



RESEARCH ARTICLE

Stability analysis and $G \times E$ interaction study in sunflower (*Helianthus annuus* L.) hybrids for yield across different environments using AMMI and GGE models

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Abstract

Stability analysis plays a vital role in plant breeding and this involves the evaluation of the genetic performance of genotypes under varying environmental conditions. Sunflower, a valuable oilseed crop primarily cultivated for its edible oil and confectionary purposes, is known for its high yield potential. However, the performance of sunflower is significantly influenced by genotype-environment interactions. Thereby, here in this study, a set of thirty-three hybrids along with three checks were evaluated across three different seasons, viz., *kharif* 2023, *rabi* 2023-2024, and summer 2024. Analysis on hybrid performance revealed that, *kharif* followed by *rabi* and summer was identified to be the most favourable. The AMMI biplots highlighted the stability of hybrids namely, H9, H22, H19, H23, H16, and checks C3, C1. Hence, based on their comparative performance, the hybrids viz., H13 and H24 exhibited higher yields in AMMI biplots across environments. Moreover, the GGE biplots, portrayed the higher stable performance of the check C1 and the hybrid H13 across environments. The hybrids, viz., H24, H13, and H32 were also identified for their high yield and moderate stability, making them desirable choices for further evaluation. In conclusion, from the «which won where» biplot it was indicated that the hybrids H13 and H24 were the stable cum desirable performers from all locations. Therefore, these genotypes could be forwarded for developing stable and high-yielding sunflower hybrids in future breeding programs.

Keywords: AMMI, GGE biplot, which won where, sunflower hybrids

Introduction

Sunflower (*Helianthus annuus* L.) is a significant oilseed crop grown worldwide for its edible oil and confectionary uses. It is the fourth most consumed edible oil and offers numerous health benefits compared to other oils (Bakari et al. 2024; Above and Edo 2024). The demand for premium sunflower seeds in the global market has risen due to its versatility. Despite its cross-pollination nature, traditional breeding continues to rely on open-pollinated varieties to maximize heterosis. Moreover, the introduction of cytoplasmic male sterile lines has significantly increased the importance of breeding for hybrids with a structured CGMS system. This leads to the exploitation of heterosis through hybrid breeding programme. This has eventually led to an increase of sunflower yield from 18 to 40 per cent.

Sunflowers are known for their wide adaptability and photo-insensitivity, allowing them to be grown in various agroclimatic regions. This versatility enables their cultivation throughout the year, across multiple seasons, and in diverse soil types and climatic conditions. However, the complex trait of seed yield is influenced by several environmental fluctuations, making the selection of hybrids ineffective

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when based solely on a single location (Shrestha et al. 2012). Therefore, the primary goal of the breeders is to develop well adapted hybrids suitable for different environments.

Evaluating the stability and performance of genotypes across different environmental conditions is crucial for identifying reliable hybrids. Various statistical methods, both parametric and non-parametric, have been developed to study the genotype × environment interactions (Kumar et al.2025). Among these methods, the AMMI (Additive Main Effect and Multiplicative Interaction) and GGE biplot have gained popularity in recent years since, it combines additive main effects to assess the average performance of hybrids across environments, along with multiplicative interaction components that capture specific interactions between genotypes and environments (Gauch 1988; Agahi et al. 2020; Singh et al. 2024). The Biplot graphs are effective tools for comparing genotype stability and adaptability to diverse environments. Further, these graphs represent the genotypes based on their principal component values as well as it includes interpretation models that visually address genotype evaluation vs. test environments (Kamal et al. 2024). Therefore, the plant breeders have found that these stability models like AMMI and GGE biplots are valuable for identifying stable hybrids across various environments (Farooq et al. 2023; Kumar et al. 2024). In a view of the above, 33 hybrids were assessed in three different seasons to identify stable hybrids with high yields using the AMMI and GGE models.

Materials and methods

The experimental material comprised of 33 hybrids generated using three lines (COSF 6A, COSF 12A, HA 89A) and eleven testers (AKSFI 174, GMU 1000, RHA 83R-6, GP 6-374, CB 19-05, RCB 19-11, GMU 498, GMU 311, GMU 500, RHA 378, GMU 379) along with three checks viz.,COH3,DRSH1 and GK 2002 raised in Completely Randomised Block Design with three replications. The experiment was conducted in three different seasons during *kharif* 2023, *rabi* 2023-2024, and summer 2024 designated as E1, E2 and E3, respectively at the Department of Oilseeds, Tamil Nadu Agricultural University, Coimbatore. Each entry was sown in a single 5 m length row by adopting a spacing of 60 × 30 cm. The agronomic practices for good crop growth were followed during the entire crop duration. Observations were recorded for seed yield from the five randomly selected plants in each hybrid which were raised in three replications.

