Evaluation of Groundnut (*Arachis hypogaea* L.) Genotypes through Different Multivariate Analyses at Eastern Ethiopia

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Abstract

Groundnut is a vital source of oil and protein. It plays an important role as food as well as cash generator crop in Ethiopia. The production of groundnut in Ethiopia has a lot of potential, but the average yield is very low due to lack of an improved high yielding variety(s). Fourteen groundnut genotypes were evaluated at two locations (Werer and Meisso) to identify the most superior and stable genotype(s) in Eastern and similar agroecology of Ethiopia. Grain yield performance of the tested genotypes was evaluated between 2012 to 2015 at Werer and Miesso using randomized complete block design with three replications in main cropping season. Multivariate analysis viz., *Principal Component Analysis (PCA), GGEbiplot, Ammi Stability Value (ASV) and Yield Stability Index (AYSI) analysis were computed. Evaluation of 14 groundnut genotypes coupled with the standard check revealed significant difference genotypes, environment and their interacting levels for key economic traits. Combined analysis of variance showed genotype (G), environments (E) and genotype by environment (GE) interaction significantly influenced the grain yield. The first two principal component analysis (PCA_1 and PCA_2) were used to create a two-dimensional GGE biplot explained by 54.676% and 24.374 %, respectively. Both GGE biplot and AMMI model identified G4, G1 and G10 as winning genotypes. The average environment coordination (AEC) views of the GGE-biplot and Yield stability index (YSI) were highly useful with AMMI stability value (ASV) that come up with the genotype high grain yield and wider adaptability identified as genotype G4 and G10 as the most stable and high yielding genotypes; whereas, genotype G6 was identified as the most stable but low yielding genotypes. GGE biplot analysis and AMMI model based on grain yield data confirmed that genotypes G4 and G10 were stable and superior to the standard check. Therefore, genotype G4 (ICGV-96346) and G10 (ICGV-97243) could be recommended for variety verification trial and release.*

Keywords: *Ammi stability value, GEI, Genotypes, GGE biplot, Groundnut, MET, PCA, Yield stability index*

Introduction

Groundnut (*Arachis hypogaea* L.) is a self-pollinated legume in the *Leguminosae* family. It is a valuable source of oil and protein-rich food and feed. There are more than 70 species of *Arachis* in nature, with only A. *hypogaea* being cultivated (Rao and Wu, 1988). The botanical varieties of cultivated groundnut are *hypogaea* and *fastigiata*. *A. hypogaea* has a basic chromosomal number (x) of 10 and is a segmental amphidiploid (2n = 4x = 40).

Groundnut seed contains 44 to 56% oil, 22-30% protein~~,~~ and 3% dietary fibre on a dry seed basis, which lowers the risk of certain cancers and aids in blood sugar regulation (Savage and Keenan, 1994). It contains half of the 13 essential vitamins for growth, including Folate, Niacin, Thiamin (B1), Pyridoxine (B6), Riboflavin (B2), and Vitamin E. Similarly, groundnut contains seven of the twenty minerals required for body growth and repair: copper, phosphorus, magnesium, iron, potassium, zinc, and calcium (Reddy, 2009).

Globally, groundnuts are grown on 32.7 million hectares, with a total annual production of 53.9 Million tons (FAOSTAT, 2021). Comprehensively; groundnut production is dominantly produced by china (32.7%), India (16.2%), Nigeria (8.4%), USA (5.2%), Sudan (4.6%), Mynammar (3.0%), Senegal (2.9%), Aregentina (2.2%), Chad (1.6%) and Indonesia (1.5%); hence this ten top groundnut producer country is covered 78.2 percent of the world production. According to FAOSTAT (2021) world groundnut area harvested is 30441035 hectare in 2020 and 32720960 in 2021, whereas production in ton is 53790839 in 2020 and 53926894 in 2021. We goes to Africa; production in hectare is 17552049 in 2020 and 18469648 in 2021; however, production in ton is declined in 2020 to 2021 is from 17201864 to 16356685 `ton of total production. Decreasing rate of groundnut production in Africa by the rate of five percent (5%). Similarly; we go to Ethiopia, dramatically drop down from 112124 hectare to 77283 hectare whereas 2029137 total production in tons to 1392784, decreased by 31 percent.

Oil seeds in Ethiopia added 4.28% (about 522,149.28 hectares) of the grain crop area and 1.65% (about 541,506.5 tons) of the production to the national grain total. Currently, groundnuts are widely produced in the Benishangul-Gumuz, accounting for (63.8%; 39.8%) of the total area in hectare and production in ton, followed by Oromia Region (22.4%; 35.1%), Amhara (12.2%; 23.2%), Southern Nation and Nationalities People (0.9%; 1.2%), and the Harari (0.9%; 0.7%) Regional Stat (CSA, 2021/22). Conversely; in Ethiopia groundnut estimated production area in hectare and in ton in 2020/21 (112124 hectare and 2029137 ton), whereas in 2021/22 is 77283 hectare and 1392784 ton (CSA, 2021/22);

hence the production and area coverage is decreasing, due to limited availability of improved high yielding variety, drought, pests, lack of seed system and poor extension attention (Abady et al. 2019; Tesfamariam, et al., 2021).The performance of a genotype is heavily influenced by the genetic makeup of the crop, the environment and their interplay (Savemore et al., 2017; Sendekie et al., 2018). Similarly, experts feel that upgrading adaptable and more productive groundnut cultivars is the greatest and most environmentally friend strategy to resolving agricultural restrictions. According to Kebede et al. (2017), seed yield in Ethiopia is extremely poor, due to a lack of high yielding cultivars, insufficient soil fertility, and limited access to external inputs. Under multi-environments trials (MET), groundnut has a strong genotype x environment interaction (GEI) (Savemore et al., 2017, Kebede et al., 2017 and Sendekie et al., 2018).

