

Genotypes by environment interaction of groundnut (*Arachis hypogaea* L.) for yield and yield related components

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ABSTRACT

Groundnut is a versatile and economically significant plant that has played a prominent role in human history. Using additive main effects and multiplicative interaction analysis, the performance of 12 groundnut genotypes was assessed in six environments across four sites. Highly significant genotypes and GE interactions were found in the mean squares of the analysis of variance for seed yield per hectare. Environment-related differences made for 53.25% of the overall variation, whereas genotype was responsible for 43.73% of it. For 84.93% of the overall variation, the biplot was responsible. The most stable models according to the AMMI model were 19748 and 19750. As a result, these genotypes are thought to be the most suitable ones for the study locations. The candidate variety 19748 is stable and high yielding, with a yield advantage of about 18 percent above the standard check Babile-2. Then suggested to release and further multiply as a commercial variety at study and similar agro-ecology.

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1. INTRODUCTION

Groundnut (*Arachis hypogaea* L.) plays an important role as a food as well as a cash crop in Ethiopia (Berhanu, H., *et al.*2020). It is a versatile and economically significant plant that has played a prominent role in human history. It ranks third in terms of importance as a source of vegetable protein and is the sixth most significant oilseed crop in the world (Singh, A. L. (2004). Cash crops like groundnut give framers a living and a means of subsistence. The crop is best adapted to well drained, loose, finable, medium texture soils (Raza, A. *et al.*, 2017). Similarly the study areas were characterized by well drained, loose with medium soil texture. Groundnut is rich in very essential source of oil (43-55%) and protein (25-28%), hence used as food and feed (Saeed, I. and Hassan, M 2009). Groundnut is a good source of edible oil as it contains about 50% oil of good quality (Gunstone, 2011). Groundnut oil is one of the best cooking oils due to its high smoking point and is desirable for use in ghee, margarine, shortening and salad oil. Groundnuts are immensely rich in potassium, calcium, phosphorus and B vitamins which offers you with a host of health benefits (Toomer, O., 2018). Groundnuts are a great blend of healthy fats, protein and fibre that curbs your appetite, lowers the risk of heart disease and regulates blood glucose levels

(Jayamali, 2021). The meal contains 25% protein and considered best meal for human consumption and livestock feed. Groundnut is also an excellent source of vitamins and contains high levels of thiamine, riboflavin and niacin (Raza, A. *et al.*, 2017).

Currently the crop is becoming one of the high value crops that are growing in the lowlands areas of the eastern Oromia. Particularly, Gursum, Babile, Fadis, Midhaga tola and other lowland areas of eastern Hararghe. However, despite the importance of the Groundnut among smallholder farmers in the country, its production has continued to decline due to the absence of improved Variety, presence of pests and diseases. Therefore this study undertaken to identify and release; stable, high yielding, tolerant to major diseases and other a biotic stresses genotypes with better agronomic performances (traits).

2. METHOD

2.1 Experimental area

The study was conducted at four locations (FARC on station “Bokko”, FARC sub-station “Erer”, MARC station and Diredawa) for two years (2018-2020).

2.2 Experimental Materials

Eleven Groundnut genotypes along with one standard check variety (Babile-2) were used. The materials were collected from Ethiopian Biodiversity Institute.

Table1. List of groundnut genotypes used as planting materials during the study

G. Code	Genotypes name	Source the Genotypes	G. Code	Genotypes name	Source the Genotypes
G1	19739	EBI	G7	19768	EBI
G2	19750	EBI	G8	19769	EBI
G3	19749	EBI	G9	19770	EBI
G4	19748	EBI	G10	19776	EBI
G5	19753	EBI	G11	24208	EBI
G6	19755	EBI	G12	Babile-2 St check	EBI

NB: - EBI=Ethiopian Biodiversity Institute

2.3 Experimental Design

The field experiment was laid out in RCBD designs with three replications. The experimental plots consisted of six rows of 4 m length with row spacing of 60 cm and 10 cm between plants. The spacing between adjacent replications, blocks and plots were 1 m, 1 m and 0.5 m, respectively. The central four rows were harvested to estimate grain yield. All the recommended agronomical practices such as fertilizer application, weeding, hoeing, harvesting and threshing were undertaken to raise the healthy crop.

