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AMMI and GGE Biplot Analysis of Multi-environmrnt Seed Yield Data in Cluster Bean [*Cyamopsis tetragonoloba* (L.) Taub.]

Manish Sharma, P.J. Patel, P.R. Patel, M.P. Patel

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ABSTRACT

Background: Cluster bean is a drought tolerant, warm season legume crop, cultivated mainly as a rain fed crop in arid and semi-arid regions of India. The productivity of guar seed is low as it is cultivated in varied and harsh environments so development of new varieties with stable performance over environments as well as identification of discriminative environments for proper testing of cultivars is absolutely essential.

Methods: In the present study, 13 guar genotypes developed by pedigree method of breeding at Pulses Research Station, SDAU, S.K.Nagar were evaluated for yield performance during *kharif* 2020, at eight different locations. Pooled analysis of variance and stability analysis was performed by AMMI and GGE biplot.

Result: The results of pooled analysis indicated the presence of significant G × E interaction (GEI) for seed yield and hence the data was subjected to stability analysis. From stability analysis, it was evident that the genotypes *viz*., G8, G4, G2 and G5 were with high mean values for the trait concerned and exhibited less variation over environments whereas other genotypes had a greater variation with the environment. Among the environments, E7 (VIJ)) was found to be the best test environment having high discriminative ability and representativeness for selecting generally adapted genotypes.

Key words: AMMI, Cluster bean, GGE biplot, Seed yield, Stability.

INTRODUCTION

Cluster bean [*Cyamopsis tetragonoloba* (L.) Taub.], commonly known as guar, an annual legume with drought hardiness, high temperature tolerance and deep root system suited to arid and semiarid regions. The qualities of the crop like high adaptation towards erratic rainfall, multiple industrial uses and its importance in different cropping system for factors such as soil enrichment properties, low input requirement have made the guar one of the most significant crops for farmers in arid and semiarid regions (Gresta *et al*., 2014, Santhosha *et al*., 2017). Guar crop has experienced a remarkable journey from a traditional crop grown on marginal lands mainly for food, animal feed and fodder to a crop with various industrial usages ranging from food, cosmetics, printing, pharma textile, *etc*. (Sharma, 2012) The unique binding, thickening and emulsifying properties of guar gum powder obtained from guar seed has made it a much sought after product in international market.

Guar is a native to the Indian subcontinent. The crop is mainly grown in the dry habitats of Rajasthan, Haryana, Gujarat and Punjab and to a limited extent in Uttar Pradesh and Madhya Pradesh. India is the major producer and exporter of guar to the world market. In India, Guar seed is being cultivated mainly in arid and semiarid regions covering about 3.4 million hectares with a production of 1.3 million tonnes with productivity of 378 kg/ha during 2018-19 (Project Co-ordinators Report, AINP on Arid Legumes 2020). The productivity of guar seed is low as it is cultivated in varied and harsh environments hence assessing the interaction between genotypes and environments resulting in high yield potential is the need of the hour. The yielding potential of the genotypes will be greatly affected if grown under different environmental conditions. The crop which performs better in varied climatic situations will be an ideal one (Gresta *et al*., 2018). Adaptability and stability of genotypes to different kinds of environments with low, marginal and average, as well as high, yielding potential can be assessed by studying phenotypic characters of the crop cultivars. Grain yield is more complicated phenomena determined by polygenes and environmental factors. The growing environment often masks the potential genetic expression, leading to poor genetic gain from artificial selection, especially for quantitative traits such as grain yield (Wankhade *et al*., 2017). Thus, it becomes necessary to understand the effect of environment on characters and its performance in a specified environmental condition, which can be achieved

Pulses Research Station, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar-385 506, Gujarat, India.

Corresponding Author: Manish Sharma, Pulses Research Station, Sardarkrushinagar Dantiwada Agricultural University, ardarkrushinagar-385 506, Gujarat, India.
Email: manisharmagpb@sdau.edu.in

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by studying genotype and environment interactions (GEI). GEI also effects the genetic gain, recommendation and selection of cultivars with wider adaptability (Lal *et al*., 2019). G × E analysis involves evaluation of novel selections across representative growing environments, which will assist breeders to recommend promising genotypes based on their narrow or broad adaptation. G × E analyses are valuable during the final stages of selection of elite breeding materials too. Several statistical techniques have been widely adapted to analyze and interpret G × E data, including the additive main effect and multiplicative interaction (AMMI) effect and the genotype main effect plus genotype-by-environment interaction (GGE) biplot analysis (Yan *et al*., 2007). Accordingly, present study aimed to evaluate the effects of G × E interaction and yield stability among advance breeding lines of guar and to identify promising genotypes with narrow or broader adaptation for grain productivity and stability.

