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Genotype by Environment Interaction and Kernel Yield Stability of Groundnut (*Arachis hypogaea L.*) Varieties in Western Oromia, Ethiopia

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Abstract: Nine groundnut varieties were tested across six environments in western Oromia, Ethiopia during 2013 main cropping season to evaluate the performance of groundnut varieties for kernel yield and their stability across environments. The varieties were arranged in randomized complete block design (RCBD) with three replications. Pooled analysis of variance for kernel yield showed significant ($p \leq 0.01$) differences among the varieties, environments and the genotype by environment interaction (GxE). Additive main effect and multiplicative interactions (AMMI) analysis showed highly significant ($p \leq 0.01$) differences for varieties, environments and their interaction on kernel yield. Similarly, the first and the second interaction principal component axis (IPCA1 and IPCA 2) were highly significant ($p \leq 0.01$) and explained 41.32 and 7.2% of the total GxE sum of squares, respectively. The environment, genotype and genotype by environment interaction accounted 14.7, 24.1 and 53.3% variations, respectively. This indicated the existence of considerable amounts of deferential response among the varieties to changes in growing environments and the deferential discriminating ability of the test environments. Shulamith and Bulki varieties showed the smallest genotype selection index (GSI) values and had the highest kernel yield and stability showing that these varieties had general adaptation in the tested environments. In the genotype and genotype by environment (GGE) biplot analysis, IPCA1 and IPCA 2 explained 63.5% and 22.4%, respectively, of genotype by environment interaction and made a total of 85.9%. GGE biplot analysis also confirmed Bulki and Shulamith varieties showed better stability and thus ideal varieties recommended for production in the test environments and similar agro-ecologies.

Keywords: Ground nut (*Arachis hypogeal*); AMMI; GGE biplot; stability analysis.

1. Introduction

Groundnut (*Arachis hypogaea* L.) is a major oil seed crop that ranks 12th among the food crops of the world. This annual crop is native of South America (Brazil), but now grown throughout the tropical and warm temperate region of the globe between latitudes of 40^0N and 40^oS [1]. Groundnut is one of the chief vegetable oil sources in the world. The cultivated groundnut is also known as peanut. The kernel of groundnut contains 46-52% oil, 25-30% crude protein and 12-18% carbohydrate [2]. About two- third of the world production of groundnut seed serves for production of oil, which is used for cooking, salad oil and margarine and lower grades of oil are used in soap manufacture [1]. Groundnut is one of the five widely cultivated oilseed crops in Ethiopia [3] predominantly by the traditional farming community under rain-fed conditions. It occupies about 79,947 hectares of land with a corresponding gross annual production of about 112,888.7 tons [2]. The yield of groundnut in Ethiopia is very low (i.e. below 1.1 ton $ha^{-1)}$ as compared to average yields on a global scale (1.52 ton ha^{-1}). In present study area of Oromia Regional state, the area covered by the crop was during 2013 was 56951 ha and productivity was 1.33 ton ha^{-1}. However, with good varieties and management practices, yields can be increased to 3.0 ton ha^{-1} [4, 5]. Amare [6] and EARO [7] reported that seed yield in Ethiopia is extremely low mainly due to lack of high yielding varieties, low soil fertility and limited access to external inputs.

The additive main effects and multiplicative interactions (AMMI), genotype and genotype by environment interaction (GGE) bi-plot models are defined powerful tools for effective analysis and interpretation of multi-environment data structure in breeding programs [8-10]. AMMI model can treat both the additive main effect and

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multiplicative interaction component employing the analysis of variance (ANOVA) and Interaction Principal Components (IPCA), respectively [11]. It has both linear and bilinear component of genotype by environment interaction and hence very useful in visualizing multi-environment data (understanding complex GEI and determining which genotype won where) and gaining accuracy (improving cultivar recommendation and accelerating progress) [12].

Genotypes exhibit fluctuating yields when grown in different environments or agro-climatic zones. This complicates demonstrating the superiority of a particular variety. Multi-environment yield trials are crucial to identify adaptable high yielding cultivars and discover sites that best represent the target environment [9]. Failure of genotypes to respond consistently to variable environmental conditions is attributed to genotype by environment interaction (GGE). Knowledge of GGE is advantageous to have cultivar that gives consistently high yield in wider range of environments and to increase efficiency of breeding program and selection of best genotypes. Genotype and genotype by environment interaction (GGE) biplot allows for assessing the performance of genotypes in the tested environments. Phenotypic variation of genotypes across environments resulted from environmental and genotypic variations and genotype by environment interaction. Environmental variation is the dominant source of phenotypic variation [13].

Lack of high yielding and stable varieties are among the major factors contributing to the low yield level. Temporal and special instability of quantities traits of crops have connection with unreliability of crop yield and thereby food insecurity at household and national level. In most cases, genotypes grown in different environments yield differently due to genotype by environment interaction (GEI). Therefore, multi-environment trials (MET) are required to identify specific and the general adaptability of genotypes. In the study area, where this research was conducted, the yield of groundnut was very low because farmers depend on low yielding local cultivars. This study is therefore, aimed to identify high yielding and stable varieties across environment and examines the influence of GEI on kernel yield of groundnut varieties.

