Indian J. Genet. Plant Breed., (2024); 84(2): 304-307

https://doi.org/10.31742/ISGPB.84.2.21

ISSN: 0975-6906

www.isgpb.org

SHORT RESEARCH ARTICLE

Dissection of genotype x environment interaction and yield stability analysis in greengram (*Vigna radiata* L.) using AMMI and GGE biplot

A. Sheeba and P. Yogameenakshi[1*]

Abstract

Nineteen green gram [*Vigna radiata* (L.) Wilczek] genotypes were evaluated for yield stability under field conditions over three seasons. The AMMI analysis revealed that genotype TM 11007 (G3) had wider adaptation for grain yield, performing well across a wide range of environments. The genotypes TM 11038 (G14) in E_1 and G3 in E_2 and E_3 were found to be highly stable and gave the highest yield in their respective mega-environments, while TM 11034 (G11) and TM 11042 (G17) located in the vertex performed better in all the three environments. E_2 was the most discriminating test environment for selecting widely adapted genotypes for yield *per se,* while E_3 was the most representative testing environment to provide unbiased information about the performance of genotypes. Based on the average versus stability graph**,** the genotype TM 11042 stands out because of simultaneous high yields and high stability.

Keywords: Green gram, stability, G x E interaction, AMMI, GGE biplot

Mungbean [*Vigna radiata* (L.) Wilczek] is a very good source of digestible protein (25–28%) and has 504 mg g^{-1} of lysine (Saini et al. 2010), which is an essential amino acid lacking in cereals. India is the largest mungbean-producing country, accounting for about 65% of the world's acreage and 54% of the production (Baraki et al. 2020). Even though green gram is an important grain legume, its productivity is very low and unstable across environments and seasons due to biotic as well as abiotic factors and scarcity of widely adaptable high-yielding varieties. Often, the high-yielding genotypes fail to realize their potential yield due to the influence of different climatic factors across the locations/seasons. Therefore, understanding the genotype × environment interaction and the crop's response to the seasonal fluctuations would provide valuable insight into environment-specific crop response (Elias et al. 2016). Hence, the present investigation aimed to evaluate the G × E interaction pattern of 19 green gram genotypes in three seasons using AMMI and GGE-biplot analyses and identify the stable and superior green gram genotypes for the targeted environment.

Nineteen green gram genotypes were evaluated at Rice Research Station, Tirur, Tiruvallur, Tamil Nadu over three different seasons *viz*., *kharif*, 2019, *rabi*, 2019 and *kharif*, 2020. The experiments were conducted in a randomized block design with three replications. Each entry was raised in a 5 m^2 plot with a 30 x 10 cm spacing. The mean data on plot yield (converted into yield/ha) under three different seasons were subjected to AMMI (Zobel et al. 1988) and GGE biplot analysis (Yan 2001). A combined analysis of variance for grain yield was performed using the Agricolae package. AMMI biplot and GGE biplot analysis were carried out using PB Tools.

Analysis of variance

Combined ANOVA indicated significant differences in the performance of genotypes across environments, variations in the environmental conditions, as well as the difference in response of genotypes to varied environmental conditions.

Krishi Vigyan Kendra, Tamil Nadu Agricultural University (TNAU), Campus Aruppukottai 626 207 Tamil Nadu, India

[1]Rice Research Station, TNAU Campus, Tirur 602 925, Tiruvallur, Tamil Nadu, India

***Corresponding author:** P. Yogameenakshi, Rice Research Station, TNAU Campus, Tirur 602 925, Tiruvallur, Tamil Nadu, India, E-Mail: pyogameenakshi@tnau.ac.in

How to cite this article: Sheeba A. and Yogameenakshi P. 2024. Dissection of genotype x environment interaction and yield stability analysis in greengram using (*Vigna radiata* L.) AMMI and GGE biplot. Indian J. Genet. Plant Breed., **84**(2): 304-307.

Source of support: Nil

Conflict of interest: None.

