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Research Article

Study on blackgram (*Vigna mungo* (L.) Hepper) genotypes for yield stability and Mungbean Yellow Mosaic Virus (MYMV) resistance

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Abstract

A total of 50 genotypes were evaluated during *Kharif* 2022 in three different locations in Tamilnadu, India. The data on seed yield per plant was subjected to AMMI and GGE biplot analysis for stability study. The IPCA values explained 100% and 98.8% variation in AMMI and GGE biplot respectively. Results from both analyses inferred that the genotypes viz., Mash 114, Mash 1008, VBN (Bg) 4 and VBN 10 were stable across the environments with high mean seed yield per plant. Hence these varieties can be utilized for cultivation in varied environments of Tamilnadu. Besides, the genotypes; MASH 1008, MASH 114, VBN (Bg) 4, VBN 8, VBN 10 and VBN 11 were found to be resistant to MYMV based on the field screening at National Pulses Research Centre, Vamban, Pudukkottai.

Keywords: Blackgram, Stability, AMMI, GGE Biplot, MYMV, Field Screening

INTRODUCTION

Blackgram [*Vigna mungo* (L.) Hepper] is an important short-duration pulse crop which is predominantly grown in South Asian regions during various seasons in rainfed-based agroecosystems (Kaewwongwal *et al.* 2015). It is packed with nutrients and forms a major component of a vegetarian diet because it contains about 24 - 26% protein in addition to other vital vitamins and minerals (USDA National Nutrient Database, 2018). India is the largest producer and consumer of blackgram (Vinothini and Kaleeswari 2022). Blackgram is grown in all seasons like *kharif*, *rabi*, summer irrigated and rice fallow situations. If a variety is suitable for all situations, it would be a gift to

the farming community to raise the crop throughout the year without seasonal boundaries. To identify genotypes with predictable performance that are responsive to environmental variations, it is essential to analyze the adaptability and stability of each genotype to minimize the effects of the GE interaction. Even though numerous superior blackgram cultivars have been cultivated, many of them have primarily fluctuated in terms of yield performance in various regions due to significant GEI. Due to the unreliable performance of genotypes across environments because of GEI, the breeding programme ends up being increasingly challenging (Ebdon & Gauch,

2002). The AMMI model is flexible and effective for comprehending GEI. It shows GEI patterns graphically and encompasses both the additive and multiplicative components of the two-way data structure (Mukherjee *et al.*, 2013). Since, it explains more G+GE than AMMI, the GGE biplot is preferable in terms of mega environment analysis and genotype evaluation. The most widely applied statistical techniques for analyzing the results of multi-environment trials are AMMI and GGE biplot (Gauch 2006; Zhou *et al.*, 2011).

Mungbean Yellow Mosaic is one of the notorious diseases that impair blackgram productivity in most South Asian nations including India, Sri Lanka, Pakistan, and Bangladesh. This disease results in 50% yield reduction in blackgram (Dikshit *et al.*, 2020). It is transmitted by the whitefly, *Bemisia tabaci* (Nene, 1972), which is manageable with prompt insecticide administration. However, the inability and high expense of pesticides make it difficult to effectively control the disease. This research was carried out to gain insight into the nature and magnitude of genotype x environment interaction utilizing AMMI and GGE biplot analysis thus, identifying the stable performer among the genotypes and to disclose the MYMV disease-resistant genotypes in natural epiphytotic conditions during *kharif* season in hotspot region.

MATERIALS AND METHODS

Stability analysis for Seed yield: The experiment was carried out in three locations during *Kharif* 2022 at Agricultural College and Research Institute, Madurai (E1), National Pulses Research Institute, Vamban (E2) and a farmer's field at Vizhuthudayan, Ariyalur district (E3). The details of the environments are presented in **Table 1**. A total of 50 diverse blackgram genotypes were collected from various sources such as National Pulses Research Centre, Vamban; Indian Institute of Pulses Research, Kanpur; Agricultural Research Station, Lam and Tamil Nadu Agricultural University, Coimbatore and were evaluated in a randomized complete block design with two replications in each environment. The data on seed yield per plant (g) was collected from 10 plants per replication and subjected to stability analysis to identify the stable genotype. The genotype x environment (GxE) interaction was studied as per the AMMI model (Zobel *et al.*, 1988) and GGE biplot (Yan, 1999 and Yan *et al.*, 2001). All the analyses were performed using the software PBtools (ver 1.3), International Rice Research Institute, Philippines.

