International Journal of Plant & Soil Science

34(23): 471-477, 2022; Article no.IJPSS.92300
ISSN: 2320-7035

Assessment of Genotypes X Environment Interaction of Black Gram (*Vigna mungo* (L.) Hepper) Using Multivariate Analysis

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Article Information

DOI: 10.9734/IJPSS/2022/v34i2331612

Open Peer Review History:
This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc are available here: https://www.sdiarticle5.com/review-history/92300

Original Research Article

Received 20 July 2022
Accepted 28 September 2022
Published 08 October 2022

ABSTRACT

Twenty black gram genotypes were evaluated at five different locations of middle Gujarat in *kharif* 2016 to assess the genotype x environmental interactions in RBD design with two replications. The data were analyzed according to the AMMI model and AMMI based stability measures (ASV $W_{i(AMMI)}$ and $ASTAB_i$). Analysis of variance on the data pooled over locations and G x E interaction was found significant indicated genotypes performed differently in different locations. IPCA1 and IPCA2 were found significant in AMMI model and both combined accounted for by 78.7% variance of GEI. Environments viz., Devgadhbaria, Derol and Dahod were found high yielding environments whereas Vadodara and Jabugam were low yielding environments. Genotypes G3, G18, G16 and G10 gave high yield in environment E3, E1 & E4, E5 and E2, respectively as they were vertex genotypes in polygon of AMMI2. According to AMMI model, ASV, $W_{i(AMMI)}$ and ASTABi, G19 was found stable and high yielding genotype, whereas G16 was unstable genotypes.

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Keywords: Black gram; AMMI; GEI; ASV; $W_{i(AMMI)}$ *and* $ASTAB_i$*.*

ABBREVIATIONS

AMMI : Additive Main effect and Multiplicative Interaction
ANOVA : Analysis of Variance
ASV : Ammi Stability Value
GE : Genotype-Environment
GEI : Genotype-Environment Interaction
I : Stability Index
IPCA : Interaction Principal Component Axes
PCA : Principal Component Analysis

1. INTRODUCTION

Black gram or urd (*Vigna mungo* (L.) Hepper) is a tropical legume grown widely in India, China, Japan and Brazil mainly for its dry seeds, dal which is an important source of easily digestible protein which supplements the staple rice diet. It is said to be poor man's meat and rich man's vegetable. In Gujarat; area, production and productivity of black gram is 64 thousand hectares, 38 thousand tones and 594 kg per hectare, respectively (www.indiastat.com). The nation to become pulse sufficient, productivity level of pulses has to be increased substantially up to 1200 kg per hectare by 2020, which is possible through the development of stable high yielding genotypes using elite parental genotypes. There are different stability methods for studying genotype × environment interaction, *viz*. parametric method and non-parametric method and multivariate method. Among parametric methods; analysis of variance (ANOVA) models like Eberhart and Russell model is mostly used for studying the G x E interaction, whereas many non-parametric methods [1,2] are commonly used for G x E interaction. But AMMI model is multivariate technique to interpret GEI using ANOVA and Principal component analysis. The analysis of variance is useful for identifying and testing sources of variability, it provides no insight into the particular pattern of the underlying interaction. The ANOVA model effectively describes the main additive effects, while interaction (residuals from the additive model) is non-additive and requires alternative techniques, such as principal component analysis (PCA) to identify interaction pattern. Thus, ANOVA and PCA models combined to constitute the Additive Main effects and Multiplicative Interaction (AMMI) model [3].

The present investigation was carried out to analyze the pattern of genotype x environment interaction (GEI) for yield, to select the stable genotypes of black gram and to compare the stability measures viz., $W_{i(AMMI)}$ [4], ASV [5] and ASTA B_i [6] were calculated based on AMMI analysis for stability of black gram genotypes.

2. MATERIALS AND METHODS

A set of twenty black gram genotypes (*Vigna mungo* (L.) Hepper) was evaluated at five different locations *viz.* Vadodara (E1), Jabugam (E2), Devgadhbaria (E3), Derol (E4) and Dahod (E5) in middle Gujarat, India during the *kharif* 2016 in randomized complete block design with two replications. The yield data of multi-locational trial (Zonal varietal trial) were subjected to stability analysis using multivariate method (AMMI).