MATERIALS AND METHODS

The study comprised of thirteen guar genotypes/lines including two checks (Table 1) developed at Pulses Research Station, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar, Gujarat, India. The purelines were mainly obtained by hybridization followed by the pedigree method of selection. The advanced strains selection was performed, focusing on the productivity of the grains, earliness, architecture of the plants, quality of the grains and resistance to diseases and pests. The present investigation was carried out during *kharif* 2020 at eight locations covering different agro-ecological zones of Gujarat (Table 2). Experimental material was evaluated in randomized complete block design with three replications in each environment. Experimental units consisted of 8 rows of 4 m length with spacing of 20 cm within and 45 cm between rows. The crops were established under rainfed conditions with supplementary irrigation as and when required. Six middle rows (net plots) were harvested to estimate grain yield per plot, later converted to yield per hectare (t ha^{-1}). The outer rows were not used for yield estimation in order to control border effects and to minimize experimental error. The data on seed yield were subjected to statistical analysis. The G × E interaction was studied as per AMMI model (Zobel *et al*., 1988) and GGE biplot (Yan *et al*., 2001). Analyses were carried out using the software, PB tools (ver 2.0) developed by International Rice Research Institute, Philippines.

Table 1: List of guar genotypes used in the study and their parentage.

Code	Genotype	Parentages
G1	GG 1612	GAUG 0013 × F-5-1
G2	GAUG 1305	GAUG 0005 × IC 370730
G3	GG 1808	GAUG 0513 × IC 370730
G4	GG 1 (C)	Mutant of Kutch 8
G5	GG 1804	GG 2 × PNB
G6	GAUG 1502	GAUG 0005 × IC 370730(I)
G7	DRLGG 13-28	Local selection
G8	GAUG 1507	HG 365 × IC 370730 (I)
G9	DRLGG 13-23	Local selection
G10	GG 1806	GAUG 0005 × IC 370502
G11	GG 2 (C)	Mutant of HG 75
G12	GG 1609	HG 365 × IC 370730
G13	GG 1802	GG 2 × IC 373497

RESULTS AND DISCUSSION

The data recorded in each of the eight environments were subjected to statistical analysis which indicated that genotypes were significant in each of the environment. Further, the data on all the locations were subjected in to pooled analysis of variance for seed yield. (Table 3). The results indicated the presence of significant G x E interaction (GEI) for seed yield and hence the data was worthy to be subjected to stability analysis. Benakanahalli *et al.* (2021) also reported similar results for seed yield in guar. The large sum of squares and significant effect for environments demonstrated that the eight locations where the experiments carried out are having diverse agro climatic conditions resulting in difference for environmental means causing variation in seed yield. This variation is useful when intending to study the effects of GEI, as well as to evaluate the phenotypic stability of genotypes. The GEI is of major concern to plant breeders because a large interaction can reduce gains from selection and make the identification of superior cultivars difficult. Measuring GEI is important to determine an optimum strategy for selecting genotypes adapted to target environments.The observed GEI in the AMMI model have been partitioned among the first and second interaction principal components axes (IPCA) which

Table 2: Different environments used in the present study.

Environment	Place	Altitude	Latitude	Longitude
E1 (SKN)	Sardarkrushinagar	164 m	24.32347395	72.31582424
E2 (DEE)	Deesa	137 m	24.2594977	72.1803348
E3 (KOT)	Kothara	38 m	23.1263951	68.9440198
E4 (DER)	Derol	88 m	22.6299886	73.4619771
E5 (RAD)	Radhanpur	29 m	23.8315668	71.6103884
E6 (DEV)	Devgadhbariya	197 m	22.7014918	73.9088415
E7 (VIJ))	Vijapur	132 m	23.5615483	72.753396
E8 (BHU)	Bachau	15 m	23.8433797	70.2626539

Table 3: Pooled ANOVA for seed yield (kg/ha) in guar.

Character	Genotype	Environment	GEI	Pooled error
	Mean sum of squares			
Degree of freedom	12	7	84	192
Seed yield (Kg/ha)	551024.47**	13423995.77**	136084.24**	4674.94

Table 4: ANOVA of stability (AMMI) for seed yield (kg/ha) in guar.

Character	IPCA 1		IPCA 2	
	MS	% explained	MS	% explained
Seed yield (Kg/ha)	214672.25**	50.7	139157.55**	29.2

were significant for Seed yield and accounted for 50.7% and 29.2%, respectively, together explaining 79.9% of the total variation (Table 4). This was in agreement with Rajalakshmi *et al*. (2021) where 90% of the total variation was explained in IPCA 1 and IPCA II for seed yield in blackgram.