Statistical analysis

The Data was subjected to pooled analysis of variance, to estimate the variance among environment, genotypes, replication, and genotype x environment. This analysis was performed using R package version 4.4.1. Further, the Multivariate stability and genotype x environment interaction were analysed using AMMI and GGE biplot.

The AMMI and GGE biplot was performed using PB Tools 1.4 version of IRRI.

Results and discussion

The pooled analysis of variance showed significant the significant G x E interaction on the yield of hybrids across locations. This illustrates performance of seed yield of hybrids vary across the environments (Table 1). Similar GxE interaction for seed yield in sunflower hybrids were studied by Farooq et al. 2023; Ma’Ali et al. 2019; Gholizadeh et al. 2022.

The AMMI biplot 1 depicts the interaction between the PCA 1 and the seed yield for hybrids (Fig. 1). The biplot illustrates the genotypes that have excelled in an environment, positioned away from the midpoint of the graph. Consequently, genotypes with higher yield values will be situated further from the centre of the biplot. However, those genotypes that are closer to the midpoint of the biplot exhibit less interaction (IPCA1=0) with the environment and are therefore considered to be stable genotypes (Ma’Ali et al. 2019).The AMMI biplot 1 depicts that the E3 had the shortest vector among all. This shows that E3 had the lowest influence on the hybrids across environments. Whereas, E1 and E2 were lying in the positive quadrant and were observed to be desirable environments for the stimulating the elite performance of hybrids.Similar results were reported by(Farooq et al. 2023; Kiruba et al. 2023). Among all, the hybrid H9 and the check C3exhibited

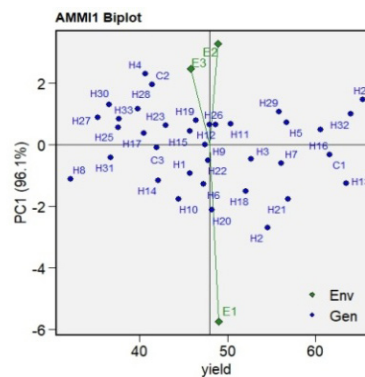


Fig. 1. AMMI biplot depicting PCA 1 vs seed yield across three environments

Table 1. AMMI analysis of variance for seed yield of 33 hybrids in three different seasons

Source	df	MSS	%TSS
Environment (E)	2	240.20**	1.72
Replication(R)	2	14.08**	0.15
Genotype(G)	35	472.48**	59.27
Gx E	70	73.88**	18.54
Error	105	4.72	1.78

lower interaction (IPCA=0) and were placed near the origin of the biplot. Successively, C1 and H3 were also observed to be stable with a high mean for seed yield. The rest of the hybrids were observed to possess a higher interaction with environments. Thus, they could be recommended for specific environments. In this case, the hybrid H13 showed high mean with negative IPCA for E1 and the hybrid H24 showed high mean with positive IPCA for E2. Thereby, these

hybrids could be recommended to be cultivated in the appropriate seasons. Similar recommendations for season specific cultivation were also suggested by [Cvejić et al. 2019](#); [Farooq et al. 2023](#); [Mengistu and Abu, 2023](#).

The biplot presented here illustrates the interaction effect of genotype with the environment, specifically IPCA 1 versus IPCA 2 as shown in [Table 2](#) and [Fig. 2](#). In this visualization, the environment scores for E1, E2, and E3 are connected to

Table 2. Mean performance of seed yield for 33 hybrids and the IPCA1 and IPCA 2 values studied in different environments

