield

Table 2. The main effects of seed rate, nitrogen, and phosphate fertilization on grain yield and some agronomic parameters of food oats in the West and North Shewa Zones, combined across years and locations

Treatments	DTH	DTM	Plh (cm)	SPL	NSP S	TSW (g)	GY (t/ha)	HL (kg/hl)
Year								
2019	91	151	99	23.4	50.9	34.42	1.77	51.84
2020	99	158	107	26.1	65.4	36.98	3.15	48.72
LSD (5%)	0.4	0.3	1.3	0.58	2.45	0.475	0.103	0.39
Location								
West Shewa Zone	94	148	97	26.3	57.9	34.16	2.13	48.89
North Shewa Zone	95	161	109	23.2	58.4	37.23	2.79	51.68
LSD (5%)	0.4	0.3	1.3	0.58	ns	0.475	0.103	0.39
Seed rate (kg/ha)								
100	95	155	103.0	25.2	59.8	35.91	2.26	49.89
125	95	154	103.7	24.7	57.0	35.61	2.50	50.46
150	94	154	102.5	24.5	57.6	35.57	2.62	50.50
LSD (5%)	0.5	0.4	ns	ns	ns	ns	0.126	0.477
Nitrogen (kg/ha)								
21	97	155	98.6	24.3	54.7	36.35	2.19	50.12
42	95	154	103.2	25.1	60.6	35.28	2.42	50.28
63	93	154	107.4	25.0	59.1	35.47	2.77	50.45
LSD (5%)	0.5	0.4	1.6	ns	3.19	0.581	0.126	ns
P₂O₅ (kg/ha)								
23	95	154	103.0	24.7	57.9	35.66	2.46	50.32
46	95	154	103.7	24.9	58.7	35.48	2.43	50.22
69	95	154	102.5	24.8	57.8	35.94	2.48	50.31
LSD (5%)	ns	ns	ns	ns	ns	ns	ns	ns
Mean	94.7	154	103.1	24.8	58.1	35.7	2.46	50.28
CV (%)	1.9	0.9	5.7	10.7	19.3	6.1	19.1	3.54

DTH=Days to 50% heading, DTM=Days to 90% physiological maturity, Plh=Plant height, SPL=Spike length, NSPS=Number of seeds per spike, TSW=Thousand seeds weight, HL=Hectoliter weight and GY=Grain yield

Table 3. The two-way interaction effects of location with seed rate on days to heading, plant height, and hectoliter weight of food oats in the West and North Shewa Zones, combined across years and locations

Location	Days to heading			Plant height (cm)		
	Seed rate (kg/ha)			Seed rate (kg/ha)		
	100	125	150	100	125	150
West Shewa Zone	94.9ab	94.4b	93.4c	97.3c	96.3c	97.5c
North Shewa Zone	95.6a	94.9ab	95.0ab	108.7b	111.0a	107.5b
	Mean= 94.7, LSD (5%)= 0.7			Mean= 103.1, LSD (5%)= 2.20		

Table 4. The two-way interaction effects of location with nitrogen fertilization on days to heading and plant height of food oats in the West and North Shewa Zones, combined across years and locations

Location	Days to heading			Plant height (cm)		
	N rate (kg/ha)			N rate (kg/ha)		
	21	42	63	21	42	63
West Shewa Zone	96.5a	93.9c	92.4d	93.2e	98.4d	99.5d
North Shewa Zone	96.7a	95.1b	93.7c	104.0c	108.1b	115.2a
	Mean= 94.7, LSD (5%)=0.7			Mean= 103.1, LSD (5%)= 0.78		

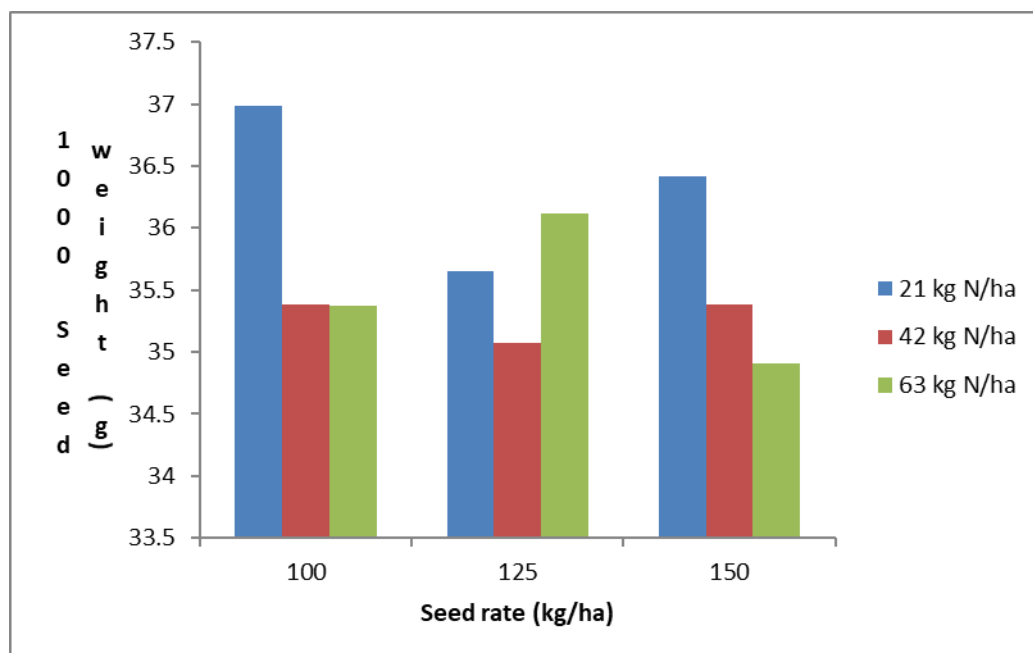


Figure 1. The combined effect of nitrogen fertilization and seed rate on 1000 seed weight (g) of food oats combined over years and locations

Grain yield was significantly affected by the main effects of year, location, seed rate, and nitrogen, as well as by the two-way interaction of year with location and by the four-way interaction of year by location by seed rate by phosphate fertilizer (Table 1). Significantly, the highest grain yields were recorded in the second year (3.15 t/ha) and in the North Shewa Zone (2.79 t/ha) (Table 2), most likely due to the presence of relatively higher soil total nitrogen and higher soil phosphorus availability in the first year. On the other hand, according to the results reported by Mohr *et al.* (2007), the response to phosphate in oats is inconsistent and often does not respond to soil test levels. In most cases, P fertilizer did not result in a significant increase in grain yield. Grain yield increased linearly by

15.93% as the seed rate increased from 100 to 150 kg/ha (Table 2). Similarly, as nitrogen fertilization increased from 21 to 63 kg/ha, there was a significant increase in grain yield from 2.19 to 2.77 kg/ha (Table 2). Also, the economic analysis revealed that the highest net benefits of 39444.00 and 42795.00 ETB/ha with marginal rates of returns of 298.29% and 718.18% were obtained under a seed rate of 150 kg/ha and a nitrogen fertilizer rate of 63 kg/ha, respectively (Table 5). Except for hectoliter weight, all parameters were positively and highly significantly ($P < 0.01$) correlated with or contributed to grain yield (Table 6). In agreement with this result, Marwan *et al.* (2019) reported the highest grain yields from the highest nitrogen level (80 kg/ha) and the highest seed rate (160 kg/ha),

justifying the contribution of the number of tillers per meter square, panicle length, and number of grains per panicle. Several scholars also reported different results. For example, Byamungu and Jo (2018) reported a linear increase in grain yield as the seed rate was increased from 100 to 160 kg/ha, while a higher grain yield was obtained at an N rate of 50 kg/ha. Islam *et al.* (2020) obtained the highest mean grain yield at 90 kg N/ha, but beyond 90 kg N/ha, the mean grain yield leveled off at a higher N rate (105 kg/ha), although the decrease was very slight. Also, Mohr *et al.* (2007) reported a higher grain yield at the higher N level of 100 kg/ha. Similarly, Gilchrist and Jack (2003) reported a significant ($p<0.001$) drop in yield for each 20 kg/ha

reduction in applied nitrogen from 100 kg/ha to 60 kg/ha. In contrast, Dawit and Teklu (2014) obtained the highest seed yield (4.48 t/ha) at a seed rate of 70 kg/ha and fertilizer rates of 50 kg Urea/ha and 100 kg DAP/ha, suggesting that the higher fertilizer rates could result in higher lodging of fodder oats and that increasing seeding rates above 70 kg/ha are more likely to reduce the size and quality of seed.

