Original Research

Genotype by Environment Interaction and Stability of Pod Yield of Elite Breeding Lines of Groundnut (*Arachis hypogaea* L.) in Eastern Ethiopia

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Abstract	Article Information
Groundnut (*Arachis hypogaea* L.) yield under small scale farming of eastern Ethiopia is low (1.04 t ha^{-1}) and highly variable over years and locations. Eleven elite breeding lines of groundnut were tested at Babile and Likale, eastern Ethiopia, in 2007, 2008 and 2009 to identify high yielding and stable genotypes. Additive main effect and multiplicative interaction (AMMI) model, cultivar-superiority measure, and genotype plus genotype by environment variation (GGE) were used to analyze multi-environment data. In the analysis of variance, all sources of variations showed statistically significant differences except year by genotype interaction indicating the possibilities for identification of best performing genotypes with specific and broad adaptability in the tested sites. AMMI analysis showed highly significant (*P*<0.01) effect of genotypes, environments and their interactions on dry pod yield. Similarly, the first and the second interaction principal component axis (IPCA 1 and IPCA 2) were highly significant (*P*<0.01) and explained 58.57 and 23.18 % of the G×E sum of squares, respectively. The environment had 84.7% effect, thereby explained high differences in genotype response to the tested environments. Genotype and genotype by environment interaction (GEI) accounted 6.6 and 8.7 %, respectively. Genotypes *BaHa-jidu* (-0.099), ICG-9251 (0.013), ICG-8644 (0.055) and *Roba* (0.057) with the lowest IPCA 1 showed the general adaptation in the mega-environment-1 (Ba2007, Ba2008 and Ba2009) and mega-environment-2 (Li2007, Li2008 and Li2009). *BaHa-gudo* had the highest mean dry pod yield (t ha^{-1}) in a mega-environment-2 and highest PCA 1 score (0.343). Genotypes *BaHa-jidu* and *BaHa-gudo* had the smallest superiority measure values and had the highest dry pod yield and stability. In GGE bi-plot, PC 1 and PC 2 explained 51.2 and 30.6% of genotype by environment interaction, respectively. ICGV-8749 and *BaHa-gudo* were vertex genotypes at mega-environment-1 and mega-environment-2, respectively, whereas *BaHa-jidu* was vertex genotype in both mega-environments.	 ***Corresponding Author:** **Amare Kebede** **E-mail:** amarekebede@gmail.com

INTRODUCTION

Groundnut (*Arachis hypogaea* L.) is an annual legume, best adapted to warm climatic conditions and is dominantly grown under rain-fed conditions in potential areas of Ethiopia. The estimated total area coverage of groundnut in Ethiopia was about 49,603 hectares with an estimated annual production of 71606.80 tons with an average dry pod yield of 1.44 t ha^{-1} in 2010/11 cropping season. East Hararghe zone accounted for 43.4% (21527.12 ha) of the national area of production and currently groundnut is replacing other major crops in East Hararghe zone of eastern Ethiopia due to its high nutritional and market value, adaptation to marginal soil types, drought tolerance and resistance to striga infestation. However, its dry pod yield is very low (1.04 tons ha^{-1}) in eastern Ethiopia as compared to the national average yield (1.44 tons ha^{-1}) (CSA, 2011). Moreover, this yield is far less than the potential (2.02 tons ha^{-1}) and highly variable over years and locations, mainly due to the various biotic and abiotic production constraints.

Among the factors contributing to the low yield level is due lack of high yielding and stable varieties. Temporal and spatial instability of quantitative traits of crops have connection with the unreliability of crop yields and thereby food insecurity at household and national level. In most cases, genotypes grown in different environments did 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.

The additive main effect and multiplicative interaction (AMMI) model involves the Additive Main effects of ANOVA along with the Multiplicative Interaction effects of principal components analysis (PCA). This model is used frequently for the analysis of multi-environmental data in plant breeding programs and more accurate in predicting future cultivar performance than cell means (Crossa *et al.*, 1990; Ebdon and Gauch, 2002).

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Cultivar-superiority measure is one of the analysis used in multi-environment trials for the selection of high yielding, stable and reliable genotypes. In cultivar-superiority measure, genotypes with the smallest values incline to be stable and better in yields (Lin and Binns, 1988).

Genotype plus genotype by environment variables (GGE) bi-plot allows for assessing the performance of genotypes in the tested environments. Phenotypic variation of genotypes across environments results from environmental and genotypic variations and genotype by environment interaction. Environmental variation is the dominant source of phenotypic variation. For single-trait data, vertex cultivars are considered to be the highest-yielding genotypes in the environments that occur in the same sector (Yan and Kang, 2003). The objective of this study was to identify high yielding, adapted and stable groundnut genotypes across different environments in eastern Ethiopia.