Genotype	Hybrid	E1	E2	E3	Combined mean	IPCA 1	IPCA 2
H1	CSFH 23002	52.28	44.16	40.89	45.77	-0.93	-0.20
H2	CSFH 23004	71.25	47.80	44.72	54.59	-2.68	-0.48
H3	CSFH 23005	56.50	52.96	48.59	52.68	-0.45	-0.36
H4	CSFH 23006	28.57	49.23	44.18	40.66	2.29	0.00
H5	CSFH 23007	53.75	60.51	55.96	56.74	0.71	-0.18
H6	CSFH 23008	55.91	44.97	41.06	47.31	-1.28	-0.41
H7	CSFH 23009	60.84	55.91	51.84	56.19	-0.60	-0.32
H8	CSFH 23010	39.55	29.04	27.67	32.09	-1.11	0.18
H9	CSFH 23011	48.57	48.64	45.28	47.50	0.00	-0.05
H10	CSFH 23012	55.72	40.37	37.26	44.45	-1.75	-0.32
H11	CSFH 23014	47.64	53.83	49.63	50.37	0.67	-0.11
H12	CSFH 23015	45.18	50.18	48.54	47.97	0.66	0.45
H13	CSFH 23017	71.82	60.23	58.51	63.52	-1.25	0.08
H14	CSFH 23018	50.00	40.83	35.49	42.11	-1.15	-0.70
H15	CSFH 23019	44.27	47.07	45.96	45.77	0.43	0.52
H16	CSFH 23020	58.94	63.39	59.47	60.60	0.48	-0.09
H17	CSFH 23021	39.29	41.51	40.75	40.52	0.38	0.59
H18	CSFH 23022	62.00	48.99	45.31	52.10	-1.51	-0.40
H19	CSFH 23023	42.93	50.04	46.25	46.41	0.79	0.00
H20	CSFH 23024	61.54	42.16	41.02	48.24	-2.12	0.05
H21	CSFH 23025	67.92	49.13	53.61	56.89	-1.77	1.36
H22	CSFH 23027	51.82	46.73	44.73	47.76	-0.51	0.15
H23	CSFH 23059	40.54	46.16	42.29	43.00	0.62	-0.05
H24	CSFH 23062	58.27	72.22	65.91	65.47	1.46	-0.44
H25	CSFH 23063	35.08	37.03	40.64	37.58	0.56	1.60
H26	CSFH 23064	45.91	51.17	48.95	48.68	0.66	0.32
H27	CSFH 23066	31.25	39.83	34.57	35.22	0.89	-0.31
H28	CSFH 23067	34.27	45.71	39.42	39.80	1.17	-0.49
H29	CSFH 23068	50.92	61.43	55.39	55.91	1.07	-0.45
H30	CSFH 23069	30.31	43.55	35.65	36.50	1.30	-0.82
H31	CSFH 23070	40.00	35.30	34.70	36.67	-0.40	0.48
H32	CSFH 23071	59.53	69.35	63.29	64.06	0.99	-0.47
H33	CSFH 23072	34.06	42.73	36.24	37.68	0.84	-0.59
C1	COH3	64.45	60.69	59.76	61.63	-0.31	0.43
C2	DRSH 1	31.16	47.38	45.84	41.46	1.95	0.71
C3	GK 2002	43.50	41.84	40.53	41.96	-0.09	0.38
Grand mean	-	49.04	48.94	45.83	-	-	-

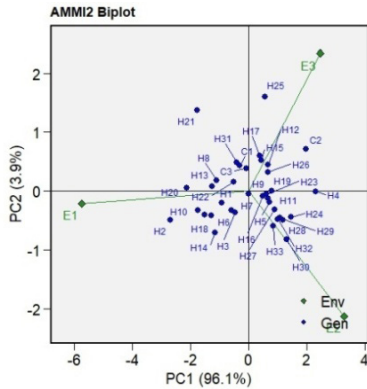


Fig. 2. AMMI Biplot depicting PCA 1 vs PCA 2 across three environments

the origin by lines. Environments with shorter lines indicate a smaller interaction between genotype and environment, and are considered to be less interactive environments. (Ansarifard et al. 2020). The results indicated that the E3 was less interactive. Further, the genotypes located close to the point zero, tended to have a less interaction and were considered to be stable across environments. Thereby, the hybrids H9, H22, H19, H23 and H16 along with the checks C1 and C3 were found with a higher IPCA 1 value closer to zero. Thus, these genotypes were considered to be stable across environments. Among all, the hybrid H25 and H30 were found to be more sensitive across environments and were found to be unreliable for adaptability. The IPCA 1 and IPCA 2 in this biplot accounted for about 96.10% and 3.90% of the total variability. Similar results for interaction effects for stability of sunflower hybrids were also reported by Farooq et al. (2023) and Mousavi et al. (2016).