MYMV Screening: The 50 blackgram genotypes were screened for mungbean yellow mosaic virus (MYMV) at National Pulses Research Centre, Vamban in *Kharif* 2022 which is a hotspot for MYMV. The susceptible check, CO 5 was raised in every 10th row to ensure the necessary spread of MYMV as per the infector row technique. All the recommended packages of practices were carried out except for insecticide spray to encourage the building of the whitefly population in the field. The scoring was performed on the 45th day and the 60th day after sowing when the susceptible check, CO 5 showed a maximum scale of 9 for MYMV. The arbitrary score scale of 0-9, proposed by Singh *et al.* (1995) which indicates 1 free (F), 2 highly resistant (HR), 3- resistant (R), 4- moderately resistant (MR), 5-moderately susceptible (MS), 6-susceptible (S), 7- susceptible (S), 8- highly susceptible (HS) and 9- highly susceptible (HS), was used for scoring.

RESULTS AND DISCUSSION

Analysis of variance for each environment revealed that the genotypes were significant in all three environments representing a greater magnitude of genetic variation for the trait, seed yield per plant (g). Further, pooled analysis of variance exhibited significant GxE interaction for seed yield per plant (**Table 2**), hence, stability analysis was performed. Genotypes typically showed variations in their performance in response to different environmental conditions. Stability analysis is an efficient tool used by the plant breeders to comprehend, how a genotype responds to its surroundings. To improve seed yield, stable-performing genotypes must be developed. When developing varieties, the relationship between genotype and environment is crucial. Adaptability and character expression may vary according to the environmental condition, leading to developmental variation in their performances across different environments. Therefore, developing varieties with stable performance across different locations of district and state will be rewarding to improve the overall productivity and production of blackgram.

The AMMI is a hybrid model that includes the two-way data structure's additive and multiplicative parts. The AMMI analysis is an invaluable tool for graphically defining GxE outlines. The biplot display of PCA scores stacked one on top of the other provides a graphic representation and interpretation of the GxE interaction. The combination of biplot presentation and genotypic stability statistics permits the grouping of genotypes based on resemblance

Table 1. Details of the environments under study

Code	Environment	Agroecological zone	Rainfall (mm)	Soil type	Latitude	Longitude	Altitude(m)
E1	Madurai	Southern	855	Sandy Clay loam	9°58' N	78°12' E	134
E2	Vamban	Southern	881	Red laterite	10°22' N	78°54' E	93
E3	Vizhuthudayan	North Eastern	1050	Red loam	11°24' N	79°20' E	45

Table 2. ANOVA for stability (AMMI) analysis for seed yield per plant (g)

Character	Df		Seed yield per plant (g)
Genotypes (G)	49		26.62**
Environment	2		18.03**
Genotype x Environment	98		5.40**
IPCA 1	50	MSS	12.91**
		% Explained	61.00
IPCA 2	48	MSS	8.59**
		% Explained	39.00
MS due to Pooled error	147		0.49

in performance through diverse locations (Mukherjee *et al.*, 2013). The analysis of variance for AMMI showed that the interaction principal component axes *viz.*, IPCA 1 and IPCA 2 were significant for the trait, seed yield per plant (g). The contribution of IPCA 1 and IPCA 2 towards interaction was observed to be 61 and 39% respectively. This revealed that both the components together fully explained the GxE interaction for seed yield per plant (g). Similar results were reported by Dhasaradhan *et al.* (2021) and Sridhar *et al.* (2023).

A stable genotype is one whose performance is constant despite variations in the environment (Karimizadeh *et al.*, 2013). Among the genotypes; G6, G8, G10, G11, G14, G16, G25, G26, G27, G30, G45, G46, G47, G48 and G49 had significantly higher mean seed yield per plant than the grand mean. However, the genotypes, Mash 1008 (25), Mash 114 (G26), VBN (Bg) 4 (G45), VBN 10 (G46) and VBN 8 (G48) exhibited higher mean and IPCA scores nearer to '0' indicating that they are stable genotypes with less environmental interaction (**Table 3** and **Fig. 1**),

