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GENOTYPIC STABILITY AND CLUSTERING ANALYSIS OF CONFECTIONERY GROUNDNUT (*ARACHIS HYPOGAEA* L.) FOR SEED AND PROTEIN YIELD IN MOISTURE-STRESS AREAS OF NORTHEASTERN ETHIOPIA

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ABSTRACT: Nine groundnut genotypes were evaluated in terminal moisture-stress areas of northeastern Ethiopia during 2005 and 2006 cropping seasons with the objective of analyzing genotypic stability and clustering of confectionery groundnut for seed and protein yield. The genotypes were evaluated on a plot size of 15 m^2 at Kobo, Mersa and Chefa testing sites of Sirinka Agricultural Research Center. The experiment was laid-out using randomized complete block design with three replications. Simple correlation analysis for seed and protein yield with other yield components were carried out using Genstat software package. Genotypic stability and clustering for seed and protein yield were computed using Additive Main effect and Multiplicative Interaction (AMMI) model. Correlation analysis depicted that seed yield exhibited positive association with number of matured pods $plant^{-1}$ ($r= 0.70^{**}$), shelling percentage ($r=0.46^{**}$) and hundred seed weight ($r=0.25^{*}$). Similarly, protein yield exhibited strong positive association with seed yield ($r=0.97^{**}$), number of matured pods $plant^{-1}$ ($r= 0.70^{**}$) and shelling percentage ($r=0.43^{**}$). Therefore, shelling percentage, number of matured pods $plant^{-1}$ and hundred seed weight could be used as indirect selection criteria for simultaneous improvement of seed and protein yield in confectionery groundnut in terminal moisture-stress environments. Clustering analysis showed that genotypes were grouped into three distinctive clusters with the highest inter-cluster distance between cluster-I and-II ($D^2=173$). Genotypic stability analysis revealed ICGV-88361 was stable for seed and protein yield across environments.

Key words/phrases: AMMI, Clustering, Groundnut, Protein, Stability.

INTRODUCTION

Groundnut (*Arachis hypogaea* L.) is an annual legume belonging to the family Leguminosae but it is so unique in bearing the pod below the surface of the soil. It suitably grows in hot and sunny areas below 1600 meter above sea level with an average temperature ranging from $20\text{-}35^0$ C. Groundnut seed is rich in oil and protein, containing 44-56% and 22-30%, respectively, on a dry seed basis (Savage and Keenan, 1994). Moreover, it is a good source of phosphorous, calcium, magnesium, potassium and some vitamins

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(Dwivedi *et al,* 1996).

Groundnut widely grows in eastern Ethiopia, whereas it is a newly introduced crop in northeastern Ethiopia. The lowland areas of northeastern Ethiopia are moderately suitable for groundnut production though the occurrence of terminal moisture stress, usually at peg formation, pod and seed development and maturity, critically curtail production and productivity of groundnut.

In a variety development, genotype x environment (GxE) interaction is an important concern to plant breeders. The magnitude and nature of GxE interaction often dictates the feature of breeders' selection and testing procedure. The phenotypic expression of most characters of crop plants is the consequence of interaction between the genes it carries for the character and the environment in which it has been grown. Quantitative characters, such as yield, the expression of which is much dependent on the very variable environmental factors, have very large environmental variances and thus mask the genetic expression of quantitative traits. Normally, all living things can make physiological adjustments which permit them to cope with the fluctuating environments (Dabholkar, 1992). The extent of physiological adjustment of genotypes to variable environments, called buffering capacity, is highly variable among genotypes indicating the variation of genotypes in genetic potential to survive under variable environments. Stability is one of the most desirable properties of a genotype to be released as a variety for wider environments (Singh and Chaudhary, 1985).

Currently, numerous computerized genotypic stability analysis models are available, of which Additive Main effect and Multiplicative Interaction (AMMI) is so unique in assigning genotypes and environments in biplot graph based on their principal component values and mean yield (Agrobase, 1999). This model involves the additive main effects of ANOVA along with the multiplicative effects of the Interaction Principal Components Axis (IPCA) analysis. The principal component model is fitted to the residual from the ANOVA and the resulting scores called IPCA are calculated for both genotypes and environments (Gauch and Zobel, 1997). The genotype-based concept is relevant, because planting the winning genotype in each environment optimizes seed yield (Gauch and Zobel, 1997). Adugna and Elias (1995) and Elias and Assefa (2005) reported the performance and stability of groundnut genotypes for pod yield. The previous reports were mainly focused on oil type groundnut genotypes under irrigation and/or in high rainfall areas. However, information on the stability and clustering of

confectionery groundnut genotypes for seed and protein yield in terminal moisture-stress environments of northeastern Ethiopia was lacking. Therefore, the objective of this experiment was to analyze the genotypic stability and clustering of confectionery groundnut genotypes for seed and protein yield in terminal moisture-stress areas of northeastern Ethiopia.