Understanding and evaluating genotype and GEI implications is required to improve crop breeding selection know-how; and multi-environmental trial (MET) also aids in the identification of genotypes with major adaptations or those that are adapted to a given environment (Yan and Kan, 2002;Yan and Tinker, 2006). As a result, groundnut agriculture has feast throughout numerous locations and habitats in Ethiopia; thus, there is a significant need to provide farmers and producers with well-adapted cultivars. The objective of the current study was to identify the most superior and stable genotype(s) in Eastern Ethiopia.

Material and Methods

Description of the study area

The experiment was carried out in Werer in Afar Regional State, and Miesso in Oromia Regional State of groundnut growing areas in Ethiopia, main growing seasons of three years from 2012 to 2015 (Table 1 and Figure 1). Important metrological data for the testing location described in Table 2.

Table 1. List and characteristic features of groundnut genotype test environments

No	Environments	Testing Year	Testing Location	Region	Altitude
1	E1	2012	Werer	Afar	745 masl
2	E2	2012	Miesso	Oromia	470 masl
3	E3	2013	Werer	Afar	745 masl
4	E4	2013	Miesso	Oromia	1470 masl
5	E5	2014	Werer	Afar	745 masl
6	E6	2014	Miesso	Oromia	1470 masl
7	E7	2015	Werer	Afar	745 masl
8	E8	2015	Miesso	Oromia	1470 masl

E= environment and masl=meter above sea level

Table 2. Minimum, Maximum and Mean Temperature, Precipitation and Evapotranspiration of the testing locations

	Werer					Miesso				
Month	TMin [°C]	TMax [°C]	TMean [°C]	Peri [mm]	PET [mm]	TMin [°C]	TMax [°C]	TMean [°C]	Peri [mm]	PET [mm]
Jan	4.26	11.03	4.26	134.39	35.4	5.42	12.25	8.54	119.96	31.99
Feb	4.17	11.4	4.17	115.19	42.96	5.78	13.21	9.19	102.43	43.24
Mar	5.32	13.22	5.32	90.42	63.04	6.89	15.59	11.14	82.52	59.52
Apr	7.32	15.91	7.32	98.46	85.83	9.25	18.86	14.03	81.65	79.23
May	10.78	20.7	10.78	77.01	119.97	11.95	23.7	17.87	63.52	110.54
June	14.69	25.78	14.69	41.35	149.43	15.49	28.15	21.83	43.1	142.12
July	17.97	29.98	17.97	19.93	187.18	18.35	31.44	24.65	13.85	171.14
Aug	18.11	29.88	18.11	21.75	169.26	18.53	31.06	24.56	26.26	151.43
Sept	15.61	26.11	15.61	53.25	118.17	16.48	28.02	22.19	43.83	97.84
Oct	11.86	20.38	11.86	106.17	72.25	13.16	22.31	17.61	127.11	63.57
Nov	7.97	14.85	7.97	148.69	44.45	9.56	16.43	13.06	179.5	39.58
Dece	5.42	12.18	5.42	139.85	35.63	7.18	13.11	9.97	157.62	30.11
Mean	10.29	19.29	10.29	87.2	93.63	11.5	21.18	16.22	86.78	85.03

Tmin=minimum temperature, TMax=maximum temperature, Tmean= mean temperature, °C] =degree centigrade and [mm] = millimeter

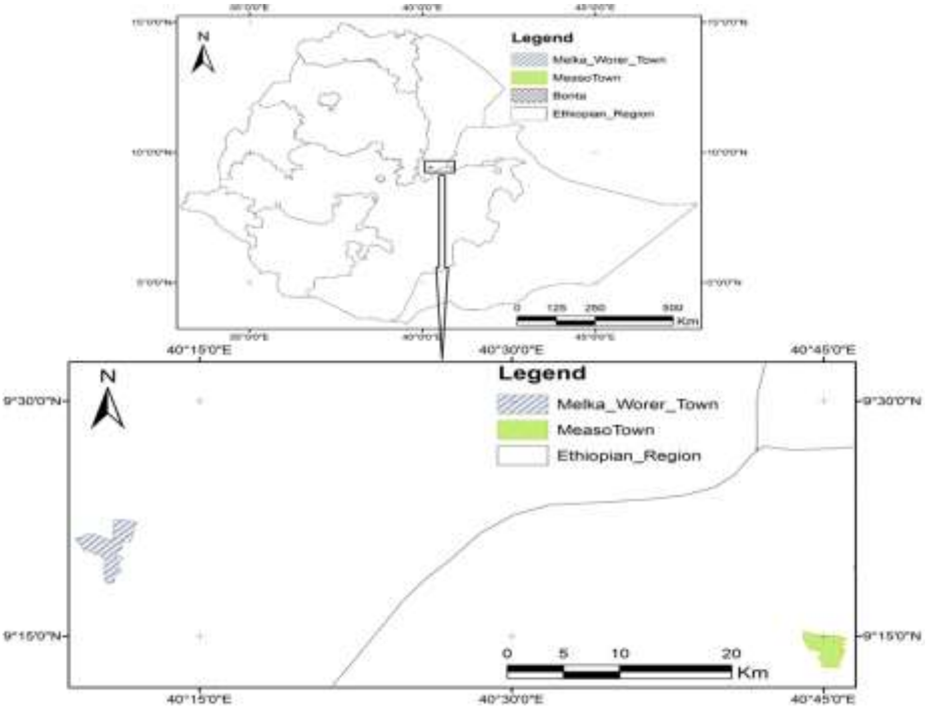

Figure 1.Study area

Experimental materials, design and procedures

The experiment was laid out in randomized complete block design (RCBD) with three replications in all testing sites. Each genotype was randomly assigned and sown in a plot area of 3meter(m) x 5meter(m) with 1m between plots and 1.5m between blocks keeping inter and intra row spacing of 60cm and 10cm. Each plot had a total area of 15m^2 and total of five rows and 9m^2 net plot area with three harvestable rows and all managements were done equally and properly as per the recommendations for the study areas.