which infer that they are suitable for all environments. An environment with the longest spoke is considered more interactive. E2 has the longest spoke of the three environments, implying that it is more interactive than the other two. The AMMI 2 biplot (**Fig. 2**) provides plenty of information about the interaction component but fails to demonstrate the additive main effects. When it comes to AMMI 2 biplots, a genotype is thought to be more stable if it is situated close to the biplot's origin, or in its centre. A genotype with a high mean yield coupled with a high IPCA value indicates the specific adaptability to environments, hence the genotypes; VBG 19-033 (G1), IPU 19-51 (G6), DPU-552 (G13) and KKB 19-005 (G31) can be recommended for cultivation in the specific environment, E2. Other high-yielding genotypes like TBU 236-6 (G9), DPU-238 (G12), CO BG 21-04 (G32) and NIC 15-26 (G34), implying that they constructively interact with the environment and can therefore be encouraged for cultivation in the favorable environment, E3. Based on the AMMI biplots 1 and 2, the genotypes; Mash 1008, Mash 114, VBN (Bg) 4 and VBN 10 were identified as stable

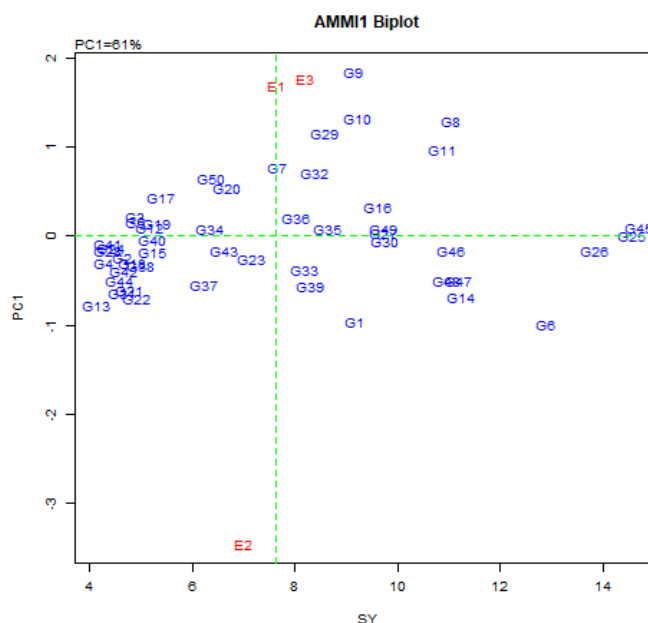
**Fig. 1. AMMI Biplot 1 for seed yield per plant (g)**

Table 3. Mean and IPCA scores of the genotypes and environments for seed yield per plant (g)

Code	Genotype	Seed yield per plant (g)			Code	Genotype	Seed yield per plant (g)		
		Mean	IPCA1	IPCA2			Mean	IPCA1	IPCA2
G1	VBG 19-033	9.17	-0.97	0.36	G29	VBG 18-099	8.58	1.16	-0.14
G2	SVU 6	4.64	-0.24	-0.90	G30	KKB 19-003	9.75	-0.05	0.03
G3	LBG 787	4.88	0.22	0.22	G31	KKB 19-005	4.64	-0.65	-0.04
G4	1PU 13-6	4.27	-0.30	-0.26	G32	CO BG 21-04	8.38	0.71	2.08
G5	VBG 17-021	4.89	0.16	-0.48	G33	N-1	8.20	-0.37	-0.64
G6	IPU 19-51	12.88	-0.99	0.10	G34	NIC 15-26	6.35	0.08	1.21
G7	IPU 18-7	7.67	0.78	-0.29	G35	PBD-103	8.64	0.09	-1.16
G8	MBG 1080	11.04	1.30	-0.34	G36	PDU-31	8.01	0.21	-0.50
G9	TBU 236-6	9.14	1.85	0.39	G37	PLU 446	6.24	-0.54	0.76
G10	C0 5	9.22	1.33	0.14	G38	PLU-1079	5.00	-0.34	-0.01
G11	CO BG 45	10.87	0.97	-0.11	G39	PLU-294	8.29	-0.56	0.24
G12	DPU-238	5.18	0.10	0.78	G40	PLU-608	5.23	-0.04	0.22
G13	DPU-552	4.13	-0.77	-0.17	G41	RU 9-195	4.35	-0.09	-0.41
G14	DPU-6	11.24	-0.68	0.12	G42	STU-22-88	4.66	-0.39	0.25
G15	DPU-99-228	5.22	-0.19	0.65	G43	CO 7	6.62	-0.16	-0.63
G16	IPU 99-224	9.62	0.33	-0.26	G44	VBG 06-019	4.58	-0.50	0.32
G17	KKG-0-3	5.40	0.43	-0.34	G45	VCN (Bg) 4	14.71	0.10	-0.30
G18	KU 9-157	4.84	-0.30	-0.21	G46	VCN 10	11.05	-0.16	-0.48
G19	KU-9-152	5.31	0.15	-1.08	G47	VCN 11	11.18	-0.50	0.22
G20	KU-9-158	6.69	0.55	0.16	G48	VCN 8	12.96	-0.50	0.13
G21	L 13-10	4.77	-0.61	0.24	G49	VCN 9	10.73	0.09	0.48
G22	L-401	4.92	-0.71	0.07	G50	VH 86-47	6.38	0.65	-0.27
G23	L-64	7.16	-0.26	0.30	E1	Madurai	8.22	1.69	-2.70
G24	LBG 17	4.42	-0.14	-0.29	E2	Vamban	7.01	-3.46	0.04
G25	MASH 1008	14.58	0.01	-0.10	E3	Vizhuthudayan	7.66	1.77	2.66
G26	MASH 114	13.85	-0.17	-0.08		Mean	7.63		
G27	MDU 1	9.72	0.03	-0.13		SE	1.49		
G28	VBG 19-010	4.36	-0.16	0.15		CD (5%)	1.87		

