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Stability Analyses using Regression and AMMI Models for Seed Yield in Blackgram

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ABSTRACT

Background: Blackgram is an important pulse crop grown in almost all agro ecological zones in India. One of the major limitations of pulse cultivation in India is lack of superior genotypes with better adaptation to local conditions. Hence developing high yielding stable blackgram genotypes becomes a necessity to improve the area and production across the country. With this background, the present study was undertaken to identify stable and superior performing blackgram genotypes over seasons.

Methods: The experiment was carried out during *kharif* 2017, *rabi* 2017-18, *kharif* 2018 and *rabi* 2018-19 at National Pulse Research Centre, Vamban. A total of 21 genotypes were evaluated in randomized block design with two replications in each environment. The data on seed yield was subjected to statistical analysis. The G × E interaction was studied as per Eberhart and Russell model, AMMI model and GGE biplot analyses.

Result: In Eberhart and Russell model, the checks VBN 6, VBN 8 and VBN 10 and genotypes VBG 17-019, VBG 17-023 and VBG 17-026 were considered as stable with average response to the environments. In biplot 1 of AMMI analysis, check VBN 8 and genotypes VBG 16-005 and VBG 17-023 were considered as stable with high mean seed yield and less interaction with environment. In biplot 2 of AMMI analysis VBG 16-005 and VBG 007 were less interactive genotypes. GGE biplots indicated that *rabi* seasons are more informative than *kharif* seasons to assess the stability of genotypes. This model identified VBG 17-007, VBG 17-024 and VBG 17-030 as ideal genotype with high mean seed yield and stability. It also identified VBG 17-023 as with high mean seed yield and moderate interaction with environment. Based on the results of all models, the genotype VBG 17-023 was considered as stable genotype with high mean seed yield. Hence, the genotype VBG 17-023 can be tested in larger environments to release for general cultivation.

Key words: AMMI, Blackgram, GGE biplot, G × E interaction, Seed yield.

INTRODUCTION

Pulses play an inevitable role in Indian diet as they are the major contributors of dietary protein particularly for vegetarian population. Higher contribution towards protein makes them as supplement to cereals. Rather being utilized as food and feed; they also involve in improving the soil physical properties and nitrogen content by fixing atmospheric nitrogen. Among the pulses, blackgram is an important pulse crop grown in almost all agro ecological zones in India. The total Indian area under blackgram cultivation is 3.06 million ha with a production of 1.7 million tonnes and productivity of 431 kg/ha (Rampal, 2017). One of the major limitations of pulse cultivation in India is lack of superior genotypes with better adaptation to local conditions. Many improved varieties developed tend to show unstable performances under different environmental conditions which was due to genotype × environment interactions (Shanthi *et al*., 2007). Hence developing high yielding stable blackgram genotypes becomes a necessity to improve the area and production across the country. Developing such stable genotypes may endorse a valuable opportunity to be utilized as a climate change strategy. With this background, the present study was undertaken to identify stable and superior performing blackgram genotypes over environments.

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MATERIALS AND METHODS

The experiment was carried out during *kharif* 2017, *rabi* 2017-18, *kharif* 2018 and *rabi* 2018-19 at National Pulse Research Centre, Vamban. A total of 21 genotypes were evaluated in randomized block design with two replications in each environment. The data on seed yield was subjected to statistical analysis. The G × E interaction was studied as per Eberhart and Russell (1966) using the software, TNAUSTAT (Manivannan, 2014). AMMI model (Zobel *et al*., 1988) and GGE biplot (Yan, 1999 and Yan *et al*, 2001) analyses were carried out using the software, PB tools (ver 1.3) developed by International Rice Research Institute, Philippines.

RESULTS AND DISCUSSION

Data on each environment were analyzed separately. The results indicated that genotypes were found to be significant in all the three environments indicating that there is greater magnitude of genetic variation for the character seed yield taken under study. Further, the data on all the three locations were subjected in to pooled analysis of variance for seed yield (Table 1). The results indicated that the genotypes and environment had significance indicating the presence of variation among the genotypes and environments taken under study. The variance due to genotype × environment was found significant indicating the influence of G × E Interaction. Hence the data was subjected into stability analyses.

Table 1: Analysis of variance (mean squares) (Eberhart and Russell, 1966).

Source of variation	df	MS
Genotype	20	57763.60*
Environment + (Genotype × Environment)	63	128651.55*
Environment	1	4496597*
Genotype × Environment	20	79895.37*
Pooled deviation	42	47870.13*
Pooled error	80	6117.19

*Significance at 5% level.