Statistical model:

$$\text{ANOVA}: \quad Y_{ij} = \mu + \alpha_g + \beta_e + \alpha\beta_{ge} + \rho_{ij} + \varepsilon_{ijk}$$

$$\text{PCA} \quad : \quad Y_{ij} = \mu + \Sigma_n \lambda_n \gamma_{gn} \delta_{en} + \rho_{ij} + \varepsilon_{ijk}$$

$$\text{AMMI} \quad : \quad Y_{ij} = \mu + \alpha_g + \beta_e + \Sigma_n \lambda_n \gamma_{gn} \delta_{en} + \rho_{ij} + \varepsilon_{ijk}$$

Where,

μ = grand mean ,
α_g = deviations of genotype(g)
β_e = deviations of environment(e)
λ_n = singular value for Interaction Principal Component Axis n (IPCA)
γ_{gn} = genotype eigenvector for axis n
δ_{en} = environment eigenvector
ρ_{ij} = residual
ε_{ijk} = error term or uncontrolled variation

The bi-plot is a graphical representation from AMMI analysis which is a useful tool to understand more complex specific pattern of genotypes and GEI or both genotypes and environments. The concept of bi-plot was first developed by Gabriel KR [7]. It is a scatter plot that graphically displays the genotype (entries) and the environments (testers) of a two-way data and allows visualization of the interrelation among the entries (genotypes) and interaction between entries and testers (environments).

2.1 $Wi_{(AMMI)}$

$Wi_{(AMMI)}$ a measure of stability is as good as Wrick'secovalence (W_i^2) was estimated as under [4].

$$W_{i(AMMI)} = \sum_{m=1}^{M} \lambda_m^2 \gamma_{mi}^2$$

λ^2_m = singular value for Interaction Principal Component Axis m (IPCA)
γ^2_{mi} = genotype eigenvector for axis n

2.2 AMMI Stability Value (ASV)

The AMMI model does not make provision for a quantitative stability measure, such a measure is essential in order to quantify and rank genotypes according their yield stability, the following measure proposed by Purchase JL [5] was estimated as under.

$$ASV = \sqrt{\left(\frac{\text{IPCA1 SS}}{\text{IPCA2 SS}} \text{ x } (\text{IPCA1score})^2\right) + (\text{IPCA2 score})^2}$$

2.3 AMMI based Selection Indices

A new stability measure and incorporated as a stability component [6]. When more than two axis are retained in AMMI model, the biplot formulation of interaction is failed. When n' of N axis are retained in the AMMI model to explain GEI, then the stability measure of i^{th} variety can be determined as the end point of its vector α^*_{1i}, α^*_{2i}, …, α^*_{ni} from the origin $0'_{nx1}$. This is a squared Euclidean distance and was calculated as under.

$$ASTABi = \alpha_{1i}^{2*} + \alpha_{2i}^{2*} + \ldots + \alpha_{ni}^{2*} = \sum_{n=1}^{n'} \alpha_{ni}^{2*} = \sum_{n=1}^{n'} \lambda_n \alpha_{ni}^2$$

A genotype is considered as highly stable when the value of ASTABi is small or closer to zero.

3. RESULTS AND DISCUSSION

The combined analysis of variance (ANOVA) of twenty black gram genotypes over five locations according to AMMI model is presented in Table 1.

Additive effects for main effects (genotypes and environments) and multiplicative effects for G x E interaction are considered. The results presented in Table 1 indicated that mean square for genotypes was found non-significant but locations (environments) and GEI were found highly significant indicating the diverse performance of genotypes over locations. The proportion of variance due to locations was the largest (58.57 per cent) followed by the variance due to G x E interaction (32.23 per cent) and genotypes (9.21 per cent). ANOVA provided no insight into the particular pattern of genotypes or environments that gave rise to interactions, but described only main effects effectively. Since G x E interaction was highly significant (Table 1), ANOVA model was combined with PCA model to further analyze the residuals (GEI) of the ANOVA model.

The GEI was highly significant and was further partitioned into three PCA axes (IPCA) which jointly contributed 92.21 per cent of GEI. The first and second PCA were found highly significant ($P < 0.01$) and contributed 62.9 and 15.8 per cent to the total GEI variance, respectively and both the IPCA jointly 78.73 per cent of GEI. The residual SS accounted 7.79 % of the interaction SS and 21 % of df for GEI [3].