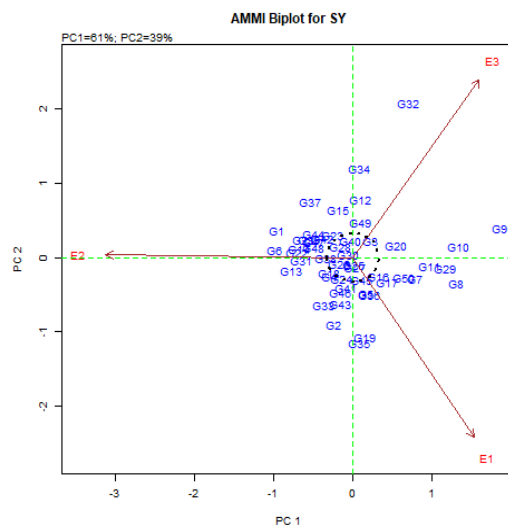


Fig. 2. AMMI Biplot 2 for seed yield per plant (g)

genotypes with high yield potential. The environment which can separate the genotypes should have a high IPCA1 and a low IPCA2. Among the environments, Madurai (E1) had the highest mean for seed yield per plant making it the most favorable environment followed by Vizhuthudayan (E3) and Vamban (E2). Vamban (E2) is the most interactive and discriminative environment so it is a good test environment to cull out the unstable genotypes.

Numerous studies showed that, the environment influences more with the highest magnitude, whereas the main genotype effect and GEI (Genotype Environment Interaction) had a lesser effect in explaining variations. Since, environment is an uncontrollable component, GGE biplot graphically visualizes G plus GE of a MET in a way that makes genotype evaluation and mega environment identification easier. GGE biplot graphically partitions the complex GEI into two distinct principal components (Yan *et al.*, 2000; Yan *et al.*, 2007). The GGE biplot effectively captured 98.8% of variation *via* PC1 (71.8%) and PC2 (27.0%) respectively. This demonstrated that the biplot constructed by the first principal component scores of genotypes and environments against the respective scores of the second principal component adequately represented the environment-centered data. These findings were in harmony with the earlier reports by Jeberson *et al.* (2022) and Parmar *et al.* (2022) in blackgram, wherein they also observed 90% of the total GGE variation in the first two principal components.

The Average Environment Axis (AEA) represents the average coordinate of all the environments being studied. The environment, E1 and AEA bring about an acute angle making it essentially representative of all test environments, whereas E2 is the least representative

environment (Fig. 3). E1 is a suitable test environment for choosing genotypes that are generally acclimated. Since E2 is the least representative and most discriminative, it can be used to rule out unstable genotypes. E1 and E3 together make up a single mega environment, whereas, E2 forms a single distinct mega environment. The Average Environment Coordination Abscissa (AEA), which has just a single arrow, implies that the mean seed yield is escalating. The AEC coordinate with two arrows on it shows the most variation in either direction. With this perspective, the genotypes, G6 (IPU 13-6), G14 (DPU-6), G17 (KKG-0-3), G25 (Mash 1008), G26 (Mash 114), G45 (VBN (Bg) 4) and G46 (VBN 10) were ideal with high mean and less interactive with the environment (Fig. 4).