Received: Oct. 2023 **Revised:** April 2024 **Accepted:** April 2024

Table 1. ANOVA for stability (AMMI) for grain yield

Source	Df	Sum of squares	Mean sum of squares	Percentage sum of squares
Genotypes	18	2153389	119633*	38.16
Environment	2	517873	258937*	9.18
G x E interaction	36	1486007	41278*	26.33
IPCA 1	19	979730	51564*	17.36
IPCA 2	17	506275	29780*	8.97
Total	92	5643274	----	100.00

Pooled ANOVA also demonstrated that the total variability in yield was majorly contributed by the genotypes (38.16%), followed by the genotype × environment interaction (26.33%) and environment (9.18%) (Table 1).

Biplot analysis

Biplot analysis is possibly the most powerful interpretive tool for AMMI models. AMMI I biplot revealed the relationship between genotype and environment; the three environments differed in both main and interaction effects. The environments E_1 and E_2 exhibited a high interaction effect, whereas E_3 had a moderate interaction effect with the other two environments for grain yield. The genotypes G13, G18, G2 and G17 showed a PCA 1 score close to zero for grain yield and are stable and adaptable in all environments. The genotypes G12, G14, G15, G16, G17, G19, G4, G5 and the environment E_1 had positive PCA 1 scores and they interacted positively. Hence, this environment was considered as the favorable environment for these genotypes(Fig. 1a and Table 2). The AMMI 2 biplot illustrated scores for PCA 1 and PCA 2. The genotypes G9 and G4 were highly interactive since these were situated away from the origins. The environments E_1, E_2 and E_3 did not form any group on the plot and they were also located far from the origin and had different interaction patterns on genotypes. The AMMI 2 analysis revealed that genotypes G3, G7 and G2 had wider adaptation for grain yield and performed well across environments, as they were less affected by G ´ E interaction(Fig. 1b, Table 2).

GGE biplot

The GGE biplot graphic analysis of 19 green gram genotypes revealed that the observed G × E interactions had been partitioned among the first and second IPCA scores, accounting for 61.8 and 24.2%, respectively, together explaining 82.0 % of the total GEI variance (Fig. 2).

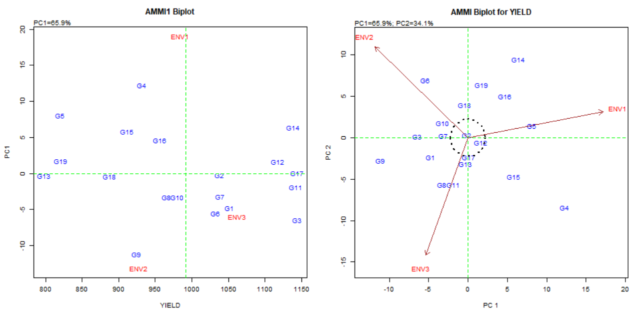
The vectors (black lines) delimited the diagram in six sectors, forming two mega-environments, ME I with the environments E_2 and E_3 and ME II with the environment E_1 (Fig. 2). By the "which-won-where" pattern of the GGE Biplot for yield, the polygon was delimited by the genotypes G9, G3, G14, G4, G5 and G13. The genotype G14 (TM 11038) in

Table 2. Estimates of stability parameters (AMMI) for grain yield

Genotype/ Environment code	Genotype/ Environment	Yield		
		Mean	PC1	PC2
G1	TM 11003	1051	-4.78	-2.34
G2	TM 11004	1037	-0.19	0.30
G3	TM 11007	1143	-6.47	0.12
G4	TM 11010	931	12.22	-8.43
G5	TM 11015	820	8.07	1.42
G6	TM 11017	1032	-5.48	6.96
G7	TM 11018	1039	-3.20	0.27
G8	TM 11019	965	-3.32	-5.70
G9	TM 11025	924	-11.19	-2.75
G10	TM 11027	980	-3.28	1.76
G11	TM 11034	1141	-1.88	-5.65
G12	TM 11035	1117	1.62	-0.60
G13	TM 11037	798	-0.32	-3.18
G14	TM 11038	1138	6.37	9.46
G15	TM 11040	911	5.79	-4.68
G16	TM 11041	956	4.64	5.02
G17	TM 11042	1144	0.11	-2.32
G18	CO 8	887	-0.44	3.94
G19	VBN 3	820	1.73	6.38
ENV1	*kharif*, 2019	985	19.07	3.52
ENV2	*rabi*, 2019	927	-13.13	12.25
ENV3	*kharif,* 2020	1062	-5.94	-15.77

