International Journal of Scientific Engineering and Science
Volume 4, Issue 5, pp. 8-17, 2020. ISSN (Online): 2456-7361

Kernel Yield Evaluation of Groundnut (*Arachis hypogaea* L.) Genotypes in North Western Part of Ethiopia

Yeshiwas Sendekie[1], Berehanu Abate[2], Mulugeta Atinaf[3]
[1]Ethiopian Institute of Agricultural Research, Pawe Agricultural Research Center, Pawe, Ethiopia
[2]Hawassa University, School of plant and horticultural science, Hawassa college of agriculture, Hawassa, Ethiopia
[3]Ethiopian Institute of Agricultural Research, Fogera Agricultural Research Center, Woreta, Ethiopia
E-mail address: yeshiwassendekie @ gmail.com

Abstract— *North western part of Ethiopia is one of the major groundnuts producing areas in Ethiopia. However, only variety Manipeter is commonly cultivated in the region even though there are 21 nationally released groundnut varieties in Ethiopia. To grow other groundnut varieties in the area multi-environment trials should be conducted to determine their adaptability and productivity. Therefore, fifteen groundnut genotypes were evaluated under multi-environment yield trials in 2017 cropping season at six locations with the objectives of identifying stable high yielding genotypes. The experiment was laid out in Randomized Complete Block Design with three replications. The analysis of variance on kernel yield at each location showed that there was significant difference among genotypes. Genotype Babile-1 at Pawe (2.35t/ha) and Dangur (2.03 t/ha), Roba at Manduara (2.3t/ha) and Dibate (1.92 t/ha), Bulgi at Guba (2.74 t/ha) and Manipeter at Bullen (2.02 t/ha) produced the highest kernel yield. Bartlett's test revealed that the variances were homogenous. Pooled analysis of variance also revealed highly significant difference among genotypes (G), environments (E) and genotype by environment interaction (GEI) for kernel yield. Stability analysis results using AMMI and GGE-biplot analysis revealed that Babile-1 variety is stable high yielding genotype across locations and it had great potential to be recommend and grown on large scale production.*

Keywords— *Genotype by environment interaction; groundnut; kernel yield.*

I. INTRODUCTION

Groundnut (*Arachis hypogaea* L.) also called the peanut and earthnut (Acquaah, 2012). It is a self-pollinated, allotetraploid (2n = 4x = 40) with little polymorphism at the molecular level (*Janila et al., 2013) and* annual herbaceous legume; belonging to the family *Leguminoceae* and sub-family *Papilionaceae* (Stalker and Wilson, 2016). It is cultivated in more than 100 countries with 33.16 million ha with a total production of 63.34 million tons during 2018 (FAO, 2019). China and India are the leading groundnut producers followed by Nigeria and USA. Groundnut is ranked fifth in area coverage among cultivated oilseed crops in the world after oil palm, soybean, rapeseed, and sunflower (FAO, 2019) and ranked third in Ethiopia after Sesame and Nuge (CSA, 2019). The total land coverage of groundnut in Ethiopia is 84,237.01 ha and the production is estimated to be 144,091.26 tons with productivity of 1.71 tons per hectare (CSA, 2019).

Nutritionally it contains 36% to 54% oil, 16% to 36% protein and 10 to 20% carbohydrates (Gregory *et al*., 1980). It supplies about 5.6 calories per kernel when consumed raw and 5.8 calories per kernel when consumed roasted (Woodroof, 1983). Groundnut haulms are rich in protein and palatable than stovers of cereals which have low N, high fibre content, and poor digestibility and therefore have low nutritive value and are used as supplementary feed (Singh *et al*., 2011).

Quantitative traits like biological and economic yields are highly determined by environmental factors varying across locations and seasons. For this reason, performance evaluations of promising cultivars are carried out in multiple years and locations. So, productivity of cultivars across environments depends on the extent of genotype by environment interaction (Bernardo, 2002). Genotype by environment interaction is an important challenge facing plant breeders that complicates varietal selection. Genotype by environment interactions occurs when two or more genotypes perform differently in different environments (Yan and Tinker, 2006; Yang, 2007). However, significant genotype by environment interaction is practically important when tested genotypes have rank change in their performance across environments (Beker, 1988). Abera *et al*., (2004) reported that performance of the crop varieties varies widely with change in the sowing dates across locations due to existence of significant genotype by environment interaction (GEI) effect.

Ethiopia is a country of different agro-ecologies and, macro and micro-climatic variability which have resulted from the wider altitude range from Danakil depression (116 m.b.s.l) to the highest mountain Ras Dashen (4620 m.a.s.l) (EBI, 2014). This wider altitudinal range has influence on temperature, rainfall amount and its seasonal distribution, soil fertility, crops distribution and their productivity across locations and over years. It may be expected that the genotype by environment interaction will also be high (Abera *et al*., 2004). Therefore, knowledge of the pattern and magnitude of GEI and stability analysis is important for understanding the response of different genotypes to varying environments and for identification of widely and specifically adapted genotypes. Various researchers have performed experiments to determine the extent of genotype by environment interaction and stability of genotypes on different crops (Naser *et al*., 2012 on lentil; Sewagegne *et al*., 2013 on rice; Mulugeta, *et al*., 2016 on lupin; Ngirazi *et al*., 2017 on groundnut).

International Journal of Scientific Engineering and Science
Volume 4, Issue 5, pp. 8-17, 2020. ISSN (Online): 2456-7361

This study was conducted to identify stable high yielding genotypes and examining the presence of genotype by environment interaction.

II. Materials and Methods

A. Experimental site and genotypes description

The study was conducted at six experimental testing sites of Pawe Agricultural Research Center during 2017 main cropping season. Those testing locations were Pawe, Guba, Dibatie, Mandura, Bullen and Dangur districts which are located in north western part of Ethiopia. Pawe is main research site which is located in north western part of Ethiopia in Benishangul-Gumuz region at 565km away from Addis Ababa at 11° 18'49.6" N latitude and 036°24'29.1'' E longitude (Fig 1). Characteristics of the experimental sites are presented in Table 1 below.

Fifteen groundnut genotypes were used for this study. The materials were obtained from Pawe Agricultural Research Center Pulse and Oil Crops Improvement Section and Haromaya University National Groundnut Research Coordinating Program. Some descriptions of the genotypes are provided in (Table 2).