MATERIALS AND METHODS

Description of the study areas

The study was conducted in terminal moisture-stress areas of northeastern Ethiopia, Viz., Kobo, Mersa and Chefa testing sites of Sirinka Agricultural Research Center (SARC) on well-drained soils during the 2005 and 2006 cropping seasons. The testing sites are located at 12^0 $9^{'}$ N and 39^0 $38^{'}$ E (Kobo) 11^0 $42^{'}$ N and 39^0 $36^{'}$ E (Mersa) and 10^0 $57^{'}$ N and 39^0 $47^{'}$ E (Chefa). The mean elevation of each site is 1470, 1580 and 1450 meters above sea level, respectively. Rainfall is usually unpredictable and erratic. Maximum rainfall was recorded in July and August while terminal moisture-stress was occurred from September onwards. Amount of rainfall received during the growing seasons is presented in Table 1. Meteorological station is not available at Mersa testing site and thus, data from the nearest meteorological station (Sirinka, 18 km away from Mersa) was used.

Table 1. Monthly rainfall (mm) during the growing season of groundnut at Mersa, Kobo and Chefa areas during 2005 and 2006 cropping seasons.

	2005			2006		
Month	Kobo	Mersa	Chefa	Kobo	Mersa	Chefa
June	2.8	26.7	25.0	3.0	8.3	7.9
July	125.2	284.7	257.0	81.2	157.0	306.9
August	190.9	283.9	239.9	223.9	223.2	300.3
September	20.1	55.6	43.7	75.4	117.8	58.9
October	8.7	36.3	5.7	12.5	38.0	23.0
Total	347.7	687.2	571.3	396.0	544.3	697.0

Plant material

Nine confectionery groundnut genotypes along with standard check (*Roba*) were evaluated at six environments (Table 2). Variety *Roba* was officially released in 1989 by the national lowland oil crops improvement program, Worer Agricultural Research Center (WARC) while the rest of the genotypes were introduced from ICRISAT through WARC.

Table 2. List and origin of confectionery groundnut (*Arachis hypogaea* L.*)* genotypes used for the experiment.

Genotypes	Origin	Status
ICGV-88390	ICRISAT	Breeding line
ICGV-88438	ICRISAT	Breeding line
ICGV-88389	ICRISAT	Breeding line
ICGV-88382	ICRISAT	Breeding line
ICGV-88358	ICRISAT	Breeding line
ICGV-88357	ICRISAT	Breeding line
ICGV-88367	ICRISAT	Breeding line
Roba	ICRISAT	Released
ICGV-88361	ICRISAT	Breeding line

Experimental design and procedures

Experimental design and data collection

The experiment was laid-out using randomized complete block design with three replications. Genotypes were space planted with inter- and intra- row spacing of 60 and 10 cm, respectively on a plot size of 15 m^2 (5 rows x 5 meter length x 0.6 meter inter-row spacing). Land preparation, weeding and earthening-up were done uniformly for all the genotypes.

Datum for number of matured pods $plant^{-1}$ (MPP) was recorded from five randomly taken plants, which were tagged ahead of flowering and computed as an average of the five plants. However, shelling percentage (SHP), hundred seed weight (HSW) and seed yield (SY) was recorded from the central three rows (a net plot size of 9 m^2) after discarding border rows. Shelling percentage was calculated from 200 g sound matured pods and computed using the formula; $SHP=\frac{SW}{PW}*100$ where, SW = shelled seed weight and PW= unshelled pod weight (which is 200 g). On the other hand, data for protein content (PC) and protein yield (PY) were taken on genotypic basis. Total nitrogen content of each genotype was determined using Kjeldahl technique as described by Dalby and Tsai (1975). Then, crude protein content was calculated by multiplying the total nitrogen content by a conversion factor of 5.46 (FAO, 2003; The United Nations University, 1980). Likewise, protein yield of each genotype was determined as the product of seed yield (kg ha^{-1}) and protein content (%) using the formula: PY = SY*PC.

Statistical analysis

Individual environment Analysis of Variance (ANOVA) for the locations

and years was carried-out using MSTAT-C statistical software program (Michigan State University, 1988) as per Gomez and Gomez (1984) using mixed model. Genotypes were considered as fixed factor while environment (location x year) was regarded as random factor. Combined analysis of variance over environments was computed after testing the homogeneity of error variance using Bartlett's test as per Gomez and Gomez (1984).

Analysis of simple correlation coefficients and clustering of genotypes and environments were carried-out using Genstat software package (Genstat, 2007). Stability analysis of genotypes for the economic traits (seed and protein yield) was computed with the Additive Main effects and Multiplicative Interaction (AMMI) model using Agrobase software program (Agrobase, 1999). The relative position of genotypes and environments in a biplot graph was analyzed using Agrobase software program (Agrobase, 1999) as per Gauch and Zobel, (1997).

RESULTS AND DISCUSSION

1. Seed size

Seed size is one of the premium quality attributes for confectionery groundnut to qualify for export standards. Sound Matured Seeds (SMS) with a minimum weight of 44 g for hundred seeds are essential for a groundnut sample to meet the criterion of its grading as Hand Picked and Selected (Reddi, 1988). In this study, genotypes showed significant variation for hundred seed weight, justifying the presence of genetic variation among the tested confectionery groundnut genotypes. Hence, it might be a good opportunity to utilize such variation to improve confectionery groundnut seed size through genotypic selection. In agreement with the current result, Gemechu *et al.* (1999) reported significant genotypic and phenotypic variations among groundnut genotypes for seed size. Similarly, GxE interaction exhibited significant variation for hundred seed weight, implying the presence of differential response of genotypes across environments (Table 3). All the tested groundnut genotypes fulfill the minimum seed size requirement ranging from 58-93 g per hundred seeds. ICGV-88390, ICGV-88438, ICGV-88389 and ICGV-88367 consistently exhibited bold seed size (Table 4) in all the environments.