Table 2: Genotypic means with stability parameters for seed yield (kg/ha).

Code	Genotype	Mean (Xi)	bi	S^2di
G1	VBG12-062	777	0.20	13724.80*
G2	VBG12-110	856	0.23	21970.31*
G3	VBG13-003	778	-0.02	14761.58*
G4	VBG14-016	874	0.36	126300.44
G5	VBG16-005	1009	1.06	11028.99**
G6	VBG17-005	824	0.67*	-1679.16**
G7	VBG17-007	970	0.68	49718.00
G8	VBG17-012	916	1.27*	10806.95**
G9	VBG17-014	721	0.23	1380.18**
G10	VBG17-019	1208	1.13	52279.23
G11	VBG17-021	835	1.81	56646.08
G12	VBG17-023	1099	1.62	92096.17
G13	VBG17-024	1007	1.82*	8021.62**
G14	VBG17-025	997	1.61	37471.35
G15	VBG17-026	1058	1.32	31305.06
G16	VBG17-029	1071	1.96*	15988.02*
G17	VBG17-030	1009	1.36*	8274.31**
G18	VBG17-032	923	0.49	39308.93
G19	VBN 6 (Check)	905	1.50	68551.17
G20	VBN 8 (Check)	959	0.64	126643.23
G21	VBN 10 (Check)	876	1.06	92212.95
	Mean	936.7		
	SE	129.4		
	CD (P=0.05)	115.4		

*Significance at 5% level; **Significance at 1% level.

Stability analysis by Eberhart and Russell model (1966)

The G × E interaction is further partitioned into linear and non-linear components. Both linear and non linear components were found to be significant indicating the presence of both stable and non stable genotypes in the study. The results were similar with the outcomes of Manivannan *et al*. (1997), Manivannan (1999), Natarajan (2001) and Manivannan *et al.* (2002).

Eberhart and Russell (1966) suggested that both linear (bi) and non-linear (S^2di) components of G × E interaction should be considered in determining the phenotypic stability of a particular genotype. In the present study, stability parameters such as mean (Xi), regression coefficient (bi) and deviation from regression (S^2di) are considered as per the suggestions of Eberhart and Russell (1966) to assess the stability of different genotypes for seed yield. The stability parameters Xi, bi and S^2di for seed yield was presented in Table 2. Among the check varieties, VBN 8 (959 kg/ha) recorded highest seed yield. Among the test genotypes *viz*., VBG 17-019 (1208 kg/ha) has the highest mean value followed by VBG 17-023 (1099 kg/ha), VBG 17-029 (1071 kg/ha), VBG 17-026 (1058 kg/ha). These genotypes showed better performance than checks where as rest of the genotypes were on par with checks.

According to Eberhart and Russell (1966), a stable genotype should have high mean with minimum S^2di. Considering the stability parameter S^2di, all the checks VBN 6, VBN 8 and VBN 10 showed non significant S^2d and hence stable. Among the high yielding genotypes, VBG 17-019, VBG 17-023 and VBG 17-026 recorded non significant S^2d and hence stable. With regard to the response to the environment, all stable genotypes had b=1, hence considered as average responsive to the environment. All the stable genotypes can be recommended to all environments.

Stability analysis suggested by Eberhart and Russell (1966) is based on additive model alone. Many researchers used this model to assess the G × E interaction and identified stable genotypes. However, due to the fact that the G × E consists of both additive and multiplicative model, the recent researchers used the AMMI model. Hence, the present data was used to analyse in both models to compare the results.

Stability analysis by AMMI model (Zobel *et al*., 1988)

The AMMI model includes both additive and multiplicative components and hence may be considered as an effective method to analyze the G × E interaction effect. By integrating the biplot and genotypic stability statistics, it ensures the grouping of genotypes having similar performances across diverse environment (Mukherjee *et al*., 2013).

The analysis of variance for AMMI analysis showed that the interaction principle component axes *viz*., IPCA1, IPCA2 and IPCA3 were significant for seed yield. Similar results were observed by Tiwari *et al* (2018) and Yihunie and Gesesse (2018). The IPCA1, IPCA2 and IPCA3 contribute 46.3%, 37.5% and 16.2% to the interaction respectively. This

indicates that all the components together fully explained the G × E interaction for seed yield.