Table 1. Analysis of Variance (ANOVA) according to AMMI model for black gram genotypes

Source of Variations	df	Sum of Squares	Mean Squares	F Ratio	% SS
Trials	99	8.242	0.083	2.38	
Genotypes	19	0.759	0.040	1.14	9.21
Environments	4	4.827	1.207**	34.53	58.57
GxE Interaction	76	2.656	0.035**		32.23
PCA I	22	1.671	0.076**	10.86	62.91
PCA II	20	0.420	0.021**	3.00	15.81
PCA III	18	0.358	0.020	2.86	13.48
Residual	16	0.207	0.013	1.86	7.79
Pooled residual	95	1.295	0.007		

*** Significant at P < 0.01*

Table 2. IPCA1 and IPCA2 scores of different back gram genotypes and locations

Sr. No.	Genotypes	Mean yield (kg plot^{-1})	Rank	IPCA1	IPCA2
G1	VUG-14	0.627	20	-0.083	-0.224
G2	VUG-18	0.729	14	0.297	0.075
G3	VUG-19	0.884	2	0.279	0.182
G4	VUG-23	0.722	15	0.089	0.073
G5	VUG-63	0.731	13	-0.312	-0.176
G6	VUG-32	0.870	3	-0.161	-0.324
G7	VUG-35	0.645	18	-0.059	0.153
G8	DERUG-16-1	0.802	9	0.258	0.100
G9	DERUG-16-2	0.862	4	0.294	-0.179
G10	DERUG-17-1	0.744	11	0.325	-0.397
G11	DERUG-17-5	0.733	12	0.184	0.099
G12	DERUG-20-4	0.704	16	-0.244	0.132
G13	DERUG-21-4	0.666	17	-0.060	0.271
G14	DERUG-27-2	0.632	19	-0.010	-0.301
G15	DBUGP-2-2	0.828	7	-0.293	0.070
G16	DBUGP-2-5	0.833	6	-0.406	-0.256
G17	DBUGP-6-1	0.850	5	-0.175	0.125
G18	DBUGP-6-2	0.927	1	-0.153	0.465
G19	T-9	0.823	8	0.062	0.209
G20	GU-1	0.784	10	0.168	-0.096
	Over all Mean	**0.770**			
	Environments				
E1	Vadodara	0.526	4	-0.154	0.532
E2	Jabugam	0.482	5	0.750	-0.352
E3	Devgadhbaria	1.001	1	0.154	0.061
E4	Derol	0.905	3	-0.142	0.409
E5	Dahod	0.935	2	-0.608	-0.650

Correlation between PC1 and PC2 = 1.25E-11 ns

The results of AMMI analysis can also be easily comprehended with the help of AMMI1 biplot as presented in Fig. 1. The mean performance of genotypes and environments vs IPCA1 score were used to construct the biplot (Table 2). According to AMMI model, the genotypes which are characterized by mean higher than the grand mean and the IPCA scores nearly zero are considered as generally adapted to all environments. However, the genotypes with high mean performance with large value of IPCA scores are considered to have specific adaptability to the environments [8-10]. Bioplot assay [7] presented in Fig. 1 identified three high yielding genotypes viz., G19, G18 and G6 having general adaptability, having mean yield >0.770 kg plot^{-1} and close to IPCA1 = 0 line. Genotypes G3, G9 and G16 were higher yielding and specially adapted to favorable environments. Genotypes G1, G7, G13 and G14 had low mean yield and positioned near to IPCA1 = 0 line indicated that they were stable but they were lower yielding genotypes.

Similar sign of IPCA1 score for both genotypes and environment imply positive interaction and thus it attributed to higher yield of genotype at particular environment [11]. IPCA scores of genotypes G3, G8, G9, G19 and G20 and of Devghadbaria (E3) location had positive sign, which indicated that these genotypes attributed higher yield at this location having positive GEI.

Environments were widely spread over scatter diagram which indicated high variability was among the locations. The environment E3, E4 and E5were high yielding potential locations, whereas, E1 and E2 were found low yielding environments [9].