Table 3. Combined analysis of variance (ANOVA) for hundred seed weight and seed yield of nine confectionery groundnut genotypes grown at six environments.

Source of variations	Degree of freedom	Mean squares	
		Hundred seed weight (g)	Seed yield (kg ha^{-1})
Environment (E)	5	**	**
Genotype (G)	8	**	ns
GxE interaction	40	*	*
IPCA1	12	-	*
IPCA2	10	-	ns
CV%		4.1	26.8
LSD at 5%	Environments	5.7	175.3
	Genotypes	4.3	ns

Contribution of IPCA1 for G x E interaction is 62.3%.

Table 4. Mean hundred seed weight (HSW), Seed yield (SY) Protein content (PC) and Protein yield (PY) of nine confectionery groundnut genotypes tested at six environments.

Genotypes	HSW (g)	SY (kg ha-1)	PC (%)	PY (kg ha-1)
ICGV-88390	78	1328	25.4	337.2
ICGV-88438	85	1243	27.5	342.4
ICGV-88389	84	1174	27.5	322.7
ICGV-88382	58	1220	26.1	318.2
ICGV-88358	67	1131	24.0	270.8
ICGV-88357	81	1093	23.0	251.3
ICGV-88367	85	1214	26.1	316.4
Roba	71	1171	24.9	292.1
ICGV-88361	71	1344	24.9	334.7
Mean	76	1213	25.5	309.5
SD	9.4	83.5	2.2	31.6

Where, HSW= Hundred seed weight, SY= Seed yield, PC= Protein content, PY= Protein yield, SD= Standard deviation

2. Seed yield

Combined analysis of variance showed non-significant variation among genotypes in seed yield, where the highest seed yield (Table 4) was obtained from ICGV-88361 (1344.2 kgha^{-1}) followed by ICGV-88390(1328.3 kgha^{-1}) and ICGV-88438 (1243.2 kgha^{-1}).

Environment-wise, the highest seed yield was recorded at Chefa-2006 (1944.9 kgha^{-1}) while, the lowest seed yield was obtained from Kobo-2006 (412.3 kgha^{-1}) (Table 6). This significant seed yield variation among environments could be mainly attributed to the variation in the amount of rainfall received and uneven rainfall distribution, more importantly at the critical periods, which is at seed establishment, peg formation, pod and seed development and maturity. Environments received low rainfall coupled with erratic rainfall distribution in July (Table 1) resulted in poor stand establishment. As a consequence, poor seed harvest was recorded in

environments that received low rainfall during seed establishment time, no matter how much total rainfall the environment received under the whole growing period. For instance, the total rainfall received in July was decreased by 35% at Kobo-2006 compared to Kobo-2005 (Table 1), which was the critical period for seed establishment. Thus, seed yield was dropped by 61.8% at Kobo-2006 as compared to Kobo-2005 (Table 6).

Table 6. Designations, IPCA scores and mean seed and protein yield of nine confectionery groundnut genotypes and six environments.

		IPCA scores		Mean yield (kg ha^{-1})	
Designations	Genotypes	SY	PY	SY	PY
a	ICGV-88390	-2.3	-4.9	1328.3	337.2
b	ICGV-88438	-2.0	-8.0	1243.2	342.4
c	ICGV-88389	-18.7	-9.7	1174.3	322.7
d	ICGV-88382	-10.4	3.0	1219.8	318.2
e	ICGV-88358	1.0	0.7	1130.5	270.8
f	ICGV-88357	10.8	8.2	1092.8	251.3
g	ICGV-88367	8.3	7.9	1214.2	316.4
h	Roba	13.4	-1.1	1171.0	292.1
i	ICGV-88361	-0.3	4.0	1344.2	334.7
	Environments				
A	Kobo-2005	-12.4	-0.4	1078.3	248.5
B	Mersa-2005	5.9	1.0	653.9	173.2
C	Chefa-2005	21.2	9.1	1400.7	325.8
D	Kobo-2006	3.1	1.8	412.3	103.3
E	Mersa-2006	-5.2	-15.4	1788.8	486.0
F	Chefa-2006	-12.6	4.0	1944.9	520.3

Where, IPCA= Interaction Principal Components, SY= Seed yield and PY= Protein yield

Therefore, the stress at the juvenile stage of the crop was believed to result in poor vegetative growth, as a consequence seed and protein yield were significantly reduced. On the other hand, Chefa-2006 received the highest rainfall during September and October with an increase of 39.7% over Chefa-2005 (Table 1) which is the crucial period for peg formation, seed and pod development and maturation. Accordingly, seed yield was boosted-up by 30% at Chefa-2006 in contrast to Chefa-2005. This result indicates that groundnut is very sensitive when stressed at peg formation, seed and pod development and maturation. The low seed yield at high drought stress could be justified by the malfunction of pegs to penetrate the dried soil, coercing them to be exposed to dry wind and high temperature and aborted. Moreover, pod and seed developments and maturity were also extremely impaired. Similar to the current finding, Craufurd *et al.* (2003) reported the sensitivity of groundnut at high temperature, resulting in pegs and pod yield reduction.