A stable genotype is one whose performance is unchanged regardless of any variation in environment (Karimizadeh *et al*., 2013). The mean and IPCA scores for the genotypes and environment under study was presented in Table 3 and Fig 1. Among check varieties, VBN 8 (959 kg/ha) recorded superior mean seed yield. Among the check varieties, VBN 6 had higher IPCA 1 values while VBN 8 and VBN 10 had relatively less IPCA1values. Hence considering the mean IPCA values, the check VBN 8 is considered as best variety with less interaction. Among high yielding genotypes, the genotype VBG 16-005 and VBG 17-023 has high mean value than the best check VBN 8 and their IPCA1 values are also nearer to zero indicating that these genotypes are stable. Hence it can be grown in all environments. Other high yielding genotypes *viz*., VBG 17-019, VBG 17-024, VBG 17-025, VBG 17-026, VBG 17-029 and VBG 17-030 had IPCA 1 values more than zero indicating that they positively interact with the environment. Hence these genotypes can be recommended for cultivation in favourable environment E2, which also has high and positive IPCA1 value.

In AMMI biplot 2 (Fig 2), the environment having the longer spoke is said to be more interactive. Among environments, E4 and E2 (both *rabi* seasons) has the longest spoke. Hence the *rabi* seasons are considered as more interactive than *kharif* seasons. Considering the genotypes, those genotypes are nearer to the origin are considered to be less interactive with environments. Based on this criterion, genotypes G5 (VBG 16-005) and G7 (VBG 17-007) were considered as less interactive genotypes with environments. Based on AMMI biplot and 1 and 2, the genotypes VBG 16-005 was identified as stable genotypes with high seed yield.

Table 3: Mean and IPCA scores for the genotypes and environments.

Code	Genotype	Mean Yield	IPCA1	IPCA2	IPCA3
G1	VBG12-062	777	-10.11	4.40	5.43
G2	VBG12-110	856	-8.33	7.51	5.99
G3	VBG13-003	778	-14.03	0.38	-3.34
G4	VBG14-016	874	-13.11	-10.01	-4.07
G5	VBG16-005	1009	-1.17	-3.17	5.31
G6	VBG17-005	824	-2.95	4.16	0.86
G7	VBG17-007	970	-2.24	2.40	-12.60
G8	VBG17-012	916	1.37	-6.21	-1.84
G9	VBG17-014	721	-7.73	7.53	-0.14
G10	VBG17-019	1208	5.14	5.31	-8.37
G11	VBG17-021	835	13.32	4.76	3.77
G12	VBG17-023	1099	1.95	-15.30	0.94
G13	VBG17-024	1007	7.47	-8.77	3.85
G14	VBG17-025	997	3.53	-10.48	5.56
G15	VBG17-026	1058	5.90	1.17	-8.05
G16	VBG17-029	1071	12.60	-3.72	-5.00
G17	VBG17-030	1009	3.23	-5.26	-3.77
G18	VBG17-032	923	-9.55	-4.17	3.41
G19	VBN 6 (Check)	905	9.52	6.85	6.41
G20	VBN 8 (Check)	959	2.12	14.79	-6.55
G21	VBN 10 (Check)	876	3.05	7.85	12.21
E1	*Kharif* 2017	706	-14.77	16.56	16.24
E2	*Rabi* 2017-18	1314	29.73	-3.48	6.54
E3	*Kharif* 2018	802	-1.20	13.35	-21.33
E4	*Rabi* 2018-19	925	-13.76	-26.44	-1.45

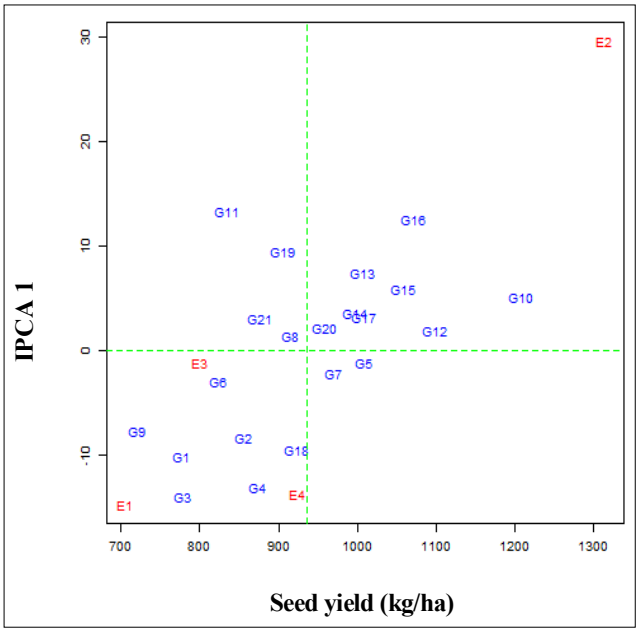

Fig 1: AMMI Biplot 1.