Fourteen groundnut genotypes in Table 1, including a check, were examined in four main seasons (2012 to 2015) total of eight environments during the main cropping season at two location (Werer and Miesso). Among these fourteen genotypes, thirteen were advanced lines and introduced through (ICRISAT) International Crop Research Institutes Semi-Arid Tropics: Patancheru-India and the standard check Werer-961 variety is released from Werer Agricultural Research Center (Table 2). The nature of genotypes is early maturing group and advanced lines used for both confectionary and oil purpose. The experiment was carried out with three replications utilizing a randomized complete block design.

Table 3. List experimental materials

No	Genotype	Seed Sources	Genotype code
1	ICGV-93429	ICRSAT	G1
2	ICGV-96333	ICRSAT	G2
3	ICGV-96342	ICRSAT	G3
4	ICGV-96346	ICRSAT	G4
5	ICGV-96352	ICRSAT	G5
6	ICGV-96390	ICRSAT	G6
7	ICGV-96395	ICRSAT	G7
8	ICGV-96399	ICRSAT	G8
9	ICGV-96442	ICRSAT	G9
10	ICGV-97243	ICRSAT	G10
11	ICGV-97245	ICRSAT	G11
12	ICGV-97257	ICRSAT	G12
13	ICGV-97262	ICRSAT	G13
14	Werer-961	Werer	Released variety

Data collection:

All pertinent agronomic data were taken from the three harvestable central rows from each plot.

Days to maturity: number of days starting from planting to the plant physiologically matured; 100 seed weight (gm): hundred seeds was randomly taken and measured in gram; Shelling %: the percentage of shelled with the total weight; Yield (kg ha^{-1}): grain yield of groundnut harvested from each plot was shelled, weighed, and the kernel moisture content (MC) was determined. The estimation of grain yield (kg ha^{-1}) at 12.5% moisture content (MC) was utilized.

Data analysis:

The collected data for quantitative traits were subjected to analysis of variance (ANOVA) and to create a graphical representation of GGE biplot (Yan and Kang, 2002) and AMMI (Ze et al., 1998); the genotypes were best suited to the testing location using the R statistical software version 4.2.3 (R Core Team, 2017). Mean values were compared with LSD test at $P<0.05$. Analysis of variance (ANOVA) for yield was carried out for combined analysis across locations. For a simple analysis of variance of a randomized complete block design, the model: $Yijk = \mu + Gi + Ej + GEij + Bij + \varepsilon ijk$ was applied; where μ is the mean, Gi is the effect of the i^{th} genotype, Ej is the effect of the jth environment, GEij is the interaction of the i^{th} genotype with the j^{th} environment, Bij is the effect of the k^{th} replication in the j^{th} environment, and εijk is the random error. The GGEbiplot and other multivariate(principal component analysis(PCA-biplot), AMMI, Ammi Stability Value and Yield Stability Index) analysis model was used in the R_Software version R.4.2.3 to graphically display the link between environments (locations by seasons) and genotypes, as well as to find high yielder and stable genotypes. In visualizing, genotype scaling was utilized for genotypic comparison, and environment-focused scaling was employed for environmental comparison. In showing the "which-won-where" pattern of multi-environment yield trials (MEYTs) data, symmetric scaling was selected (Yan and Kan, 2002; Yan and Tinker, 2006).

Results and Discussion

A combined analysis of variation across locations and seasons revealed that there were substantial differences in location, year and location by year, genotypes and GEI (Table 4). Similarly; many scholars' reported that groundnut genotype highly influenced by genotype and genotype by environment interaction (Savemore et al., 2017, Kebede et al., 2017 and Sendekie et al., 2018).

Table 4.Combined analysis mean square values of grain yield at two locations over four year

	Grain Yield		
Sources of variation	Degree of freedom	Sum square %	Mean square
Genotypes(G)	13	2194	169^{**}
Environments(E)	7	44322	6332^{**}
Genotype by Environment(GEI)	91	4232	47^{**}
Residuals	55	1305	24.00
Mean	4282		
CV (%)	25.57		
LSD (at 5%)	622		

CV=coefficient of variation, LSD=least significant analysis

Ethiopia has different climatic circumstances in terms of altitude, soil type, and climate unpredictability, making it challenging for Ethiopia's plant-breeding program to generate stable cultivars with more adaptability. In the current study, the combined analysis of variance of four seasons of data from the Werer and Miesso stations shows that the grain yield performances of promising genotypes was considerably influenced by year, location~~,~~ and GEIs. The difference in grain production seen between genotypes is attributable to a genotypic and GEI effect that must be considered during analysis. Several strategies for selecting genotypes with improved stability for diverse ranges of settings have been established which can be used to measure their performance in similar scenarios. The combined analysis of genotype by environment revealed; the presence of GEI, which influences the grain yield performance of genotypes across locations (Tables 5 and 6). Overall mean yield and yield component across locations over the course of a year. The genotype performance at Werer and Miesso, genotypes G4 (ICGV-96346), G1 (ICGV-93429) and G10 (ICGV-97243) performed best (Table 5 & 6). GEI is a major element that frustrates breeders and geneticists since it complicates the plant variety development program for most crops, making it difficult to establish a stable variety across multiple seasons (Yan and Tinker, 2006).

