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Research Article

Development of stable blackgram [*Vigna mungo* (L.) Hepper] genotypes by deciphering genotype × environment interaction using Eberhart-Russell and AMMI models

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Abstract

The genotype and environment ($G \times E$) interaction is a key area of research for creating stable cultivars as it has a major impact on crop yield performance. In this study, we examined the stability and adaptability of the seed yields of elite blackgram genotypes in four Agricultural Research Centers of PJTSAU consisting of diverse environments in Telangana, India during *Rabi* 2019-20 using Eberhart-Russell and Additive Main effects and Multiplicative Interaction (AMMI) models. A combined analysis of variance showed significant differences between the varieties and the interactions between the varieties and locations for seed yield. Both Eberhart and Russell and AMMI1 model analyses of G×E interaction identified G1 (LBG-752) as the stable variety with respect to yielding ability suitable for cultivation under diverse conditions. Environments A, B, and C were found to be ideal environments for genotypes G7, G8, and G6, respectively, based on AMMI 2. The selected elite varieties based on different stability analyses could be used for further exploitation for cultivar release.

Keywords: G × E interaction, Adaptability, AMMI I, Eberhart & Russell, Seed yield, Vigna mungo.

INTRODUCTION

Blackgram [*Vigna mungo* (L.) Hepper] is an important pulse crop in Asian countries and is of Indian origin. It is considered the "King of the Pulses" because of its flavour and numerous other healthy attributes. In India, it is cultivated on 4.50 million hectares with an annual production of 2.83 million tonnes (MULLaRP, 2019). It meets the protein requirements of India's vegetarian population. It has been cultivated in almost all agroecological zones of India. Despite the development of numerous improved varieties, most of them exhibit variable performance under a variety of environmental and climatic conditions as a result of genotype environment interactions (Shanthi *et al.*, 2007). It is claimed that one of the significant factors influencing the decline in pulse production in India is the lack of suitable varieties and genotypes with adaptation to local conditions (Sivaprakash *et al.*, 2004).

Phenotypically stable genotypes are essential because environmental conditions change from year to year and from season to season. Stable performance of blackgram

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genotypes for seed yield across various environments is crucial for efficient cultivar production (Yousaf and Sarwar, 2008). An important criterion for selecting stable and high-yielding genotypes is the combination of genetic stability and yield performance *per se* (Yihunie and Gesesse, 2018). Understanding the relationship between genotype and the genotype x environment interaction and determining how different genotypes respond to environmental changes is crucial for crop improvement in black gram. The identification of cultivars with predictable performance and their responses to environmental variations in specific or broad situations require an analysis of adaptability and stability, making the selection of cultivars more reliable (Cruz *et al.*, 2012).

In order to recommend the genotypes that consistently outperform and yield higher across various locations, stability analysis methods have been presented to address $G \times E$ interactions. The Additive Main effects and Multiplicative Interaction (AMMI) analysis is an efficient model to determine stable and high yielding genotypes, and it provides information on main and interaction effects (Zobel *et al.*, 1988).

In blackgram breeding, the adaptability and stability analyses have not been extensively studied. To provide reliable estimates of yield and agronomic traits and to assess yield stability, or the ability to withstand both predicted and unexpected environmental variation ($G \times E$ interaction), stability analysis is performed (Singh *et al.*, 2020). The current study set out to analyze a number of elite blackgram genotypes for their adaptability and stability to seed yield using the Eberhart and Russell (1966) as well as AMMI models (Zobel *et al.*, 1988; Gauch, 1992) in order to recommend stable genotypes for cultivation and their use in breeding programs for enhancing blackgram yields.

MATERIALS AND METHODS

Eight elite blackgram varieties were evaluated at four different agro climatic centres (**Table 1**) in Telangana, namely, Regional Agricultural Research Station (RARS), Warangal; Agricultural Research Station (ARS), Adilabad; Agricultural Research Station (ARS), Madhira and Regional Sugarcane & Rice Research Station (RS&RRS), Rudrur during *rabi*, 2019-2020. The experimental material was planted in a randomized block design (RBD) with three replications adopting row-row and seed-seed spacing of 30 cm and 10 cm, respectively. For healthy

Table 1. Description of four test locations

crop growth, all the recommended package of practices was followed.