TABLE 1. Description of testing sites

Location	Altitude (m.a.s.l)	Coordinate		Rain fall (mm)/ uni-modal	Temperature (o_c)		Soil type
		Latitude(N)	Longitude(E)		Mean (max)	Mean (min)	
Pawe	1120	11° 18' 49.6"	036°24' 29.1"	1000-1600	32.6	16.5	Nito soil
Guba	799	11°16'17.04"	035°21'00.86"	500-1000	38.2	22.5	sandy
Dibatie	1572	10°47'00.582"	036°16'48.786"	1500-1700	28	14	Nito soil
Bullen	1323	10°32'00.000"	035°54'22.452"	1300-1700	28.1	14.8	Sandy loom
Mandura	1455	11°04'17.858"	036°25'55.800"	1100-1800	33	15	Nito soil
Dangur	1167	11°16'12.588"	036°15'07.836"	1000-1500	35.5	21.2	Nito soil

m.a.s.l = meters above sea level, E=east, N=north, Min=minimum, Max=maximum, T=temperature, °c= degree centigrade, mm=millimeter, '= minute, "=second
Source; Pawe Agricultural Research Center (2018)

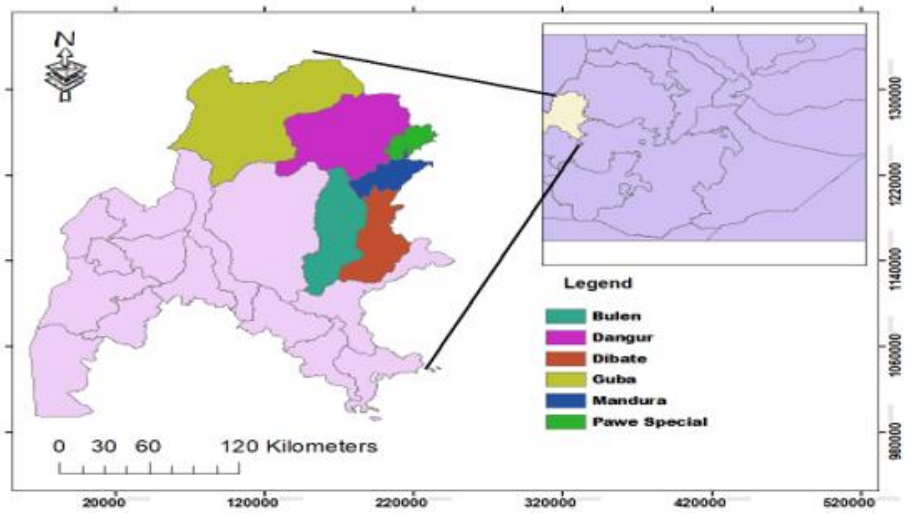

Figure 1. Map of test locations

TABLE 2. List of genotypes used for the study

Number	Variety name	Year of release	Growth habit	Source of genotypes
1	Manipeter	-	Bunch type	PARC
2	Bulgi	2002	Bunch type	HU
3	Lotte	2002	Bunch type	HU
4	Roba	1989	Bunch type	PARC
5	Werer-962	2004	Bunch type	HU
6	Faxo	-	Bunch type	HU
7	NC-343	1986	Bunch type	HU
8	BaHa-jidu	2012	Runner type	HU
9	BaHa-gudo	2012	Bunch type	HU
10	Fetene	2009	Bunch type	HU
11	Werer-961	2004	Bunch type	HU
12	Babile-2	2016	Bunch type	PARC
13	Babile-1	2016	Bunch type	PARC
14	Werer-963	2004	Bunch type	HU
15	Babile-3	2016	Bunch type	PARC

PARC = Pawe agricultural research center, HU= Haromaya University,
Source; MoANR (2017)

International Journal of Scientific Engineering and Science
Volume 4, Issue 5, pp. 8-17, 2020. ISSN (Online): 2456-7361

B. Experimental Design and Management

Randomized complete block design (RCBD) with three replications was used to conduct the experiment. Plot size was 9.6 m^2 consisting of 4 rows each 4 m long. The inter-row and intra-row spacing was 60 cm and 10 cm, respectively. The distance between plot and replication was 0.8m and 1.5 m, respectively. One seed per hill seed rate was used. 100kg DAP fertilizer per hectare which is 96gm per plot basis was used and all applied during planting. Data were collected from two middle rows (4.8m^2) and these rows were harvested to record yield and related traits. All possible agronomic management practices were applied properly.

C. Data Collected

According to IBPGR and ICRISAT (1992), the following data were collected. Days to emergence, days to flowering, days to maturity, number of branches per plant, number of mature pods per plant, number of seeds per pod, hundred seed weight, dry pod yield, Shelling percentage and kernel yield. Only kernel yield is used for this particular study.

D. Statistical Analysis

Analysis of variance for kernel yield for each location and pooled analysis of variance over locations were performed by the PROC GLM procedure in SAS (2011) versions 9.3 software to assess the difference among the tested varieties. First, normality of the data Shapiro-Wilk W test checked using SAS (2011) versions 9.3 software for each location based on the assumption that the distribution is normal. Secondly, analysis of variance for each location was conducted, and the homogeneity of variance (error mean square) among the locations was tested by Bartlett's test and pooled analyses of variance was performed for the traits whose variance (error mean squares) is homogenous. Mean separation was carried out using least significant difference (LSD at 0.05α).

For combined data analysis, the linear model used was;

$$Y_{ijk} = \mu + g_i + l_j + (gl)_{ij} + r_k(l) + e_{ijk}$$

Where, Y_{ijk}= the observed value of the trait Y for the i^{th} genotype in the j^{th}; location and k^{th} block; μ= the grand mean of trait Y in the experiment; g_i= the effect of the i^{th} genotype; l_j = the effect of the the j^{th} location; $(gl)_{ij}$= the genotype-by-environment interaction effect; $r_k(l)$= effect of block across location; e_{ijk}= experimental error

a. Genotype by environment interaction and stability analysis

In this study, to determine the effects of genotypes, environments and their interaction and to identify stable high yielder genotype, both AMMI and GGE bi-plot were employed (Gauch and Zobel, 1988; Yan *et al*., 2000, 2001; Yan, 2001). AMMI and GGE bi-plot were analyzed and graphed using Plant Breeding Tools version 1.4 software. AMMI stability value

The mathematical statement of AMMI model is given by the following formula:

$$\bar{Y}ijk = \mu + G_i + E_j + \sum_{k-1}^{m} \lambda k \alpha ik \gamma jk + P_{ij}$$

Where; $\bar{Y}ijk$ = the yield of the i^{th} genotype in the j^{th} environment in k^{th} axis; Gi = the mean of the i^{th} genotype minus the grand mean; Ej = the mean of the j^{th} environment minus the grand mean; λk = the square root of the eigen value of the k^{th} IPCA axis; αik and γjk = the principal component scores for IPCA axis k of the i^{th} genotypes and the j^{th} environment; Pij = the deviation from the model

The AMMI stability value (ASV) as described by Purchase *et al*. (2000) was calculated using Microsoft excel (2010) as follows:

AMMI Stability Value (ASV)

$$= \sqrt{\left[\left(\frac{\text{IPCA1ss}}{\text{IPCA2ss}}\right)(\text{IPCA1 score})\right]^2 + (\text{IPCA2 score})^2}$$

Where: ASV= AMMI's stability value; ss =sum of squares; IPCA1 and IPCA2= the first and the second interaction principal component axes, respectively.