Depending on both agronomic and economic analysis results, the highest grain yield was obtained from the highest seeding rate and nitrogen level. Hence, further study using higher seed and fertilizer rates needs to be considered, as the higher grain yield was obtained from higher levels.

Table 5. Dominance and marginal rate of return analysis for the effect of seed rate and nitrogen fertilization on grain yield (t/ha) of food oats in the West and North Shewa Zones, combined over years

Seed rate (kg/ha)	GY (t/ha)	GY adjusted (10% down) (t/ha)	GB (Birr/ha)	TVC (Birr ha ⁻¹)	NB (Birr ha ⁻¹)	MRR (%)
Seed rate (kg/ha)						
100	2.26	2.04	36634.84	2000.00	34634.84	
125	2.50	2.25	40452.53	2500.00	37952.53	663.54
150	2.62	2.36	42444.00	3000.00	39444.00	298.29
Nitrogen (kg/ha)						
21	2.19	1.97	35478.00	693.00	34785.00	
42	2.42	2.18	39204.00	1386.00	37818.00	437.66
63	2.77	2.49	44874.00	2079.00	42795.00	718.18

Table 6. Correlation coefficients between food oats studied characters

	DTH	DTM	Plh (cm)	SPL	NSPS	TSW (g)	HL (kg/hl)	GY (t/ha)
DTH	-							
DTM	0.563**	-						
Plh (cm)	0.296**	0.703**	-					
SPL	0.128*	-0.27**	0.022ns	-				
NSPS	0.202**	0.105ns	0.228**	0.575**	-			
TSW (g)	0.496**	0.668**	0.545**	-0.217**	-0.051ns	-		
HL (kg/hl)	-0.465**	0.130*	0.043ns	-0.306**	-0.059ns	-0.218**	-	
GY (t/ha)	0.521**	0.633**	0.743**	0.173**	0.353**	0.5024**	-0.125*	-

DTH=Days to 50% heading, DTM=Days to 90% physiological maturity, Plh=Plant height, SPL=Spike length, NSPS=Number of seeds per spike, TSW=Thousand seeds weight, HL=Hectoliter weight and GY=Grain yield

Quality parameters

The hectoliter weight/test weight, which is a measure of the density or specific weight and is thought to be an indicator of grain quality, particularly potential extract yield (Burke *et al.*, 2021), was significantly affected by the main effects of year, location, and seed rate, as well as by the two-way interaction of year with location, and by the three-way interactions of year by seed rate by nitrogen, and location by seed rate by nitrogen, as well as by the four-way interaction of location by seed rate by nitrogen by phosphate fertilization (Table 1). Significantly, the heaviest hectoliter was recorded in the first year (51.84 kg/hl) as well as in the North Shewa Zone (51.68 kg/hl) (Table 2). It increased linearly by 1.22% as the seed rate increased from 100 to 150 kg/ha, but the difference between seed rates of 125 and 150 kg/ha was not significant (Table 2). In contrast, increasing seeding rates from 100–175 kg/ha linearly decreased the hectoliter weight of malt barley (Senait *et al.*, 2020). Nitrogen and phosphorus fertilization showed a non-significant effect on hectoliter weight. However, the heaviest hectoliter was

obtained at the North Shewa Zone at all seed rates and nitrogen fertilization levels, as shown in Table 7.

The highest/heaviest hectoliter was recorded at the combination of the North Shewa Zone with a seed rate of 125 kg/ha and a nitrogen fertilization rate of 21 kg/ha, while the lowest hectoliter weight was recorded at the combination of the West Shewa Zone with a seed rate of 100 kg/ha and a nitrogen fertilization rate of 21 kg/ha. From the results, it can be concluded that the North Shewa Zone could be more favorable for producing quality seeds. In practice, food oats are widely produced in the North Shewa zone, where the altitudes are higher and cooler than in the West Shewa zone. In general, as stated above, the hectoliter weight is a common measure of grain quality in oats (*Avena sativa* L.), and it measures the weight per unit volume of grain and is positively associated with nutritional value and milling quality (Pixley, 1990). On the other hand, the quality of oat grain depends on genetic factors and environmental conditions throughout the growing season (Peterson *et al.*, 2005, Zeki *et*

al., 2018). According to the codex quality standards (1995), the minimum acceptable test weight for oats is at least 46 kg/hl. Accordingly, the results of the present experiment

demonstrated an acceptable test weight for both zones, but preferably at the North Shewa Zone (Tables 2 and 7).

Table 7. The three-way interaction effects of location by seed rate by nitrogen fertilization on hectoliter weight (kg/hl) of food oats in the West and North Shewa Zones, combined over years and locations

Location	Seed rate kg/ha	Nitrogen (kg/ha)	Hectoliter weight (kg/hl)
West Shewa Zone	100	21	48.29c
West Shewa Zone	125	21	48.44c
West Shewa Zone	150	21	49.16c
West Shewa Zone	100	42	48.81c
West Shewa Zone	125	42	48.87c
West Shewa Zone	150	42	48.97c
West Shewa Zone	100	63	48.99c
West Shewa Zone	125	63	49.14c
West Shewa Zone	150	63	49.32c
North Shewa Zone	100	21	51.51ab
North Shewa Zone	125	21	52.52a
North Shewa Zone	150	21	50.81b
North Shewa Zone	100	42	50.90b
North Shewa Zone	125	42	51.89ab
North Shewa Zone	150	42	52.22a
North Shewa Zone	100	63	50.87b
North Shewa Zone	125	63	51.89ab
North Shewa Zone	150	63	52.49a

Conclusions

In the present study, seed rate and nitrogen rate showed a significant effect on most of the studied parameters, while phosphate fertilization had no significant effect on all the studied parameters. Based on higher agronomic and economic yield, the lowest phosphate fertilizer rate of 23 kg P₂O₅/ha together with a seed rate of 150 kg/ha and nitrogen rate of 63 kg/ha was found to be optimum for food oat production in the West and North Shewa Zones. In addition, further study needs to consider using a zero phosphate

fertilizer rate and higher seed rates and nitrogen levels.