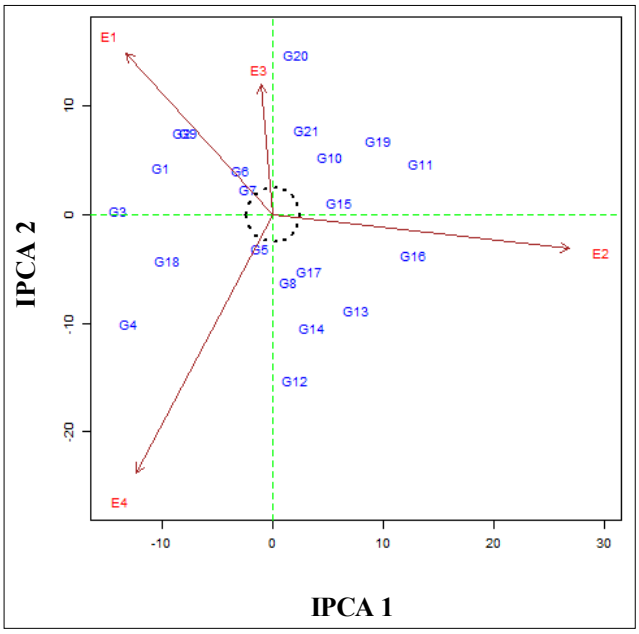

Fig 2: AMMI Biplot 2.

Stability analysis by GGE Biplot

The GGE-Biplot approach is preferred to AMMI since only G and G×E are important and E is not important and therefore only these components must be simultaneously considered (Yan *et al*. 2007). GGE biplot helps in identifying G×E interaction pattern of data and provides us with clear picture of which genotype performs best in which environments and thus facilitates mega-environment identification than AMMI. Otherwise, both GGE and AMMI models are equivalent as far as their accuracy is concerned (Gurmu *et al*. 2012).

Relationship among test environment

In the Fig 3, among the environmental vectors E2 and E3, E2 and E4 are found to be positively correlated (acute angle) whereas, E1 and E2, E1 and E3, E1 and E4 vectors form obtuse angle and hence they are negatively correlated. Environments E3 and E4 form right angle and hence not correlated between them. Longer the distance between environmental vectors indicates that they are dissimilar in discriminating the genotypes. From the Fig 3, E2 and E3 form one group whereas E1 and E4 form two different groups. This indicated that the season wise performance has lot of difference over years. The environment vector of E2 is the longest indicating that it is the environment with most discriminating ability followed by E4 while E3 and E1 is least discriminating environment. This indicated that the *rabi* season has more discriminating environment than the *kharif* season.

Representativeness of environment

Average environmental axis (AEA) is the average coordinates of all test environments. It passes through the origin and average environment. From Fig 4, the environment E2 forms smaller angle with AEA indicating that E2 is the most representative of all test environments while E1 is least representative. E2 is both discriminating and representative and hence it is the good test environment for selecting generally adapted genotypes. E4 is also discriminating environment but less representative environment. Hence this environment is useful to select specifically adapted genotypes and cull out unstable genotypes. These results indicated that *rabi* seasons are more informative than *kharif* seasons to assess the stability of genotypes.

Ideal test environments and mega environments identification

The centre of the concentric circles is a point on the AEA at the distance of the longest environmental vector from the origin in the positive direction. E2 is the closest to this point and therefore it is the ideal test environment for selecting genotypes adapted to all environments. E1 is the poorest environment. From Fig 4, E2 and E3 form a single mega environment whereas E1 and E4 form a mega environment each.

Genotype evaluation based on GGE biplot

In the Fig 5, both genotype and environmental vectors are taken into account for understanding the specific interaction between genotype and environment. The performance of the genotypes G1, G2, G3, G6, G9, G11, G19, G20 and G21 are better than average (acute angle) in E1. G18 is near average performer (right angle) in E1 while rest of the genotypes are poorer than average in E1. In E2, the genotypes; G5, G8, G10, G11, G12, G13, G14, G15, G16, G17, G19 and G20 are above average performers. G21 is near average performer while rest of the genotypes are poorer than average in E2. In E3, the genotypes; G10, G11, G13, G14, G15, G16, G17, G19, G20 and G21 are above average performer while G12 is near average performer.