AMMI analysis of variance (Table 3) exhibited significant variation ($p<5\%$) in GxE for seed yield, inferring the presence of differential responses of genotypes over different environments. The crossing-over effect of genotypes and environment necessitates to stratify environments to nearly homogenous mega-environment and to single-out "which-won-where" (Gauch and Zobel, 1997). This result is in agreement with the previous research report of Inamullah *et al*. (2006) who found significant differences among the testing environments and genotype x environment interaction.

3. Protein content and protein yield

In addition to seed size and SMS, seeds with low oil content, high protein and sugar contents are also the most important quality attributes to meet the standards for international trade (Rajgopal *et al,* 2000). Accordingly, genotypes varied in protein content ranging from 23.0 to 27.5% where ICGV-88438 and ICGV-88389 gave the highest protein content (Table 4).

Similarly, genotypes appreciably differed in protein yield varying from 251.3 to 342.4 kg ha^{-1} where ICGV-88438 gave the highest protein yield followed by ICGV-88390 and ICGV-88361 (Table 3), implying the presence of genetic variation among the tested groundnut genotypes for the trait under study. Hence, it is a good opportunity to utilize such variation for protein yield improvement through selection. This result is in conformity with previous findings (Dwivedi *et al*., 1996; Savage and Keenan, 1994) elucidating significant genetic variation among confectionery groundnut genotypes for total protein.

Environment-wise, protein yield was recorded highest at Chefa-2006 and lowest at Kobo-2006 (Table 6), where protein yield was negatively corresponded to the intensity of drought stress. Similar to the justification made for seed yield, the variation in protein yield among environments could be mainly associated with the amount of rainfall received and the number of rainy days at critical periods (Table 1). Early cessation of rainfall enforced false-maturity with considerably high seed abortion, and low seed and protein yield. Sanders (1980) reported the negative influence of drought stress against the protein composition of groundnut genotypes, more importantly; protein composition gets declined when the genotypes suffered drought stress at maturity stage. Dwivedi *et al*. (1996) also reported that terminal drought affects the composition of protein and oil contents of groundnut genotypes, confirming the sensitivity of various traits of groundnut to the increasing degree of terminal drought stress.

4. Associations of characters with seed and protein yield

Correlation coefficient of seed and protein yield with other yield-related characters is presented in Table 5. Seed yield exhibited positive association with hundred seed weight ($r = 0.25^{*}$), number of matured pods plant^{-1} ($r = 0.70^{**}$) and shelling percentage ($r = 0.46^{**}$), implying positive contribution for seed yield improvement in confectionery groundnut genotypes in terminal moisture-stress environments. These traits are therefore, could be used as important yield components for confectionery groundnut seed yield improvement. The present study is partly in agreement with previous reports. Pod yield, which is positively associated with seed yield, exhibited positive significant association with hundred seed weight (Deshmukh *et al*., 1986; Korat *et al.*, 2010), number matured pods plant^{-1} (Deshmukh *et al*., 1986; Liao et *al*., 1989) and shelling percentage (Kataria *et al*., 1984; Yadava *et al*., 1984).

Table 5. Correlation coefficients of seed and protein yield with yield components in confectionery groundnut genotypes evaluated under moisture-stress areas (2005-2006).

Characters	SY	PY	HSW	MPP	SHP
Seed yield (SY)	1	-	-	-	-
Protein yield (PY)	0.97**	1	-	-	-
Hundred seed weight (HSW)	0.25*	0.22	1	-	-
Matured pods plant-1 (MPP)	0.70**	0.70**	0.03	1	-
Shelling percentage (SHP)	0.46**	0.43**	0.45**	0.49**	1

Where, SY= Seed yield, PY= Protein yield, HSW= Hundred seed weight, MPP= number of matured seeds plant^{-1} and SHP= Shelling percentage

Similarly, protein yield showed strong positive correlation (Table 5) with seed yield ($r = 0.97^{**}$), number of matured pods plant^{-1} ($r = 0.70^{**}$) and shelling percentage ($r = 0.43^{**}$). Significant and positive associations of these characters with protein yield suggested that any improvement for these traits might improve protein yield of confectionery groundnut in terminal moisture-stress areas. Similarly, shelling percentage exhibited significant positive association with hundred seed weight ($r = 0.45^{**}$) and number of matured pods plant^{-1} ($r = 0.49^{**}$). Therefore, shelling percentage, number of matured pods plant^{-1} and hundred seed weight could be used as indirect selection criteria for simultaneous improvement of seed and protein yield in confectionery groundnut variety development under terminal moisture-stress environments. Korat *et al.*, (2010) reported hundred seed weight was among the most important yield contributing characters in groundnut.

In the present study, the strong positive correlation between seed and protein yield deviated from the previous findings of non-stressed environments. In

ideal environment where water deficit is not the major limiting factor for groundnut production, seed and protein yield had negative association. The probable reasons for the deviation of the current result from previous findings could be varietal difference, timing and intensity of drought stress or the difference in gene expression profile in drought-stress environment. Normally, when plants face biotic and abiotic stresses, some genes might be induced up- or down- regulated. It is also a common phenomenon to observe high temperature stress when the soil water level gets declined. Therefore, though it requires transcriptomics analysis for confirmation, the strong positive and significant correlation between seed and protein yield in terminal drought stress might be hypothesized as the up-or down- regulation of drought stress responsive genes that have pleiotropic effects on both seed and protein yield. Hence, stress responsive genes might possibly up-regulate both seed and protein yield related genes simultaneously or down-regulate the oil content-related genes, hence favouring for seed and protein yield related genes to be turn-on. This logical justification is in support of previous research findings. Green (1986) and Golombek *et al*. (1995) reported the reduction of oil content at high temperature during seed filling stages. Holley and Hammons (1968), Tai and Young (1975), Dwivedi *et al.* (1996) reported the presence of significant negative correlation between protein and oil content where the relative protein composition was improved at the expense of oil content.