III. Results And Discussion

A. Analysis of Variance

The experimental result in (table 4) showed that, there was highly significant (p≤ 0.001) difference among genotypes in all environments. The highest mean kernel yield was recorded at environment Guba which is 2178.2 kg ha^{-1} and the lowest was recorded at environment Dibate which is 1512.7 kg ha^{-1}.

Bartlett's test result revealed that error variance was homogeneous for kernel yield across six environments (Table 3). It allowed to proceed further for pooled analysis of variance.

TABLE 3. Homogeneity of variance test results across six locations on kernel yield.

Parameter	Kernel yield
DF	5
Chi-square	9.05
Pr >chisq	0.11

Where, DF= degree of freedom, Pr= probability value

Pooled analysis of variance revealed that the main effect of genotypes (G), environment (E), and genotype by environment interactions (GEI) were highly significant (p≤ 0.01) on kernel yield of fifteen groundnut genotypes (Table 5) this was similar with the finding of Alemayehu *et al*, (2016). Therefore, superior genotypes across environments cannot be identified by considering their mean kernel yield performance because GEI is highly significant. Yan *et al*. (2000) indicated that since GEI minimize the usefulness of genotypes, it is thus imperative that yield levels, adaptation and stability are taken into account in multi-location trials. GEI is an important aspect of plant breeding programs and it is important for plant breeders to identify specific genotypes adapted or stable to across environments (Yan *et al*., 2007). Similar results were reported by (Dolinassou *et al*., 2016; Mulugeta *et al*., 2016 and Ngirazi *et al*., 2017).

Genotypes Babile-1, Roba and NC-343 were top yielder genotypes with mean values of 2103.5kg ha^{-1}, 2094.9kg ha^{-1} and 2040.8kg ha^{-1}, respectively. Genotype Fetene had the lowest mean kernel yield with value of 1451.6kg ha^{-1}. The overall mean kernel yield was 1744.53kg ha^{-1}. In general, all genotypes showed inconsistent performances across the tested environments. For example, the genotype Roba ranked 1st in environment Pawe, but it ranked 4th in environment Mandura for mean kernel yield (Table 4). Therefore, the presence of

International Journal of Scientific Engineering and Science
Volume 4, Issue 5, pp. 8-17, 2020. ISSN (Online): 2456-7361

genotype by environment interaction was clearly evident on kernel yield of tested genotypes across environment.

TABLE 4. Mean kernel yield (kg ha^{-1}) of genotypes evaluated at six locations

No	Genotypes	Locations						
		Pawe	Dangur	Mandura	Guba	Dibatie	Bullen	Overall mean
1	Manipeter	1748.2^{cd}	1621.3^{cde}	1935.7^{bc}	1997.7^{efg}	1389.4^{c-f}	2021.9^{a}	1785.7^{c}
2	Bulgi	1679.9^{d}	1677.2^{bcd}	2058.2^{ab}	2743.6^{a}	1573.7^{a-e}	1727^{abc}	1909.9^{b}
3	Lotte	1770.7^{cd}	1976^{a}	1941.8^{bc}	1829.4^{fg}	1517.4^{b-e}	1639.5^{bcd}	1779.1^{c}
4	Roba	2289.8^{a}	1707.3^{bcd}	2299.4^{a}	2445.3^{bc}	1919.7^{a}	1907.9^{ab}	2094.9^{a}
5	Werer-962	1876.9^{bc}	1782.8^{abc}	1908.1^{bc}	2177.1^{de}	1715.3^{abc}	1642^{bc}	1850.4^{bc}
6	Faxo	2263.1^{a}	1905^{ab}	1603.1^{de}	2331.1^{cd}	1417.2^{c-f}	1469.1^{cde}	1831.4^{bc}
7	NC-343	2283.5^{a}	1612^{cde}	2117.4^{ab}	2717.4^{a}	1674.9^{a-d}	1839.4^{ab}	2040.8^{a}
8	BaHa-jidu	1759.1^{cd}	1410.4^{efg}	1782.4^{cd}	1815.8^{g}	1272.4^{ef}	1798.6^{ab}	1639.8^{d}
9	BaHa-gudo	2231.7^{a}	1528.2^{de}	1260.8^{g}	2301.2^{cd}	1620.5^{a-e}	1625.2^{bcd}	1761.3^{c}
10	Fetene	1405.7^{e}	1188.6^{g}	1379.5^{efg}	2272.6^{cd}	1121.8^{f}	1341.3^{de}	1451.6^{e}
11	Werer-961	1200.6^{f}	1479.7^{def}	1346.4f^{g}	2022.4^{ef}	1320.2^{def}	1034.8^{f}	1400.7^{e}
12	Babile-2	2022.5^{b}	1688.2^{bcd}	1566.3^{def}	2188.9^{de}	1588.4^{a-e}	1452.3^{cde}	1751.1^{c}
13	Babile-1	2348.3^{a}	2025.5^{a}	2043.9^{b}	2553.4^{ab}	1834.6^{ab}	1815.4^{ab}	2103.5^{a}
14	Werer-963	1194.1^{f}	1403.6^{efg}	1260.1^{g}	1435.1^{h}	1091.4^{f}	1296.1^{ef}	1280.1^{f}
15	Babile-3	1787.8^{d}	1271.2^{fg}	1186.1^{g}	1842.1^{fg}	1633^{a-d}	1206.2^{ef}	1487.8^{e}
	Mean	1857.5	1618.5	1712.6	2178.2	1512.7	1587.8	1744.5
	CV%	6.3	9.3	8.6	5.3	14.2	11.2	9.1
	LSD	195.4	252.5	245.8	194.6	358.7	298.4	103.8
	F-test	**	**	**	**	**	**	**

Where, *= significant difference, **= highly significant difference at p<0.01, CV=coefficient of variation, LSD = Least significance difference and means within a column followed by same letter(s) are not significantly different at 5 % according to LSD.

From the total variation explained was 30.46% due to environment, 36.44% due to genotype and 22.17% due to genotype by environment interaction for kernel yield (Table 5). For kernel yield genotype had largest contribution for variations which accounts 36.44%. This indicates the influence of genotype was higher than environment. so that, genotype selection needs more effort, this is similar with the finding of Alemayehu *et al*, (2016). The high percentage of the genotype sum square indicated that yield performance across location highly influenced by genetic potential of genotypes across environments. The presence of significant variations among the genotypes indicates the differences in the inherent genetic potential of the genotypes that makes selection possible, whereas differences among the environments showed the variability in potential suitability of the test locations for groundnut production.