Visualization of which-won-where pattern of MLT data is important for studying the possible existence of different mega-environments. The polygon was drawn by connecting the markers of the genotypes that were far away from the biplot origin such that all other genotypes were contained in the polygon. The rays in Fig. 2 were lines that were perpendicular to all the sides of the polygon. These five rays divided the biplot into five sectors and the environments were distributed in the four sectors. The interesting feature of this view of GGE biplot is that the vertex genotype for each sector was the best for the environment fall in the same sector than the others in all environments [12]. Thus, environment E1 and E4 fell into sector III delineated by Rays 2 and 3 and the vertex genotypes for this sector was G18 suggesting that G18 was the winner high yielding genotype for Vadodara (E1) and Derol (E4) locations. Similarly, for environment E2 (sector I) the vertex genotypes was G10 which was the best for Jabugamlocation (E2). Sector IV delineated by Rays 3 and 4 contained the environment E5 and the winning genotypes for Dahod (E5) location was G16, which was higher yielding genotype. The discrepancy between the results of vertex genotype and higher yielding one may be because of the biplot explained 78.7% to variation of GEI and the remaining 22.3% variation was unaccounted [9,13].

3.1 AMMI Stability Value (ASV)

The ASV is the distance from the co-ordinate point to the origin in two dimensions of IPCA1 scores against IPCA2 scores in the AMMI model. Genotype G4 followed by G7, G19 and G1 were the most stable, while genotype G16, G10 and G5 were undesirable in terms of stability (Table 3). Among the stable genotypes, yield of genotype G19had higher mean than over all mean of grain yield. Similarly in unstable genotypes G16 had higher grain yield while G10and G5 had lower grain yield than mean grain yield. Thus, present findings are in accordance with those reported by different workers [9,13,14].

3.2 $W_{i(AMMI)}$ Measure

The different $W_{i(AMMI)}$ values presented in Table 3 indicated that ranks of $W_{i(AMMI)}$ superimposed on ranks of AVS measures. According to the value of $W_{i(AMMI)}$, G4, G7 and G19were the most stable, while genotype G16, G10 and G5 were most unstable [15].

3.3 AMMI Based Selection Index (ASTABi)

ASTABi [5] stability measures (squared Euclidean distance) were calculated using the retained ‘n’ (3) axis out of ‘N’ total axis and presented in Table 3. Genotype G19 had the lowest value of ASTABi followed by G14 and G7considered as stable. Among these genotypes, only G19 had higher grain yield than overall mean grain yield. The highest values of ASTABi were observed for G16, G10 and G7 which indicated their instability over environments.