5. Stability and clustering analysis

5.1. Stability of genotypes for seed and protein yield

5.1.1. Seed yield

The G×E interaction was further partitioned into IPCA1 and IPCA2, of which IPCA1 component was significant and accounted for 62.3% of the total G×E interaction sum of squares (Table 3). IPCA score of a genotype is an indication of stability over diverse environments. The higher the IPCA score of a genotype, either negative or positive, the more specifically adapted the genotype is. The more the IPCA scores approximate to zero, the more stable the genotype is over all the environments (Crossa *et al*., 1990). Thus, based on the mean seed yield and IPCA scores, genotypes and environments were plotted on a biplot graph. Genotypes and environments positioned at the right side of the ordinate yielded above average seed yield while those placed at the left side of the ordinate yielded below average seed yield. ICGV-88361 exhibited small IPCA value with above average seed yield (Table 6 and Fig.1) thus, plotted near the x-axis on the biplot graph,

implying the presence of minimum GxE interaction. On the other hand, ICGV-88367 and ICGV-88382 had higher IPCA values with above average seed yield, thus plotted away from the abscissa, indicating the sensitivity of the genotypes to variable environments. Hence, these genotypes had specific adaptation to relatively potential environments.

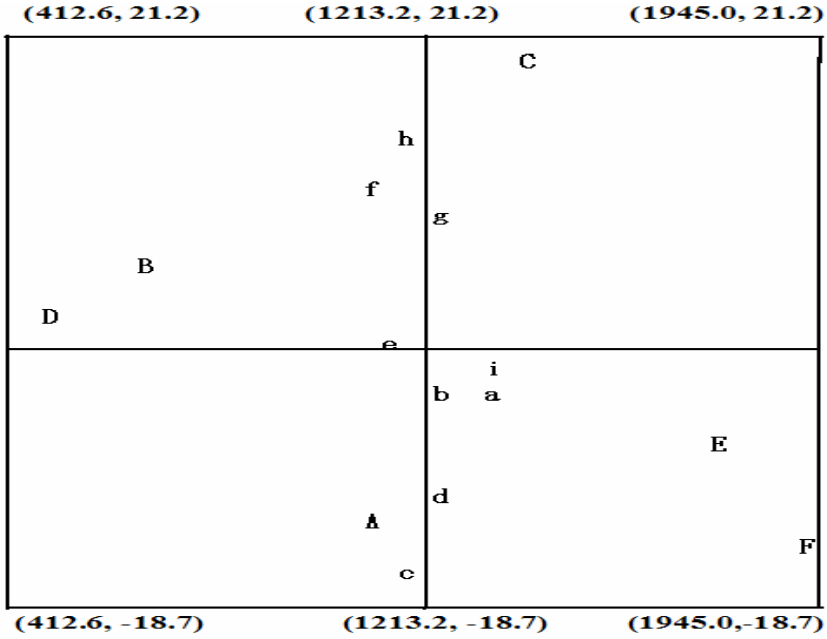

Fig. 1. Assignment of genotypes plotted as a,b,c, etc and environments as A,B,C, etc in biplot graph using **mean seed yield** (412.6 to 1945.0 kg ha^{-1}) and **IPCA axis scores** (-18.7 to 21.2).

Environment-wise, high IPCA scores were revealed at Chefa testing site for both 2005 and 2006 cropping seasons, signifying Chefa could discriminate genotypes in terms of genetic main effect. Favorable environments should have larger IPCA scores, which is an indication of more discriminative power for the genotypes (Gauch and Zobel, 1997; Ilker *et al*., 2009).

5.1.2. Protein yield

Protein yield, being quantitative trait, is strongly affected by environmental factors. Thus, identifying the winning genotype for each environment is imperative to maximize protein yield in confectionery groundnut. Based on the IPCA scores and mean protein yield of genotypes and environments

(Table 6), biplot stratified genotypes and environments to the biplot graph (Fig. 2). ICGV-88438, ICGV-88390 and ICGV-88389 gave above average protein yield plotted away from the x-axis at the first quadrant of the graph along with Mersa-2006, revealing the presence of specific adaptation to Mersa and other similar areas. On the other hand, ICGV-88361, ICGV-88382 and ICGV-88367 gave above average protein yield, thus plotted at the fourth quadrant of the graph along with Chefa-2005 and Chefa-2006. The genotypes were found responsive to potential environment and specifically adaptable to Chefa and similar environments. ICGV-88358 exhibited minimum sensitivity to environmental fluctuations. However, protein productivity of ICGV-88358 is below average and hence can't be recommended for production. On the other hand, ICGV-88361 consistently exhibited the highest protein yield relatively with low IPCA scores. Thus, ICGV-88361 was identified superior genotype that is able to adapt to variable environments with reasonable protein fluctuation. A genotype is said to be stable and desirable if it performs well relative to other genotypes under adverse environmental conditions and if it has the ability to respond to favorable environments (Eberhart and Russell, 1966).