2. Material and Methods

Nine groundnut varieties (eight released and one local cultivars) were evaluated at six environments (Uke, Chewaka, Bako, Haro-sabu, Kombo and Guliso) in 2014 main cropping season. The varieties were NC- 4X, Were-962, Tole-2, Shulamith, Werer-964, Sedi, Bulki, Manipinter and local cultivar. The latitudes, longitudes, average temperature and the total annual rain fall for each of the environments are presented in Table 1**.** The seeds of groundnut varieties were obtained from Melka Werer Agricultural Research Center. The planting was done early June across location and the design was randomized complete block with three replications. The plot size was five rows of 4m long with 60cm between rows and 10cm between plants but only the three middle rows was harvested and used for data collection. Fertilizer was applied at the rate of 100kg DAP (diammonium phosphate) per hectare. Kernel yield and other yield related traits were recorded. Unshelled pod were sun dried for two weeks and shelled to estimate kernel yield.

Table-1. Description of six locations used for evaluation of Groundnut varieties.

Locations	**Environment label**	**Geographical position**		**Altitude (m.a.s.l)**	**Average rain fall(mm)**	**Soil type**
		Latitude	**Longitude**			
Bako	E3	09˚06'N	37˚09'E	1650m	1431mm	Sandy clay
Uke	E1	09.41824N	036. 53975E	1333m	NI	sandy loam
Chewaka	E2	09.98285N	036.11703E	1259m	NI	Sandy loam
Haro sabu	E4	08^{0}52,919’N	035^{0}13,930’E	1550m	1200mm	Sandy clay
Kombo	E5	08^{0}51,192’ N	035^{0}06,809’E	1440m	1300mm	Sandy loam
Guliso	E6	NI	NI	1600m	1500mm	Sandy loam

NI= not identified

Multivariate method, Additive Main Effects and Multiplicative Interaction (AMMI) model was used to assess genotype by environment interaction (GEI) pattern. The AMMI model equation is:

$Y_{ger} = \mu+\alpha g+\beta e+\Sigma n\lambda n\gamma gn\delta en+ \varepsilon ger+\rho ge$;

where, Y_{ger} is the observed yield of genotype (g) in environment (e) for replication (r);

Additive parameters**:** μ is the grand mean; αg is the deviation of genotype g from the grand mean, βe is the deviation of the environment e;

Multiplicative parameters: λn is the singular value for IPCA, γgn is the genotype eigenvector for axis n, and δen is the environment eigenvector; εger is error term and ρge is PCA residual. Accordingly, genotypes with low magnitude regardless of the sign of interaction principal component analysis scores have general or wider adaptability while genotypes with high magnitude of IPCA scores have specific adaptability [14, 15].

AMMI stability value of the ith genotype (ASV) was calculated for each genotype and each environment according to the relative contribution of $IPCA_1$ to $IPCA_2$ to the interaction SS as follows [16]:

$$ASV = \sqrt{[(SS_{IPCA1} \div SS_{IPCA2})(IPCA1score)]^2 + (IPCA2score)^2}$$

Where, SS_{IPCA1}/SS_{IPCA2} is the weight given to the $IPCA_1$ value by dividing the $IPCA_1$ sum of squares by the $IPCA_2$ sum of squares.

Based on the rank of mean grain yield of genotypes (RYi) across environments and rank of AMMI stability value (RASVi) a selection index called Genotype Selection Index (GSI) was calculated for each genotype, which incorporates both mean grain yield (RYi) and stability index in single criteria (GSIi) as suggested by Farshadfar [17].

$$GSIi = RASVi + RYi$$

Environmental index (Ii) was obtained by the difference among the mean of each environment and the general mean.Analysis of variance was carried using statistical analysis system (SAS) version 9.0 software [18]. Additive Main Effect and Multiplicative Interaction (AMMI) analysis and GGE biplot analysis were performed using Gen Stat 15th edition statistical package [19].

3. Result and Discussion

3.1. Combined Analysis of Variance

Analysis of variance showed statistically significant differences (P<0.01) among varieties, environments and their interaction for kernel yield (Table 2). This indicated the presence of genetic variation among varieties and possibility to select high yielding and stable variety (s), the environments are variable and the differential response of groundnut varieties across environments. Similar result was reported for groundnut varieties [13, 20].

Table-2. Combined Analysis of variance for kernel yield of groundnut varieties evaluated across six environments during 2013 main cropping season.