Table 5. Mean based on statistical analysis of yield (kg ha^{-1}) of groundnut genotypes at Werer and Mieso (2012 to 2015)

No	Treatment	Werer					Miesso					Over all Means
		2012	2013	2014	2015	Mean	2012	2013	2014	2015	Mean	
G1	ICGV-93429	7570	9077	3941	7233	6955	2674	3628	1367	3272	2735	4845
G2	ICGV-96333	6207	6753	5456	4770	5796	1786	3111	2000	3125	2505	4151
G3	ICGV-96342	7080	7755	4410	6194	6360	2169	3336	1217	3774	2624	4492
G4	ICGV-96346	6800	9060	7198	6256	7329	2237	3431	1403	3313	2596	4962
G5	ICGV-96352	7100	5892	5885	5003	5970	1685	2778	1703	3283	2362	4166
G6	ICGV-96390	5833	7161	4289	3557	5210	1400	2547	958	3141	2012	3611
G7	ICGV-96395	4633	6939	5225	3595	5098	1817	2825	1564	3727	2483	3791
G8	ICGV-96399	7313	6545	5322	6404	6396	1772	3039	1114	3780	2426	4411
G9	ICGV-96442	5867	7483	5428	5958	6184	1941	3539	1891	3475	2711	4448
G10	ICGV-97243	6983	8049	6416	6565	7004	2035	3003	1561	3697	2574	4789
G11	ICGV-97245	6353	8139	5520	5266	6320	2006	2830	1881	3755	2618	4469
G12	ICGV-97257	4943	55.95	5182	4450	5043	2029	2328	1575	2936	2217	3630
G13	ICGV-97262	5790	5761	3892	4679	5030	1950	2883	1394	2989	2304	3667
G14	Werer-961	6457	9061	6318	4562	6600	2002	3875	606	3286	2442	4521
	Mean	6352	7376	5320	5321	6092	1964	3082	1445	3397	2472	4282
	CV	13.93	11.62	26.85	24.16	24.99	19.32	14.94	34.89	10.35	38.93	25.57
	LSD	1485	1438	2398	2150	1228	637	773	846	590	776	622

Table 6. Combined analysis and mean based on statistical analysis of yield and yield components of groundnut trial at Werer and Miesso stations (2012 to 2015)

S. N.	Genotypes	100seed weight	Days to Maturity	Shelling percentage	Yield (kg/ha)
G1	ICGV-93429	49.29	121.96	68.6	4845
G2	ICGV-96333	47.83	110.63	69.9	4151
G3	ICGV-96342	46.21	108.96	69.2	4492
G4	ICGV-96346	50.13	111.63	67.8	4962
G5	ICGV-96352	46.67	107.96	73.6	4166
G6	ICGV-96390	41.17	86.29	67.6	3611
G7	ICGV-96395	50.54	115.96	69.4	3791
G8	ICGV-96399	40.25	103.63	68.5	4411
G9	ICGV-96442	41.83	120.63	70.3	4448
G10	ICGV-97243	51.13	115.96	67.9	4789
G11	ICGV-97245	54.29	109.63	67.5	4469
G12	ICGV-97257	43.04	97.29	72.1	3630
G13	ICGV-97262	44.42	102.63	69.7	3667
G14	Werer-961	47.08	127.63	69.4	4521
	Mean	46.70	110.05	69.4	4282
	CV%	17.94	8.19	22.13	25.57
	LSD	4.76	5.12	3.85	622

CV=coefficient of variation, LSD=least significant analysis

Scree plot: is a multivariate statistics, shows the eigenvalues on the y-axis and the number of factors on the x-axis. It always displays a downward curve. The point where the slope of the curve is clearly leveling off (the "elbow") indicates the number of factors that should be generated by the analysis. As a result, this result showed that we have four principal component analyses (Fig.2).

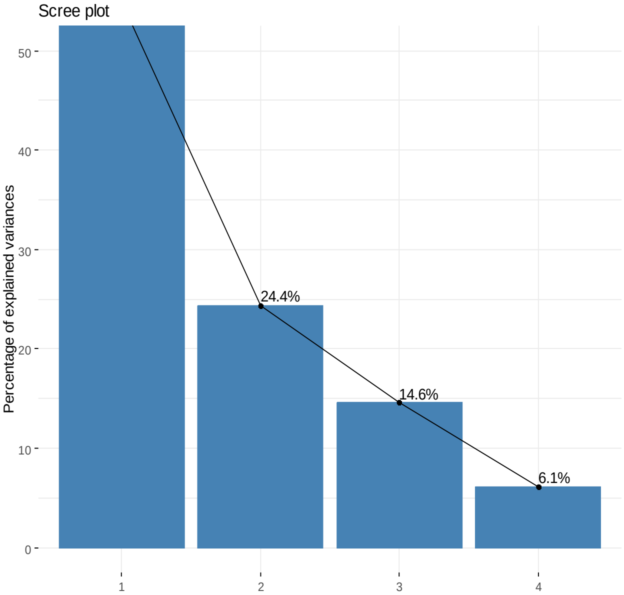

Figure 2: Scree plots of groundnut genotypes

Principal Component Analysis (PCA): is one of multivariate analysis to identify the principal components having a major contribution to the total variation. The first two principal components with eigenvalues greater than one accounted for 79.35 % of the total variation (Table 7). The first principal component analysis (PCA1) had high positive loading for seed yield per hectare, hundred seed weight and pods per plant. It accounted for 54.676 % of the variability and the major attributing characters include yield, hundred seed weight and pods per plant. Likewise, 24.374 % of the total variability among genotypes accounted for the second principal component analysis (PCA2) originated maturity date. The second PCA2 had high loading for days to maturity. Therefore, seed yields, hundred seed weight, pods per plant and maturity date are the major contribution to the total variation (Table 7).

Table 7. The principal component analysis of the major contributing variables

Variables	PC1	PC2	PC3	PC4	eigenvalue	Variance %	Cumulative. Variance~~.~~ %
HSW	-0.514	0.017	-0.842	-0.164	2.199	54.979	54.979
DM	-0.535	-0.503	0.189	0.652	0.975	24.374	79.354
SP	-0.323	0.863	0.145	0.359	0.582	14.561	93.914
YLD	-0.588	-0.032	0.484	-0.647	0.243	6.086	100.000

Principal components of the variable and its association: biplot analysis is a multivariate analysis that tries to compress information and shows them in ~~C~~cartesian coordinates using Principal Component Analysis (PCA). PCA is a tool for identifying the main axes of variance within a data set and allows for easy data exploration to understand the key variables in the data and spot outliers. PCA1 representing the most variation in the data and PCA2 representing the second most variation in the data. Seed yield in kilogram per hectare strongly contributed dimension one (PCA1) followed by hundred seed weight and numbers of pod per plant; and positively associated for each other. While plant height weakly contributed in PCA2. Days to maturity strongly contributed to PCA2; and negatively correlated with others, indicating that as the days to maturity increased, the yield and yield component decreased due to the short rainy season. As a result, early maturing material will be used to escape the short rain period in the area (Fig. 3).