The “which won-where” biplot as a polygon (Fig. 5) is the best way to interpret the interaction patterns between genotypes and environments and give comprehensive information. The polygon is drawn by joining the farthest genotypes from the biplot origin in such a way that all the other genotypes are within the polygon. The perpendicular lines connecting the sides of the polygon generate parts of genotypes and environments (Hernandez and Crossa 2000). The genotypes on the polygon’s vertices indicate which genotypes perform more effectively in specific environments. The winning genotypes are situated on the vertices of each sector. E1 and E3 are grouped under a single mega environment while, E2 in a separate mega environment with respective winning genotypes at the vertex. The genotype, G1 (VBN 19-033) and G6 (IPU 19-51) are the winning genotypes in the mega environment comprising of E2, whereas, G25 (Mash 1008), G26 (Mash 114) and G45 (VBN (Bg) 4) are winning genotypes in mega environment comprising E1 and E3. Hence, for different mega environments, different genotypes can be identified and suggested for cultivation in the respective locations.

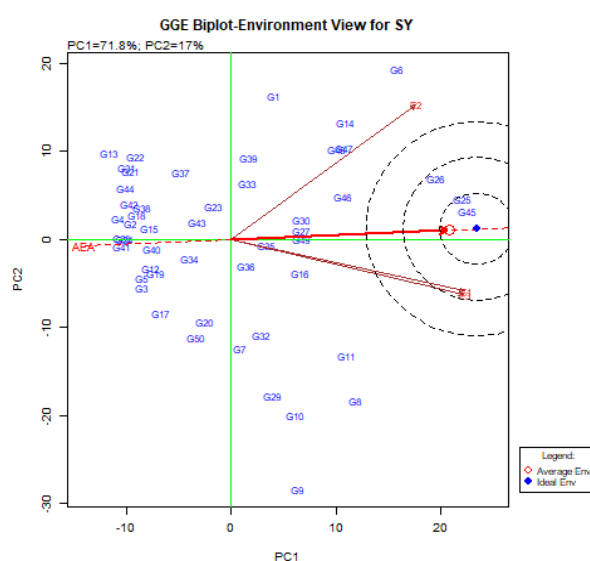


Fig. 3. GGE Biplot- Environment view for seed yield per plant (g)

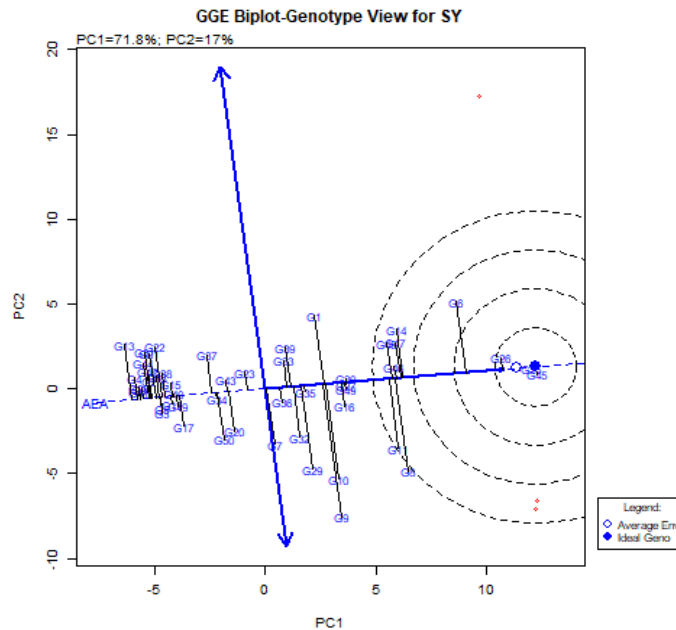


Fig. 4. GGE Biplot- Genotype view for seed yield per plant (g)