SOV	DF	Mean square of kernel yield
Environments	5	2775196.15^{**}
Genotypes	8	2742283.32^{**}
Block within environment	12	62752.42^{ns}
GXE interaction	40	1177513.08^{*}
Error	96	2775196.15^{**}
CV(%)		16.4
LSD		167.2
R^2		93%

DF= Degree of freedom and SOV= Source of variation, LSD=Least Significant differences, CV=coefficient of variation, GxE= genotype by environment interaction, *=significant at P≤0.05, **=significant at P≤0.01, ns=non significant

3.2. Yield Performance of Groundnut Varieties Across Environments

It appears that some varieties consistently performed best in a group of environments [21]. The average kernel yield ranged from the lowest of 988kg ha^{-1} at Bako site to the highest of 1889 kg ha^{-1} at Guliso site with grand mean of 1536 kg ha^{-1} (Table 3). The average kernel yield across environments ranged from the lowest of 774 kg ha^{-1} for Tole- 2 variety to the highest of 2000kg ha^{-1} for Shulamith variety (Table 3). This difference could be due to their genetic potential of the varieties. Shulamith variety was the top ranking variety at two environments (Chewaka and Guliso), Maniinter ranked first at Haro-sabu and Kombo, Werer-962 at Uke site and Bulki variety at Bako site (Table 3). The difference in yield rank of varieties across the environments revealed the high crossover type of GxE interaction [22, 23].

Table-3. Mean kernel yield (kg ha^{-1}) of groundnut varieties evaluated at six environments

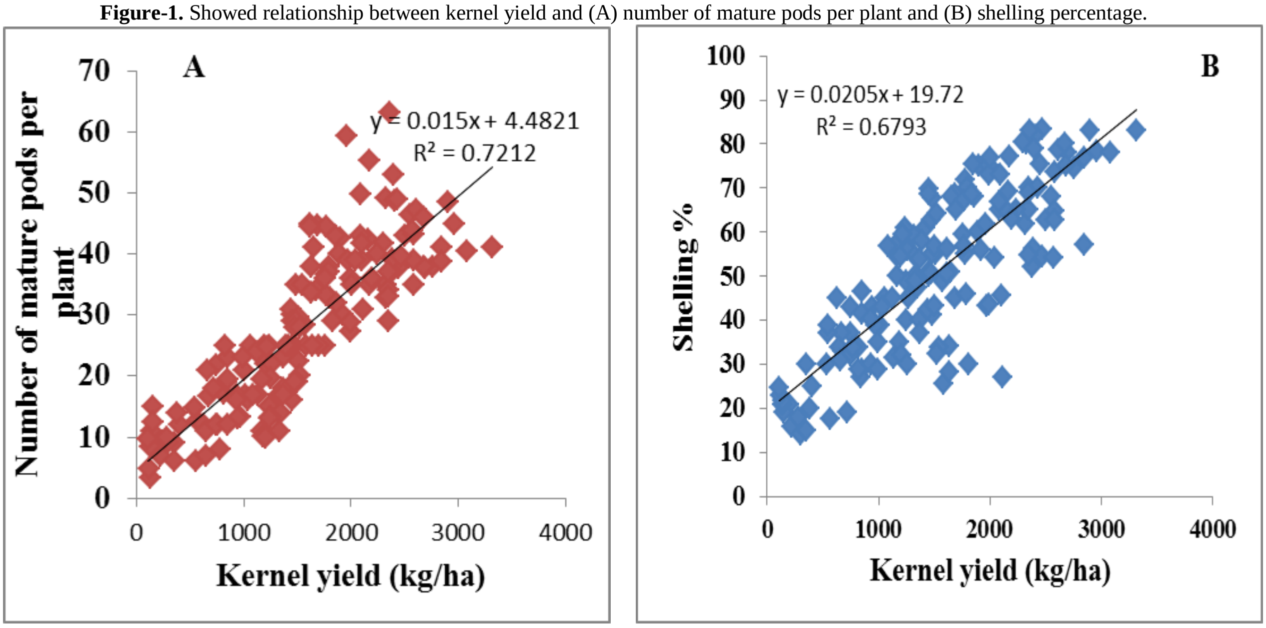
Variety	Mean kernel yield over locations						Mean
	E_1	E_2	E_3	E_4	E_5	E_6	
NC-4X	2584	2468	847	1203	1349	2366	1803^{b}
Werer-962	**2587**	2168	1599	641	982	2367	1733^{b}
Tole-2	1164	932	127	650	762	1007	774^{c}
Shulamith	2380	**2848**	1425	1444	1301	**2601**	**2000^{a}**
Werer-964	1836	1522	134	1356	1232	1524	1267^{c}
Sedi	748	692	1345	2155	1792	1128	1310^{c}
Bulki	1614	2105	**1656**	1970	1837	1896	1837^{ab}
Manipinter	377	192	312	**2194**	**2745**	2325	1358^{c}
Local	2266	2073	1443	1495	1389	1782	1742^{b}
Mean	1728	1667	988	1457	1488	1889	**1536**

Key: 'E' stands for environments E_1= Uke, E_2= Chewaka, E_3= Bako, E_4= Haro sabu, E_5= Kombo and E_6= Guliso

3.3. The Relationship of Kernel Yield with Number of Mature Pods and Shelling Percentage

The kernel yield showed highly significant positive relationships with number of mature pods per plant and shelling percentage. This indicates that plants with more number of pods per plant and high shelling percentage provide more kernel yield than those of less number of pods and shelling percentage (Fig 1).

Figure-1. Showed relationship between kernel yield and (A) number of mature pods per plant and (B) shelling percentage.