The significance effect of GEI on kernel yield suggested the need to assess the stability of genotypes across environments. AMMI and GGE-biplot stability analysis models were used in this study. Dagnachew *et al*. (2014), used these two multi-variate stability analysis methods in his study on finger millet varietal selection for selection of high yielder and stable genotypes.

TABLE 5. Pooled analysis of variance for kernel yield (kg ha-1) of groundnut genotypes evaluated across six locations

Source of variation	df	SS	%ss	M S	F Value	Pr > F
Replication with in E	12	597501.11	1.37	49791.8		
Environment(E)	5	13323590.8	30.46	2664718	107.02	<.0001
Genotypes(g)	14	15936995.7	36.44	1138357	45.72	<.0001
G X E	70	9695333.6	22.17	138505	5.56	<.0001
Error	168	4182889.79	9.56	24898.15		
Total	269	43736311	100			
CV (%)				9.05		
LSD (5%)				103.84		
R^2(%)				90.4		

CV= coefficient of variation, df= degree of freedom, E= environment, SS= sum of square, MS= Mean square, LSD= least significant difference,

B. Additive main effects and multiplicative interaction (AMMI)

AMMI comprises two basic biplots, the AMMI 1 biplot, where the main effect (Genotype and Environment means) and IPCA-I scores are plotted against each other (Fig. 2) and AMMI 2 biplot, where scores of IPCA-I and IPCA-2 are plotted against each other (Fig 3). In AMMI 1 biplot, the differences among genotypes in terms of direction and magnitude along the X-axis (yield) and Y axis (IPCA 1 scores) are important. The AMMI analysis of variance for kernel yield indicated highly significant differences for environments, genotypes and genotype by environment interaction (Table 6). The F-test was highly significant for all IPCA. The IPCA are ordered according to decreasing importance.

The Gollob's test that has been used to separate the pattern and noise in GEI has revealed that the all IPCAs were highly significant (P<0.001), indicating that the total information contained in GEI can be explained using these IPCAs (Table 6). The pattern in GEI of the given groundnut data set was predicted by the first two principal components axis of genotypes and environments, since IPCA1 and IPCA2 were cumulatively accounted for 66.1% for kernel yield (Table 6) which was greater than half of a total GEI, which is consistent

with other studies (Gauch and Zobel, 1996 and Yan *et al*., 2000), they recommend the most accurate model for AMMI can be predicted using the first two IPCAs and that rest IPCAs mostly captured noise.

TABLE 6. AMMI analysis of variance for mean kernel yield (kg ha^{-1}) of genotypes tested across six locations

Source of variation	Df	SS	MS	GEI explained (%)	Cumulative (%)	Variation Explained (%)
Total	269	43736311				
Replication with in E	12	597501.11	49791.8**			1.37
Environment(E)	5	13323590.8	2664718**			30.64
Genotypes(g)	14	15936995.7	1138357**			36.44
G X E	70	9695333.6	138505**			22.17
IPCA1	18	3691813.5	205100.75**	38.1	38.1	
IPCA2	16	2713887.6	169617.98**	28	66.1	
IPCA3	14	1770841.3	126488.67**	18.3	84.4	
IPCA4	12	834983.6	69581.97**	8.6	93	
IPCA5	10	68387.5	68380.75**	7.1	100	
Error	168	4182889.79	24898.15			

a. AMMI-1 bi-plot analysis for kernel yield

In the AMMI 1 bi-plot model, the IPCA 1 scores of genotypes and environments have been plotted against their respective means for kernel yield (Fig. 2). The IPCA scores for both genotypes and environments were plotted against the mean yield for genotypes and environments. Genotypes or environments on the right side of the midpoint of the axis have higher yield than those on the left-hand side. The greater the IPCA scores, negative or positive, (as it is a relative value), the genotype are specifically adapted to certain environments (large interaction). The more the IPCA scores approximate to zero, the more stable or adapted the genotype is over all the environments sampled (Crossa *et al*., 1990; Gauch and Zobel, 1996).

AMMI1 bi-plot of Kernel yield presented in (Fig. 2) showed that, genotypes G4 , G10 , G7 , G11, G5, G2 and G13 exhibit small interactions (smaller scores close to zero) and appear close to the horizontal axes and therefore, are relatively stable indicating that these genotypes were less influenced by environments. However, among these widely adopted or stable genotypes, high mean performance exceeding grand mean were exhibited by G13, G4, G7, G2, G5 and G3 genotypes, while genotypes G10, G8 and G11 were the low yielder. Conversely, genotypes such as G8, G12, G15, G6, G14, G3, G9 and G1 are relatively far apart from the origin (greater IPCA1 scores) and thus they had strong location interaction effects and are unstable or specifically adopted (Fig. 2). The result is in agreed with Sharma *et al*., (2009) and Verma *et al*. (2016) findings.

Environments with IPCA score located near to the origin in the bi-plot were less interacting with the genotypes, while environments with IPCA score located away from the origin in the bi-plot were more interacting with the genotypes and make the selection difficult. Accordingly, among six environments E2 and E4 located relatively near to the origin and they were less interacting environments, they contribute less amount of variation to the total GEI (Fig. 2). Conversely, the environments E1, E5, E6 and E3 had the IPCA1 score located far apart from the origin in the bi-plot was the most interactive environments meaning that contribute higher amount of variation to the total GEI, this finding was in harmony with Sharma *et al*. (2009) and Suneetha *et al*. (2013).

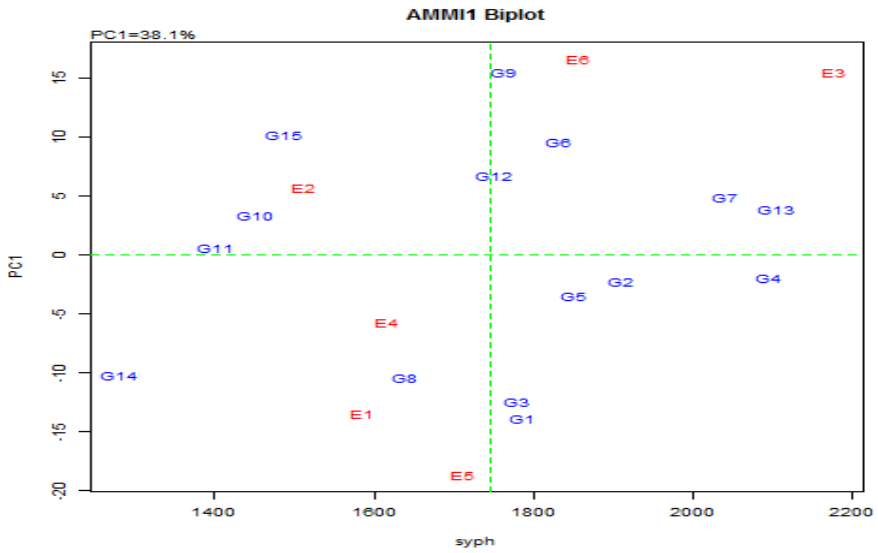

Figure 2. AMMI bi-plot of IPCA1 against kernel yield of groundnut genotypes across six locations