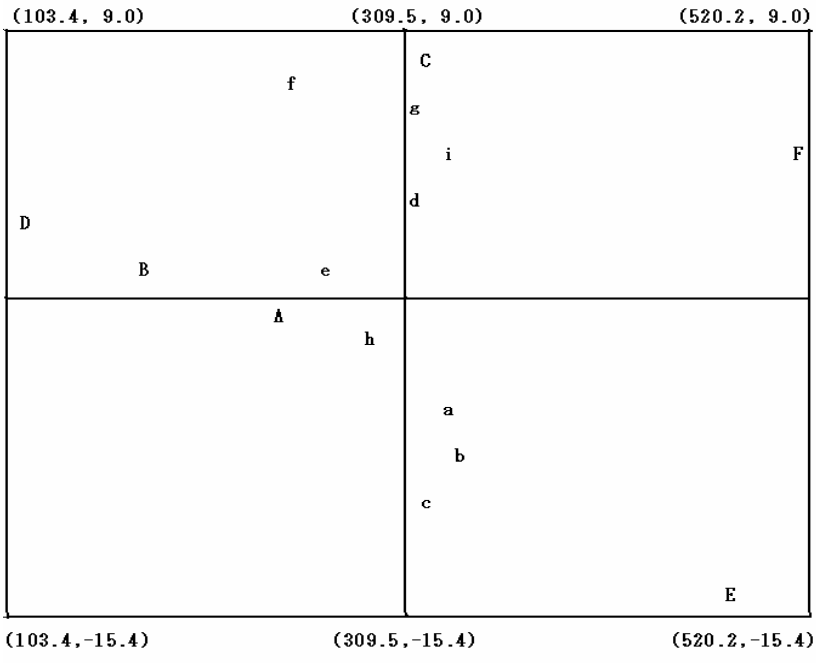

Fig. 2**.** Assignment of genotypes plotted as a,b,c, etc and environments as A,B,C, etc in biplot graph using **mean protein yield** (103.4 to 520.2 kg ha^{-1}) and **PCA axis scores** (-15.4 to 9.0).

Environment-wise, it was observed that Kobo-2005, Kobo-2006 and Mersa-2005 gave below average protein yield, where protein yield was decreased as the severity of drought increased (Fig.2). On the other hand, Chefa-2005 and Chefa-2006 plotted at the fourth quadrant of the graph showing the environment was relatively favourable for confectionery groundnut production. In a nutshell, protein yield showed a drastic decreasing trend as the severity of drought got worse. Dwivedi *et al.* (1993) and Mozingo *et al.* (1988) reported the influence of location, cultivar and season, particularly soil moisture and temperature during crop growth and seed maturation on seed quality.

5.2. Clustering of genotypes and environments

5.2.1. Clustering of genotypes

Based on seed yield and yield related traits, genotypes were grouped into three clusters (Table 7). Cluster-I, with an intra-cluster distance (D^2=46), comprised four confectionery groundnut genotypes (ICGV-88390, ICGV-88361, ICGV-88382 and ICGV-88367). This cluster is generally characterized with having high mean seed yield (1277 kg ha^{-1}), high protein yield (327 kg ha^{-1}), high number of matured pods $plant^{-1}$ (25.9), relatively small seed size (73 g HSW^{-1}) and high shelling percentage (59.6%). Cluster-II encompassed three groundnut genotypes (ICGV-88438, ICGV-88389 and ICGV-88358) possessing intra-cluster distance (D^2=27). Genotypes grouped under cluster-II, epitomized with average characteristics for seed yield (1183 kg ha^{-1}), protein yield (312 kg ha^{-1}), number of matured pods $plant^{-1}$ (24.5) and shelling percentage (57%) and bold seed size (78.8 g HSW^{-1}). Cluster-III exhibited the lowest intra-cluster distance (D^2=13), implying genotypes grouped under this cluster showed some relatedness. Cluster-III consisted of two groundnut genotypes (ICGV-88357 and *Roba*) having the least mean seed yield (1132 kg ha^{-1}), protein yield (kg ha^{-1}), few number of matured pods $plant^{-1}$ (22.1), average seed size (76.8 g HSW^{-1}) and low shelling percentage (53.5%).

Table 7. Clustering of genotypes, intra-cluster distances (**bolded diagonal values**) and inter-cluster distances (off diagonal values) and mean cluster values for seed yield and yield related traits.

Cluster	Genotypes $cluster^{-1}$	Intra- and Inter-cluster distances			Mean values of traits $cluster^{-1}$				
		I	II	III	SY	PY	MPP	HSW	SHP
I	a, d, g, i	**46**	173	164	1277	327	25.9	73.0	59.6
II	b, c, e		**27**	106	1183	312	24.5	78.7	57.0
III	f, h			**13**	1132	272	22.1	75.8	53.5

Where SY= Seed yield (kg ha^{-1}), PY= Protein yield (kg ha^{-1}), MPP= Number of matured seeds $plant^{-1}$, HSW= Hundred seed weight and SHP= Shelling percentage.