3.4. Additive Main Effects and Multiple Interaction (AMMI) Model

Combined analysis of variance revealed highly significant ($P \leq 0.01$) variations among environments, genotype x environment interaction, IPCA-1 and IPCA-2 (Table 4). This result revealed that there was a differential yield performance among groundnut varieties across testing environments and the presence of strong genotype by environment interaction. The GEI posed significant effect on the kernel yield of groundnut, which explained 53.3% of the total variation while the varieties contributed 24.1% of the variation. Only 14.7% of the total variation is attributed to the environmental effect (Table 4). This also indicated the existence of a considerable amount of deferential response among the varieties to changes in growing environments and the differential discriminating ability of the test environments. Similar results were reported by Yayis, *et al.* [24] and Akande, *et al.* [25]. Substantial percentage of G x E interaction was explained by IPCA-1 (41.34%) followed by IPCA-2 (7%) and therefore used to plot a two dimensional GGE biplot. Gauch and Zobel [11] and Amare and Tamado [13] suggested the most accurate model for AMMI can be predicted by using the first two IPCA.

Table-4. Partitioning of the Explained Sum of square (SS) and Mean of square (MS) from AMMI analysis for Kernel yield of nine groundnut varieties evaluated at six environments

SOV	DF	SS	Ex. SS%	Mean square
Total	161	89.05	100	0.553
Treatments	53	82.14	92.2	1.550**
Genotypes	8	21.5	24.14	2.687**
Environments	5	13.17	14.7	2.635^{**}
Block	12	0.77	0.86	0.064^{ns}
Interactions	40	47.47	53.3	1.187^{**}
IPCA1	12	36.82	41.34	3.069^{**}
IPCA2	10	6.47	7.2	0.647^{**}
Residuals	18	4.18	4.6	0.232^{**}
Pooled error	96	6.14		0.064

Key: ns= non- significant, **= significant at 1% and *= significant at 5% probability level. MS= mean square, SS= sum of square, SOV= source of variation, DF= degree of freedom, Ex. SS%= Explained sum of square in percent

The IPCA-1 and IPCA-2 scores for each variety and also the AMMI Stability Value (ASV) with its ranking for nine varieties are presented in Table 5. In ASV method, genotype with least ASV score is the most stable [16]. Accordingly, Tole-2, Werer-964 and Bulki were the most stable, but Manipinter and Sedi were the most unstable. This measure is essential in order to quantify and rank of varieties according to their seed yield stability. The least Genotype Selection Index (GSI) is considered as the most stable with high grain yield [17, 26]. Based on the GSI result, the most desirable variety for selection of both stability and high kernel yield was Bulki followed by Shulamith, which was in accordance with the result of AMMI biplot and with most estimation stability parameters.

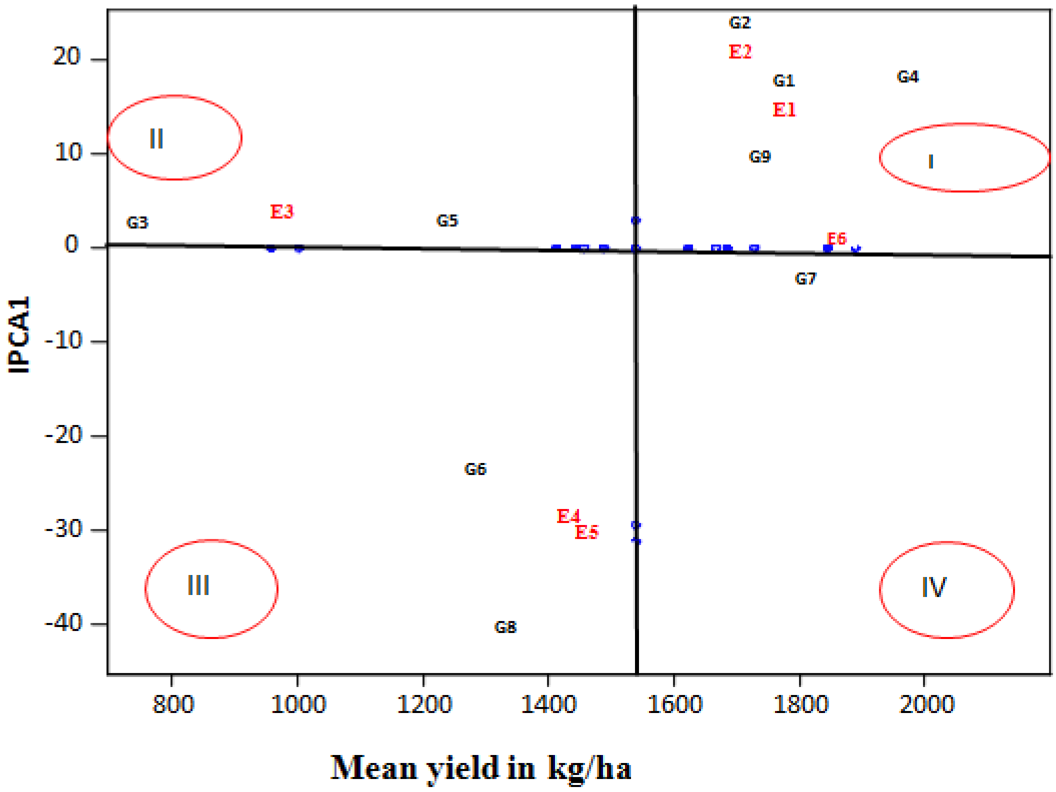
Table-5. IPCA-1, IPCA-2 scores, AMMI stability value (ASV) and Genotype Selection Index (GSI) of nine groundnut varieties.