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On-farm Improved Common Bean Variety Demonstration and Evaluation in Central Rift Valley of Ethiopia: Case of Bora and Adami Tullu Jido Kombolcha Districts

Abebe Teshome, Berhanu Amsalu and Endriyas Gabrekiristos

Ethiopian Institute of Agricultural Research, Addis Ababa, Ethiopia

E-mail: abebegurmu3@gmail.com

Abstract

Common bean played a vital role in the national economy and used as food and cash sources for the smallholder households. Various common bean varieties were developed by the national lowland pulse research program. Nevertheless, most of the farmers had little chance to know and make their own choice from the ranges of available common bean varieties developed. This study was, therefore, proposed to introduce improved common bean technologies to farmers in major common bean growing areas in the central rift valley of Ethiopia, particularly in Adami Tullu Jido Kombolcha and Bora districts. The districts were purposively selected based on their common bean production potential and variety releasing and the registration committee's recommendation regarding suitable areas for which the demonstrated improved common bean varieties can be adapted. The target demonstration kebeles and sites were further selected purposively depending on their common bean production potential and accessibility of the site for researchers' monitoring, evaluation and other non-host farmers' visit, respectively. The farmers' selection was based on landholding and ownership of the farmers, willingness of the farmers to conduct experiments properly under the regular follow-up of the researchers and their capability to transfer knowledge and create awareness about the varieties among their neighbor and surrounding non-host farmers. Three improved common bean varieties namely, KAT-B1, KAT-B9 and Batu (standard check) were demonstrated side by side on an area of 200m² each. The result shows that KAT-B9 and KAT-B1 give a yield of 1300 and 1250 Kg/ha which is significantly higher than that of the standard check (940kg/ha). The varieties are preferable over the standard check regarding to yield, early maturity, tolerance to disease and insect infestation, drought tolerance and food test. Hence, promotion and popularization of the varieties in the study areas and areas with the same agroecology should be given an emphasis.

Keywords: Common Bean, Demonstration, Preference Score, Standard Check

Introduction

Common Bean is one of the most important pulse crops grown in different parts of Ethiopia; Oromia, Amhara and Southern Nations (SNNP). Area under common bean

production in Ethiopia in 2007/2008 was 231,443.06 hectares and has reached 306,186.59 hectares in 2017/2018 with production of 2,414,17.6.4 and 5,209,79.3. tons, respectively (CSA, 2018). Ethiopia ranked third in common bean

production in Eastern and Southern Africa. The country exports 40 percent of its total common bean production in 2010 (FAOSTAT, 2015). Common bean producers (farmers) prefer the crop because of its fast-maturing characteristics that enable households to get the cash income required to purchase food and other household needs when other crops have not yet matured (Berhanu *et al.*, 2018). Moreover, the crop is preferred by most farmers, since it is an important cash crops and source of protein for farmers in many lowlands and mid-altitude zones.

Market-oriented production system as a way to increase smallholder farmer's income has been in a policy spotlight of many developing countries including Ethiopia (Tufa *et al.*, 2014). Thus, Agricultural Research Institutes plays an important role in releasing and disseminating an improved agricultural technologies which are significant to enhance the growth and development concerns of the agricultural sector (Logan, 2014). Ethiopian Institute of Agricultural Research (EIAR) is one of the institutes working in agricultural sector in Ethiopia which contributes to the sector through development of a wide range of the high-yielding and multi-disease resistant bean varieties to enhance production and productivity for both domestic and export markets.

Varietal adaptation under the Ethiopian Institute of Agricultural Research

resulted in the release of high-yielding improved common bean varieties that are potentially suitable for a range of agro-ecologies, from lowlands to highlands (Teha *et al.*, 2006). So far, many common bean varieties were developed by the national lowland pulse research program in collaboration with the national and international partners in different parts of the country which are suitable for common bean production including the central rift valley of Ethiopia with the objectives of addressing both market and consumer demand. Nevertheless, newly released common bean technologies with better yields and relatively good traits like early maturity, disease resistance, less susceptibility to insects and tolerance to stressed conditions (drought) are not sufficiently introduced and promoted to the potential production sites and most of the farmers had little chance to make own choice from the ranges of available common bean varieties developed. On the other side, most of the farming community had little chance to know and make their own choice from the ranges of available common bean varieties developed. Farmers' selection criteria for the common bean varieties were not sufficiently evaluated and assessed in the study area. Therefore, this research was designed to evaluate the performance of the newly released common bean varieties through on-farm variety demonstration, to assess farmers' variety selection criteria (trait preference) and recommend the most important criteria or traits for future

the research in common bean variety development and improvement.

Material and Methods

Description of the study area

The demonstration was conducted in Adami Tullu Jido Kombolcha and Bora districts. Adami Tullu Jido Kombolcha district is found in the east shewa zone of Oromia region at about 168Km south of Addis Ababa. The district is located in the central rift valley of Ethiopia with an elevation of 1636 meters above sea level. The lean area of the woreda is estimated to 1487.6 Km² which is divided into 38 administrative rural kebeles and five towns. Batu town is the administrative center of the woreda. It is bordered by Southern Nations, Nationalities and Peoples' Regional State (SNNPRS) in the West and North West, Dugda district in the north, Arsi Zone in the east and Arsi-Negele district in the south. According to the 2007 national census report, the district has a total population of 141, 405 of which 85.2% live in rural areas. Crop production is the dominant agricultural practice in the area. Maize and common bean are the major crops grown in the smallholding subsistence farming system in the district. Maize is used mainly for food while, haricot bean is used as a cash crop.

Bora district is located in east shewa zone of Oromia regional state. The total area of the district is estimated to 48, 469 hectares. Alemtena is the administrative center of the district which is located at 117Km south of

Addis Ababa. The district has a latitude of 8.30°N and a longitude of 38.95°E. with an elevation of 1611meter above sea level. It is bordered by Lume, Lake Koka and Dodota in the east, Dugda woreda in the west, Liben in the north and Zeway Dugda and lake zeway in south. According to the national census report of 2007, the district has a total population of 58,748 of which 30, 487 were male and 28, 261 were females. Of the total population 47, 345 were living in rural areas. The district is mostly known for the production of vegetable crops, wheat, maize, common bean and teff.

Description of the varieties

KAT-B1(Ada)and KAT-B9 (Dandesu) are improved common bean varieties which released in 2013 and were demonstrated alongside the standard check (Batu) which was released in 2008. The seed color of the varieties is yellow and red, respectively. The varieties have acceptable grain size and weight Moisture stress areas and short rainy season areas of the central rift valley and lowland areas of Ethiopia were the main adaptation areas of the varieties. The varieties are expected to perform well at an altitude of 1300-1650 m above sea level and rainfall of 400-750 mm. The recommended seed rate used was 100 kg per hectare with the recommended spacing of 40cm between rows and 10 cm between plants (MOA, 2014). It matures within 75-78 days and is tolerant to major diseases such as Common

Bacterial Blight (CBB), Hallow Blight (HB) and rust.

Identification of demonstration site and participant farmers.

The demonstration was conducted in central rift valley of Ethiopia, Adami Tulu Jido kombolcha and Bora districts. Two kebeles from each district and a total of four kebeles were addressed. The demonstration was conducted on each kebele for two consecutive years. The districts were selected purposively depending on the potential of bean production and crop adaptation area. Target demonstration kebeles further selected purposively depending on their common bean production potential and accessibility for researchers' monitoring, evaluation and other non-host farmers' visit. Accordingly, Anano Shisho, Gerbi Wedana from Adami Tullu Jido kombolcha and Dalota Mati and Tuka Langano kebeles from Bora district were selected for demonstration. The farmers' selection was based on landholding and ownership of farmers, willingness of the farmers to conduct experiment properly under the regular follow up of the researchers and their capability to transfer knowledge and create awareness about the varieties among their neighbors and surrounding non-host farmers. Three improved varieties of common bean namely, KAT-B1 (Ada), KAT-B9 (Dandesu) and Batu (standard check) were demonstrated.

Design of the demonstration activity

The varieties were demonstrated side by side. A plot of 600 m² was used for demonstrating the three varieties in which each variety was demonstrated on area of 200 m². The demonstration was replicated on 4 four farmers in each target location (Kebeles) for the consencutive two years. A total of 32 farmers participated in demonstration.