On the other hand, the highest inter-cluster distance (D^2 =173) was recorded between cluster-I and cluster-II (Table 7). Crossing of distantly related genotypes possessing useful traits could complement each other and would yield transgressive segregants with good combination of traits. Therefore, crossing of genotypes from cluster-II (ICGV-88438 or ICGV-88389) with cluster-I (ICGV-88390 or ICGV-88361) could yield good combination of segregants having high seed yield, high protein yield, high shelling percentage and bold seed size. In agreement with the current finding, Arega *et al.* (2010) reported genetically divergent genotypes in durum wheat possessing good combination of complementary traits that can be used as parents for hybridization and are able to yield superior progenies at segregating generations. Increasing parental distance implied a greater number of contrasting alleles at the desired loci, and then to the extent that these loci recombine in the F_2 and F_3 generations following a cross of distantly related parents, the greater will be the opportunities for effective selection for yield (Ghaderi *et al.*, 1984).

5.2.2. Clustering of environments

The six environments are generally clustered into two mega-environments, comprising three homogenous environments each. Mega-environment-I consisted of Kobo-2005, Mersa-2005 and Kobo-2006; which was generally characterized with low annual rainfall within the growing season (Table 1), high temperature and low relative humidity. Thus, the performance of confectionery groundnut genotypes for seed and protein yield was very poor. On the other hand, Chefa 2005, Mersa-2006 and Chefa 2006 were clustered under mega-environment-II, which was identified with relatively better rainfall amount and distribution. Thus, the response of genotypes was explicitly in favor of mega-environment-II and fairly expressed their genetic potential for the traits considered.

However, Mersa is clustered at both mega-environment-I and -II, indicating that clustering of environments may not be directly corresponded to geographical locations. Environment refers to the interaction of all biophysical factors involved at a certain location that have direct or indirect effect on the adaptation and performance of an organism. Of the three testing sites, Mersa exhibited strong and unpredictable environmental fluctuations, thus clustered at both mega-environment-I and -II. Therefore, Kobo and Chefa could be used as a testing site for future groundnut breeding, representing severely moisture stressed and relatively potential environments, respectively. Gauch and Zobel (1997) recommended the need

to use mega-environment analysis to group diverse environments into nearly homogeneous sub-regions having similar GxE interactions. Stratification of heterogeneous environments into smaller, more homogenous sub-regions is the primary strategy in developing specifically adapted improved varieties (Mohammadi *et al.*, 2007).

CONCLUSION

To maximize production and productivity of confectionery groundnut at different environments, selection of best adapted groundnut genotype possessing superior agronomic and quality traits is vital. In northeastern Ethiopia, farmers usually faced yield fluctuation owing to unpredictable and terminal moisture stress. Thus, identifying stable groundnut genotype that can do well across environments is the best option to minimize the risk of yield inconsistency. However, it is hardly easy to find genotype that can do well across diverse environments. This necessitates screening out specifically adapted genotype for each environment. Identifying specifically adapted genotype could also answer the problem of yield instability, which results from environmental fluctuation.

Hence, genotype ICGV-88361 was found stable for both seed and protein yield across environments. The current research result showed strong positive correlation between seed and protein yield in moisture-stress environments, which deviates from previous research reports. The probable reason might be the difference in varieties used, the intensity and time of drought stress occurred and the expression of stress responsive genes that have simultaneous effect on both seed and protein yield.

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REFERENCES

Adugna Wakjira and Elias Urage. (1995). Stability of pod yield in groundnut. *Sebil* 24-29.

Agrobase. (1999). The database management and analysis system for plant breeders and agronomists. Agromix software, Inc. Winnipeg, Manitoba, Canada.

Arega Gashaw, Hussien Mohammed and Singh, H. (2008). Analysis of genetic divergence in durum wheat (*Triticum durum* Desf.) and selection of elite parents for hybridization. *Ethiop. J. Biol. Sci.* **7**(2): 111-121.

Craufurd, P.Q., Prasad, P.V.V, Kakani, V.G., Wheeler, T.R. and Nigam, S.N. (2003). Heat

tolerance in groundnut. *Field Crop. Res.* **80**: 63-77

Crossa, J. (1990). Statistical analysis of multi-location trials. *Adv. Agron*. **44**: 5585.

Dabholkar, A.R. (1992). **Elements of Biometrical Genetics**. New Delhi.

Dalby, A. and Tsai, C.Y. (1975). Acetic anhydride requirements in the colorimetric determination of tryptophan. *Anal. Biochem.* **63**: 283-285.

Dwivedi, S.L., Jambunathan, R., Nigam, S.N., Raghunath, K., Shankar, K.R. and Agabhushanam, G.V.S. (1990). Relationship of seed mass to oil and protein contents in peanut *(Arachis hypogaea* L.). *Peanut Science* **17**: 48-52.

Dwivedi, S.L., Nigam, S.N., Jambunathan, R., Sahrawat, K.L., Nagabhushanam, G.V.S. and Raghunath, K. (1993). Effects of genotypes and environments on oil content and oil quality parameters and their correlations in peanut (*Arachis hypogaea* L.). *Peanut Science* **20**: 84-89.

Dwivedi, S.L., Nigam, S.N., Nageswara Rao, R.C., Singh, U. and Rao, K.V.S. (1996). Effect of drought on oil, fatty acids and protein contents of groundnut (*Arachis hypogaea* L.) seeds. *Field Crop. Res.* **48**: 125-133.

Eberhart, S.A. and Rusell, W.L. (1966). Stability parameters for comparing varieties. *Crop Sci.* **6**:36-40.