Variety	Varietal labeling	Mean yield	RYi	IPCA1	IPCA2	ASVi	RASVi	GSIi
NC-4X	G1	1803	3	23.7	17.4	102.1	5	8
Werer-962	G2	1733	5	26.4	8.1	137.8	7	12
Tole-2	G3	774	9	-8.8	31.8	10.7	1	10
Shulamith	G4	2000	1	27.3	5.6	103.2	6	7
Werer-964	G5	1267	8	1.1	27.7	16.9	2	10
Sedi	G6	1310	7	-22.1	-1.4	148.5	8	15
Bulki	G7	1837	2	5.2	-4.3	29.3	3	5
Manipinter	G8	1358	6	-32	19	245.6	9	15
Local check	G9	1742	4	-8.6556	5.3151	51.9	4	8

The stability and high yielding ability of the varieties has been graphically depicted by the AMMI biplot. Environments Uke & Chewaka relatively showed high IPCA scores and contributed largely to GEI. These environments were favorable for high yielding varieties based on mean yield as they had more than the grand mean. Environment Bako (E3) is the least favorable environment for almost all the varieties with low yield & smaller IPCA-1 score (Fig 2).

The variation of yield for each variety was significant at different environments. Varieties Shulamith, Bulki, Nc-4x and Werer-962 were specifically adapted to high yielding environments (Fig 2). Considering the IPCA-1 score, Werer-962 was the most unstable variety and also adapted to higher yielding environments. Bulki was more stable in comparison to other varieties. Variety Werer-964 was adapted to low yielding environments and also relatively stable (Fig 2). Manipinter, Tole-2 and Sedi were adapted to low yielding environments but not stable. Bulki variety was near to zero $IPCA_1$ by which it was shown to have a higher stability for kernel yield than other varieties (Fig 2). Shulamith had highest kernel yield followed by Bulki and Nc-4x. It also had higher $IPCA_1$ score than others except of Werer-962. Shulamith had higher GEI at environments of Uke (E1) and Chewaka (E2) with a repeatable performance across both locations, whereas low GEI at Bako (E3) (Fig 2).

Figure-2. Biplot of interaction principal component axis ($IPCA_1$) against mean kernel yield of nine groundnut varieties evaluated across six environments.