MATERIALS AND METHODS

The local check (*Oldhale)* and ten elite breeding lines of groundnut, which have been imported from the International Crops Research Institute for Semi Arid Tropics (ICRISAT), were evaluated in a multi-environment under rain fed conditions at Haramaya University research sites, namely Babile and Likale in 2007, 2008 and 2009 main cropping seasons. Thus, combinations of the locations (Babile and Likale) and years (2007, 2008 and 2009) were treated as six environments (Ba2007, Ba2008, Ba2009, Li2007, Li2008 and Li2009). For ease of assessment, genotypes were coded as

Genotype	Pedigree	Code	Genotype	Pedigree	Code
BaHa-jidu	NC-AC-2748xChico	G1	ICG-9251	ICG-9251	G7
GRRP-16	GRRP-16	G2	ICG-8644	ICG-8644	G8
BaHa-gudo	ICGV-88357	G3	*Werer-962*	ICGS20 Xl.NO95-A	G9
ICGV-8749	ICGV-8749	G4	*Roba*	ICG-7794	G10
NC-5	NC-5	G5	*Oldhale*	Local cultivar	G11
ICGS-62	ICGS-62	G6			

Site Description

Location	Geographical coordinates		Altitude (m.a.s.l)	Soil textural class
Babile	09°13'09"N	042°19'25"E	1642	Sandy loam
Likale	09°10'53"N	042°21'58"E	1612	Sandy loam

The experiment was arranged in randomized complete block design with three replications. The spacing between rows and between plants was 0.60 m and 0.10 m, respectively. The number of rows per plot was 5 and the dry pod yield was collected from middle three rows.

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

$$Y_{ijl} = \mu + G_i + E_j + (\sum \lambda_k \alpha_{ik} \gamma_{jk}) + d_{ij} + e_{ijl}$$

Where λ_k is k^{th} eigenvalue, α_{ik} is the principal component score for the ith genotype for the kth principal component axis, γ_{jk} is principal component score for the jth environment for the kth principal component axis, d_{ij} is residual G×E, not explained by model.

In addition, a cultivar-superiority measure was used to compute stability coefficients for genotype by environment data of each genotype. It is computed as the sum of the squares of the differences between its mean in each environment and the mean of the best genotype there, divided by twice the number of environments (Lin and Binns, 1988).

Genotype plus genotype by environment variation (GGE) was used to assess the performance of genotypes in different environments. The environmental effects were removed from the data and results obtained from the data were used to calculate environment and genotype scores and these scores were used to plot the standard principal component bi-plots (Yan and Kang, 2003).

Statistical Analysis

Analysis of variance was carried out with a statistical analysis system (SAS) version 9.0 software (SAS Institute Inc., 2002). Additive Main Effect and Multiplicative Interaction (AMMI) analysis, cultivar-superiority measure, and GGE bi-plots were performed using GenStat 15th edition statistical package (VSN International, 2012).

RESULTS AND DISCUSSION

Analysis of variance was carried out to determine the effect of genotype, location, year and their interaction on dry pod yield of groundnut genotypes (Table 1). Accordingly, except year by genotype interaction, all sources of variances showed statistically significant differences.

Table 1: Mean squares from combined analysis of variance for dry pod yield over two locations and three years.

Source of Variance	Df	Mean Square
Location	1	21.39**
Year	2	9.93**
Year×Location	2	22.94**
Rep (Year×Location)	18	0.58**
Genotype	10	0.68**
Location×Genotype	10	0.39**
Year×Genotype	20	0.07ns
Year×Location×Genotype	20	0.18**
Error	180	0.086
CV (%)		16.6

** and *significant level at *P*<0.01 and *P*<0.05, respectively, and ns=not significant
df=degree of freedom, CV= coefficient of variation.

Genotype by location interaction showed a highly significant difference indicating the need for independent breeding program to identify best performing genotypes for each tested sites. In the combined analysis, interactions among year, location and genotype were highly significant which indicates response variation among genotypes in the tested environments.

AMMI analysis of dry pod yield of eleven genotypes in six environments showed that genotypes, environments and their interactions were highly significant ($P<0.01$). IPCA 1 and IPCA 2 were also statistically significant ($P<0.01$) and explaining 58.57 and 23.18% of the GxE sum of squares, respectively (Table 2).