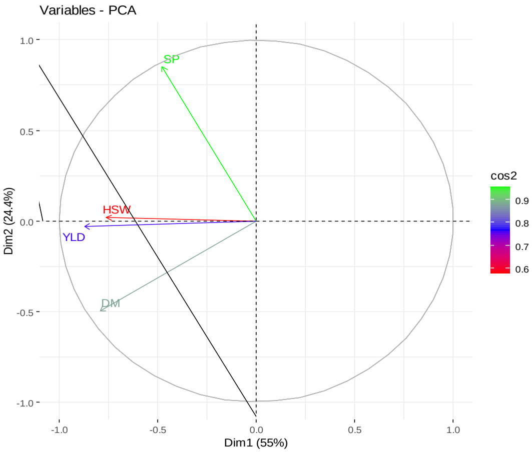

Figure 3. The contribution of the variables each dimension

Performance of the genotypes associated with the variable in PCA_biplot: the performance of the genotype associated with the variables; hence, genotype 10 and 1 had identified as high yielder, whereas genotype 14 is late maturing compared to the fourteen genotype. Further; genotype 5 and 2 had the longest; whereas, genotype 4 has the highest number of pods (Fig.4)

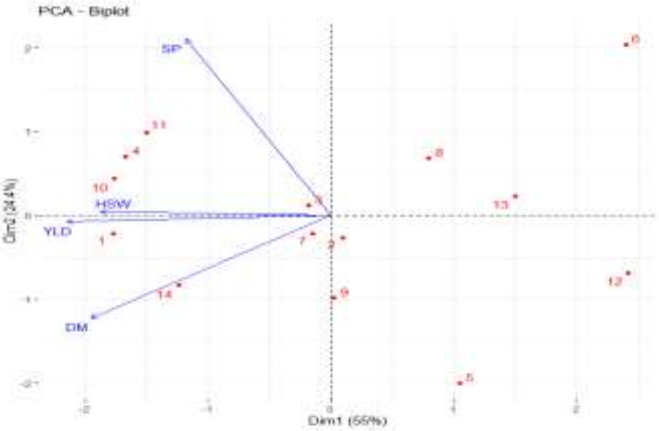

Figure 4. Performance of the genotypes associated with the variable in PCA-biplot

GGEbiplot analysis of groundnut genotypes: genotype performance in specific situations in figure 5 depicts both genotypes and environment vectors, illustrating the particular interactions between genotypes and environments. According to Yan and Tinker (2006), a genotype performs better than average in an environment when the angle between its vector and the environment's is 90°; it performs worse than average if the angle is greater than 90°; and it performs near average if the angle is less than 90°. Environment vectors are the lines that connect the test environments to the biplot origin. The correlation between two environments is approximated by the cosine of the angle between their vectors. As a result, E1 and E2 in figure 5a & b; shown to be positively associated (an acute angle) (Fig.5a & b); whereas, E1 and E7 explains negatively correlated, since wide obtuse angles (high negative correlations) between test environments indicate strong crossover GE. Consequently, the biggest angle in this case is slightly greater than 90° (between E2 and E7), indicating that the GE is relatively large (Fig.5a & b).

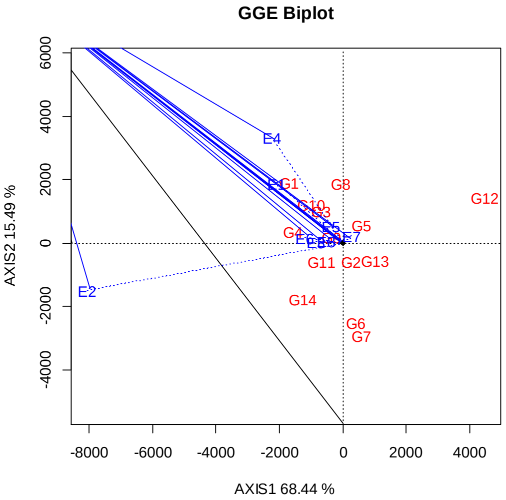

Figure 5a. Performance of the genotypes associated with the variable in PCA1 vs PCA2

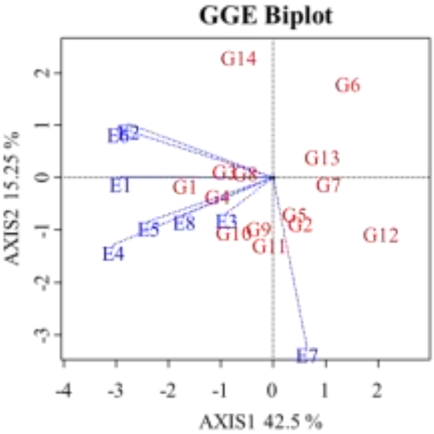

Figure 5b. Performance of the genotypes associated with the variable in PCA1 vs PCA3

Relationship among test environment: it is based on an environment-centered (centering = 2) G by E table without any scaling (scaling = 0). GGEbiplot explained: 42.5% the variation in PCA 1, whereas 15.25% of variation in PCA2. Total of 58% variation of the environment-centered explained by GE. Environment two (E2) and Environment four (E4) were positively correlated; while Environment two (E2) and Environment seven (E7) were negatively correlated (obtuse angle); moreover; E4 & E7 were not correlated (a right angle) (Fig.6). According to Yan and Tinker (2006) described that the presence of wide obtuse angles (i.e., strong negative correlations) among test environments is an indication of strong crossover GE. The presence of close associations among test environments (i.e. E1, E2, E4, E5, E6 & E8) suggests that the same information about the genotypes could be obtained from fewer test environments, and hence the potential to reduce testing cost (Yan and Tinker, 2006).

