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Genotype by Environment Interaction and Stability Analysis in Sunflower Genotypes

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Abstract: The study was conducted during the main cropping season of 2019/2020 to evaluate advanced sunflower genotypes for its stability over multiple environments. The study was carried out at six locations namely; Holeta, Debrezeit, Fenoteselam, Arsi Negele, Kulumsa and Ambo. Randomized complete block design with four replication was used in layout of the experiment. Data were collected for seed yield and yield related components and subjected to analysis using R-software. AMMI and GGE-biplot were used to estimate the stability of genotypes across test environments. The results from AMMI analysis of variance showed that there is significant difference for environment, genotype and genotype by environment interaction for seed yield. AMMI analysis of variance for oil content revealed the significant differences for genotypes, genotype by environment interaction and non-significant for environment. The Gollob's test showed that total variation greater than 70% was explained together by PC1 and PC2 for both seed yield and oil content. AMMI 1 bi-plot analysis for seed yield revealed that E1 and E5 was high seed yielder than others and genotypes, G4, G5 and G2 were stable genotypes relative to others. AMMI2 Bi-plot showed genotypes G3, G1, G6 and G8 were stable for seed yield whereas, G7, G8 and G1 were stable for oil content.

Keywords: AMMI, Genotype X Environment Interaction, Stability, Sunflower, Ethiopia

1. Introduction

Sunflower (*Helianthus annuus* L.) 2n=30 is one of the most important oil crops in the world [1]. The origin of the crop is thought to be North America from where it was introduced to Europe and then to Africa. The sunflower use as an oil crop started in the 1960s; however, intensive research work on the crop was started in the 1980s with the production of hybrid seeds. Sunflower which is primarily cultivated for edible oil has several industrial applications such as a basic component for polymer synthesis, biofuel, emulsifier or lubricant [2]. It is also used as meal for livestock[2] and has esthetic and ornamental values [3]. As rising of world human population increases the demand for food and causes hunger, starvation and disease outbreak there is a need to improve crops genetic potential through plant breeding for maximum food production [4].

Plant breeding is essentially the selection of plants among germplasm in the target environment. The development of genetic material is considered to be an essential part of enhancing the genetic potential of cultivated sunflower. The genotype by environment interaction is very important for plant breeders to identify the general and specific adaptability of the genotypes in crop plant improvement [5-7]. AMMI and GGE-biplot are an important and widely used by different scholars to identify the most stable genotype and environment [8-12] Yield enhancement in crop genetic resources are currently of great interest to ensure food security.

Therefore it is important to consider the target environment and best genotypes through genotype by environment interaction analysis.

2. Materials and Methods

2.1. Experimental Materials and Study Locations

A total of eight genotypes including one standard check (Ayehu) were grown at six locations namely, Holeta, Ambo, Debrezeit, kulumsa, Arsi Negelle and Finoteselam (Table 1).

Table 1. Experimental Materials and Study Locations.

Treatments	CODE	ENVIRONMENT	CODE
Adadi-2	G1	Holetta	E1
Adadi-1	G2	Ambo	E2
VSFH-2074	G3	Fenotselam	E3
VSFH-2006	G4	Debrezeit	E4
VSFH-180	G5	Kulumsa	E5
PR63LL06	G6	Arsi Negelle	E6
R-black	G7		
Ayehu	G8		

2.2. Experimental Design and Trial Management

The experiment was laid out using randomized complete block design with four replications. Five rows of 3m length with the spacing of 25cm between plants and 75cm between rows was used to raise the crop. The seeds of the genotypes were sown by dibbling method putting two seeds per hill. Hand thinning to one plant per hill was done after emergence at 4-6 leaf stage. All recommended agronomic practices were followed throughout the growing period of the crop. The three central rows were harvested for all plots of each entry at each location.

3. Results and Discussion

The AMMI analysis of variance showed that there is highly significant differences ($p<0.01$) for environment, genotype and GEI (Table 2). Most of the sum of squares was explained by genotype by environment interaction followed by genotype and then environment indicating that most of the causes in the variation of yield were due to interaction of genotype by environment. Highly significant differences were observed for genotype and genotype by environment interaction whereas the environment was non-significant for oil content (Table 2).