Table 2: AMMI analysis for eleven groundnut genotypes studied in six environments

Sources of variation	Df	SS	MS
Blocks within environment	18	10.45	0.581**
Treatments	65	102.84	1.582**
Genotypes	10	6.80	0.680**
Environments	5	87.11	17.422**
G × E	50	8.93	0.179**
IPCA 1	14	5.23	0.374**
IPCA 2	12	2.07	0.173*
Residual	24	1.62	0.068
Error	180	15.51	0.086

** and *significant level at $P<0.01$ and $P<0.05$, respectively
df = degree of freedom, SS = sum of squares, MS = mean squares

The environment had the highest effect (84.7%) of the treatment sum of squares indicating the environments were diverse and caused most of the variation in dry pod yield. Such highest variability due to the environment were also reported on groundnut and other crops (Crossa *et al.* 1990; Casanoves, 2005; Aina *et al.*, 2007). On the other hand, genotypes and GxE accounted only 6.6% and 8.7% of the treatment sum of squares, respectively.

Genotypes *BaHa-jidu (-*0.099*)*, ICG-9251 (0.013), ICG-8644 (0.055) and *Roba* (0.057) had IPCA 1 values close to zero showing that these genotypes had general adaptation in the tested environments. However, based on best dry pod yield performance, *BaHa-jidu* (2.02 t ha^{-1}) was recommended for production. *BaHa-gudo* (0.579) had a highest IPCA 1 score, which indicates its highest interaction with the specific environment, best in mean dry pod yield, and consequently recommended for production (Table 3). Similarly, high yielding groundnut genotypes were obtained in a unique mega-environment (Casanoves *et al.,* 2005). Mitrovic *et al.* (2012) also followed the same procedure to select specific and broad adaptable maize hybrids.

Among studied varieties, *BaHa-jidu* (0.026) and *BaHa-gudo* (0.044) had smallest superiority measure values, which showed their best yield performance and dry pod yield stability (Table 3).

In the AMMI selection of genotypes, *BaHa-jidu* took the third position in Li2007 and the second best position in all other environments. Accordingly, *BaHa-jidu* showed dynamic stability, but its relative performance was consistent and predictable across environments, which is desirable characteristics for crop production at various

levels of agricultural inputs. This narrow change of the differential response of *BaHa-jidu* in different environments is an indication of its wide adaptability. *BaHa-gudo* took the first position in the mega-environment-2 indicating consistent and predictable dry pod yield performance in the specific environment (Table 4). The report indicated that the interaction pattern of some locations across crop species are consistent so that they are highly predictable in year to year interaction with genotypes (Ebdon and Gauch, 2002). In this line, the Babile and Likale research sites were found good selection sites for broad and specific based adapted groundnut genotypes. Similarly, Aina *et al.* (2007) identified sites suitable for crop improvement program based on genotype performance.

Table 3: Mean dry pod yield, IPCA scores and stability coefficients for eleven genotypes tested in six environments

Genotype	DPY (t ha^{-1})	IPCA 1	IPCA 2	Genotype superiority measure
BaHa-jidu	2.02	-0.099	0.009	0.026
GRRP-16	1.82	-0.366	0.320	0.109
BaHa-gudo	1.97	0.579	0.343	0.044
ICGV-8749	1.81	-0.559	-0.117	0.126
NC-5	1.76	-0.200	0.088	0.107
ICGS-62	1.78	-0.204	-0.196	0.108
ICG-9251	1.85	0.013	-0.420	0.066
ICG-8644	1.51	0.055	0.259	0.254
Werer-962	1.69	0.341	-0.202	0.121
Roba	1.74	0.057	0.235	0.110
Oldhale	1.46	0.384	-0.317	0.275

IPCA 1 = first interaction principal component axis, IPCA 2 = second interaction principal component axis, DPY= dry pod yield.

Table 4: First four AMMI selections of genotypes per environment

Environment	Mean DPY (t ha^{-1})	Genotype rank			
		1	2	3	4
Ba2007	1.774	G2	G1	G4	G5
Ba2008	2.175	G7	G1	G4	G6
Ba2009	2.197	G4	G1	G7	G6
Li2007	2.167	G3	G9	G1	G7
Li2008	1.715	G3	G1	G2	G10
Li2009	0.556	G3	G1	G7	G2

DPY= dry pod yield

In GGE bi-plot (Figure 1), PC 1 and PC 2 explained 51.2 and 30.6%, respectively, of genotype by environment interaction and made a total of 81.8%. The other study conducted on the same crop showed 79 to 85% total of PC 1 and PC 2 (Casanoves, 2005). Environments Ba2007, Ba2008 and Ba2009 were ellipse rounded identifying the homogeneity of the environments (mega-environment-1). Similarly, environments Li2007, Li2008 and Li2009, were ellipse rounded, showed the similarity of the environments (mega-environment-2).