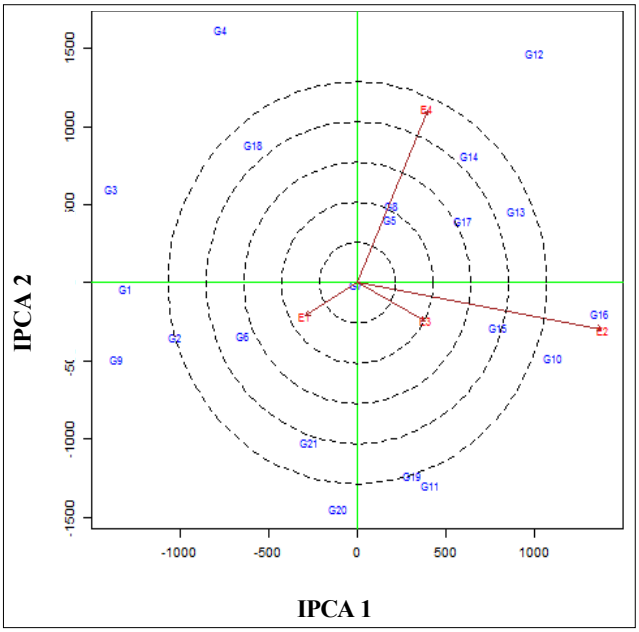

Fig 3: GGE Biplot-Environment view for seed yield kg/ha.

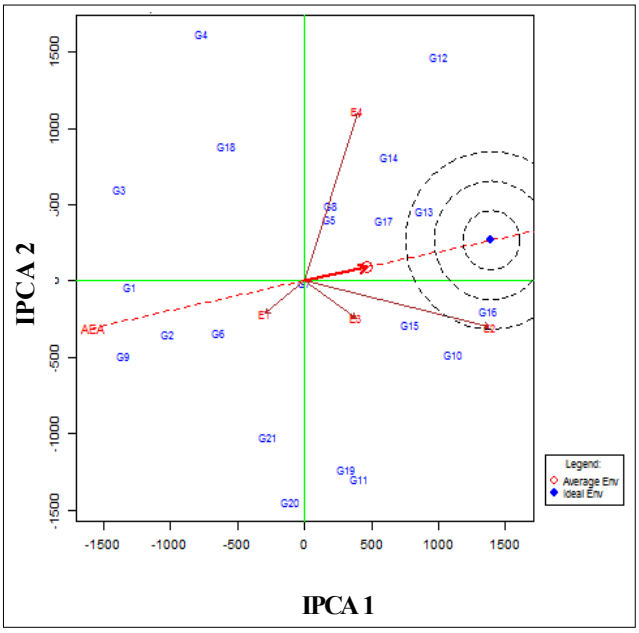

Fig 4: Environment view for yield.

In case of E4, genotypes G4, G5, G8, G12, G13, G14, G16, G17 and G18 are above average in performance while G3 and G15 are near average performer. Rest of the genotypes has below average performance in E4.

Mean performance and stability of the genotype

Single arrowed line is the Average Environment Coordination abscissa (AEC) (Fig 6). It points to higher mean yield across environments. The double arrowed line is the AEC coordinate representing highest variation in either direction. Hence the genotypes, G2, G5, G6, G7, G8, G9, G13 and

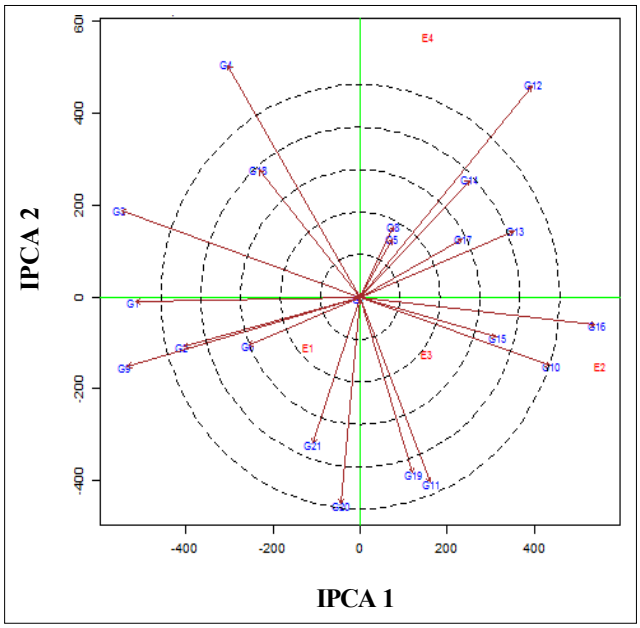

Fig 5: Genotype view for seed yield kg/ha.