E_1 and genotype G3(TM 11007) in E_2 and E_3 are found to be highly stable in their respective environments and these genotypes are suggested as the winners and highest-yielding genotypes in their mega-environments, while genotypes G11 (TM 11034) and G17 (TM 11042) located in the vector performed better in all the three environments. The genotypes located in the sectors that do not have any environment were the low-yielding genotypes in some or all of the environments (Yan et al. 2000). Baraki et al. (2020) and Jeberson et al. (2022) identified winning genotypes in different mega environments using which-wins-where GGE biplot in pulse crops. The study indicated the presence of wide, obtuse angles (*i.e.*, strong negative correlations) among test environments E_1 and $E_{2,}$ which is an indication of strong crossover GE and the existence of acute angles (*i.e.*, strong positive correlations) among test environments E_2 and E_3 which is an indication of no crossover GE (Fig. 3).

The representativeness and discrimination of the environments is based on the length of the vectors (Yan andRajcan2002). In the present study, the test environment E_2 was identified as the most discriminating environment,



Figs. 1a and b. AMMI 1 and AMMI 2 biplot for yield in green gram genotypes

which provided much information about differences among genotypes and is considered as good test environment for selecting widely adapted genotypes for yield *per se*.Both environments E_2 and AE(represented by the small circle at the end of the arrow) lie on the same concentric circle and have similar discriminating abilities. E_3 which had smaller angle with the AEA is the most representative testing environment for grain yield, whereas E_1 was identified as the least representative among the testing environments (Frutos et al. 2014).

Average-Environment Axis" (AEA), indicates the genotypes that exhibited greater mean yield performance (Yan and Tinker 2006). The line perpendicular to the AEA, indicates greater variability (lower stability) in any direction. In addition, it allows separation of the genotypes that are above or below the mean. The genotypes that had higher grain yield are G3, G11, G17, G14, G12, G1, G7, G2 and G6. In contrast, G10, G8, G16, G4, G9,G15, G18, G19, G5 and G13 had the lowest yields, with performance lower than the mean. In relation to stability, the genotypes G2, G13, G17, G 18 were the most stable, while the genotype G9 is the least. The genotype G17 (TM 11042) stands out because of