2.4 Data Collection

Days to maturity, pod per plants, seed per pod, number of branches per plants and grain yield were collected and analysed.

2.5 Analysis of variance (ANOVA)

Analysis of variance was done using Proc lattice and Proc GLM procedures of SAS version 9.0, (SAS, 2002). The differences among treatments means were compared using DMRT at 5% probability level. The AMMI stability value (ASV) as described by Purchase (2000) and calculated as follow:

$$ASV = \sqrt{[(IPCA1 \text{ sum of square} \div IPCA2 \text{ sum of square}) * IPCA1 \text{ score}]^2 + (IPCA 2 \text{ Score})^2}$$

3. RESULTS AND DISCUSSION

3.1 ANOVA for seed yield and yield related traits

Analysis of variance revealed that Location, year and interaction of location by year were showing highly significant variation, while Genotypes, Genotypes by Location and interaction of Genotypes and location by year shows significant variation. Similarly, Akley, E., (2022) reported highly significant effects of genotype, environment, and genotype by environment interaction were observed for traits studied.

Table 2. Analysis of variance Seed of Groundnut tested across years and location

Source of variation	d.f.	Sum square	Mean square	F pr.
Replication	2	37.02	18.51	
Genotypes	11	377.85	34.35	0.003
Location	3	6652.75	2217.58	<.001
Year	1	1180.41	1180.41	<.001
Genotypes*Location	33	774.11	23.46	0.005
Genotypes*Year	11	146.45	13.31	0.382
Location*Year	1	159.55	159.55	<.001
Interaction	11	293.85	26.71	0.019
Residual	142	1750.86	12.33	
Total	215	11372.85		

ANOVA stated that significant variations were observed among the genotypes for days to maturity, number of pods per plant, number of seeds per pod, hundred seeds weight and seed yield.

Table 3. Combined mean of seed yield and other parameters for GXE, of Groundnut at three locations over two years

Genotypes	Days to Maturity	Pods/plant	Seeds/pod	HSW(g)	Seed yield(qt/ha)
19739	173.9a	54.88ab	1.83bc	42.48e	20.1d
19750	172.5ab	59.61a	1.83bc	50.94ab	23.78ab
19749	172.9ab	51.52bc	1.87ab	49.58bc	21.26cd
19748	174.8a	55.37ab	1.91ab	52.98a	24.12a
19753	172.0ab	55.26ab	1.83bc	49.18bc	21.95a-d
19755	171.8ab	51.86bc	1.89ab	45.28d	20.5d
19768	173.0ab	55.37ab	1.87ab	48.49bc	21.28cd
19,769	173.6a	49.29b-d	1.91ab	48.70bc	21.6b-d
19770	171.9ab	54.69ab	1.86a-c	48.92bc	21.48cd
19,776	172.9ab	47.85cd	1.86a-c	51.01ab	22.95a-c
24208	173.9a	50.21b-d	1.78c	48.28c	21.24cd
Babile-2	169.6b	44.37d	1.92a	49.11bc	20.07d
CV	3.5	20.9	8.2	8.8	16.7
LSD	3.699	6.68	0.1	2.6	2.217

Maximum number of pods per plant were counted from the genotype G4 (59.61) followed by G2 (55.37), G7 (55.37) and G5 (55.26) whereas the minimum number of pods per plant was counted from standard check Babile-2 (44.37). Similar study reported by Borkar and Dharanguttikar 2014 The genotypes, ICG-8075 (43.90), ICG-8539 (42.00) and ICG-8506 (41.40) recorded highest number of pods per plant. Significant variation was observed for hundred seeds weight among the genotypes. Accordingly, heavy seed weight was measured for G2 (52.98) and followed by G10 (51.01) and G4 (50.94) While, minimum weight of hundred seeds weight was measured from G1 (42.48). Highly significant variations were obtained among the genotypes for seed yield. Accordingly three genotypes namely G2 (19748) (2.4 ton ha⁻¹) G4 (19750) (2.38 ton ha⁻¹), and G10 (19776) (2.29 ton ha⁻¹) are a stable, and high yielding genotypes with yield advantage of 18%, 15% and 12% over the standard check, G12 (Babile-2) (2.01ton ha⁻¹) respectively.

3.2 Mean seed yield of groundnut Genotypes

Significant variation was found among the genotypes for seed yield (Table 2). According maximum seed yield was harvested from G4 (19748) 24.12qt/ha followed by G2 (19750) 23.78qt/ha.