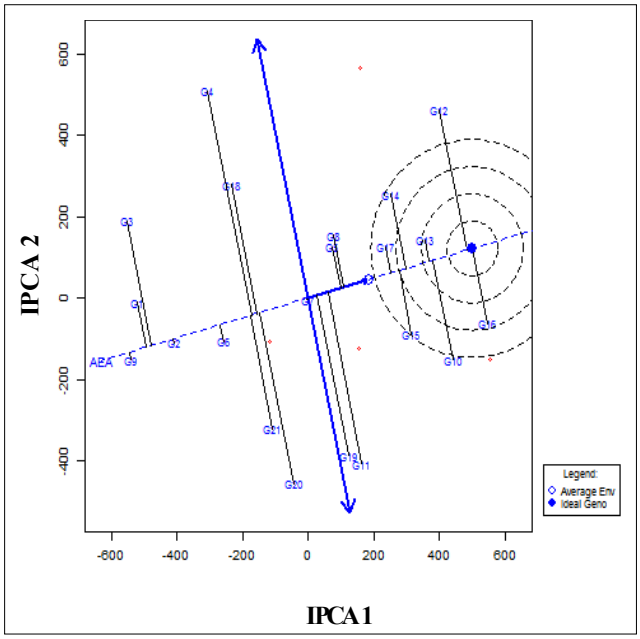

Fig 6: Genotype view for seed yield kg/ha.

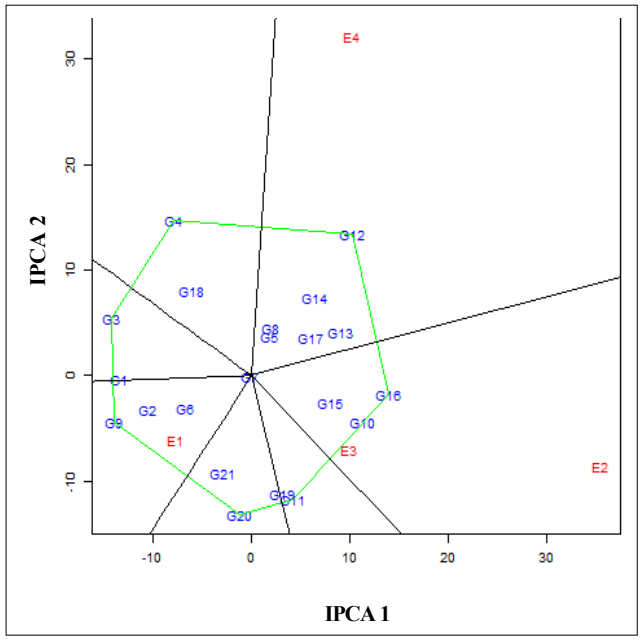

Fig 7: What-won where biplot for seed yield kg/ha.

G17 are stable whereas others are highly interactive with environment. Ideal genotype should have high mean and stability across environments. Hence the genotypes G7 (VBG 17-007), G13 (VBG 17-024) and G17 (VBG 17-030) are found to be ideal with high mean and stability. Genotype VBG 17-023 is identified as high mean with moderately interactive with environment.

Which-won-where: GGE biplot

The genotype on the vertices of the polygon indicates that they are either best or poorest performers in one or more environments (Fig 7). G12 is best performer in E4. Genotypes G11 and G16 are best in E2 and E3 whereas G9 and G20 are best in E1. These genotypes perform poorer in other environments. The equality line divides the biplot into different sectors and winning genotypes are located on the vertex of each sector. G12 (VBG 17-023) in mega environment consisting E4; G11 (VBG 17-021) and G16 (VBG 17-029) in mega environment containing E2 and E3; G9 (VBG 17-014) and G20 (VBN 8) in mega environment containing E1 are the winning genotypes. Hence for different mega environments, different genotypes have to be selected and deployed for each.

CONCLUSION

Based on the foregoing discussion on various stability modeles, it can be concluded that genotype VBG 17-023 was found as stable genotypes with high seed yield. Hence, it can be tested in larger environments to release for general cultivation.

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