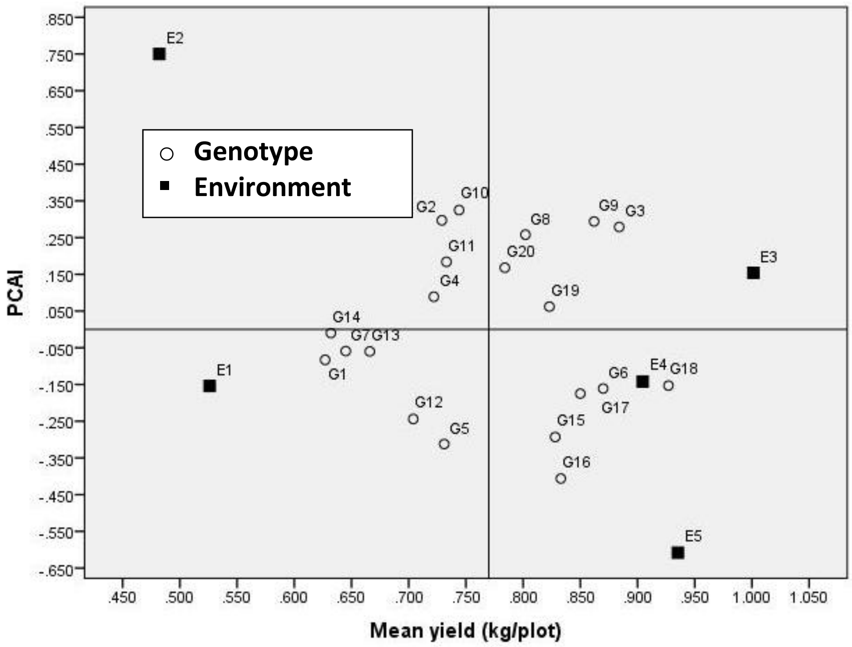

Fig. 1. AMMI1 biplot for black gram genotypes and locations

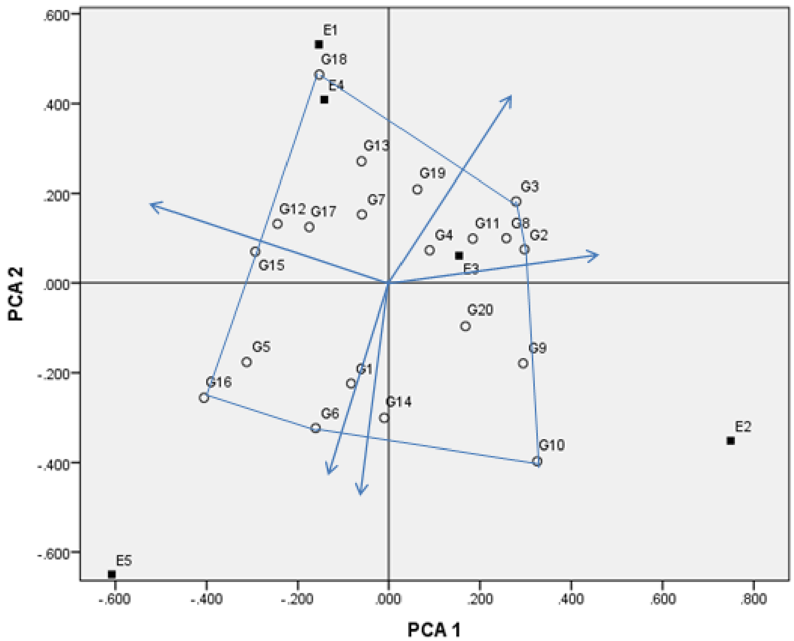

Fig. 2. AMMI2 biplot for black gram genotypes and locations

Table 3. Selection of genotypes based on different indices based on AMMI model for blackgram genotypes

Sr. No.	Genotype	Mean yield (kg plot^{-1})	Rank	ASV	Rank	$W_{i(AMMI)}$	Rank	$ASATB_i$	Rank
G1	VUG-14	0.627	20	0.279	4	0.033	4	0.042	5
G2	VUG-18	0.729	14	0.596	16	0.149	16	0.252	17
G3	VUG-19	0.884	2	0.586	14	0.144	14	0.232	14
G4	VUG-23	0.722	15	0.192	1	0.015	1	0.033	4
G5	VUG-63	0.731	13	0.646	18	0.175	18	0.280	18
G6	VUG-32	0.870	3	0.456	10	0.087	10	0.091	7
G7	VUG-35	0.645	18	0.192	2	0.016	2	0.032	3
G8	DERUG-16-1	0.802	9	0.524	12	0.115	12	0.188	13
G9	DERUG-16-2	0.862	4	0.613	17	0.158	17	0.250	16
G10	DERUG-17-1	0.744	11	0.760	19	0.243	19	0.324	19
G11	DERUG-17-5	0.733	12	0.380	9	0.061	9	0.098	9
G12	DERUG-20-4	0.704	16	0.503	11	0.106	11	0.170	12
G13	DERUG-21-4	0.666	17	0.296	5	0.037	5	0.052	6
G14	DERUG-27-2	0.632	19	0.302	6	0.038	6	0.021	2
G15	DBUGP-2-2	0.828	7	0.588	15	0.145	15	0.241	15
G16	DBUGP-2-5	0.833	6	0.850	20	0.304	20	0.473	20
G17	DBUGP-6-1	0.850	5	0.371	8	0.058	8	0.092	8
G18	DBUGP-6-2	0.927	1	0.556	13	0.130	13	0.107	11
G19	T-9	0.823	8	0.243	3	0.025	3	0.019	1
G20	GU-1	0.784	10	0.349	7	0.051	7	0.101	10

4. CONCLUSION

Yield is a not a trait but it is cumulative effect of all other quantitative trait that is strongly affected by environment. AMMI statistical model might be a best tool to select the most high yielding and stable genotypes for specific as well as for across the environments. In the present study, AMMI model has shown that the largest proportion of the total variation in seed yield was attributed to environments. Overall results suggested that genotype G19 (T-9) was high yielding and stable genotype which can be recommended for all five locations. Genotypes G4 (VUG-23) and G7 (VUG-35) gave low yield but they were stable. Out of all environments, Derol, Devgadh baria and Dahod are high seed yielding environments whereas Vadodara and Jabugam are low seed yielding environments for blackgram.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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