Data collection and analysis

The type of data collected includes grain yield and farmers' feedback on the technologies (varieties) regarding different parameters or traits like yield, early maturity, drought tolerance, tolerance to disease and food tests.

Descriptive statistics were employed to anlyze the data. Graphs and tables were used to illustrate the result. T-test was employed to understand the existence of a significant mean yield difference between the improved common bean varieties and the standard check. A three-point Linkert scale method used to determine the farmers' perception score regarding the trait preference of the varieties. The perception level of a given statement is evaluated based on the comparison between the median of the Likert scales (levels) and the mean perception score of that statement (Nguthi, 2007). The farmers' level of variety and varietal trait preference was based on the median of the three-point Linkert scale. Therefore, two is the median of the three-pint Likert scale, which is used as a cut point to

say whether the variety is better or poor in a given trait.

Results and Discussion

The overall yield performance of different common bean varieties

KAT-B9 (Dandesu) was performed best and an outstanding variety in grain yield than all other varieties of common bean demonstrated. KAT-B1

(Ada) was also good in grain yield next to KAT-B9. The mean yield of KAT-B1 (Ada) and KAT-B9 (Dandesu) is 12.3Qt/ha and 13Qt/ha with the standard deviation of 5.0 and 5.7 respectively. The mean yield of Batu (standard check) is low when compared with the mean yield of the other two varieties which is 9Qt/ha with a standard deviation of 5.20 (Table 1).

Table 1. Yield performance of different common bean varieties in Kg (n=31)

Variety	Min.	Max.	Mean	Std. Deviation	Mean difference	t	Sig.(2-tailed)
KAT B-1	350	2400	1230	4961	330	3.693	0.001
KATB-9	300	2300	1300	5672	400	3.930	0.000
Batu	300	2100	940	4989	<i>Comparison group: Batu. df=30</i>		

Source: Demonstration data

As indicated in table 1, there is a significant mean yield difference among the varieties. The mean yield of KAT-B9 was significantly higher than that of the standard check (Batu). KAT-B1 gives significantly higher than that of the standard check (Table1). This shows that improved common bean varieties have a significant yield advantage over the standard check. The resulting match with Dembele E. and Ashenafi D, (2018) who reported that the improved common bean varieties had a significant yield advantage over the local variety or the standard check. The finding is further in line with Kassahun A., Asmamaw K., (2021) who found that KAT B-9(Dandessu) had the best yield performance since, it is tolerant to major biotic and abiotic factors mainly diseases such as Common Bacterial Blight (CBB), Hallow Blight (HB) and rust.

Yield performance across locations

KAT-B9 performed outstanding variety in yield than all other varieties of common bean in all locations. However, it gave a higher mean yield in Bora than Adami Tullu Jido Kombolcha. KAT-B1 was also given a higher mean yield in all locations next to KAT-B9 (Dandessu). However, the standard check (Batu) was giving a lower mean yield than KAT-B9 and KAT-B1 varieties across all locations (Fig 1). The finding is consistent with Teame et al., (2017) who stated that improved common bean varieties are the high-yielding varieties with better performance than the local variety. Furthermore, the result is in agreement with Gurmu (2007), who stated that low common bean yield is mainly attributed to lack of improved common bean varieties

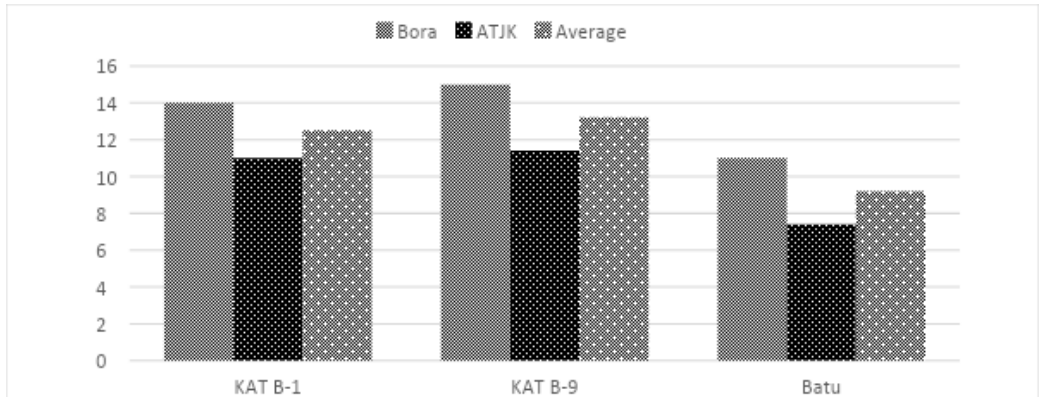


Figure 1. Yield performance of improved common bean varieties across locations in qt/ha

Trait preference of farmers (host and non-host) for different common bean varieties

The demonstration farmers were aware of the selection criteria and they know how to select and rank the varieties. They prefer best-performed varieties among different varieties of common bean depending on different parameters used for comparisons such as insect pest resistance, disease resistance, drought tolerance, food test, grain yield and others. Both the demonstration host farmers and non-host farmers were contacted at field day events and asked how they perceive the demonstrated common bean varieties concerning the above

criterion. Most of the farmers prefer KAT-B1 over other varieties for its drought tolerance, food test, tolerance to disease, seed size and seed color. KAT-B9 is also preferred by most of the farmers next to KAT-B1 in relation to all of the above parameters. KAT-B9 is preferred by most of the farmers over the other two varieties (KAT-B1 and Batu) about Yield, Early maturity, withstanding shattering problems and susceptibility to insect infestation. KAT-B1 is also preferred by the farmers next to KAT-B9 about all of the above parameters. However, Batu was not preferred by the farmers as the other two varieties (KAT-B1 and KAT-B9), since it performed less with regard to the given parameters.

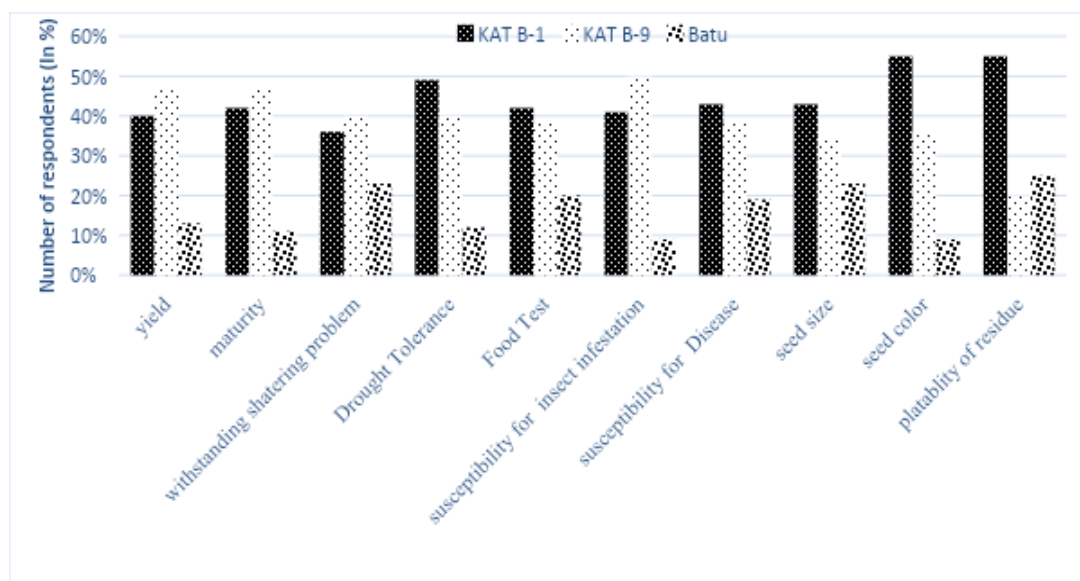


Figure 2. Farmers' variety preference based on set of parameters/criterion

As shown in figure 2, KAT-B9 is preferred in yield, early maturity and tolerance to insect infestation. Fifty percent of the respondents indicated that, KAT-B9 is not easily susceptible to insect infestation like the rest two varieties. A larger proportion of the respondents (47%) preferred this variety over the other two in grain yield. It was also preferred by 47% of the respondents in early maturity relative to the other two varieties (KAT-B1 and Batu). KAT-B1 is also preferred by 40% and 42% of the respondents in yield and early maturity, respectively next KAT-B9 (Dandessu). On the other hand, KAT-B1 takes a leading position in drought tolerance, seed size, seed color and food test. It was preferred by 43% and 42% of the respondents by seed size and food test respectively. A larger proportion of the sample (55%) preferred this variety due to its yellow seed color.