GGE biplots

The GGE Biplot, which provides a genotypic view of the relationship between genotypes and test environments for seed yield, is illustrated in Fig. 3. This biplot utilizes genotype and genotype-environment ($G \times E$) interaction components on an XY graph. The first two IPCA scores are selected to represent both environments and genotypes (ref). A genotype is considered to excel in a given environment when the angle between its corresponding vectors is less than 90° , indicating acute angles (Khan et al. 2021). Here the results showed that the genotypes namely H16, H32, H5, H24 and C1, were acute to the angles between their environments E2, and E3. Further, H13 and H7 were acute in E1 respectively. Hence these hybrids and checks were found to perform better than average in E2, E3 and E1 environments, respectively (Gholizadeh et al. 2022; Hemmati et al. 2018; Ma’Ali, et al. 2019).

Subsequently, ranking of 33 hybrids along with checks across average environment based on their mean performance and stability is shown in Fig. 4. This ranking was assessed using the Average Environment coordination

(AEC) method. The average environment is represented by a circle, which is calculated using the PC 1 and PC 2 scores from all environments (Yan and Hunt 2002). In order to determine the direction of higher average grain yield, a line known as the Average Environment Axis (AEA) is drawn through the average environment and biplot origin. To ascertain the direction of higher average grain yield, a line called the Average Environment Axis (AEA) is drawn through the average environment and biplot origin. Another line, perpendicular to the AEA and passing through the origin with double arrows, signifies the stability of genotypes (Manivannan et al. 2023). An ideal genotype should possess high mean performance and high stability locating itself inside the circle of the biplot across environments (Takele et al. 2025). As a result, it is evident that the hybrids namely, H24, H32, H13, C1, H16 points to a higher mean yield across environments with above average stability in the biplot and could be recommended for further breeding trials. Selection of stable hybrids from GGE biplot based on rankings were

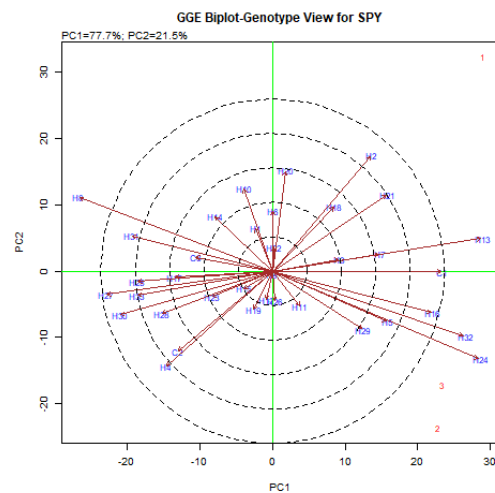


Fig. 3. GGE Biplot analysis depict genotypic view representing the relationship of genotypes with test environments

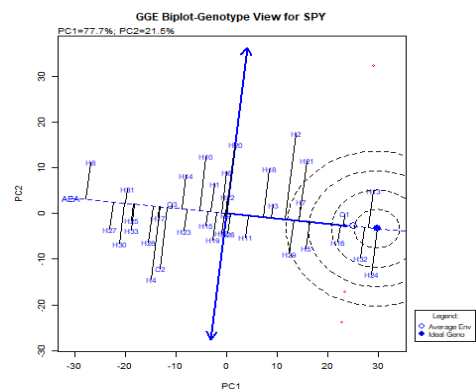


Fig. 4. Ranking of hybrids & checks across average environment based on their mean performance and stability

also performed earlier by several researchers (Farooq et al. 2023; Mousavi et al. 2016; Ma'Ali et al. 2019; Gholizadeh et al. 2022; Hemmati et al.2018).

The environmental vector view depicting the relationship among the three environments is presented in Fig. 5. The environments were connected to the biplot origin by lines called vectors which helps to find the mutual relations among the environments. The PC 1 and PC 2 components exhibited 77.70 % and 21.50% of the total variance. The angle between the two environment vectors depicts the correlation coefficient between them (Ansarifard et al. 2020; Jocković 2019; Kamal et al. 2024) thereby, the angles between the two environment vectors E2 and E3, E1 with E3, E2 with E1 were acute and hence they were observed to be correlated with each other. Similar results were reported by Mullualem et al. (2024) and Gholizadeh et al. (2022). Further, the measure of discriminating ability would be determined by the length of the environment vectors, which represents the standard deviation within each environment. This metric provides valuable insight into the effectiveness of discrimination within different environments. Thereby in this study; E1 was the most discriminating followed by E2 and E3. The distance between the vectors indicated that the E2 and E3 were lying in the same quadrant. Thus, E2 and E3 were found to have similar interaction effects and any one of these environments could be used in further breeding programs along with E1.