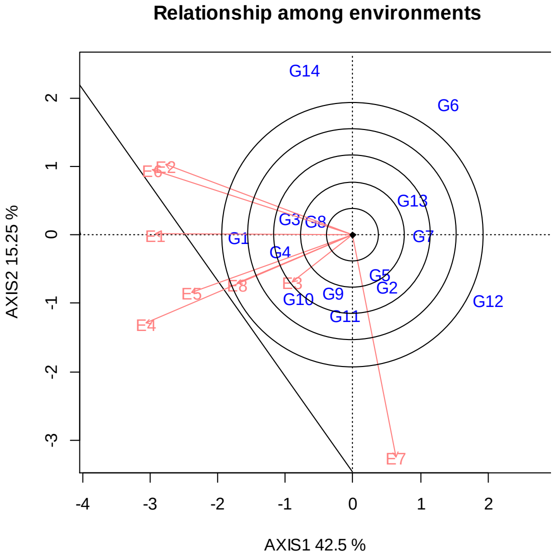

Figure 6. Relationship among environment in PCA1 vs PCA3

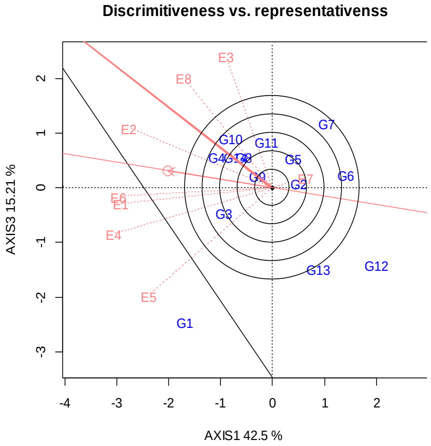

Figure 7. The environment-vector view of the GGE biplot to show similarities among test environments in discriminating the genotypes

Discriminating and representative ability of test environments: 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 eight environments E1, E2, E4, E5, E6 and E8) were most discriminating (informative); while E7 representative or non-discriminating: provide little information on the genotypes. A test environment that has a smaller angle with the Average Environment Axis (AEA) is more representative of other test environments. Thus, E7 is most representative is good test environments for selecting generally adapted genotypes (Fig.7).

Ranking Genotypes Based on Performance of the Environment

Ranking the genotypes based on their performance in an environment, a line is drawn that passes through the biplot origin and the environment. This line is called the axis for this environment, and along it is the ranking of the genotypes. Ranks the genotypes based on performance in E5 (Fig.8). Genotypes G6, G7, G12 and G13 had lower than average yield; G2, G5 and G9 had near average yield, and all others had higher than average yields. The highest mean yield was recorded in most of the environments were G4, G10 and G1 in PCA1 vs PCA2 (Fig. 8a); likewise, in PCA2 vs PCA3 (Fig. 8d); whereas G1, G4 & G10 in PCA1 vs PCA3 (Fig. 8b); further, G4, G1 & G3 in PCA2 & PCA4 (Fig. 8c); while, an ideal genotype should have both high mean performance and stability across environments to be a point on the AEA and has a vector length equal to the longest vectors of the genotypes on the side of AEA ("highest mean performance"). Thus, genotypes (G4, G1 & G10) were more desirable higher average yield (Fig.8 (a, b, c & d)).

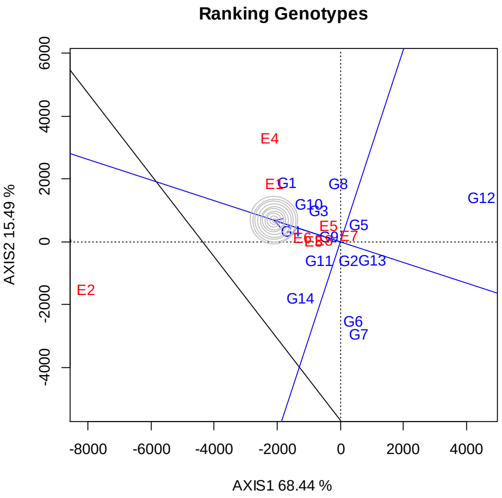

Figure 8a. Relationship among environment in PCA1 vs PCA2

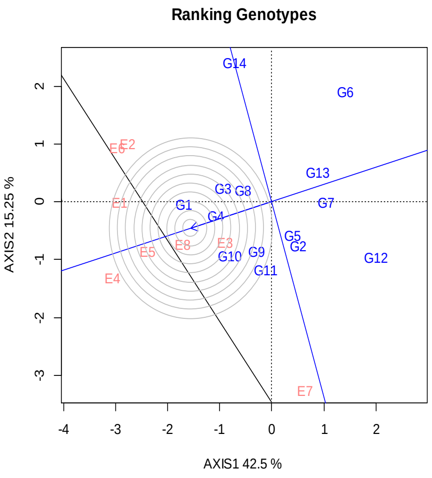

Figure 8b. Relationship among environment in PCA1 vs PCA3

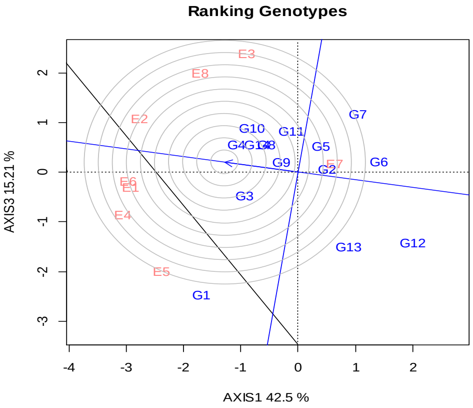

Figure 8c. Relationship among environment in PCA1 vs PCA3

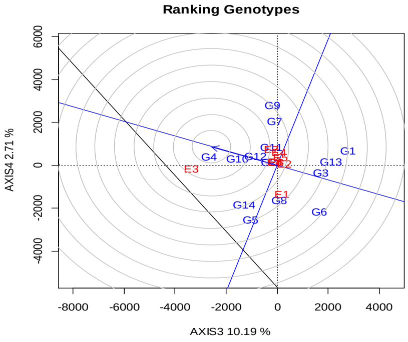

Figure 8d. Relationship among environment in PCA2 vs PCA3

Ranking of environment: it is based on an environment-centered (centering = 2) G by E table without any scaling (scaling = 0). GGE biplot explained: 68.44% the variation in PCA 1, whereas 15.19 % of variation in PCA2. Total of 83.63% variation of the environment-centered explained by GE (Fig.9a). GGE biplot explained: 42.5% the variation in PCA 1, whereas 15.25 % of variation in PCA3 (Fig.9b). Ranking of the environment near to the concentric circle environment 4, 5, 1 and 8 respectively (Fig.9b).