International Journal of Scientific Engineering and Science
Volume 4, Issue 5, pp. 8-17, 2020. ISSN (Online): 2456-7361

Where, syph= seed/kernel yield per hectar, E1= Bullen, E2= Dibatie,E3= Guba,E4= Manbuk,E5= Mandura,E6= Pawe, G1= Manipeter,G2= Bulgi,G3= Lotte,G4= Roba,G5= Werer-962,G6= Faxo,G7= NC-343,G8= BaHa-jidu,G9= BaHa-gudo,G10= Fetene,G11= Werer-961,G12= Babile-2,G13= Babile-1,G14= Werer-963,G15= Babile-3

b. AMMI-2 bi-plot for kernel yield

AMMI 2 bi-plot for kernel yield presented in (Fig. 2) indicated that, genotypes G4, G13, G5 and G11 were stable plotted relatively close to each other at the center or origin. Among these widely adopted or stable genotypes, only genotypes G13 and G4 were exhibited higher yield above grand mean. Therefore, only genotypes G13 and G4 were considered as a high yielding and widely adopted genotypes indicating their minimum contribution to the total GEI variance. On the other hand, genotypes like G8, G12, G15, G6, G14, G3, G9, G10, G2, G7 and G1 far away from center of bi-plot, which indicated that they were unstable and among them G2, G9 and G3 were relatively distant from the origin and have considerable contribution to the GEI variance considered as specifically adopted to their respective favorable environments or unstable.

The AMMI 2 bi-plot showed that, E3, E5, and E6 far from the origin indicating that these environments contribute higher amount of variation to the total GEI. Particularly E3 were the most discriminating environment. However, due to their longest distance between its marker and the origin (high IPCA score), genotype variability at this environment may not exactly reflect the average genotypes performance across environments. On the contrary, E1, E4 and E2 located close to the origin indicating their lower contribution to the GEI variance (Fig. 3). This indicated that they are favorable environment and the least discriminating environment.

Genotypes that are close to each other tend to have similar performance and those that are close to environment indicates their better adaptation to that particular environment. Hence, genotypes G1 and G8 were relatively adapted to environments E1; genotypes G12, G13, G6 and G15 were relatively adapted to environments E2; genotypes G2, G7 and G10 were relatively adapted to environments E3; genotypes G3 and G14 were relatively adapted to environments E4; genotypes G1, and G8 were relatively adapted to environments E5; genotype G9 were relatively adapted to environments E6 (Fig. 3), this finding was in harmony with Sharma *et al*. (2009).

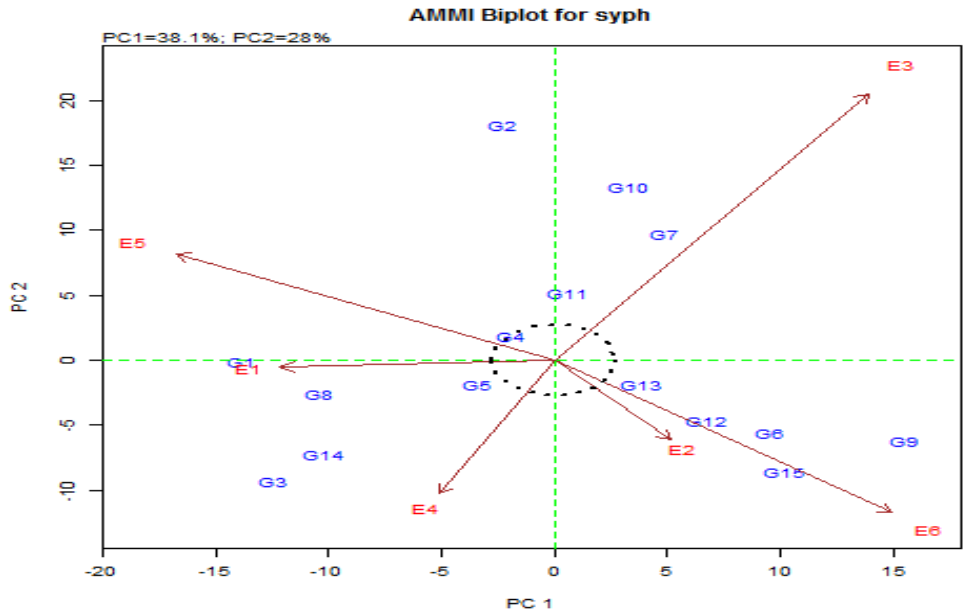

Figure 3. AMMI2 bi-plot of IPCA1 against IPCA2 for kernel yield of genotypes tested across six locations

Where, E1= Bullen, E2= Dibatie, E3= Guba, E4= Manbuk, E5= Mandura, E6= Pawe, G1= Manipeter,G2= Bulgi, G3= Lotte, G4= Roba, G5= Werer-962, G6= Faxo, G7= NC-343, G8= BaHa-jidu, G9= BaHa-gudo, G10= Fetene, G11= Werer-961, G12= Babile-2, G13= Babile-1, G14= Werer-963, G15= Babile-3

B1. AMMI stability value (ASV)

AMMI model does not make a provision for a quantitative stability measure. The AMMI is the distance from the coordinate point to the origin in a two-dimensional plot of IPCA1 scores against IPCA2 scores in the AMMI model. In the ASV method, genotypes with least ASV value were considered as the most stable (Purchase *et al*., 2000). Accordingly, Werer-961 was found to be the most stable genotype, followed by Roba, Werer-962 and Babile-1 genotypes using this method (Table 7). The highest yielding genotype ICGV-98412 ranked fourth according to ASV. so that, ASV is not effective in selecting high yielder as stable and the results were in line with the findings of Abdurahman (2009) in maize and Souina *et al*., 2016 on groundnut. Generally, the highest yielding genotypes were less stable according to ASV, so that selection solely for high seed yield could result in discarding many stable genotypes.

International Journal of Scientific Engineering and Science
Volume 4, Issue 5, pp. 8-17, 2020. ISSN (Online): 2456-7361

TABLE 7. Mean kernel yield (kg ha^{-1}) AMMI Stability Value (ASV), and IPCA1 and IPCA2 scores of the 15 groundnut genotypes tested across six environments.