Table 4. Mean performance of Seed yield of Groundnut Genotypes across testing environments in regional variety trial against standard checks over locations and years

Genotypes	Testing Environments							Mean
	(E1)Fadis 2018	(E2)Dire 2018	(E3)Mechara 2018	(E4)Dire 2019	(E5)Fadis 2019	(E6)Erer 2019	E7(Mechara 2019)	
19739	10.69	17.78	29.78	16.71	19.5	16.1	30.15	20.1
19750	15.16	16.85	36.11	25.49	19.33	25.13	28.37	23.78
19749	15.07	13.18	35.78	15.05	21.18	17.67	30.93	21.26
19748	17.04	14.92	26.78	25.84	24.98	22.79	36.52	24.12
19753	9.38	15.55	33.67	17.06	23.9	18.38	35.7	21.95
19755	11.71	17.85	34.22	17.62	16.87	15.44	29.81	20.5
19768	13.26	13.44	35.67	15.4	21.27	15.72	34.19	21.28
19,769	14.28	15.92	31.37	17.42	21.04	17.93	33.22	21.6
19770	16.45	12.7	33.22	16.9	21.39	19.64	30.04	21.48
19,776	16.49	16.05	30.07	24.55	20.17	20.61	32.74	22.95
24208	10.57	13.89	29.85	18.73	22.61	18.05	35	21.24
Babile-2	12.79	15.44	32.22	16.24	24.63	16.26	26.41	20.07

Mean 10.69 17.78 29.78 16.71 19.5 16.1 30.15 21.69

A large yield variation explained by environments also indicated the existence of diverse mega environments, i.e., a group of environments which share the same cultivars that consistently performed the best with large differences among environmental means, causing most of the variation in grain yield (Ajay, B *et al.*, 2020). The average environmental seed yield across genotypes ranged from the lowest of 10.69 Qtha⁻¹ at E1 (Fadis 2018) to the highest of 30.15 Qtha⁻¹ at E7 (Mechara 2019), with a grand mean of 21.69 Qtha⁻¹ (Table 4). The genotype average Seed yield across environments ranged from the lowest of 20.1 Qtha⁻¹ for G1 (19739) to the highest of 24.12 Qtha⁻¹ for G2 (19748) (Table 4). This difference could be due to their genetic potential of the genotypes. G2 (19748) was the top ranking genotypes at three environments E1 (Fadis 2018), E4 (Diredawa 2019) and E7 (Mechara 2019) as well as G4 was ranked first at two environments E3 (Mechara 2018) and E6 (Erer 2019).

3.3 Additive Main Effects and Multiple Interaction (AMMI) model:

The Groundnut yield data were subjected to AMMI analysis which is a combination of analysis of variance and multiplication effect analysis. Briefly, analysis of variance is used to partition variance into three components: genotype deviations from the grand mean, environment deviations from the grand mean, and GE deviations from the grand mean. Subsequently, multiplication effect analysis is used to partition GE deviations into different interaction principal component axes (IPCA), which can be tested for statistical significance through ANOVA.

Table 5. Analysis of variance for grain yield using AMMI model

Source of variation	df	Sum square	Mean square	%TSS
Total	251	16508	65.8	
Treatments	83	14265	171.9**	11.55
Genotypes	11	372	33.8*	43.73
Environments	6	12351	2058.4**	53.25
Block	14	300	21.5	1.57
Interactions	66	1543	23.4**	1.72
IPCA 1	16	619	38.7**	3.32
IPCA 2	14	449	32*	1.96
Error	36	475	13.2	0.92
Pooled Error	154	1942	12.6	

*, ** significant at 0.05 and 0.01 probability levels, respectively df= degree of freedom, IPCA1=Interaction Principal Component Axis