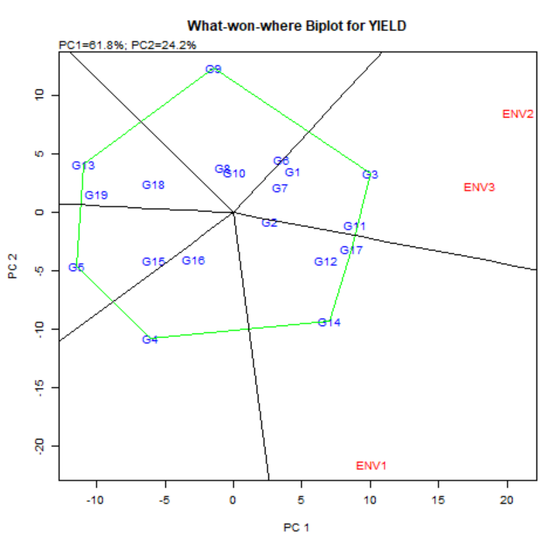


Fig. 2. GGE Polygon view of green gram genotypes

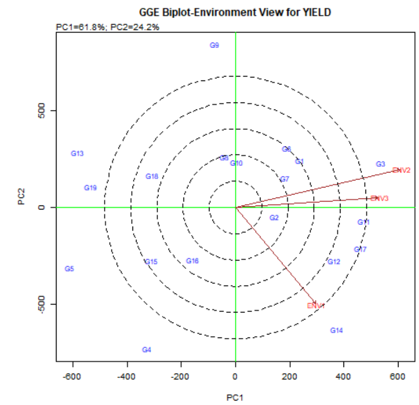


Fig. 3. Association of test environments

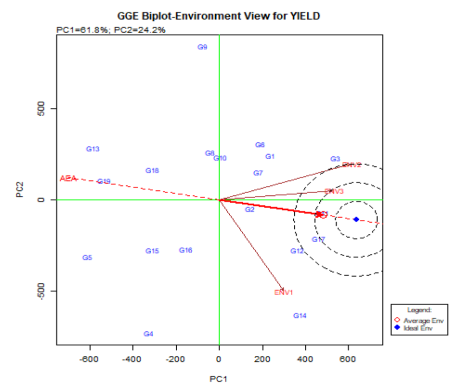


Fig. 4. Discriminating vs. representativeness view of the GGE bi-plot

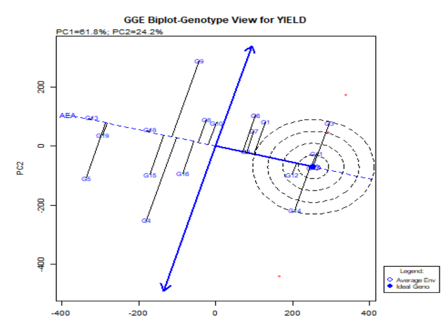


Fig. 5. Average versus stability" GGE biplot

simultaneous high yields and high stability (Fig. 5).

Compared to AMMI, the GGE biplot is superior in mega environment analysis and genotype evaluation because it combines the two main effects, *i.e.,* genotypes (G) plus the G × E interaction (GE). Among the environments, E_3 was identified as the most representative testing environment, which was able to provide unbiased information about the performance of the tested genotypes. Though the genotypes G13, G18, G2 and G17 are stable across environments, the genotype G17 (TM 11042) stands out because of simultaneous high yields and high stability.

Authors' Contribution

Conceptualization of research (AS); Designing of the experiments (AS); Contribution of experimental materials (AS); Execution of field/lab experiments and data collection (AS); Analysis of data and interpretation (AS, PY); Preparation of the manuscript (AS, PY).

References

Baraki F., Gebregergis Z., Belay Y., Berhe M. and Zibelo. 2020. Geotype x Environment interaction and yield stability analysis of mungbean (*Vigna radiata* (L.) Wilczek) genotypes in Northern Ethiopia. Cogent Food Agric., **6**: 172. DOI: 10.1080/23311932.2020.1729581

Elias A. A., Robbins K. R., Doerge R. W. and Tuinstra M. R. 2016. Half a century of studying genotype × environment interactions in plant breeding experiments. Crop Sci., **56**: 2090–2105. doi: 10.2135/cropsci2015.01.0061

Frutos E., Gallindo M.P. and Leiva V. 2013. An interactive biplot implementation in R for modeling Genotype-by-environment interaction. Stoch. Environ. Res. Risk Assess., **28**: 1629-1641. Doi:10.1007/s00477-013-0821-z

Jeberson M.S., Parihar A.K., Shashidhar K.S., Dev J., Dar S.A. and Gupta S. 2022. Selection of Suitable Genotypes of Urdbean (*Vigna mungo* L.) for Targeted Environments of Hilly Terrains of India using GGE Biplot and AMMI Analysis. Legume Res., **45**(6): 669-675.

Saini M., Singh S., Hussain Z.and Sikka V. 2010. RAPD analysis in mungbean [*Vigna radiata* (L.) Wilczek.] II: A comparison of efficiency parameters of RAPD primers. Indian J. Biotech., **9**: 276–282.

Yan W. and Tinker A. 2006. Biplot analysis of multi environment trial data: principles and applications. Canad. J. Plant Sci., **86**: 623-645.

Yan W., Hunt L.A, Sheng Q. and Szlavnics Z. 2000. Cultivar evaluation and mega-environment investigation based on the GGE Biplot. Crop Sci., **40**: 597- 605.

Yan W. 2001. GGE biplot-A windows application for graphical analysis of multi-environment trial data and other types of two-way data. Agron. J., **93**: 1111–1118. doi:10.2134/agronj2001.9351111x

Yan W. and Rajcan I. 2002. Biplot analysis of test sites and trait relations of soybean in Ontario. Crop Sci., **42**: 11–20

Zobel R. W., Wright M. G. and Gauch H. G. 1988. Statistical analysis of a yield trial. Agron. J., **80**: 388–393. doi:10.2134/agronj1988.00021962008000030002