No	Genotype	Mean kernel yield	IPCA1	IPCA2	ASV	ASV Rank
1	Manipeter	1785.7	-13.83	-0.13	63.57	14
2	Bulki	1909.9	-2.28	18.1	20.92	6
3	Loti	1779.1	-12.44	-9.35	57.94	13
4	Roba	2094.9	-1.9	1.9	8.94	2
5	Werer-962	1850.4	-3.5	-1.9	16.20	3
6	Faxo	1831.4	9.54	-5.63	44.21	9
7	NC-343	2040.8	4.91	9.72	24.57	7
8	BaHa-jidu	1639.8	-10.43	-2.59	48.01	12
9	BaHa-gudo	1761.3	15.48	-6.22	71.43	15
10	Fetene	1451.6	3.31	13.4	20.27	5
11	Werer-961	1400.7	0.57	5.17	5.80	1
12	Babile-2	1751.1	6.76	-4.7	31.43	8
13	Babile-1	2103.5	3.83	-1.9	17.71	4
14	Werer-963	1280.1	-10.22	-7.27	47.54	11
15	Babile-3	1487.8	10.16	-8.6	47.49	10

IPCA1= interaction principal component axis one, IPCA2= interaction principal component axis two and ASV= AMMI stability value

A. Genotype main effect and genotype by environment interaction (GGE) bi-plot analysis

The GGE bi-plot is an excellent tool for multi-environment data analysis for different crop improvement (Mohammadi *et al*., 2011on durum wheat; Mulugeta *et al*., 2016 on Lupin; Yirga 2016 on sesame). The partitioning of genotype and genotype by environment interaction through GGE bi-plot analysis showed that, IPCA 1 and IPCA 2 explained 79.6% (PCA1 = 65.4% and PCA2 = 14.2%) of total variation for kernel yield (Fig. 4), indicated that there is strong and complex GEI in this multi-environment yield trial data. GGE bi-plot is an effective tool for identification of ideal environments, ideal genotypes and best genotypes and their adaptable environments (Yan and Hunt, 2001).

a. Evaluation of genotypes

GGE bi-plot genotype view (Fig. 4) showed that, G4 was the "ideal" genotype and the highest mean kernel yield. G4 considered the most stable across variable environments. Genotypes closer to the ideal genotype G13 and G7 were also the stable ones, while genotypes far from the ideal genotypes were the unstable. Genotype is more desirable if it is located closer to the ideal genotype. Similar result was reported by (Ngirazi *et al*., 2017).

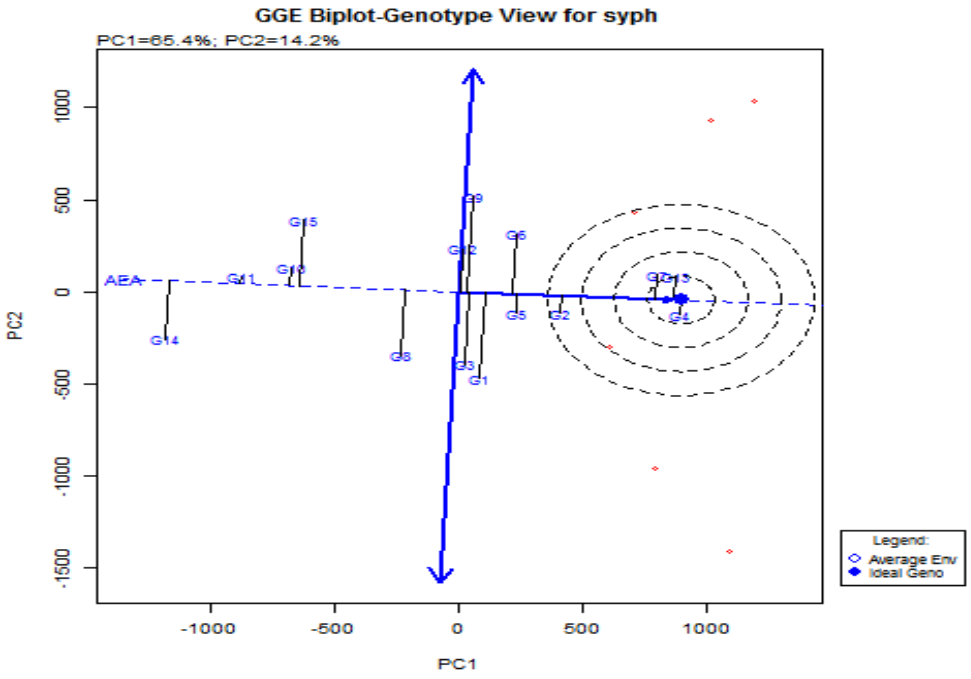

Figure 4. GGE-bi-plot showing the "ideal" genotype for kernel yield

Where, G1= Manipeter, G2= Bulgi, G3= Lotte, G4= Roba, G5= Werer-962, G6= Faxo, G7= NC-343, G8= BaHa-jidu, G9= BaHa-gudo, G10= Fetene, G11= Werer-961, G12= Babile-2, G13= Babile-1, G14= Werer-963, G15= Babile-3

b. Evaluation of environments

The environment view (Fig. 5), showed that, environment E6 (Pawe) and E5 (Mandura) had the longest environmental vector, implying that they were most discriminating

environment. Environments E4 (Dangur) and E2 (Dibatie) had the shortest vector with small IPCA, which near to the concentric circles was considered as an ideal environment. An environment with a small angle to the average environment axis (AEA) is more representative than other test environments, this finding was in harmony with Sharma *et al*., (2009) and Naroui *et al*. (2013) findings. According to Sharma *et al*., (2009), any two environments can be positively, negatively or not correlated if the angles between their vectors are less than 90°, more than 90° or equal to 90° respectively. In this trial all test environments share the angle less than 90^0 so that environments were positively correlated for kernel yield (Fig. 5).