The seed yield data from all the test sites were subjected to biometrical analysis using Windostat 8.6 version statistical package. The stability of the genotypes for each trait was calculated using the Eberhart and Russell model (1966). The significance of the regression coefficient (b_i) was tested using the t-test, whereas the significance of the deviation from regression (s^2d_i) was tested using the F test. The AMMI model (Zobel *et al.*, 1988), which is a combination of conventional analysis of variance and principal component analysis, was used to analyze G× E interaction.

RESULTS AND DISCUSSION

Significant differences in the genotypes for the seed vield (kg/ha) were observed by the pooled analysis of variance (Table 2) of the data. The environment + (genotype × environment) interaction was significant for seed yield indicating the distinct nature of environments and genotype × environment interactions in phenotypic expression. The environment (linear) was found to be significant for seed yield indicating the differences between environments and their influence on genotypes for the expression of the character. The genotype × environment (linear) interaction component revealed non-significance, which demonstrated genotype-specific differences for linear response to environments (b) and the inability to predict genotype behaviour across environments. The significant mean square obtained from pooled deviation from regression revealed that the performance of several of the genotypes was not stable across environments. These findings were in accordance with the reports of Shobanadevi et al. (2021), Rita et al. (2016) and Joseph et al. (2015).

Grain yield is a very complex trait which is strongly influenced by genotype (G), environment (E) and genotype × environment (G×E) interaction (Toker *et al.*, 2004). Environmental variation has a major effect on the variation of yield (up to 80% or higher) in test genotypes with narrow genetic base (Temesgen *et al.*, 2015). A comparison of average blackgram seed yields across test locations revealed that Warangal had very low yields while Adilabad had high yields (**Table 3**). The variety G3 recorded the highest seed yield (2059 kg/ha) followed by G4 (2028 kg/ha) when compared to others in the Adilabad location (**Table 3**). However, the seed yields of these

Location	Environmental code	Latitude	Longitude	Soil type
Adilabad	А	19°20' N	78°80' E	Clay
Rudrur	В	18°38' N	77°55' E	Clay loam
Madhira	С	16°55' N	80°22' E	Clay loam
Warangal	D	17° 58' N	79°28' E	Sandy loam

Source of variation	Degrees of freedom	Seed yield (kg/ha)	
Replications within Environment	8	7322.875	
Genotypes	7	52367.640*	
Environment + (G × E)	24	253651.600***	
Environments	3	1823592.000***	
G×E	21	29374.430	
Environments (Linear)	1	547075.000***	
G × E (Linear)	7	43483.110	
Pooled Deviation	16	19530.080**	
Pooled Error	56	6400.883	
Total	31	208200.400	
SE±		98.818	
CD @ 5 %		209.483	

Table 2. ANOVA showing mean sum of squares for seed yield in blackgram

***Significant at P ≤ 0.001

Table 3. Performance of all elite blacke	ram genotypes evaluated during ra	abi, 2019-20 with respect to seed v	vield
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Genotype	Genotypic code	Seed yield (kg/ha)			
	-	Adilabad	Rudrur	Madhira	Warangal
LBG-752	G1	1960	1565	1211	1180
MBG-1094	G2	1804	1652	1203	1120
MBG-1084	G3	2059	1690	796	886
MBG-1080	G4	2028	1580	735	829
LBG-787	G5	1845	1535	692	893
MBG-1091	G6	1675	1423	1149	674
MBG-207	G7	1967	1418	808	691
PU-31	G8	1420	1643	753	807

genotypes were comparatively lower in Rudrur followed by Madhira. The genotype G6 had the lowest seed yield (674 kg/ha) at Warangal and across the locations.