From the result, it was understood that the demonstration farmers select KATB-1 and KAT B-9 based on their selection criteria. This is substantiated by the report of Gemechu et al., (2002), who reported that farmers have their common know-how in best-performed variety selection which should be effectively exploited in the research process. Furthermore, the finding agrees with Teame et al., (2017) who stated that farmers can select the top-ranking and adapted variety based on their own selection criteria. The finding is further supported by Fekadu (2013), who reported that the farmers preferred the best performed common bean varieties based on its seed color, seed size, early maturity drought tolerance, disease and pest resistance and market demand for the variety.

Demonstration host farmers' overall varietal preference

The demonstration host farmers were giving more weight for yield from the

existing parameters. Accordingly, KAT-B9 (Dandessu) was preferred by the majority (55%) of the farmers due to yield potential as compared to other two varieties (KAT-B1 and Batu). KAT-B1 (Ada) was also preferred by

43% of the farmers next to KAT-B9 (dandessu). However, Batu (standard check) was less preferred than the two varieties. It was preferred only by two percent of farmers.

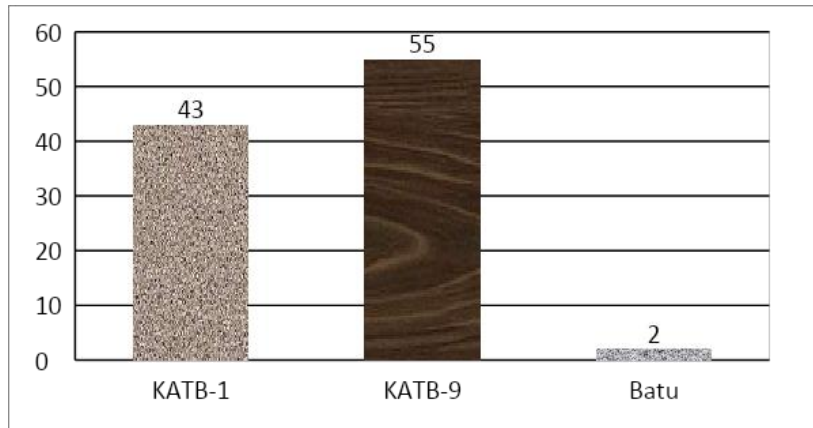


Figure 3. Overall preference of host farmers for each common bean variety

Farmer's preference ranking of the varieties

Farmers gave less score (1.08) for Batu variety for yield trait. This shows that Batu has less yield potential as compared to the other two varieties. However, it is better than the other two varieties in early maturity with the highest perception score of 2.73 (Table 3). The demonstration host farmers' perception scores on all of the given variety traits of KAT-B1 and KAT-B9 were higher than the median of a given three-point Likert scale (2). This implies that KAT-B1 and KAT-B9 were the preferred common bean varieties over the standard check (Batu) in relation to all of the variety traits except for early maturity. The overall mean perception score of KAT-B9 and KAT-B1 was 2.26

and 2.24, respectively (Table 2). The standard check recorded the mean perception score of 1.67 which is lower than the other two varieties (KAT-B9 and KAT-B1). Based on the overall perception score indicated, KAT-B9 and KAT-B1 given the first and second preference rank, respectively. Hence, the farmers are given a rank for the varieties based on the relative importance of each criterion or trait they consider during their evaluation. This is in conformity with Shiferaw et al., (2020) who reported that the farmers select the common bean varieties based on the relative importance of the important traits like yield, pod load and filling, drought-tolerant, seed color, size and shape, earliness, insect and diseases resistance, food taste and cooking time.

Table 3. Farmer's preference ranking for the varieties with respect to different criterion, Year

Criteria	KAT B-1				KATB-9				Batu			
	1	2	3	score	1	2	3	score	1	2	3	score
Yield	2(2)	10(20)	14(42)	2.46**	1(1)	13(26)	12(36)	2.42**	23(23)	2(4)	1(3)	1.15*
Maturity	2(2)	12(24)	12(36)	2.38**	3(3)	9(18)	14(42)	2.42**	1(1)	5(10)	20(60)	2.73**
Drought tolerance	5(5)	11(22)	10(30)	2.19**	5(5)	10(20)	11(33)	2.23**	22(22)	1(2)	3(9)	1.30*
Disease resistance	9(9)	6(12)	11(33)	2.08**	8(8)	8(16)	10(30)	2.08**	16(16)	2(4)	8(24)	1.70*
Food taste	6(6)	12(24)	8(24)	2.08**	7(7)	8(16)	11(33)	2.15**	17(17)	4(8)	5(15)	1.54*
Mean score	4.8(4.8)	10.2(20.4)	11(33)	2.24**	4.8(4.8)	9.6(19.2)	11.6(34.8)	2.26**	15.8(15.8)	2.8(5.6)	7.4(22.2)	1.68*
Rank		2				1				3		

Notice: preference ranking based on scores out of 3 points with 1= low score (not preferred in trait), 2= Moderate score (fair in trait) and 3= high score (preferred in trait). **= preferred in trait, *= Not preferred in trait. Figure in parenthesis shows the perception score for the given statement on each given level of Likert scale

Source: Farmers' feedback.

Conclusion

Common bean is one of the most important pulse crops grown in different parts of Ethiopia. The crop is preferred by the farmers due to its maturing characteristics that enable the household to get an immediate cash source required to purchase food and other household needs when other crops have not yet matured. It is one of the most important cash crops and used as a source of protein for farmers. Common bean is widely intercropped with other crops like maize and sorghum to supplement the farmers with an additional income and to maintain soil fertility.

Melkassa Agricultural Research Center releases common bean varieties having better production and productivity, to address the technology gap and fulfill both the bean market and consumer demand. A wide range of improved common bean technologies was released and disseminated to farmers in Central Rift Valley and other major common bean growing areas of Ethiopia. Nonetheless, the technologies were not sufficiently introduced to the potential production sites and most of the farmers had little chance to know and make their own choice from the ranges of available common bean varieties developed.

Based on the above facts, two improved common bean varieties (KAT-B9 and KAT-B1) were demonstrated alongside the standard check (Batu) on the area of 600m² in which each variety was allocated with

200m² of land. A total of 32 farmers have participated in demonstration. The result indicates that KAT-B9 and KAT-B1 give a higher yield than the standard check. The result shows that KAT-B9 and KAT-B1 give a yield of 1300 and 1250 Kg/ha which is significantly higher than that of the standard check (940kg/ha). The farmer's feedback on the variety shows the varieties are preferable over the standard check based on parameters such as yield, drought tolerance, tolerance to disease and food taste. A higher mean perception score was given to KAT-B9 and KAT-B1 as compared to the standard check (Batu). The varieties are preferable over the standard check regarding the farmers' selection criteria such as yield, early maturity, tolerance to disease and insect infestation, drought tolerance and food test. This indicates that the varieties are suitable for the study area and areas with similar agro ecologies.