The Gollob's test for seed yield showed that the first IPCA was significant whereas the remaining five IPCAs were non-significant (Table 2). To remove the noise six PCA were fitted to the interaction matrix GE. PC1explained 50.93% of total variation and PC2 proportioned 27.19%. PC1 and PC2 together explained 78.13 % of the variability. Whereas; for oil content genotype PC1 and PC2 explained 49.22 % and 23.41 % respectively (Table 3).

Table 2. AMMI Analysis of variance for mean seed yield (kg/ha) of 8 sunflower genotypes tested across six environments during 2019/20.

	DF	SS	MS	Explained %	Cumulative %	F
ENV	5	24569347.6	4913870**	26.68368	26.68368	18.25464
GEN	7	30603726.8	4371961**	33.23735	59.92103	16.24149
ENV*GEN	35	36903234	1054378**	40.07897	100	3.91693
PC1	11	5844541.46	531322*	50.93521	50.93521	1.96322
PC2	9	3120212.05	346690.2^{ns}	27.19266	78.12787	1.28101
PC3	7	1268175.57	181167.9^{ns}	11.05216	89.18003	0.66941
PC4	5	823245.004	164649^{ns}	7.17458	96.35462	0.60837
PC5	3	354925.08	118308.4^{ns}	3.09317	99.44779	0.43715
PC6	1	63363.1045	63363.1^{ns}	0.55221	100	0.23412
Residuals	411	110634908	269184.7	0	0	

**=highly significant at 0.01,*=significant at 0.05, ns= non-significant, DF=degree of freedom, SS=sum of squares, MS=mean square

Table 3. AMMI Analysis of variance for mean oil content (%) of 8 sunflower genotypes tested across six environments during 2019/20.

	DF	SS	MS	Explained %	Cumulative %	F
ENV	5	43.02725	8.60545ns	2.59819	2.59819	0.84837
GEN	7	859.8227	122.8318**	51.92021	54.5184	12.10936
ENV*GEN	32	753.1964	23.53739**	45.4816	100	2.32043
PC1	11	184.2542	16.75038	49.21705	49.21705	1.64426
PC2	9	87.64558	9.7384	23.41145	72.6285	0.95594
PC3	7	62.78264	8.96895	16.77018	89.39868	0.88041
PC4	5	24.38467	4.87693	6.51351	95.91219	0.47873
PC5	3	13.15832	4.38611	3.51479	99.42698	0.43055
PC6	1	2.14524	2.14524	0.57302	100	0.21058
Residuals	243	2464.881	10.14354	0	0	

**= significant at 0.01,, *=significant at 0.05, ns=non-significant, DF=degree of freedom, SS=sum of squares, MS=mean square

3.1. AMMI 1. Bi-Plot Analysis for Seed Yield and Oil Content

In the AMMI1 bi-plot model the IPCAs scores for genotypes and environments were plotted against the mean seed yield. The genotypes or environments on the right side of the midpoint of the axis have high seed yield than those on the left side. Accordingly environments E1 and E5 have similar interaction and gives high yield than others and they could be treated as high seed yield potential locations (Figure 1). On the other hand environments E1, E2, E3 and E6 were found on the left quadrant and regarded as low yield locations (Figure 1)

Genotypes with IPCA1 scores close to zero express broad adaptation and the larger score depicted narrow adaptation [13]. The greater the IPCA scores, negative or positive the genotypes are specifically adapted to certain environment (large interaction). The more the IPCA scores close to zero

the more stable or adapted over all environments sampled [14]. Hence genotype G4, G5 and G2 were stable and well adapted. They exhibited small interaction indicating these genotypes were less influenced by the environments.