The mean performance (µ), regression coefficient (b_i) and deviation from regression (S²d_i) have been presented in Table 3 and 4. The Eberhart and Russell (E-R) (1966) regression model has been widely used in the past few decades mainly because variability in performance of any genotype could be subdivided into predictable (regression) and unpredictable (variation from regression) components. Hypothetically, the E-R method considers both yield (regression) and stability (variation from regression), with regression being predicted and to some extent controlled by selecting specific genotypes for specific locations. In this study, among all the varieties, G2, G3, G6 and G8 were shown to have significant deviations from regression (s²d₁) (solid dots in Fig. 1) and were found to be unstable as their performance across the tested environments was unpredictable. The varieties G1, G5, G7 and G4 showed non-significant deviations from regression (Hollow dots in Fig. 1). Among these

four stable yielders, genotypes G1 and G5 which had b_i value near unity are considered to be adaptable over the tested locations. However stable genotype G1 had higher pooled mean yield than the overall mean. Other stable varieties, G5, G7 and G4 exhibited b_i values of above unity (b_i > 1) and were found to be specifically adapted to high yielding environments. Genotype G2 had b_i values below unity (b_i < 1) and it is specifically adapted to low yielding environments. It also showed significant deviation from regression and hence the stability is unpredicted. Even though the genotypes G6 and G8 showed b_i values near to one, their stability cannot be predicted accurately as they showed significant deviation from regression (**Fig. 1 and table 4**). Similar results were previously reported by Rita *et al.* (2016).

The AMMI analysis provides a graphical representation or biplot to summarize information on the main effects and the first principal component scores of the interactions (IPCA1) of both genotypes and environments simultaneously (Kempton, 1984). The main effects are displayed in the abscissa, while the interaction effects

Genotype code	Pooled mean seed yield (kg/ha)	Regression coefficient (b _i)	Deviation from regression (s²d _i)
G1	1479	0.75	2561
G2	1445	0.70	-5119
G3	1658	1.29	-2110
G4	1293	1.29	101
G5	1242	1.11	7711
G6	1230	0.81	43881
G7	1221	1.22	6174
G8	1156	0.83	50914





X-axis indicates the b_i (Regression coefficient) value of a genotype and Y-axis indicates the s^2d_i (Deviation from the regression) value of the genotype.

are represented by the IPCA 1 scores in the ordinate (**Fig. 2**). Genotypes and environments with IPCA 1 scores that tend towards zero have small interaction effects and are considered stable, while genotypes with large IPCA 1 scores in either a positive or negative direction are highly interactive (Odewale *et al.*, 2013). Genotype and environment combinations with IPCA1 scores of the same sign produce positive specific interaction effects, whereas combinations of opposite signs have negative specific interactions (Ersullo, 2016).

The elite genotype G1, which recorded high seed yield with IPCA1 scores near zero, had little interaction across environments, indicating its broad adaptations and hence is considered stable throughout all environments, *viz.*, Adilabad, Rudrur, Madhira, and Warnangal. The other high yielding genotype, G2, however, showed a large IPCA1 score further away from zero and was hence considered unstable (**Fig. 2**). Since the genotypes G5, G7, and G8 showed modest IPCA scores, they could be fairly stable. The other elite genotypes, G3, G4, and





Fig. 2. AMMI 1 biplot for additive effects vs. IPCA1 in 8 elite varieties of blackgram from four environments

G6, were also considered unstable across testing sites as they exhibited high IPCA1 scores that were farther away from zero. The two environments, *viz.*, A and B, recorded above average mean seed yields (**Fig. 2**) that were considered potential sites for higher blackgram production, while environments C and D, which showed the lowest seed yields than the average, were found to be unsuitable for high production. Nevertheless, the IPCA 1 scores of all the test environments revealed that only high yielding environment B showed a near zero value and was found to be stable.