Recommendations

The demonstrated improved common bean varieties are preferred by most the farmers over the standard checks based on set of parameters such as grain yield, disease resistance, resistance/tolerance to insects, drought tolerance, food test, seed size and seed color. This draws an implication regarding the need of advancing towards the preferred traits during the variety development.

Research should exert further effort in the creation of awareness about the

varieties among the non-host farmers by demonstrating the varieties in other areas with the same agroecology, preparing farmers' field visit exchange, field days, training and an inclusive stakeholders' platforms. Moreover, the government agricultural extension should work in strong linkage with research for the further promotion and popularization of the varieties among wider farmers in major common bean growing areas of Ethiopia. The non-governmental organization working on agricultural sector with a special focus on improving productivity, production and livelihood of smallholder common bean producers should intervene in promotion and dissemination of the varieties in common bean growing potential areas. Furthermore, different stakeholders which engaged in seed sector like seed enterprises at different levels should work with full effort to secure the farmer's access to quality seeds of the varieties.

The farmers were aware of the selection criteria and they know how to select and rank the varieties. They want the variety that best fits to their criteria and needs. Hence, the research should consider the farmer's participation in the common bean improvement and variety development program so that it considers farmers' selection criterion and trait preference to develop farmers-need based varieties that can be widely disseminated and easily adopted by the farmers.

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Spatial Mixed Model Analysis in Varietal Selection Field Trials

Tarekegn Argaw Woldemeskel¹ and Berhanu Amsalu Fenta²

¹Department of Biometrics, Ethiopian Institute of Agricultural Research (EIAR), Addis Ababa, Ethiopia,

² Ethiopian Institute of Agricultural Research (EIAR), Melkassa Agricultural Research Center, EIAR, Adama, Ethiopia; E-mail: tare.aragaw@gmail.com

Abstract

Spatial variation is common in varietal selection field trials and is a central problem confronting a plant breeder when comparing the varieties' genetic potential. If spatial variability is not taken into account, it can strongly bias variety estimates and result in large standard errors. There have been many methods developed for accounting for spatial variation. Of these, the spatial mixed model approach proposed by Gilmour et al. (1997) has received particular attention as it simultaneously considers three types of spatial variation to be modeled: local, global, and extraneous variations. Despite the recommendations by several authors, spatial mixed model techniques are not widely used in the crop variety evaluation program as a routine data analysis platform. We present a spatial mixed model analysis using field trials from Ethiopia. Results of spatial analysis are compared to that of randomized complete block (RCB) analysis. The investigated spatial mixed models show better data fitting, resulting in a smaller error variance than that of RCB model analysis and a substantial improvement in heritability. Thus, spatial mixed models must be routinely employed in analyzing field trials to accurately and efficiently select superior varieties that contribute to agricultural productivity.

Keywords: Spatial analysis, Spatial mixed models, Field trial, Heritability, Error variance

Introduction

Agricultural varietal selection field trials are popular in plant preceding and evaluation programs, but their design and analysis continue to provide challenges for researchers. Spatial variation is common in these field trials and is a central problem confronting a plant breeder when comparing differences between varieties. Spatial variability, if not taken into consideration, can severely bias variety estimates and create huge standard errors (Girma and Niuho,

2007 and 2008; Hawinkel *et al.*, 2022). The problem of spatial variability can be addressed by sound experimental design, careful trial management, and appropriate statistical analysis (Stringer *et al.* 2012). An important aim of the analysis of varietal selection field trials is to obtain good predictions for variety performance by correcting for spatial effects (Rodriguez-Alvarez *et al.*, 2016).

Spatial variability can be attributed to different sources, such as inherent

variability in the experimental units and variation induced in the units through experimental processes (Cobb, 2014). The spatial variation would be more inflated when the size of the field experiment increased at the expense of plot homogeneity in the field trials, and this would definitely produce bias and inefficiency in the parameter estimation and statistical tests. Experimental designs could account for systematic variation in the plots through the process known as blocking, and it could generally increase the precision and accuracy of experiments. However, the disadvantage of blocking is that it decreases the number of degrees of freedom associated with the residual error component, so it can reduce the power of an experiment if the number of experimental units is small. Blocking also has the potential to increase the variance if it is implemented in a non-orthogonal way (Bailey, 2008). Many elements, however, remain as spatial variation that can't be handled by blocking, strongly influencing yield and other traits. It is necessary to correct for them when analyzing field trials.

There have been many methods developed for accounting for spatial variation, including early methods that included adjacent plot yields as covariates. Papadakis (1937) proposed a covariate adjustment procedure for neighboring plots, which was later examined by Bartlett (1938) and Williams (1952). Wilkinson *et al.* (1983) proposed a smooth trend plus

independent error model with the trend being removed through differentiating the data. Removing trends by differencing neighboring plots was also used by Green *et al.* (1985) and Besag & Kempton (1986). There have been many other approaches to spatial analysis, including the one dimensional models of Gleeson & Cullis (1987), where trends were modelled using time series models, and their extension to two dimensions by Cullis & Gleeson (1991), using a separable correlation structure.

Gilmour *et al.* (1997) developed spatial models by proposing three key types of spatial variation to be modeled: local, global, and extraneous variation. Data from plots close together is more similar to those further apart, resulting in a local smooth trend that may represent changes in soil fertility, moisture, or depth. Extraneous variation is frequently caused by poor trial management or experimental procedures, for example, poor seed planting, harvesting, or fertilizer application. To model global trend and extraneous variation, Gilmour *et al.* (1997) proposed applying polynomial or spline functions to row or column co-ordinates. The authors used a correlation structure for the residuals modeled with a separable process involving a first order autoregressive model for both rows and columns to represent local trends.

Taye and Njuho (2008) proposed a non-parametric technique for fertility

trend using P-spline smoothing. They also advocated modeling fertility trends and local variation simultaneously. To model local variation, they employed Papadakis and kriged covariates.

The aim of this paper is to present spatial analysis of individual field trials using the spatial mixed model approaches proposed by Gilmour *et al.* (1997), with a focus on three scales: global, local, and extraneous variation. The paper will also help bridge the gap between the development and application of method of spatial analysis in the analysis of individual field trials. More importantly, the paper provides the first step of analysis, called separate analysis, for individual trials enhanced with spatial analysis, which will then be combined and subjected to GxE analysis.

Material and Methods

Motivating field trials' dataset

The spatial analysis is illustrated using grain yield data from the 2019 and 2020 common bean variety trials conducted across four locations (Arsinegele, Asasa, Hawassa, and Melkassa) by the Ethiopian lowland pulses research program. Table 1 presents a summary of five trials (location by year combination). The minimum and maximum number of varieties sown across these trials was 75 and 110, respectively. The trials were designed as a randomized complete block (RCB) experiment with three replications and set out in a rectangle (row x column) array of plots, with each block being a complete duplicate. The number of common entries across trials (trial connectedness) is large (Table 2), and GxE analysis is doable, but this is not our objective in this paper.