3.2. AMMI 2. Bi-Plot Analysis for Yield and Oil Content

Genotypes located closer to the bi-plot origin are less responsive and had broad adaptation [15]. AMMI2 bi-plot for seed yield presented in (Figure 2) indicated that, genotypes G3, G1, G6 and G8 were stable plotted relatively close to each other and center or origin. On the other hand Genotypes G7, G2, G5 and G4 were far from the center of the bi-plot indicating that they are unstable for seed yield (Figure 2). The AMMI 2 bi-plot for seed yield indicated in Figure 2 showed that, E5, E3, and E4 are far from the origin indicating that these environments contribute higher amount of variation to the total Genotype by environment interaction.

The AMMI-2 bi-plot for oil content showed that G7, G8 and G1 were stable relative to each other as they are close to the midpoint (Figure 3). G5, G2, G3, G4 and G6 are far from the center showing that they are unstable for oil content (Figure 3).

3.3. Evaluation for Genotypes and Environments Using GGE-Bi-Plot Analysis for Seed Yield

The partitioning of genotype by environment interaction for seed yield using GGE-bi-plot showed that IPCA1 and IPCA282.27 % (PCA1=53.91, PCA2=28.36) of total variation for seed yield (Figure 4). GGE-bi-plot view showed that genotype G4 is the ideal and most stable across variable environment whereas, genotypes far from the ideal genotype G1, G6, G7, G3 and G8 are unstable genotypes (Figure 4).

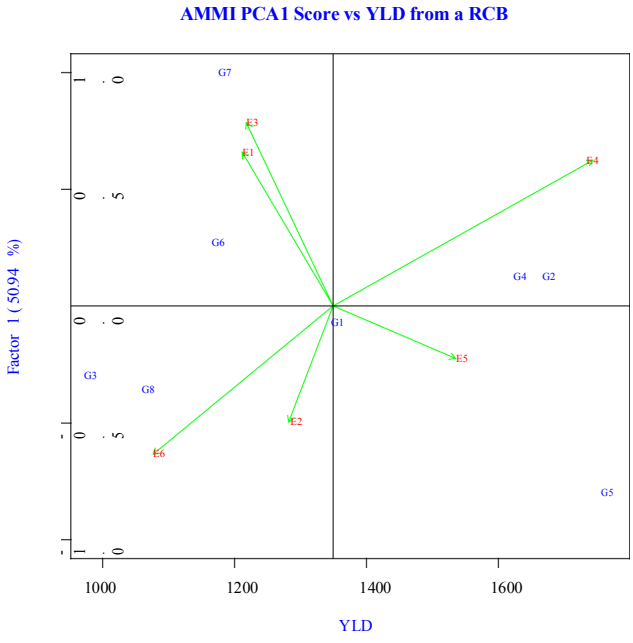

Figure 1. *AMMI 1 bi-plot (PC1 vs. PC2) model for seed yield (kg/ha) showing the means of genotypes and environments against IPCA1 and IPCA2 scores.*

Environments with longer vectors are known to be discriminative of the genotypes than with short vectors [16]. Hence, GGE-bi-plot in this study showed that E6, E4 and E 5are most discriminating environments as they have long environmental vectors. E2 and E3 had the shortest vector and considered as an ideal environments as they show inability to discriminate genotypes based on their genotypic performance.

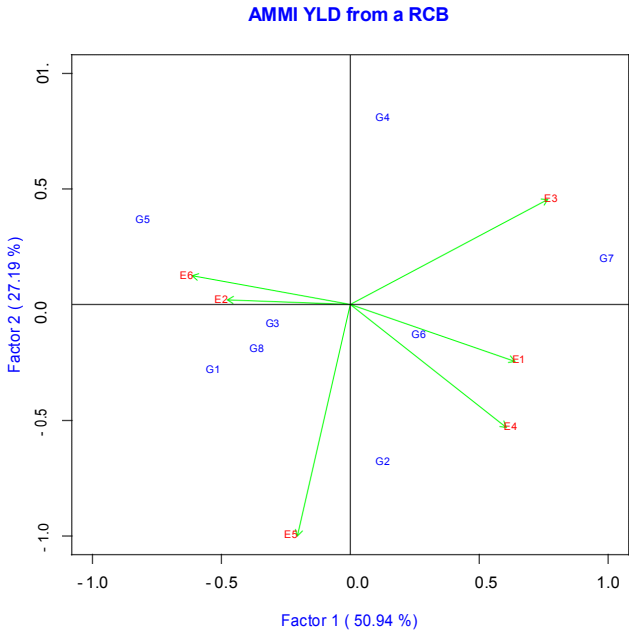

Figure 2. *AMMI 2 bi-plot (PC1 vs. PC2) model for seed yield (kg/ha) showing the means of genotypes and environments against IPCA1 and IPCA2 scores.*