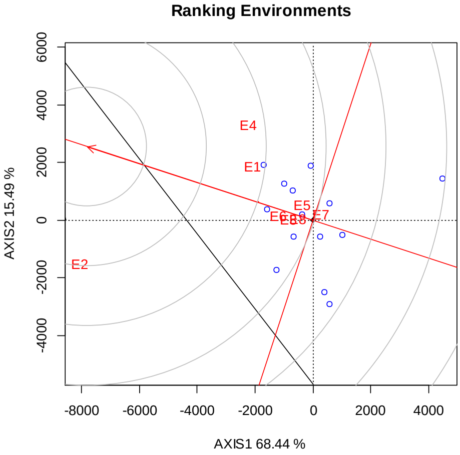

Figure 9a. Relationship among environment in PC1 vs PC2

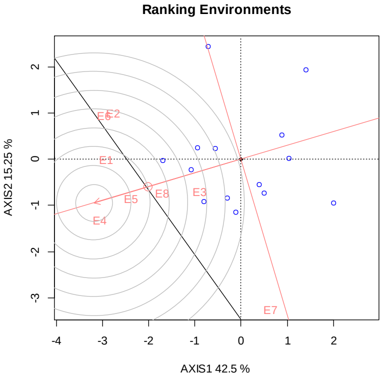

Figure 9b. Relationship among environment in PC1 vs PC3

Mean Performance and Stability of the Genotypes

Genotype (G1) had higher mean performances followed by G4, G10 and G3, whereas G5 and G2 had near average to relative mean performances, while G6, G12, G13 and G7 had the least mean performance. Comparison among all genotypes in (Fig.10) is the distance between two genotypes approximates the Euclidean distance between them, which is a measure of the overall dissimilarity between them. As a result, G1 (ICGV-93429) and G6 (ICGV-96390) are very different; while, G1 (ICGV-93429) and G4 (ICGV-96346); or G10 (ICGV-97243) and G4 (ICGV-96346) are relatively similar genotypes.

The dissimilarity can be due to difference in mean yield genotype and/or an interaction with the genotype by environments (GE). The biplot origin represents a "virtual" genotype that undertakes an average value in each of the environments. This "average" genotype has zero contributions to both genotype and genotype by environment interaction; as a result G2 (ICGV-96333) and G5 (ICGV-96352) are relatively the virtual genotypes. Therefore, the length of the genotype vector, which is the distance between a genotype and the biplot origin, measures the difference of the genotype from the "average" genotype, i.e. its contribution to either G or GE or both. Hence, genotypes located near the biplot origin have little contribution to both G and GE; and genotypes with longer vectors have large contributions to either G or GE or both (Yan and Tinker, 2006). Therefore, genotypes with the longest vectors are either the best G1 (ICGV-93429), G4 (ICGV-96346) and G10 (ICGV-97243) or the poorest are G6 (ICGV-96390), G7 (ICGV-96395), G12 (ICGV-97257) and G13 (ICGV-97262).

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 dataset (Fig.11). The vertex genotypes furthest from the biplot origin is the most responsive to the environment. According to Yan and Tinker (2006) genotypes located on the vertices of the polygon performed either the best or the poorest in one or more environments. Hence, genotypes (G1, G4, G10, G7 & G12) is the vertex genotypes furthest from the origin; whereas G1 is best performed in E5, E4, E1 and E6 whereas, G4 is best in E2 and G10 is best in E8 and E3; however, G7 and G12 are best in E7. Therefore, G1>G4>G10; while: G9 is near to the origin; as result this genotypes is stable almost in all environment (Fig.11). A polygon is first drawn on genotypes that are furthest from the biplot origin so that all other genotypes are contained within the polygon. Then perpendicular lines to each side of the polygon are drawn, starting from the biplot origin (Yan and Tinker, 2006). The perpendicular lines are equality lines between adjacent genotypes on the polygon, which facilitate visual comparison of them. Therefore, equality line between G4 and G10 indicates that G4 was better in E2; whereas G10 were better in E3 & E8; whereas G1 in E1, E4, E5 and E6 (Fig.11).

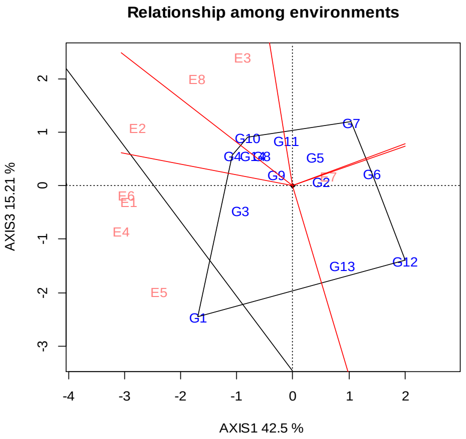

Figure 10. Mean & Stability in PC1 vs PC3

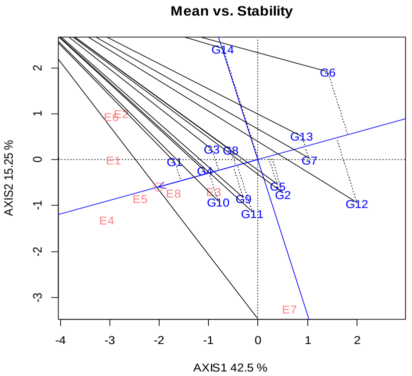

Figure 11. Which-Won-Where & relationship among environment in PC1 vs PC3

AMMI Stability Values (ASV) and Yield Stability Index (YSI) (%)