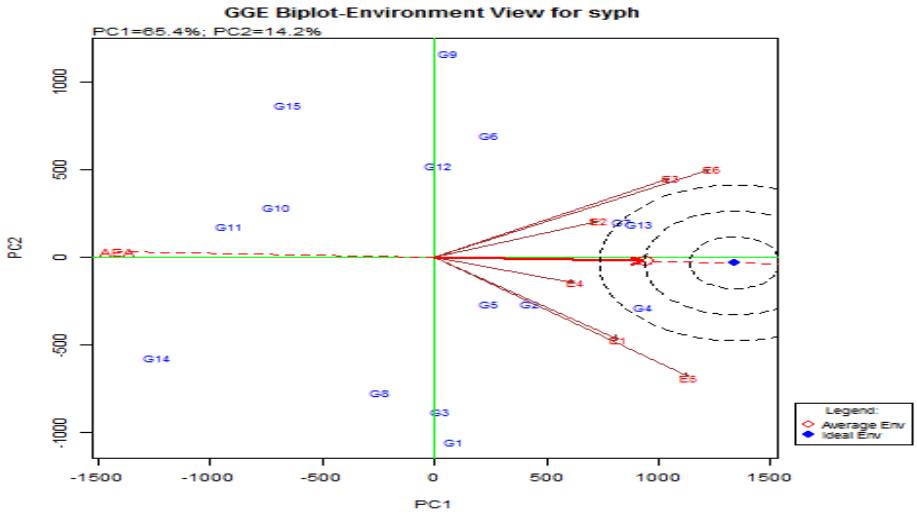

Figure 5. Average environment axis (AEC) in view of GGE bi-plot graph for kernel yield

Where, E1= Bullen, E2= Dibatie,E3= Guba,E4= Manbuk,E5= Mandura,E6= Pawe, G1= Manipeter,G2= Bulgi,G3= Lotte,G4= Roba,G5= Werer-962,G6= Faxo,G7= NC-343,G8= BaHa-jidu,G9= BaHa-gudo,G10= Fetene,G11= Werer-961,G12= Babile-2,G13= Babile-1,G14= Werer-963,G15= Babile-3

c. The "which-won-where" patterns of kernel yield

The polygon view of the GGE bi-plot showed the best genotype in each environment. There are six rays which divided the bi-plot into six sections (Fig. 6). The six environments fell into two sectors with different winner genotypes and genotypes fell into six sections. The bi-plot showed that eight vertex genotypes, G1, G4, G13, G9, G15 and G14. The vertex genotype of each sector is the one that gave the highest yield for the environments which fall within that sector. The GGE bi-plot identified two different groundnut growing mega-environments. The first environment containing E2, E3 and E6 with a vertex genotype G13; the second environment contains E1, E4 and E5 with winner genotype G4. It had also been observed that no environments fell into sectors where genotype G1, G14, G15, and G9 were the vertex genotypes, indicating that these genotypes were not the best in any of the test environments (Fig. 6).

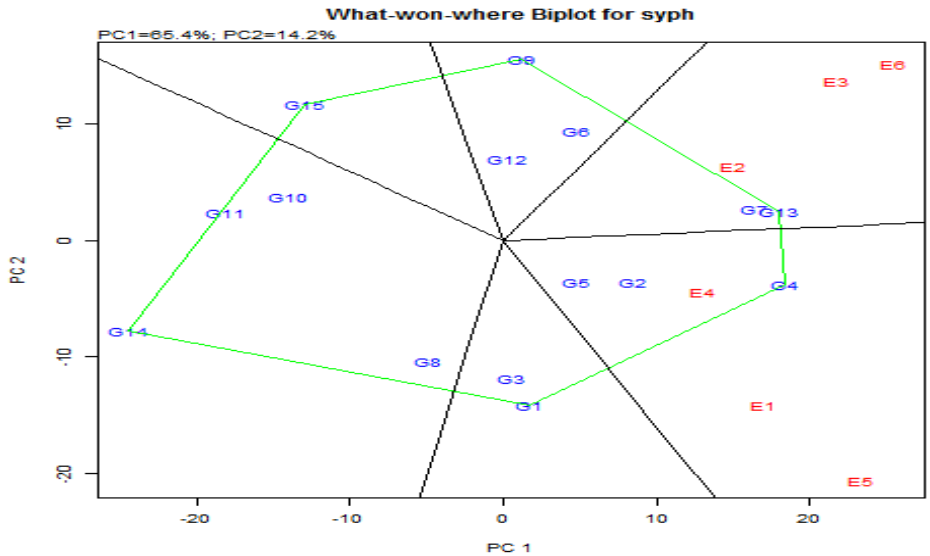

Figure 6. "Which won where" for kernel yield of genotypes evaluated in six environments

Where, E1= Bullen, E2= Dibatie,E3= Guba,E4= Manbuk,E5= Mandura,E6= Pawe, G1= Manipeter,G2= Bulgi,G3= Lotte,G4= Roba,G5= Werer-962,G6= Faxo,G7= NC-343,G8= BaHa-jidu,G9= BaHa-gudo,G10= Fetene,G11= Werer-961,G12= Babile-2,G13= Babile-1,G14= Werer-963,G15= Babile-3

IV. Conclusion and Recommendation

Accordingly, the pooled analysis of variance revealed that genotypes (G), locations (E) and genotype by location interactions (GEI) effects were highly significant on kernel yield of fifteen groundnut genotypes. The presence of significant genotype and environment interaction leads to perform kernel yield stability and adaptation analysis of the different genotypes. AMMI and GGE bi-plot were useful in concisely characterizing the environments and the genotypes. They characterized the environments in terms of stability and productivity. AMMI and GGE bi-plot analysis identified NC-343 (G7), Roba (G4) and Babile-1 (G13) genotypes as stable and high yielder for kernel yield with 2040.8 kg ha^{-1}, 2094.9 kg ha^{-1} and 2103.5 kg ha^{-1} values respectively, from which Babile-1 was the most productive genotype. So, we recommended this genotype for production in North western parts of Ethiopia. However, repeating this experiment for one more year will help recommendation of specifically adapted varieties in the region; and other quality parameters like protein content, oil content, milk quality, *Aspergilus flavus* resistance needs to be examined.

Acknowledgement

It is my pleasure to acknowledge Ethiopian Institute of Agricultural Research (EIAR) for financing this research. I would like to thank Hawassa University for hosting the study. I would also like to thank and appreciate all workers of Pawe Agricultural Research Center Staff who helped me during planting, data collection and field management of the experiment.

References

[1] Abera W., Rensburg, J. van, B.J., Labuschagne, M. T. & Maartens H., 2004. Genotype by environment interactions and yield stability analyses of maize in Ethiopia, South African Journal of Plant and Soil 21:4, 251-254.

[2] Acquaah, G., 2012. Principles of plant genetics and breeding 2nd - ed. First published by John Wiley & Sons, Ltd. 740p.

[3] Alemayehu D., Birru A., Zerihun A., Dagnachew L., 2016. Genotype by Environment Interaction and Kernel Yield Stability of Groundnut (*Arachis hypogaea* L.) Varieties in Western Oromia, Ethiopia. Journal of Agriculture and Crops, 2016, 2(11): 113-120

[4] Bernardo, R., 2002. Genotype by environment interaction. In: Bernardo, R. (ed.). Breeding for quantitative traits in plants. Stemma Press. Wood bury, MN. pp. 147-171.