The importance of applying AMMI analysis to investigate the main effects of genotypes and environment and the complex patterns of their interaction was demonstrated through this experimental study. AMMI analysis of variance for seed yield of twelve groundnut genotypes tested in seven testing environments showed that environments, IPCA 1 and their interaction effects were significantly different ($P < 0.01$) (Table 5). The Environment significant effect on the seed yield of groundnut, which explained 53.3% of the total variations while, the genotypes contributed 43.7% of the variation. This indicate the existence of a considerable amount of deferential response among the genotypes to changes in growing environments and the differential discriminating ability of the test environments. Similar result was reported by (Rezene, Y *et al.*, 2014). The interaction of the twelve groundnut genotypes with six environments was best predicted by the first 2 principal components of genotypes and environments. IPCA₁ was also statistically significant ($P < 0.01$) while PCA₂ statistically significant ($p < 0.05$) and explaining 3.32% and 1.96% for seed yield (Table 5). Because of their maximum, the first two principal components (IPCA₁ and IPCA₂) were used to plot a two-dimensional GGE bi-plot (Amare *et al.*, 2014) suggested that the most accurate model for AMMI can be predicted by using the first two IPCAs.

Table 6. Analysis of variance using AMMI model for grain yield and other yield related characters

Source of variation	df	DM	PPP	SPP	HSW	GY
Total	251	253	173.1	0.03597	26.58	65.8
Treatments	83	691**	275.3**	0.06236**	42.83**	171.9**
Genotypes	11	37*	362.4**	0.03668	153.47**	33.8*
Environments	6	9117**	986.7**	0.55658**	126.92**	2058.4**
Block	14	63	159.7	0.03131	8.96	21.5
Interactions	66	34	196.1*	0.02171	16.74	23.4**
IPCA 1	16	73	405.2**	0.03704	43.23	38.7**
IPCA 2	14	39	175.9	0.02417	14.96	32*
Error	36	14	111	0.01394	5.67	13.2
Pooled Error	154	34	119.3	0.02217	19.43	12.6

Analysis of variance for AMMI shows highly significant variation for Environment in number of pods per plant, number of seeds per pods, hundred seeds weight and seed yield traits. Significant variations for genotypes in terms of days to maturity, number of pods per plant and number of seeds per pod.

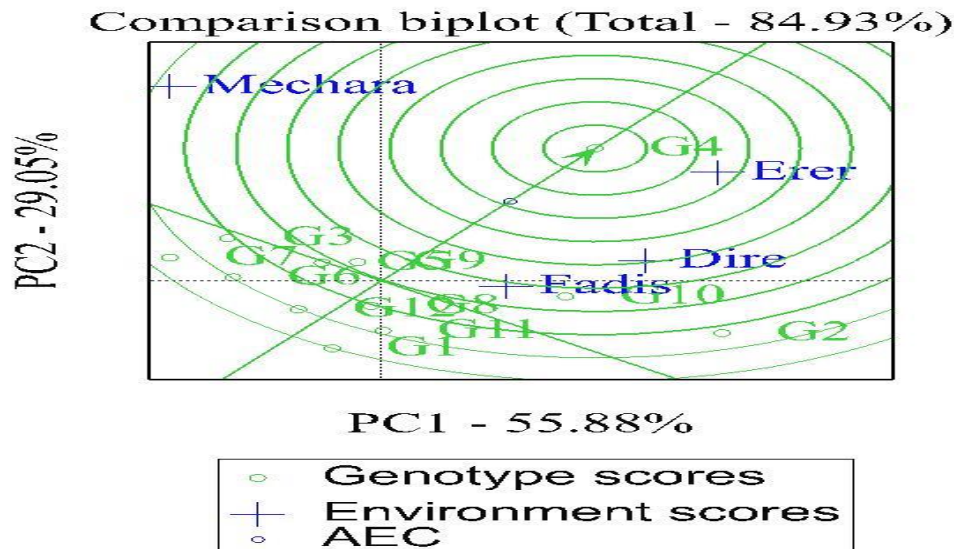


Figure 1. GGE Biplot of the seed yield of Groundnut tested at different locations and Years

Environments and genotypes that fall in the central (concentric) circle are considered ideal environments and stable genotypes, respectively (Yan, W., & Rajcan, I. 2002). Accordingly the genotype found in the concentric circle G4 was most stable, and high yielding.

4. CONCLUSION

ANOVA revealed that significant variation were obtained among the varieties for genotype, environment and their interaction. AMMI analysis shows highly significant ($P < 0.01$) variation for Environment, Interaction and IPCA1 while Genotypes and IPCA 2 shows significant ($P < 0.05$). The candidate variety 19748 is stable and high yielder having about 18% of yield advantage than the standard check Babile-2. Then suggested to release as a commercial variety.

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