Elias Urage and Assefa Zeleke (2005). Genotype x Environment interaction and stability of elite groundnut (*Arachis hypogaea* L.) varieties in North Omo Zone. *Sebil* 63-66.

FAO (Food and Agriculture Organization of the United Nations) (2003). Food energy–methods of analysis and conversion factors. FAO Food and Nutrition paper 77. Report on a technical workshop 3-6 December, 2002, Rome, Italy.

Gauch, H.G. and Zobel, R.W. (1997). Identifying mega-environments and targeting genotypes. *Crop Sci.* **37**:311-326.

Gemechu Keneni, Belay Simane and Getinet Gebeyehu (1999). Genetic variability in groundnut. *Sebil* **8**: 42-47.

Genstat (2007). **Genstat discovery**. Ed. 3. Lawes Agricultural Trust, Rothamsted, UK.

Ghaderi, A., Adams, M.W. and Nassib, A.M. (1984). Relationship between genetic distance and heterosis for yield and morphological traits in dry edible bean and faba bean. *Crop Sci.* **24**: 37-42.

Golombek, S.D., Sridhar, R. and Singh, U. (1995). Effect of soil temperature on the seed composition of three Spanish cultivars of groundnut *(Arachis hypogaea* L.). *J. Agr. Food Chem.* **43**: 2067-2070.

Gomez, A.K., and Gomez, A.A. (1984). Statistical Procedures for Agricultural Research. 2nd ed. John Wiley and Sons. Inc., New York. 680 p.

Green, A.G. (1986). Effect of temperature during seed maturation on the oil composition of low-linoleic genotypes of flax. *Crop Sci.* **26**: 961-965.

Holley, K.T. and Hammons, R.O. (1968). Strain and seasonal effects on peanut characteristics. Research bulletin No. 32, Georgia Agri. Exp. Sta., Tifton, GA, pp 5-27.

Ilker, E., Aykut, T, F., Caylak, O., Tosun, M. and Ozmen, I. (2009). Assessment of genotype x environment interactions for grain yield in maize hybrids using AMMI and GGE BIPLOT analysis. *Turk. J. Field Crops* **14**(2): 123-135.

Inamullah, H., Ahmad, F., Mohammad, G., Hassan, S. and Gul, R. (2006). Diallel analysis of the inheritance pattern of agronomic traits of bread wheat. *Pakistan J. Bot.* **38**(4): 1169-1177.

Korat, V.P., Pithia, M.S, Savaliya, J.J., Pansuriya, A.G., Sodavadiya, P.R. (2010). Studies on characters association and path analysis for seed yield and its components in

groundnut (*Arachis hypogaea* L.). *Legume Res.* **33**: 211-216

Mohammadi, R., Mohammad, A., Akbar, S. and Amir, D. (2007). Identification of stability and adaptability in advanced durum genotypes using AMMI analysis. *Asian J. Plant Sci.* **6**(8): 1261-1268.

Mohammed, F., Abdalla, O.S., Rajaram, S. and Yaljarouka, A. (2011). Additive main effect and multiplicative analysis of synthetic-derived bread wheat under varying moisture regimes. *Pakistan J. Bot.* **43**(2): 1205-1210

Mozingo, R.W., Coffelt, T.A. and Wynne, J.C. (1988). Market grade effects on fatty-acid composition of five peanut cultivars. *Agron.J* **80**: 73-75.

Michigan State University (1988). User's guide to MSTAT-C: A software program for the design, management, and analysis of agronomic research experiment. USA.

Rajgopal, K., Chandram, K., Misra, J.B., Bhalodia, P.K. and Mathur, R.S. (2000). Evaluation of bold-seeded groundnut accessions for confectionery attributes. *International Arachis Newsletter* **20**: 18-20.

Reddi, S.G.H. (1988). Cultivation, storage and marketing. In*:* **Groundnut**, pp. 318-383 (Reddy, P.S., ed.). India Council of Agricultural Research, New Delhi.

Sanders, T.H. (1980). Fatty acid composition of lipid classes in oils from peanuts differing in variety and maturity. *J. Am. Oil Chem. Soc.* **57**: 12-15.

Savage, G.P. and Keenan, J.I. (1994). The composition and nutritive value of groundnut kernels. In: **The groundnut crop: A scientific basis for improvement,** pp. 173-213 (Smart, J., ed.). Chapman and Hall, London,

Singh, R.K. and Chaudhary, B.D. (1985). **Biometrical methods in quantitative genetics analysis.** Kalyani Publishers, New Delhi-Ludhiana.

Solomon Admassu, Mandefro Nigussie and Habtamu Zelleke (2008). Genotype-Environment interaction and stability analysis for grain yield (*Zea mays* L.) in Ethiopia. *Asian J. Plant Sci.* **7**: 163-169.

Tai, Y.P. and Young, C.T. (1975). Genetic studies of peanut proteins and oils. *J. Am. Oil Chem. Soc.* **52**: 377-385.

The United Nations University (1980). Analytical methods for the determination of nitrogen and amino acids in foods. In: **Nutritional evaluation of protein foods**, (Pellett, P.L. and Young, V.R., eds.). A report of a working group sponsored by the International Union of Nutritional Sciences and the United Nations University World Hunger Program. The United Nation University, Japan.

Vargas, M. and Crossa, J. (2000). The AMMI analysis and graphing the biplot. Biometrics and statistics Unit. CIMMYT.