[5] Central Statistical Agency, 2018. Agricultural sample survey; report on area and production of crops. Volume I. Addis Ababa, Ethiopia. Statistical bulletin 584.

[6] Crossa, J., 1990. Statistical analyses of multi-location trials. Advances in agronomy 44: 55-85.

[7] Crossa, J., Gauch, H.G. and Zobel, R.W., 1990. Additive main effects and multiplicative interaction analysis of two international maize cultivar trials. Crop Science 30: 493500.

[8] Dagnachew Lule, Masresha Fetene, Santie de Villiers and Kassahun Tesfaye, 2014. Additive Main Effects and Multiplicative Interactions (AMMI) and genotype by environment interaction (GGE) bi-plot analyses aid selection of high yielding and adapted finger millet varieties. Journal of Applied Bioscience 76: 6291– 6303.

[9] Dolinassou Souina, Jean Baptiste Noubissié Tchiagam, Alain Djiranta Kemoral and Nicolas Njintang Yanou, 2016. Genotype by environment interaction and kernel yield-stability of groundnut (*Arachis hypogaea* L.) in Northern Cameroon. Journal of Applied Biology & Biotechnology 4 (1): 001-007.

[10] Ethiopian Biodiversity Institute, 2014. Ethiopia's revised national biodiversity strategy and action plan. Addis Ababa Ethiopia.

[11] FAO, 2018. Food and Agricultural Organization Statistical Database. available at www.faostat.org; accessed on May 2018.

[12] Gauch, H.G. and Zobel, R.W., 1996. AMMI analysis of yield trials. In: Genotype by environment interaction. Kang, M.S., and Gauch, H.G Jr. (eds). Pp.85-122.

[13] GEA-R (Genotype by environment Analysis with R), version 4.0 software, 2016. Center of International Maiz and Wheat Improvement Center (CIMMYT').

[14] Gregory, W. C., Krapovickas, A. and Gregory, M. P., 1980. Structure, variation, evolution, and classification in *Arachis.* Advances in legume science edited by: Summer field RJ, Bunting AH. Kew, England: Royal Botanical Gardens 469- 481.

[15] IBPGR and ICRISAT, 1992. *Descriptors for groundnut.* International Board for Plant Genetic Resources, Rome, Italy. International Crops Research Institute for the Semi-Arid Tropics, patancheru, India. ISBN 92-9043-139-3.

[16] Janila, P., Nigam, S. N., Pandey, M. K., Nagesh, P., and Varshney, R. K., 2013. Groundnut improvement: use of genetic and genomic tools. Front. Plant Sci. 4:23.

[17] Ministry of Agriculture and Natural Resources (MoANR), 2016. Plant variety release. Protection and seed qual1ty control directorate. Crop Variety Register Issue No. 19.

[18] Mohammadi, R, M Armion, D. Sadeghzadeh, A. Amri and Nachit M., 2011. Analysis of genotype- by-environment interaction for agronomic traits of durum wheat in Iran. Plant Prod Sci. 14: 15-21.

[19] Mulugeta Atnaf, Dagne Wegary, Kifle Dagne, Kassahun Tesfaye, 2016. Genotype by environment interaction and kernel yield stability of Ethiopian white lupin (*Lupinus albus* L.) Landraces. Experimental Agriculture.

[20] Naser Sabaghnia, Rahmatollah Karimizadeh, Mohtasham Mohammadi, 2012. Genotype by environment interaction and stability analysis for kernel yield of lentil genotypes. Žemdirbystė=Agriculture 99: 305–312.

[21] Ngirazi N. Savemore, Manjeru P. and Ncube B., 2017. Pod yield stability and adaptation of groundnut (*Arachis hypogaea* L.) genotypes evaluated in multi environmental trials in Zimbabwe. African Journal of Plant Science 11(5): 174-184.

[22] Plant Breeding Tools version 1.4 softwa, 2014. Biometrics and breeding informatics plant breeding, genetics and biotechnology division International Rice Research Institute.

[23] Purchase, J.L., Hatting, H. and Van Deventer, C.S., 2000. Genotype× environment interaction of winter wheat (Triticum aestivum L.) in South Africa: II. Stability analysis of yield performance. South African Journal of Plant and Soil, 17(3):101-107.

[24] SAS Institute, 2011. SAS/STAT software 9.3, SAS Institute, Cary, NC, USA.

[25] Sharma RC, Morgounov A, Baun H, Beyhan A, Mesut A, Dedoshvili D, Ahmet B, Martius C, Maarten V G., 2009. Identifying high yielding stable winter wheat genotypes for irrigated environments in Central and West Asia. Euphytica 171(1): 53-64.

[26] Stalker H. T. and Wilson Richard F., 2016. Peanuts Genetics, Processing, and Utilization. AOCS Press. Published by Elsevier Inc. ISBN 978-1-63067-038-2.

[27] Suneetha, K., Singh, S.S., Mohapatra, T., Singh, A.M., Brajendra, Bhadana, V.P., Ravichandran, S., 2013. Genotype × environment interaction analysis for Kernel yield in new plant type (NPT wheat derivatives). SABRAO Journal of Breeding and Genetics 45(3), 382–390.

[28] Verma, A., Tyagi, B.S., Meena, A., Gupta, R.K., Chatrath, R., 2016. Durum wheat genotypes stratification by AMMI analysis for irrigated conditions of central zone. International Journal of Tropical Agriculture 34(4), 1087–1092.

[29] Woodroof, L.G., 1983. Peanuts processing products. 3rd edition. AVI Publishing, Connecticut 54-56.
[30] Yan, W. and Tinker, N. A., 2006. Bi-plot analysis of multi-environment trial data: Principles and application. Canadian Journal of Plant Science 86: 623-645.
[31] Yan, W., and L.A. Hunt, 2001. Genetic and environmental causes of genotype environment interaction for winter wheat yield in Ontario. Crop Sci 41:19–25.
[32] Yan, W., Kang, M.S., Ma, B., Woods, S. and Cornelius, P.L., 2007. GGE Bi-plot vs. AMMI analysis of genotype by environment data. Crop Sci. 47: 643-655.
[33] Yan,W., L. A. Hunt, Q., Sheng,and Z. Szlavnics, 2000. Cultivar evaluation and mega environment investigation based on the GGE bi-plot. Crop Sci. 40:597–605.
[34] Yang R.C., 2007. Mixed-model analysis of crossover genotype by environment interactions. Crop Sci. 47, 1051–1062.
[35] Yirga Belay, 2016. Genotype by environment interaction and yield stability of white seeded sesame (*sesamum indicum* L.) genotypes in northern Ethiopia. M.Sc. Thesis submitted to graduate studies of Haramaya University, Haramaya, Ethiopia.