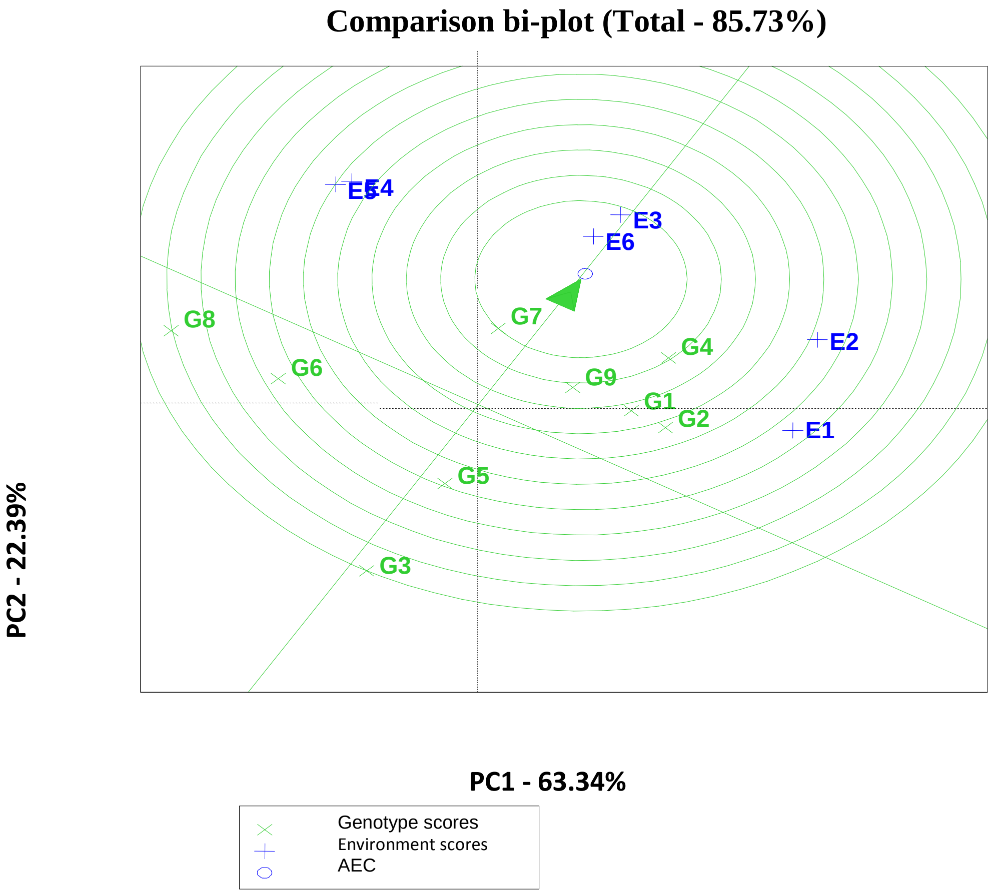


Key: ***Variety:*** G1 (NC-4X), G2 (Werer-962), G3 (Tole-2), G4 (Shulamith), G5 (Werer-964), G6 (Sedi), G7 (Bulki), G8 (Manipinter) and G9 (Local check). ***Environment:*** E_1= Uke, E_2= Chewaka, E_3= Bako, E_4= Haro sabu, E_5= Kombo and E_6= Guliso

3.5. Genotype and Genotype by Environment Interaction (GGE) Biplot Analysis

In GGE biplot (Fig 3), IPCA-1 and IPCA-2 explained 63.5 and 22.4%, respectively, of groundnut variety by environment interaction and made a total of 85.9%. The other study conducted on the same crop explained an interaction of 81.8% extracted from IPCA-1 and IPCA-2 [13]. Environments and genotypes that fall in the central (concentric) circle are considered as ideal environments and stable genotypes, respectively [27]. A genotype is more desirable if it is located closer to the ideal genotype. Thus, using the ideal genotype as the center, concentric circles were drawn to help visualize the distance between each genotype and the ideal genotype. Therefore, the ranking based on the genotype-focused scaling assumes that stability and mean yield are equally important [28]. Accordingly, variety Bulki (G7) fell into the center of concentric circles and thus ideal genotype/variety in terms of higher yielding ability and stability, compared with the rest of varieties. In addition, G4 and G9, located on the next concentric circle, may be regarded as desirable varieties. An environment is more desirable and discriminating when located closer to the center circle or to an ideal environment [29].

Figure-3. GGE bi-plot based on genotype-focused scaling for comparison of genotypes for their yield potential and stability.



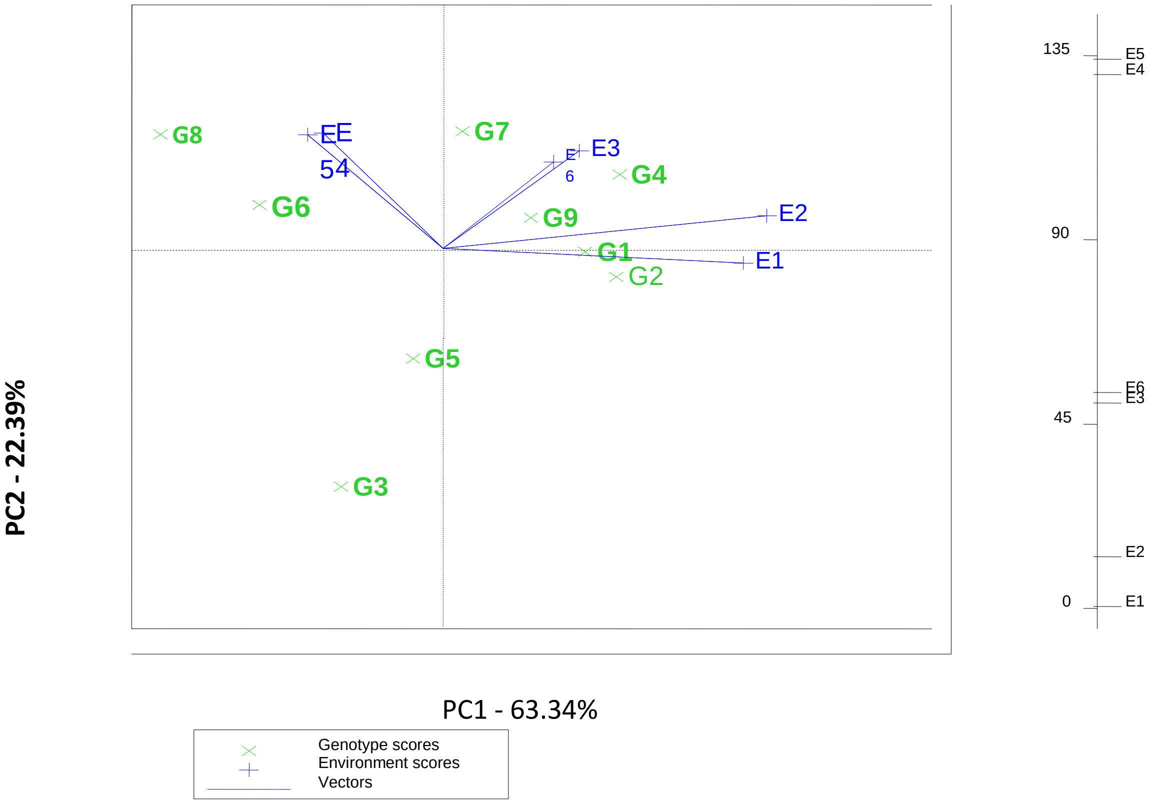
Key: E_1= Uke, E_2= Chewaka, E_3= Bako, E_4= Haro sabu, E_5= Kombo and E_6= Guliso