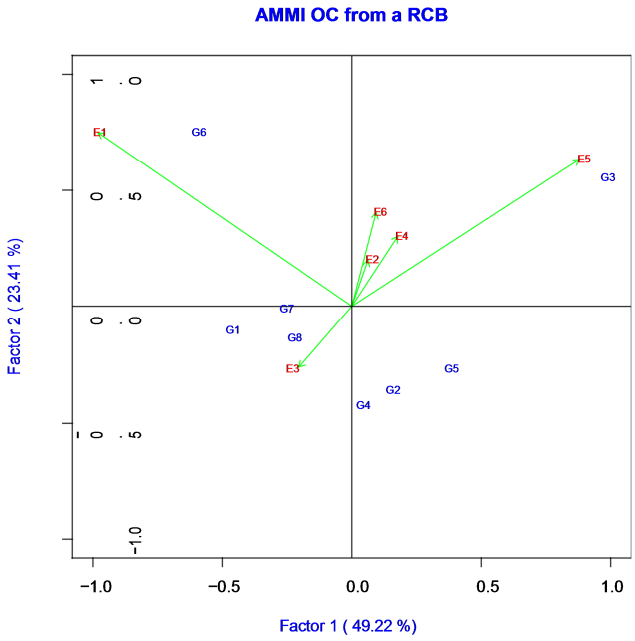

Figure 3. *AMMI 2 bi-plot (PC1 vs. PC2) model for oil content (%) showing the means of genotypes and environments against IPCA1 and IPCA2 scores.*

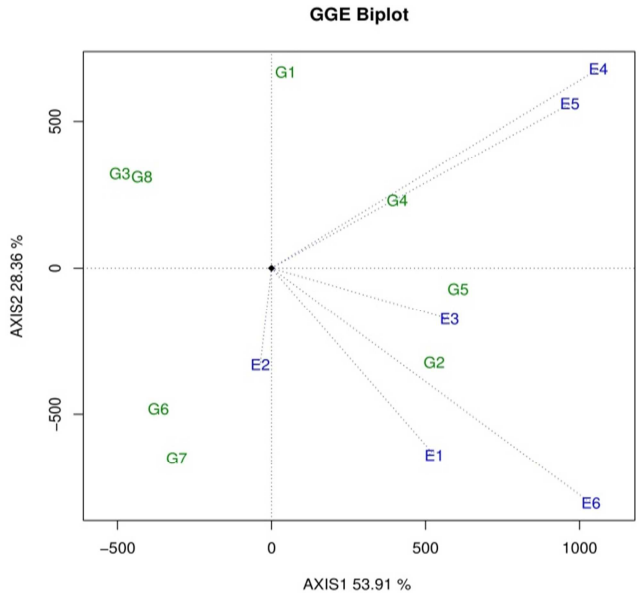

Figure 4. *Average environment axis (AEC) in view of GGE bi-plot graph for seed yield.*

4. Conclusion

The results obtained from this study revealed that the seed yield of sunflower is strongly influenced by the genotype, environment and genotype by environment interaction than oil content. The AMMI analysis showed that the genotype, environment and GXE interaction explained 33.237, 26.68, and 40.078 percent respectively for seed yield. The total explained variation of genotype, environment and genotype by environment interaction for oil content was 51.92, 2.598 and 45.48 percent respectively. The GGE-biplot analysis showed that genotype G4 is the most stable genotype and environments E6, E4 and E5 are the most discriminating environments whereas; E2 and E3 are considered as ideal environments.

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