AMMI 2 analysis is used to evaluate the interaction between genotypes and environments using two axes, IPCA1 and IPCA2 (Purchase, 1997). The two AMMI components, *viz.*, genotypic and environmental scores, were used to create this model (Odewale *et al.*, 2013). In the present investigation, **Fig. 3** shows the AMMI-2 biplot for blackgram seed yields along with the IPCA 1 and IPCA 2. Environments and genotypes that were plotted far from their origin have greater beneficial interactions with one another. In **Fig. 3**, the convex hull is drawn on genotypes that are relatively distant from the biplot origin, so that all other genotypes are contained within the convex hull. This figure also contains a set of lines perpendicular to each side of the convex hull. A perpendicular line does

not necessarily intersect the convex-hull side; it may only intersect the extension of the convex-hull side, *i.e.*, the convex-hull side that connects genotypes. These perpendiculars divide the biplot into sectors, and the environments invariably fall into those sectors. There are six sectors in this plot, with genotypes G2, G3, G4, G6, G7, and G8 as the corner or vertex genotypes. The genotype G1, which was located close to the origin, is considered a stable genotype. Environment A was located in the sector whose vertex genotype was genotype G7. This indicates that the ideal genotype for Environment A is genotype G7. The best genotypes for Environments B and C were G8 and G6, while the best genotype for Environment D was G5. However, genotypes such as G2, G3, and G4 were not superior in any environments that fell into the sector, demonstrating that none of the environments favoured those genotypes and suggesting the poor performance of the genotypes across all or part of the environment(s).

In the present study, four extremely varied environments were used to evaluate blackgram elite varieties. Different test genotypes reacted differently to each environment. Seed yields varied significantly among test sites. Diverse seed yields in blackgram have been reported in previous studies (Shobanadevi *et al.*, 2021). Breeders can characterize the mega environments and find





Fig. 3. AMMI 2 biplot showing the two main axes of interaction (IPCA2 vs. IPCA1) in 8 elite blackgram varieties from four environments

cultivars with specific environmental adaptations or broad adaptability by using multi environment trials, which are an essential component of crop improvement. (Flores et al., 2012 and 2013). It is important that we focus on the mean performance of genotypes that have traits of economic importance under various environments while conducting stability analysis. The stability analyses carried out in the current study made it possible to document genotypes with regard to their yield potential (Table 3) and identify genotypes that are stable and high yielders under various environmental conditions. A stable genotype should perform better than average and remain consistent across environments (Gedif et al., 2014). The stability parameters of the eight genotypes represent various seed yield groups with various adaptation tendencies. The non-significant S²D, value was obtained from the Eberhart and Russell model, and it represents the genotype's predictability for a given environment. It has been noted that deviation from the regression was the most appropriate indicator of stability and that the linear regression could be viewed as a measure of responsiveness to a particular genotype (Jatasra and Paroda, 1979). In order to identify the stable genotypes for seed yield, the mean value, b,, and s²d, were taken into consideration due to the significance of the linear component of the G × E interaction. Similar findings for steady seed yields in blackgram have been reported by

Shobanadevi et al., 2021; Mohanlal et al., 2019; Rita et al., 2016 and Abraham et al., 2013. Plant breeders frequently use GGE biplot analysis to find the best test sites, lower the cost of breeding and testing methods, and identify genotypes that are broadly or particularly adapted. A significant G×E interaction is evident from the partitioning of the total sum of squares obtained in our analysis, which reveals that blackgram genotypes performed differently in terms of seed yield across environments. This interaction might make genotype evaluation and selection methods less accurate (Gauch, 2012). In the present study, two AMMI biplots were used to interpret the stability of elite blackgram genotypes. AMMI1 evaluates stability in the y-axis (IPCA1), according to Duarte and Vencovsky (1999), whereas AMMI2 analysis revealed stable environments and genotypes near the origin, with low scores for the two axes of the interaction (IPCA1 and IPCA2). Accordingly, variety G1 was the most stable, as indicated by values close to the IPCA1 axis, which point to a lesser contribution to the G × E interaction (Fig. 3). The classification of blackgram genotypes for their stability based on the AMMI biplot was earlier reported by Dhasarathan et al. (2021); Joseph et al. (2015).

The AMMI analysis results also showed that environmental variation is sufficiently varied and causes more significant variation in blackgram yield. A significant G × E interaction

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represents the adaptation of the yield trait for a specific environment, demonstrating high genotypic response variations across environments. We can draw attention to the environment's minimal influence on the interaction in the B region. Other environments significantly increased (A and C) the G × E interaction (Fig. 2). Only the A and B environments, which produced the majority of the blackgram seed yields, had average yields that were higher than the overall mean yield. The better availability and distribution of rainfall in these regions or better crop management during the initial establishment and flowering phases are most likely to be responsible for the high seed yields observed in these environments (Oliveira et al., 2014). Similar results were previously reported by Alam et al. (2015), Tonk et al. (2011), and Vaezi et al. (2017).