3.6. Discriminating Ability of the Test Environment and Genotype Stability

The Average-Environment Axis (AEA) or Average-Tester-Axis (ATA) is the line that passes through the average environment and the bi-plot origin [27, 30]. A test environment with a small angle with the AEA is more representative than other environments [27]. In the present study, Bako and Guliso were the most discriminating and representative environments (Fig 3). Haro-sabu and Kombo were non-discriminating and less representative sites. This implied that, varietal stability could be challenged not only due to the change in the test environment but also due to differential response of tested varieties per environment. Similarly, Dagnachew, *et al.* [31] reported that two environments were stable, representative and discriminating among four environments for the performance of Finger millet genotypes evaluated in Ethiopia.

The varieties that connect the biplot origin and the markers for the environments are called environment vectors. The angle between the vectors of two environments is related to the correlation coefficient between them. The cosine of the angle between the vectors of two environments approximates the relationship between them [27, 31]. Based on the angles of environment vectors, the six environments are grouped in to three groups. Group one includes E1 and E2. Group two involve E3 and E6. Group three includes E4 and E5 (Fig 4). For example, the smallest angle between E3 and E6, E4 and E5 is implying that there is the highest similarity or positive correlation between them. The angles between E1 and E5, for instance, are bigger than others showing the negative correlation or highest dissimilarity between them (Fig 4). Two criteria are required to suggest existence of different mega-environments. First, there are different winning genotypes in different test locations. Second, the between-group variation should be significantly greater than the within-group variation, common criteria for clustering. Dividing the target environment into different mega-environments and deploying different genotypes in different mega-environments is the best way to utilize GxE interaction.

Figure-4. The vector view of the GGE bi-plot based on environment focused scaling for environments to show relationship among testing environments. G and E letters stand for genotypes and environments respectively.



4. Conclusion

Among testing environments, the minimum mean kernel yield (988kg ha^{-1}) was obtained from E3 (Bako) while the maximum mean yield of 1889 kg ha^{-1} was from E6 (Guliso). The mean performance of tested varieties across all environments ranged from 774 kg ha^{-1} for G3 (Tole-2) to 2000 kg ha^{-1} for G4 (Shulamith) with an average yield of 1536 kg ha^{-1}. The Analysis of variance indicated that genotype by environment interaction was the most important source of variation, accounted for 53.3% for the total variance. The first and the second principal components explained 63.5 and 22.42%, respectively. Biplot view of relation among test environments showed that environment Bako (E3) showed more association with environment Guliso (E6); environment Uke (E1) with Chewaka (E2), and Haro-sabu (E4) with Kombo (E5).

References

[1] Pradhan, D. M., 2011. "Genetic Variability for oil content, oil quality and other yield traits in Advance Breeding Lines of Groundnut (Arachis hypogaea L.)." *Department of Genetics and Plant Breeding College of Agriculture, Dharwad University of Agricultural Sciences. Master of Sciences,* p. 130.

[2] Central Statistical Authority (CSA), 2013/14. *Estimation of area production and yield of crops for 2013/2014 Meher season*. Ethiopia: Addis Ababa.

[3] Kudama, G., 2013. "Economics of groundnut production in east hararghe zone of Oromia Regional State, Ethiopia." *Star Journal,* vol. 2, pp. 135-139.

[4] Central Statistical Authority (CSA), 2009. *Estimation of area production and yield of crops for 2009/2010 Meher season*. Ethiopia: Addis Ababa.

[5] FAOSTAT, 2009. "Research on Grain Legumes (Groundnut Pigeon pea and Chickpea). Addis Ababa, Ethiopia." Available: http://faostat.faoorg

[6] Amare, 1987. " Effect of inoculation and nitrogen fertilization on yield of common bean in Ethiopia." In *Proceedings of a workshop on bean Research in Eastern Africa.* CIAT African Workshop Series. Mukono, Uganda. pp. 152-159.

[7] EARO, 2000. *Lowland pulses research strategy*. Ethiopia: Addis Ababa. pp. 1-39.

[8] Ebdon, J. S. and Gauch, H. G., 2002. "Additive main effect and multiplicative interaction analysis of national turfgrass performance trials: I. Interpretation of genotype x environment interaction." *Crop Science*, vol. 42, pp. 489-496.

[9] Yan, W., Hunt, L. A., Sheng, Q., and Szlavnics, Z., 2000. "Cultivar evaluation and mega-environment investigation based on the GGE biplot." *Crop Science,* vol. 40, pp. 597-605.

[10] Zobel, R. W., Wright, M. J., and Gauch, H. G., 1988. "Statistical analysis of a yield trial." *Agronomy Journal,* vol. 80, pp. 388-439.