A great deal of previous research into quantifying and substantiate AMMI1 and AMMI2 has results AMMI stability values (ASV) and yield stability index (YSI) were also calculated. The ASV values and yield stability index (YSI) showed variations in groundnut yield stability among the fourteen groundnut genotypes (Table 8). According to Purchase et al. (2000) stable cultivars are defined as cultivars with an AMMI stability score (ASV) close to zero, but the AMMI model does not provide a determination or a quantitative measure of stability, and thus in order to quantify ASV was proposed. Consequently, the genotypes G9 was the most stable genotype followed by G11 and G6, while genotype G1, G7 and G14 were the least stable (Table 8). Studies have used for ASV data to finds out similar results with finding of Worede et al. (2020). YSI which incorporate ASV and mean grain yield in a single non-parametric index were the most desirable indices for discriminating the most stable genotypes with high grain yield (Mahmodi et al., 2011). The stability results based on YSI were further substantiated that out of selected stable genotypes namely; G9, G10, G11 and G4 are candidate with wider adaptability (Table 8). The YSI index was observed more pertinent to identify stable and ideal genotypes after applying AMMI and ASV (Kumar et al., 2018).

Table 8. Ranking of 14 groundnut genotype based on mean grain yield (kg ha^{-1}), AMMI stability value (ASV), and yield stability index (YSI) at 2012 to 2015 main cropping season

Genotype	Grand mean	Rank (A)	IPCA1	IPCA2	ASV	ASV rank (B)	YSI (A+B)	YSI rank
G1	4845	2	-4.19	0.76	5.9	14	16	8
G2	4151	10	1.27	0.40	1.8	5	15	7
G3	4492	5	-1.91	1.07	2.9	10	15	6
G4	4962	1	-0.80	-2.57	2.8	9	10	4
G5	4166	9	1.33	1.52	2.4	7	16	10
G6	3611	14	0.57	-0.69	1.0	3	17	11
G7	3791	11	2.65	-1.12	3.8	13	24	14
G8	4411	8	-0.92	1.95	2.3	6	14	5
G9	4448	7	0.08	0.17	0.2	1	8	3
G10	4789	3	-0.84	-0.41	1.2	4	7	1
G11	4469	6	0.07	-0.78	0.8	2	8	2
G12	3630	13	2.39	1.06	3.5	11	24	13
G13	3667	12	0.71	2.20	2.4	7	19	12
G14	4521	4	-0.40	-3.57	3.6	12	16	9

Where: IPCA1 score = interaction principal component axis one score, IPCA1 score = interaction principal component axis two score, ASV = AMMI stability value, and YSI = yield stability index

The additive main effects and multiplicative interaction model groundnut genotype examined by the environment. As a result, in five of the eight environments, genotype four was ranked first (Table 9). Furthermore, according to the first five AMMI selections per environment, genotype four was chosen in environments 2,3,4,5, and 8 in the second AMMI, while genotype ten was chosen three times in environment 3 and three times in the third (Table 9 and 10).

Table 9. AMMI-estimates per environment genotype rank

No	Genotype examined by the environment							
	E1	E2	E3	E4	E5	E6	E7	E8
1	G1	**G4**	**G4**	**G4**	**G4**	G5	G1	**G4**
2	G3	G10	G14	G10	G14	G2	G3	G10
3	G8	G1	G1	G1	G7	G10	G8	G5
4	G10	G8	G10	G14	G11	G9	G10	G9
5	**G4**	G9	G11	G11	G10	G8	**G4**	G11
6	G9	G3	G3	G9	G9	G12	G9	G8
7	G11	G11	G9	G3	G2	G11	G11	G2
8	G5	G5	G8	G8	G5	G4	G5	G3
9	G14	G2	G6	G2	G12	G7	G13	G1
10	G2	G14	G2	G5	G6	G13	G14	G14
11	G13	G7	G7	G7	G3	G3	G2	G7
12	G6	G12	G5	G12	G8	G1	G6	G12
13	G12	G13	G13	G13	G1	G14	G12	G13
14	G7	G6	G12	G6	G13	G6	G7	G6

Table 10. Summary of the first four AMMI selections per environment

Number	Environment	Mean	Score	1	2	3	4
5	E5	53.20	2.808	G4	G14	G7	G11
6	E6	14.45	2.634	G5	G2	G10	G9
8	E8	33.97	1.506	G4	G10	G5	G9
2	E2	19.64	0.808	G4	G10	G1	G8
4	E4	30.82	0.340	G4	G10	G1	G14
1	E1	63.52	-2.033	G1	G3	G8	G10
3	E3	73.76	-2.748	G4	G14	G1	G10
7	E7	53.21	-3.316	G1	G3	G8	G10

Conclusion and Recommendations

Environments with above-average mean yields were judged beneficial, whereas those with below-average mean yields were rated unfavorable. Stable genotypes were adaptable to a wider range of environments and produced consistent mean yield across all locations evaluated. As a result, G9 (ICGV-96442) was discovered to be approximately nearest to the origin and the most stable, with little responsiveness to the GEI. Genotypes (G10 (ICGV-97243), G4 (ICGV-96346), and G1 (ICGV-93429)) were selected as the most stable with high mean yield and suggested for wider groundnut growing settings based on the stability models GGE biplot. Having GGE biplot, AMMI, ASV and YSI; G4 (ICGV-96346) and G10 (ICGV-97243) were found the most promising and best adapted varieties in the eight tested environment. AMMI Stability Value and Yield Stability Index models were essential tools in selecting the high yielding and stable genotype(s). As a result, G4 (ICGV-96346) and G10 (ICGV-97243) can be recommended for variety verification, release and registration in Ethiopia.

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