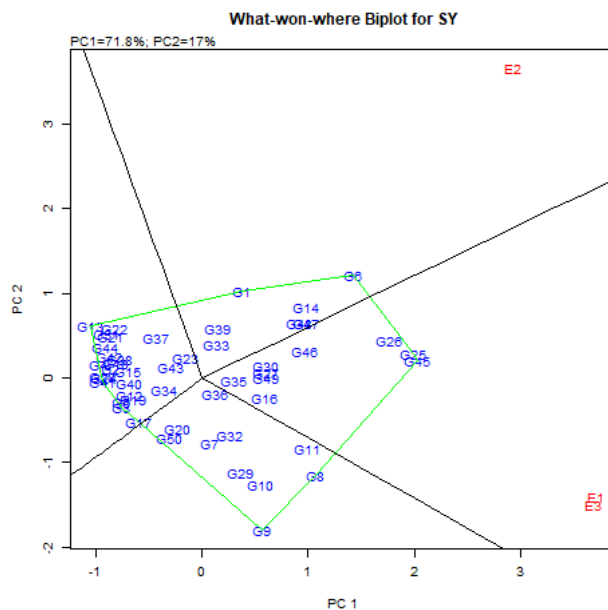


Fig. 5. GGE Biplot- Which won where plot for seed yield per plant (g)

Field screening for MYMV disease resistance: Yellow Mosaic Virus was initially discovered in 1960 in Dolichos (Capoor and Varma, 1950) and in mungbean (Nariani, 1960). It is one of the most destructive viral diseases that lowers productivity of the crop. The reduction in yield is largely due to susceptibility to MYMV (Alam *et al.*, 2014). The phenotypic scoring for MYMV was performed according to Singh *et al.* (1995).

A total of 50 genotypes were categorized into 6 groups based on the MYMV score. The genotypes *viz.*, MASH 1008, MASH 114, VBG 18-099, VBG 06-019, VBN (Bg) 4, VBN 10 and VBN 8 were highly resistant whereas, the genotypes; VBG 19-033, SVU 6, DPU-238, DPU-552, DPU-6, DPU-99-228, L 13-10, L-401, KKB 19-005, PDU-31, PLU-294, PLU-608, VBN 11 and VBN 9 were resistant to MYMV (Table 4). Similarly, Mash 114 has been

Table 4. MYMV disease reaction of the 50 genotypes based on Singh et al. (1995)

S. No.	Mymv Score	Disease Reaction	Number Of Genotypes	Genotypes
1.	2	Highly Resistant (HR)	7	MASH 1008, MASH 114, VBG 18-099, VBG 06-019, VBN (Bg) 4, VBN 10, VBN 8
2.	3	Resistant (R)	14	VBG 19-033, SVU 6, DPU-238, DPU-552, DPU-6, DPU-99-228, L 13-10, L-401, , PDU-31, KKB 19-005, PLU-294, PLU-608, VBN 11, VBN 9
3.	4	Moderately Resistant (MR)	9	1PU 13-6, VBG 17-021, IPU 19-51, KU 9-157, KU-9-152, PLU 446, PLU-1079, RU 9-195, CO 7
4.	5	Moderately Susceptible (MS)	7	LBG 787, IPU 18-7, IPU 99-224, KKG-0-3, L-64, VBG 19-010, KKB 19-003
5.	6	Susceptible (S)	3	N-1, PBD-103, STU-22-88
6.	7	Susceptible (S)	4	VH 86-47, MBG 1080, TBU 236-6, CO BG 45
7.	8	Highly Susceptible (HS)	3	CO BG 21-04, NIC 15-26, MDU 1
8.	9	Highly Susceptible (HS)	3	C 5, KU-9-158, LBG 17

reported to be highly resistant to MYMV by Gill (2018). Nine genotypes viz., 1PU 13-6, VBG 17-021, IPU 19-51, KU 9-157, KU-9-152, PLU 446, PLU-1079, RU 9-195 and CO 7 were identified to be moderately resistant while the other genotypes fall under susceptible category. Hence, the varieties that were highly resistant to MYMV can be utilized as resistant donors in breeding programs.

With regard to the graphical models of AMMI and GGE, the genotypes; Mash 1008, Mash 114, VBN (Bg) 4 and VBN 10 were found to be stable and also had high yield potential. The stable genotypes identified from this study can be used for future breeding programs. High-yielding genotypes for specific environments may be investigated in larger plots and can be used for recombination breeding to obtain ideal segregants for sustainable blackgram production. Besides, the genotypes; MASH 1008, MASH 114, VBG 18-099, VBG 06-019, VBN (Bg) 4, VBN 10 and VBN 8 were highly resistant to mungbean yellow mosaic virus. So, in combination of yield stability and MYMV resistance, the varieties, Mash 1008, Mash 114, VBN (Bg) 4 and VBN 10 were adjudged as best and can be recommended for cultivation for all three environments and also can be used in hybridization to evolve superior, stable and MYMV resistant blackgram genotypes.

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