[11] Gauch, G. and Zobel, R. W., 1996. *AMMI analysis of yield trials. In: Genotype by environment interaction (Kang, M. and Gauch, H. eds.)*. New York.: Boca Raton. CRC Press. pp. 85-122.

[12] Gauch, G., 2006. "Statistical analysis of yield trials by AMMI and GGE." *Crop Science,* vol. 46, pp. 1488-1500.

[13] Amare and Tamado, T., 2014. "Genotype by environment interaction and stability of pod yield of elite breeding lines of groundnut (Arachis hypogaea L.) in Eastern Ethiopia." *Star Journal,* vol. 3, pp. 43-46.

[14] Gauch, G., 1992. *Statistical analysis of regional yield trials: Ammi analysis of factorial designs*. Amsterdam, The Netherlands: Elsevier Science Publishers.

[15] Umma, K., Jamil, H., Ismail, H., and Niaz, F. R., 2014. "Stability for BRRI developed Promising Hybrid Rice for Yield and it's Related traits." *Journal of Applied Science and Agriculture,* vol. 9, pp. 56-62.

[16] Purchase, J. L., Hatting, H., and Vandenventer, C. S., 2000. "Genotype by environments interaction of wheat in South Africa: stability analysis of yield performance." *South Africa Journal of Plant Science,* vol. 17, pp. 101-107.

[17] Farshadfar, E., 2008. "Incorporation of AMMI stability value and grain yield in a single non-parametric index (GSI) in bread wheat." *Pakistan Journal of Biological Sciences,* vol. 11, pp. 1791-1796.

[18] SAS, 2002. "System analysis software. Version 9.0. SAS Inst. Inc., Cary, North Carolina, USA."

[19] VSN International, 2012. "GenStat for Windows 15th Edition. VSN International, Hemel Hempstead, UK." Available: www.genStat.co.uk

[20] Tulole, L. B., Erasto, S., Theofora, M., and Leah, M., 2008. "On-farm evaluation of promising groundnut varieties for adaptation and adoption in Tanzania." *African Journal of Agricultural Research,* vol. 3, pp. 531-536.

[21] Tamene, T., Gemechu, K., Tadese, S., Mussa, J., and Yeneneh, B., 2013. "Genotype x environment interaction and performance stability for Grain Yield in Field Pea (Pisum sativum L.) Genotypes." *International Journal of Plant Breeding,* vol. 7, pp. 116-123.

[22] Yan, W. and Hunt, L. A., 2001. "Interpretation of genotype × environment interaction for winter wheat yield in Ontario." *Crop Science,* vol. 41, pp. 19-25.

[23] Asrat, A., Fekadu, G., and Mulugeta, A., 2009. "AMMI and SREG GGE biplot analysis for matching varieties onto soybean production environments in Ethiopia." *Scientific Research and Essay,* vol. 4, pp. 1322-1330.

[24] Yayis, R., Agdew, B., and Yasin, G., 2014. "Genotype x environment interaction and Additive main effect and multiplicative interaction analysis for Field pea yield stability in SNNPR state, Ethiopia." *International Journal of Sustainable Agricultural Research,* vol. 1, pp. 28-38.

[25] Akande, S. R., Taiwo, L. B., Adegbite, A. A., and Owolade, O. F., 2009. "Genotype x environment interaction for soybean grain yield and other reproductive characters in the forest and savanna agro-ecologies of South-west Nigeria." *African Journal of Plant Science,* vol. 3, pp. 127-132.

[26] Hagos, T. and Fetien, A., 2011. "Additive main effects and multiplicative interactions analysis of yield performance of sesame genotypes across Environments in Northern Ethiopia." *Journal of the Dry lands,* vol. 4, pp. 259-266.

[27] Yan, W. and Rajcan, I., 2002. "Biplots analysis of the test sites and trait relations of soybean in Ontario." *Crop Science,* vol. 42, pp. 11-20.

[28] Ezatollah, F., Hassan, Z., and Reza, M., 2011. "Evaluation of phenotypic stability in chickpea genotypes using GGE-Biplot." *Annals of Biological Research,* vol. 2, pp. 282-292.

[29] Naroui, R. M. R., Abdul, K. M., Rafii, H. M. Y., Jaafar, N. M. R., and Farzaneh, A., 2013. "Genotype × environment interaction by AMMI and GGE biplot analysis in three consecutive generations of wheat (Triticum aestivum) under normal and drought stress conditions." *Aust. J. Crop Sci.,* vol. 7, pp. 956-961.

[30] Khodadad, M., Seyedsadegh, H. I., and Mahdi, Z., 2011. "Stability analysis of rice genotypes based gge biplot method in North of Iran." *Journal of Appl. Sciences Research,* vol. 7, pp. 1690-1694.

[31] Dagnachew, L., Masresha, F., Santie, d. V., and Kassahun, T., 2014. "Additive Main Effects and Multiplicative Interactions (AMMI) and genotype by environment interaction (GGE) biplot analyses aid selection of high yielding and adapted finger millet varieties." *Journal of Applied Biosciences,* vol. 76, pp. 6291– 6303.