In the present study, G1 (LBG-752) was found to be the most stable genotype when taking into account the average of the four environments based on two methods, in addition to its high yield potential. This is true even though both models have produced conflicting results when used to evaluate the stability and adaptability of tested blackgram elite varieties. Both models showed that genotypes such as G5 and G7 were fairly stable for seed yield, whereas genotypes such as G2, G3, and G6 were found to be unstable. The stable genotype(s) identified in this study may be utilized in future breeding programs and for understanding the genetic control of trait expression. In addition, the genotypes developed in this study could be useful for blackgram improvement programs in Telangana.

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REFERENCES

- Abraham, B., Vanaja, M., Reddy, P.R.R., Sivaraj, N., Sunil, N., Kamala, V. and Varaprasad, K.S. 2013. Identification of stable and high yielding genotypes in black gram (*Vigna mungo* L. Hepper) germplasm. *Indian Journal of Genetics and Plant Breeding*, **73** (3): 264-269. [Cross Ref]
- Alam, M.A., Sarker, Z.I., Farhad, M., Hakim, M.A., Barma, N.C.D., Hossain, M.I., Rahman, M.M. and Islam, R. 2015. Yield stability of newly released wheat varieties in multi-environments of Bangladesh. *Int. J. Plant Soil Sci*, 6: 150–161. [Cross Ref]
- Cruz, C.D., Regazzi, A.J. and Carneiro, P.C.S. 2012. Modelos biométricos aplicados ao melhoramento genético. UFV, Viçosa, **1**: 514.

- Dhasarathan, M., Geetha, S., Karthikeyan, A., Sassikumar, D. and Meenakshiganesan, N. 2021. Development of novel blackgram (*Vigna mungo* (L.) Hepper) mutants and deciphering genotype × environment interaction for yield-related traits of mutants. *Agronomy*, **11**: 1287. [Cross Ref]
- Duarte, J.B. and Vencovsky, R. 1999. Genotype × environment interaction: an introduction to AMMI analysis = Interação genótipos × ambientes: uma introdução à análise AMMI. Sociedade Brasileira de Genética, Ribeirão Preto, SP, Brazil (in Portuguese).
- Eberhart, S.A. and Russell, W.A. 1966. Stability parameters for comparing varieties. *Crop Science*, **6**: 36–40. [Cross Ref]
- Ersullo, L.J. 2016. Genotype × environment interaction for grain yield of some field pea genotypes in central and north eastern zones of south region, Ethiopia. *Greener Journal of Plant Breeding and Crop Science*, **4** (3): 071-080. [Cross Ref]
- Flores, F., Hybl, M., Knudsen, J.C., Marget, P., Muel, F., Nadal, S., Narits, L., Raffiot, B., Sass, O., Solis, I. and Winkler, J. 2013. Adaptation of spring faba bean types across European climates. *Field Crops Research*, **145**: 1-9. [Cross Ref]
- Gauch Jr, H.G. 1992. Statistical analysis for regional yield trials: AMMI Analysis of Factorial Designs. Elsevier, Amsterdam; The Netherlands.
- Gedif, M. and Yigzaw, D. 2014. Genotype × environment interaction analysis for tuber yield of potato using a GGE biplot method in Amhara region, Ethiopia. *Potato Journal*, **41**: 41–51.
- Jatasra, D.S. and Paroda, R.S. 1979. Stability analysis for synchrony traits in wheat (*Triticum aestivum* L.). Indian Journal of Genetics and Plant Breeding, 39: 378-383.
- Joseph, J., Francies, R.M., Santhoshkumar, A.V., Sunil, K.M. and Dayalakshmi, E.M. 2015. Stability of black gram (*Vigna mungo* L. Hepper) varieties for seed yield. *Electronic Journal of Plant Breeding*, **6** (4): 899-903.
- Kempton, R.A. 1984. The use of biplots in interpreting variety by environment interactions. J. Agril. Sci, 103:123-135. [Cross Ref]
- Mohanlal, V.A., Saravanan, K. and Sabesan, T. 2019. Linear regression model for stability analysis in blackgram (*Vigna mungo* L. Hepper) Germplasm. *Journal of Pharmacognosy and Phytochemistry*, **8** (2): 1481-1483.