Table 1. Summary of trials: trial dimension, number of entries, trial mean yield (t/ha), and number of missing values

Trial name	Trial dimension		Number of entries	Mean yield (t/ha)	Number of Missing values
	Column	Row			
AN19CBN1	22	22	110	2.54	0
AN20CBN1	15	15	75	2.55	0
AS19CBN1	15	9	45	6.57	6
HW20CBN1	15	6	30	1.66	0
MK20CBN1	15	15	75	2.7	0

Table 2. Common entries between trials

	AN19CBN1	AN20CBN1	AS19CBN1	HW20CBN1	MK20CBN1
AN19CBN1	110				
AN20CBN1	69	75			
AS19CBN1	45	28	45		
HW20CBN1	28	30	28	30	
MK20CBN1	69	75	28	30	75

Spatial mixed model

Consider a grain yield dataset collected from a varietal selection field trial in which m varieties are grown. The trial consists of n_{plots} arranged in a rectangular array with c columns by r rows ($n = c \times r$). Let $\mathbf{y}$ be the $(n \times 1)$ data vector for a trial, ordered as rows within columns

The linear mixed model for $\mathbf{y}$ can be then written as

$$\mathbf{y} = \mathbf{X}\boldsymbol{\alpha} + \mathbf{Z}\mathbf{u} + \boldsymbol{\varepsilon} \quad (1)$$

where $\boldsymbol{\alpha}$ is vector of fixed effects (including terms for the grand mean, global spatial trend, and other fixed effects) with an associated design matrix $\mathbf{X}$ (assumed to be full column rank), $\mathbf{u}$ is the a vector of random effects (including terms for variety, replication, extraneous spatial variation, and other random effects) with associated design matrix $\mathbf{Z}$, and $\boldsymbol{\varepsilon}$ is the $(n \times 1)$ vector of residual errors ordered as for the data vector.

The random effects from the linear mixed model (equation 1) are assumed to follow a Normal distribution with mean zero vector and variance-covariance matrix, that is

$$\sigma^2 \begin{bmatrix} \mathbf{G} & \mathbf{0} \\ \mathbf{0} & \mathbf{R} \end{bmatrix},$$

Where $\mathbf{G}$ is variance matrix for random effects and $\mathbf{R}$ is the variance-covariance matrix of the residual error

Individual trial residual effects can be analyzed employing spatial methods of analysis that account for local or plot-to-plot variation. $\mathbf{R}$ in this case will have its own spatial covariance structure. Spatial mixed model provides for a much more realistic correlation structure between plots. In the linear mixed model, we partition the $(n \times 1)$ vector of residual errors $\boldsymbol{\varepsilon}$ into a vector $\boldsymbol{\psi}$ ($n \times 1$) of spatially correlated effects, and a vector $\boldsymbol{\zeta}$ of independent technical or measurement errors. Thus, for variety field trials that have row by column arrangement and ordered as rows within columns, the spatially correlated effects can be modelled using a two dimensional separable correlation structure (Gilmour *et al.*, 1997). Thus, the covariance matrix for $\boldsymbol{\psi}$ is given by

$$\text{var}(\boldsymbol{\psi}) = \boldsymbol{\Sigma} = \sigma^2 \boldsymbol{\Sigma}_c(\boldsymbol{\rho}_c) \otimes \boldsymbol{\Sigma}_r(\boldsymbol{\rho}_r) \quad 2$$

Where $\boldsymbol{\Sigma}_c$ and $\boldsymbol{\Sigma}_r$ represent spatial correlation structures with parameters in $\boldsymbol{\rho}_c$ and $\boldsymbol{\rho}_r$ for the column and row directions, respectively. In both the row and column directions, we typically use an autoregressive spatial structure of order one, with in $\boldsymbol{\rho}_c$ and $\boldsymbol{\rho}_r$ each containing a single autocorrelation parameter.

For spatial auto-correlation in the row direction only, the model simplifies to $\boldsymbol{\Sigma} = \sigma^2 \mathbf{I}_{n_c} \otimes \boldsymbol{\Sigma}_r(\boldsymbol{\rho}_r)$ where n_c is the number of columns for the trial. Similarly, $\boldsymbol{\Sigma} = \sigma^2 \boldsymbol{\Sigma}_c(\boldsymbol{\rho}_c) \otimes \mathbf{I}_{n_r}$ would

be the reduced form for spatial auto-correlation in the column direction only where n_r is the number of rows for the trial. We can have also no spatial covariance in either direction. Thus, the model simplified to an IID variance structure of the form $\Sigma = \sigma^2 \mathbf{I}_{n_c} \otimes \mathbf{I}_{n_r} = \sigma^2 \mathbf{I}_n$.

Heritability formula

Following the approach of Cullis *et al.* (2006), the heritability (H^2) value for the trial can be calculated from a generalized formula that takes unbalanced data into account, as

$$H^2 = 1 - \frac{A}{2\sigma_g^2} \quad (3)$$

Where A is the average pairwise prediction error variance of genetic effects is σ_g^2 is the genetic variance.

Estimation, testing and software

Estimation in the linear mixed model involves estimating the fixed and random effects, α and $\mathbf{u}$ and the variance-covariance parameters in $\mathbf{G}$ and $\mathbf{R}$. This involves two linked processes, in which the variance parameters of the model are estimated using residual maximum likelihood (REML, Patterson & Thompson 1971), and the fixed and random effects are estimated using best linear unbiased estimation (BLUE) and best linear unbiased prediction (BLUP) respectively. The Residual Maximum Likelihood Ratio Test (REMLRT) can be used to test the significance of random effects in the linear mixed

model. The REMLRT can only be used to compare the fit of two models that are nested and have the same fixed effects.

The Wald test may be used to determine the significance of fixed effects in a linear mixed model. The classic Wald statistic has an asymptotically chi-squared distribution. This test is often seen as anti-conservative (Butler *et al.*, 2009). Kenward and Roger (1997) introduced an adjusted Wald statistic along with a F approximation that worked well in a range of scenarios. ASReml in the R environment was used to estimate the variance parameters from the linear mixed model using REML (Butler *et al.*, 2009). The Average Information (AI) algorithm is implemented by ASReml (Gilmour *et al.*, 1995).

Results and Discussion

The first model fitted was a randomized complete block (RCB) model with random block/replication and variety effects, and the residual correlation structure is denoted by $\text{id}(\text{Column}).\text{id}(\text{Row})$, where id refers to the identity matrix. This model reflects the RCB analysis based on mixed model approach. And, the next step was to model the spatial variation. Thus, a spatial model to the residuals using a separable autoregressive process in the column and row dimensions was first fitted over the RCB model for the local variation. The spatial model for extraneous variation was then fitted along the

column and row by retaining significance terms for local variation. The significance of each fitted spatial model for both local and extraneous variation was tested using the REMLR test. And finally, the spatial models for global variation were fitted and tested with the Wald test.

The presence of global and extraneous variation associated with the row and column direction can be checked with the help of model diagnosis tool, in particular the sample variogram (Gilmour *et al.* 1997). A sample variogram as a typical model diagnostic plot for trial AN20CBN1 using the Metplot package, which is a part of ASReml-R, is depicted in Figure 1. In the row direction, the plot has a saw-toothed up-down pattern. This trend, as demonstrated by Stefanova *et al.* (2009), is most likely the presence of extraneous variation within the trial, implying random row effects. By including a random column effect in the mixed model, this effect can be accommodated in the model. There is also evidence of a global trend in the row direction, with the variogram steadily increasing. This global trend may be accounted for in the model by employing linear or polynomial regression over a centered row number, denoted *lrow*.

Table 3 presents the Wald test for global variation and the REMLR test for local and extraneous spatial variation. The spatial variation were appropriately modeled for AN19CBN1 along the row and column (p-value <0.001), for

HW20CBN1 along the row (p-value=0.017), and for MK20CBN1 along the column (p-value=0.01). The global and extraneous spatial variation were found to be significant along the row direction at AN20CBN1 (p-value =0.019 and <0.001, respectively). This demonstrates how spatial variation is a crucial component of plant breeding trials that must be considered. The estimates of the local spatial correlation parameters were positive ($\rho_1=(0.33, 0.57)$, $\rho_2=0.38$, $\rho_3=0.18$, see Table 3), suggesting what was noted in De Faveri (2013) that plots near together are more likely to be comparable than plots further apart. Negative spatial correlation values would imply inter-plot competition, as shown in Stringer and Cullis (2002), but there was no indication of it here.