In dry pod yield data, *BaHa-jidu* was the vertex variety of both mega-environments. *BaHa-gudo* was vertex variety yield in the mega-environment-2. These reveal that *BaHa-jidu* and *BaHa-gudo* were the best varieties in dry pod yield in their respective environments (Figure 1).
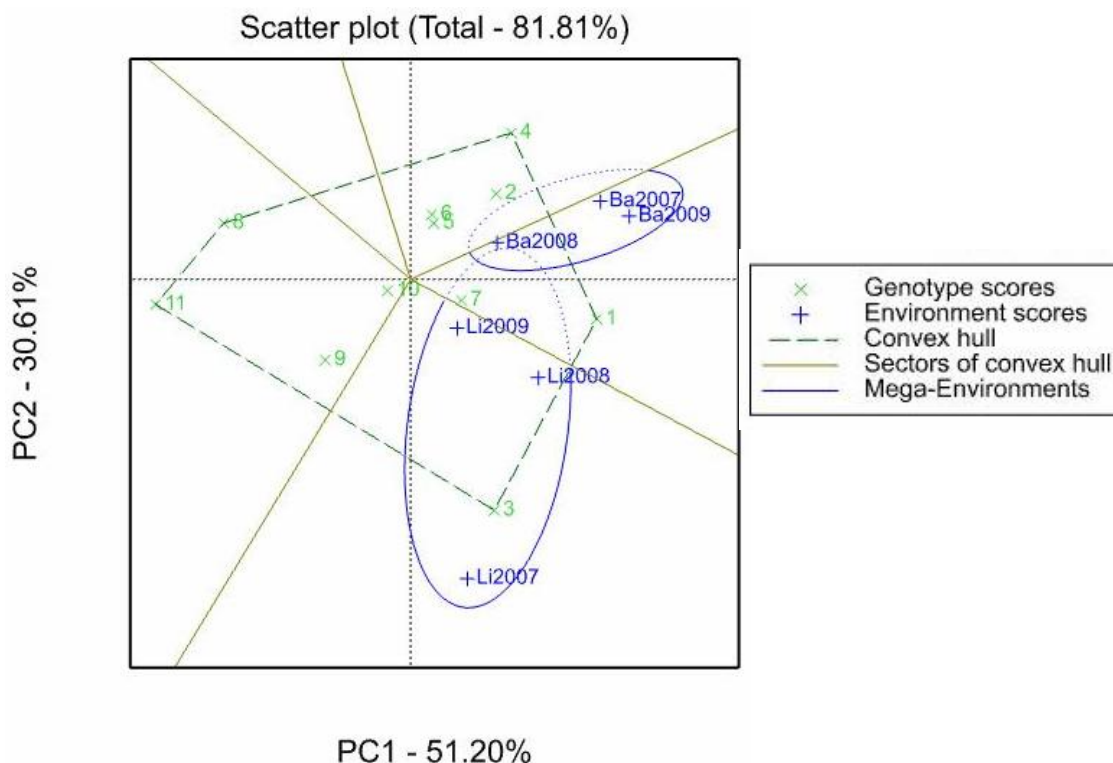
Figure 1: Genotype plus genotype by environment variation (GGE) bi-plot showing the performance of genotypes in different environments. G1, G2, G3, G4, G5, G6, G7, G8, G9, G10 and G11 are designated as 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 and 11, respectively. Dashed ellipse lines indicated the extension of ellipse in another sector.

CONCLUSIONS

The tested environments were diverse and had the greatest effect on dry pod yield variation among groundnut genotypes. Babile and Likale research sites to be suitable for the identification of best performing groundnut genotypes with broad and specific adaptability. Moreover, trials for extended years at the tested sites would not be required to select best performing genotypes. *BaHa-jidu*, ICG-9251, ICG-8644 and *Roba* had general adaptation in the mega-environment-1 (Ba2007, Ba2008 and Ba2009) and mega-environment-2 (Li2007, Li2008 and Li2009). Among which, *BaHa-jidu* showed highest dry pod yield performance and recommended for production. *BaHa-gudo* showed highest interaction with the specific mega-environment and highest dry pod yield. Consequently, recommended for production. In general, *BaHa-jidu* showed wide adaptability, highest, consistent and predictable dry pod yield across environments. Similarly, *BaHa-gudo* showed highest, consistent and predictable dry pod yield in the mega-environment-2.

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