The success of the breeding program hinges on carefully selecting optimal environments to identify superior genotypes. Khan et al. (2021) suggested that the key factors of the test environment would be fits discriminating ability between genotypes and representativeness. This differentiation is depicted in the Fig.6. Based on the vector length of the environments, E1 had a unique interaction with the genotypes and this environment could be more desirable in selecting genotypes/hybrids to cull out unstable genotypes.

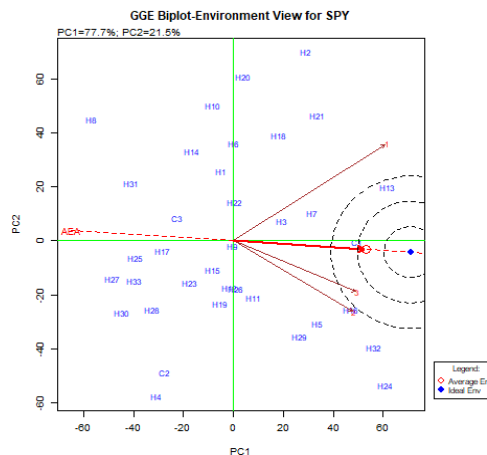


Fig. 6. GGE Biplot of Discriminateness vs Representativeness

Which won where – Polygon view for yield

The GGE biplot constructs consist of a polygon representing the G × E interaction. This polygon was formed by connecting all genotypes that are located at a distance from the origin, ensuring that all genotypes are included in the polygon (Reshma et al. 2024; Yan 2002). This is the best method to find out the interaction between the genotypes and environments and also to interpret which genotype/ hybrid has won in which environments, facilitating mega environment identification (Farooq et al. 2023; Mousavi et al. 2016; Ma'Ali et al. 2019; Gholizadeh et al. 2022 ; Hemmati et al. 2018). From the polygonal view in Fig. 7, the genotype H13 established a high yield in E1. The hybrid, H24 had a higher yield in E2 and E3. Since E2 and E3 were placed in the same quadrant in the biplot, they were considered as a mega environment and E1 was placed in the adjacent quadrant was found to be another mega environment. Thus, H13 and H24 were considered to be winning hybrids for the environments viz., E1, E2 and E3, respectively.

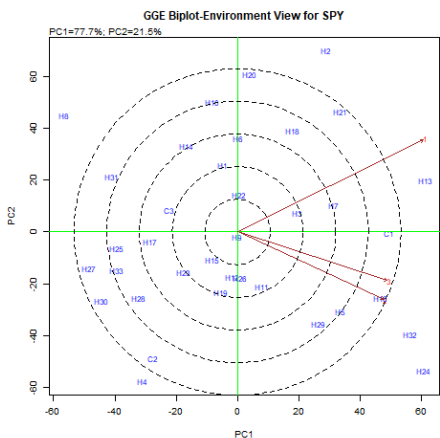


Fig. 5. Environmental vector view depicting the relationship among the three environments

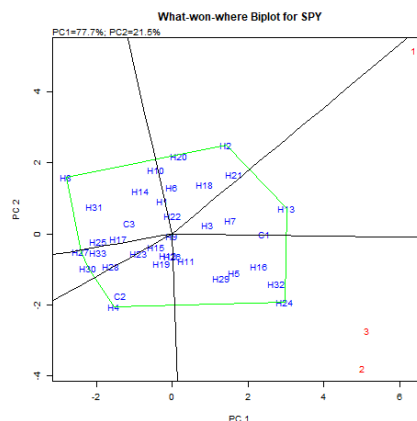


Fig. 7. What-won-Where Biplot for single plant yield across different environments

The present study showed that the combined analysis of variance has shown significant results for G x E, indicating that a substantial amount of variation was attributed due to environmental factors. Utilizing models such as AMMI and GGE can greatly enhance the accuracy and reliability of selecting superior sunflower hybrids. Upon evaluating the discriminating ability versus representativeness, it was determined that the *kharif* season was more discriminating but less representative. This environment proves to be more valuable for selecting hybrids that are well-suited to specific conditions.

Authors' contribution

Conceptualization of research (RS); Designing of the experiments (RS); Contribution of experimental materials (RS); Execution of field/lab experiments and data collection (KBS, GJ, TN); Analysis of data and interpretation (KBS, GJ, TN); Preparation of the manuscript (RS, KV).

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