Control non-genetic variability by blocking, which is based on observable factors like soil type and topography, is commonly used in designing experiments, but several possible inputs are unknown or unmeasured, which stresses the importance of incorporating spatial information into the analysis of each trial to improve the precision of variety evaluation. As noted in Girma (2005), spatial analysis is critical for field trials in Ethiopia, where the variability of soil and environment is very high, even within a very small area. If this spatial variation is unaccounted for, it leads to biased and inefficient results for variety valuation.

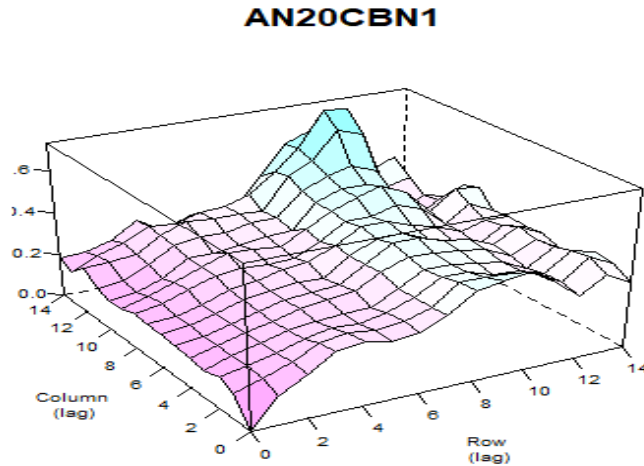


Figure 1. Sample variogram plot of the residuals from a base model for yield at trial MK18N.

Table 3. Summary of spatial analysis: spatial variation, fitted model term, Wald and REML test statistic and P-value

Trial name	Spatial variation	Model terms	Wald ^a /REMLR ^b test statistics	P-value
AN19CBN1	Local	ar1(Column):id(Row)	47.59	<0.001
		ar1(Column):ar1(Row)	65.27	<0.001
	Global	lrow	7.18	0.019
AN20CBN1	Extraneous	Row	16.74	<0.001
AS19CBN1	Extraneous	Column	4.17	0.041
HW20CBN1	Local	id(Column):ar1(Row)	5.68	0.017
MK20CBN1	Local	ar1(Column):id(Row)	6.58	0.01

$$\rho_1=(0.33, 0.57), \rho_2=0.38, \rho_3=0.18$$

^aTest for global trend after significant terms for extraneous variation and local trend are fitted

^bTest for extraneous variation and local trend after significant terms for global trend are fitted

ρ_1 , ρ_2 and ρ_3 are estimates for autoregressive order 1 (AR1) spatial correlations parameters at, AN19CBN1, HW20CBN1 and MK20CBN1, respectively

The genetic variance, error variance and heritability estimates for each trial from both methods of analysis (RCB and spatial analysis) are presented in Table 4. All results are REML estimates, and are unbiased for the corresponding variance component parameters. In the RCB analysis the estimates ranged from 0.044 to 0.297 for genetic variance, from 0.076 to 5.686 for error variance, from 29.49 to 63.33 for heritability. Similarly, in the spatial analysis the estimates ranged from 0.044 to 1.215 for genetic variance, from 0.08 to 4.246 for error variance, and from 42.82 to 76.92 for heritability. At AS19CBN1, both analyses revealed very high genetic and error variance, as well as low heritability. This might be because the spatial variation captured in the spatial analysis was considerable, and the remaining variability of the experimental units (plots) was also extremely large. The RCB analysis gives low genetic variance for most of the trials. This is not

surprising since the RCB analysis is quite inferior to the spatial analysis to efficiently explaining the genetic variance and spatial variations in the data.

As compared to RCB analysis, the spatial analysis gave relatively small error variance for all trails. It substantially also increased heritability in all trials as it clearly depicted in Figure 2. This in general reveals that the spatial analysis will improve the precision and accuracy of varieties evolution by capturing non-genetic variation associated with agricultural field plot variability (Smith and Cullis, 2018; Cullis *et al.* 2010).

Table 4. Trial genetic variance, error variance and heritability from RCB and spatial analysis

Trial name	RCB analysis			Spatial analysis		
	Genetic variance	Error variance	Heritability	Genetic variance	Error variance	Heritability
AN19CBN1	0.297	0.564	61.21	0.297	0.555	76.92
AN20CBN1	0.103	0.339	47.71	0.125	0.175	66.94
AS19CBN1	0.835	5.686	29.49	1.215	4.246	42.82
HW20CBN1	0.044	0.076	63.33	0.044	0.08	67.55
MK20CBN1	0.059	0.188	48.6	0.057	0.08	48.68

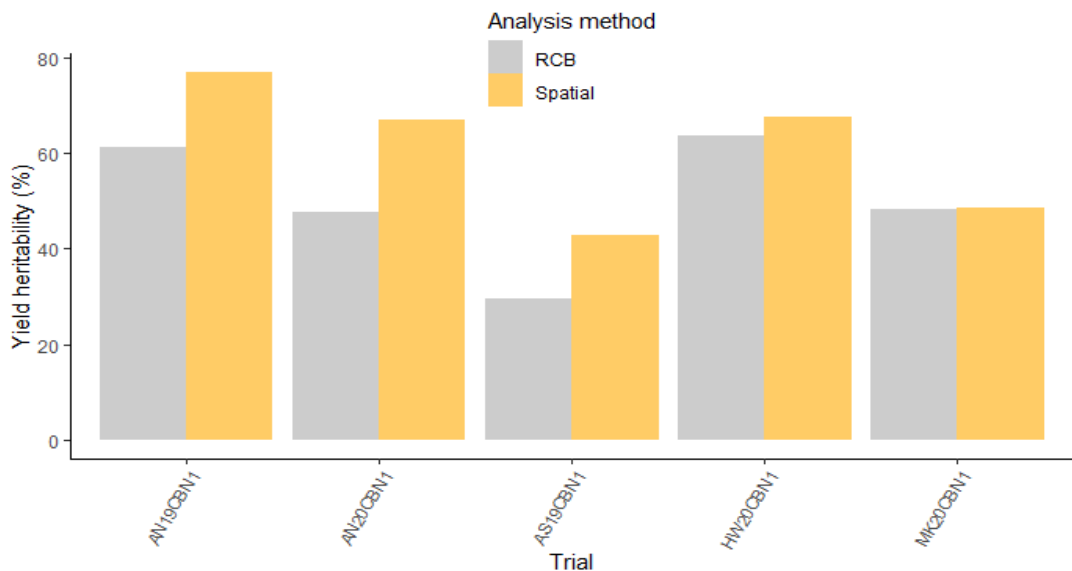


Figure 2. Heritability of yield at each trial using RCB and spatial analysis.

Conclusion

Agricultural field trial data (such as variety trials) may not be balanced or

may be big trials at the expense of plot homogeneity, and ANOVA-based approaches may not be appropriate for their analysis. Spatial variation is

clearly evident in varietal trials. If this spatial variation is not taken into account, variety selection will worsen. As a result, more efficient spatial analysis approaches must be used. The linear mixed model provides a strong framework for dealing with unbalanced as well as relaxing the distributional assumptions surrounding the residual error by employing spatial analysis. The investigated spatial models show better data fitting, resulting in a smaller error variance than that of RCB model analysis and a substantial improvement in heritability. For each individual variety trial, spatial variation on three scales: global, extraneous, and local trend must be considered to obtain accurate and efficient results for variety evaluation.

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