https://doi.org/10.37992/2023.1401.031

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- MULLaRP, 2019. Project Coordinator Report (2018-19) All India Coordinated Research Project on MULLaRP. 46.
- Odewale, J.O., Ataga, C.D., Agho, C., Odiowaya, G., Okoye, M.N. and Okolo, E.C. 2013. Genotype evaluation of coconut (*Cocos nucifera* L.) and mega environment investigation based on additive main effects and multiplicative interaction (AMMI) analysis. *Research Journal of Agricultural and Environmental Management*, 2 (1): 001-010.
- Oliveira, E.J.D., Freitas, J.P.X.D. and Jesus, O.N.D. 2014. AMMI analysis of the adaptability and yield stability of yellow passion fruit varieties. *Scientia Agricola*, **71**:139-145. [Cross Ref]
- Purchase, J.L. 1997. Parametric analysis to describe Genotype × environment interaction and yield stability in winter wheat. Ph.D. Thesis, Department of Agronomy, Faculty of Agriculture, University of the Free State, Bloemfontein, South Africa.
- Rita, N., Kigwie, S., Noren, K., Brojen, N. and Pramesh, K. 2016. Stability analysis of high yielding varieties of black gram (*Vigna mungo* L. hepper). *Electronic Journal of Plant Breeding*, **22** (1): 1-9. [Cross Ref]
- Shanthi, P., Jebaraj, S. and Murugan, E. 2007. Stability analysis in blackgram (*Vigna mungo* L.Hepper). *Legume Research*, **30** (2): 154-156.
- Shobanadevi, C., Elangaimannan, R. and Vadivel, K. 2021. Stability analysis for yield and its component characters in blackgram [*Vigna mungo* (L.) Hepper]. Indian Journal of Agricultural Research, 1: 3. [Cross Ref]
- Singh, B., Das, A., Parihar, A., Bhagawati, B., Singh, D., Pathak, K., Dwivedi, K., Das, N., Keshari, N. and Midha, R. 2020. Delineation of genotype-byenvironment interactions for identification and validation of resistant genotypes in mungbean to root-knot nematode (*Meloidogyne incognita*) using GGE biplot. *Scientific Reports*, **10**: 1–14. [Cross Ref]
- Sivaprakash, K. R., Prashanth, S. R., Mohanty B.P. and Parida, A. 2004. Genetic diversity of black gram (*Vigna mungo*) landraces as evaluated by Amplified Fragment Length Polymorphism markers. *Current Science*, **86** (10): 1411 – 1415.
- Tonk, F.A., Ilker, E. and Tosun, M. 2011. Evaluation of genotype × environment interactions in maize hybrids using GGE biplot analysis. *Crop. Breed. Appl. Biotech*, **11**: 01–09. [Cross Ref]
- Vaezi, B., Pour-Aboughadareh, A., Mohammadi, R., Armion, M., Mehraban, A., Hossein-Pour, T. and Dorii, M. 2017. GGE biplot and AMMI analysis of barley yield performance in Iran. *Cereal Res. Commun*, **45**: 500–511. [Cross Ref]

- Yihunie, T.A. and Gesesse, C.A. 2018. GGE Biplot analysis of genotype by environment interaction in field pea (*Pisum sativum* L.) genotypes in northwestern Ethiopia. Journal of Crop Science and Biotechnology, **21**: 67-74. [Cross Ref]
- Yousaf, A. and Sarwar, G. 2008. Genotypic × environmental interactions of cowpea genotypes. *International Journal of Environmental Research*, **2**: 125-132.
- Zobel, R.W., Wright, M.J. and Gauch, H.G. 1988. Statistical analysis of a yield trial. *Agronomy Journal*, **80**: 388-393. [Cross Ref]