Evaluation of different genotypes in a multi-environment and/or year is not only important to determine high-yielding cultivars but also to identify sites that best represent the target environment. Therefore in AMMI 1 biplot, Yan et al., (2007) demonstrated that genotypes that appear almost on a perpendicular line have similar means and those that fall almost on a horizontal line have similar interaction patterns. Further genotypes with large IPCA 1 scores in both positive as well as negative directions have high interactions, whereas genotypes with IPCA 1 scores near zero have small interactions. Therefore AMMI 1 biplot (Fig 1), depicted that four of the eight environments (E1 (SKN), E3 (KOT), E4 (DER) and E8 (BHU)) had below-average main effects and were poor. Environments E5 (RAD), E2 (DEE) and E7 (VIJ)) had the highest main effects and were favorable to the performance of most of the genotypes. Most preferable environment, having higher main effect values and lower interactions was E5 (RAD) while E3 (KOT) was the most undesired one. Considering the genotypes, G1, G2, G4, G6 which recorded high mean and IPCA values near zero were considered stable. With regard to AMMI 2 biplot (Fig 2) the high yielding genotypes, G1, G5 and G9 were nearer to the origin and hence less interacting with the environment. Considering both biplots, three genotypes G1, G5 and G9 can be recommended for cultivation in these diverse locations as they are stable across environments. Cruz *et al*. (2020) also classified genotypes and environments accordingly and obtained similar results in cowpea.

Stability analysis by GGE biplot

The GGE-Biplot of Yan *et al*. (2000) was utilized for evaluating GEI and stability of the genotypes under study. When using the GGE Biplot method in the selection of high-yielding wheat genotypes Yan *et al*., (2000) reported the occurrence or formation of mega-environments, suggesting the recommendation of genotypes more adapted in a specific way, according to the tested environments, being able to explore better performances and consequently greater productivity. The GGE-Biplot approach is preferred to AMMI since only G and GEI are important and E is not important and therefore only these components must be simultaneously considered. (Yan *et al.,* 2007). Moreover GGE biplot best interprets GEI pattern and gives an obvious view of which variety performs best in which environment and thus facilitates mega-environment identification than AMMI (Gurmu *et al*. 2012).

Environment evaluation based on GGE biplots

Relationships among test environments

The lines that connect the test environments to the biplot origin are called environment vectors and the cosine of the angle between the vectors of two environments approximates the correlation between them. From Fig 3, E4 (DER) and E6 (DEV) were positively correlated, similarily E2 (DEE), E1 (SKN) and E5 (RAD) were positively correlated while this group was negatively correlated to E4 (DER) and E6 (DEV) implying that the GE is moderately large. Thus we can classify eight environments into two groups, one comprising of E4 (DER) and E6 (DEV) and remaining one having all other environments. This close association among second group of environments implies that the same information about the genotypes can be obtained from fewer test environments.

Discriminating power and the representativeness of the environments

The study assessed the discrimination power and the representativity of the environments. From Fig 3 it is indicated that environments E7 (VIJ)) and E2 (DEE) are the most discriminating while E8 (BHU) is the least discriminating hence such a non discriminating test environment should not be considered as they provide little information on the test genotypes. From Fig 4, it is observed that E7 (VIJ)) is the most representative since it forms a smaller (acute) angle with average environment axis (AEA) while E1 (SKN) and E6 (DEV) are the least representative

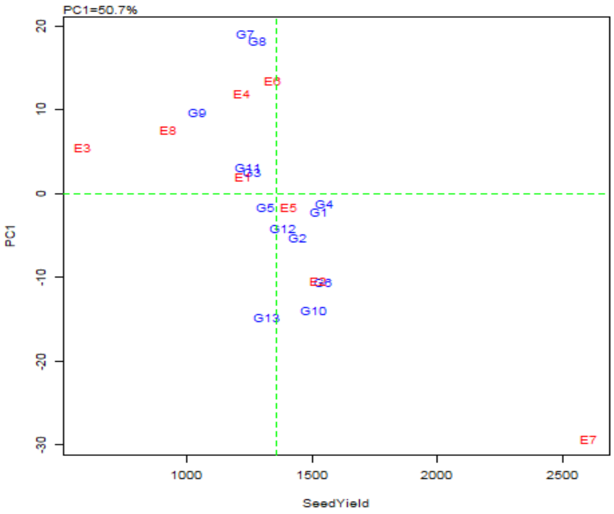

Fig 1: AMMI biplot 1 for seed yield.

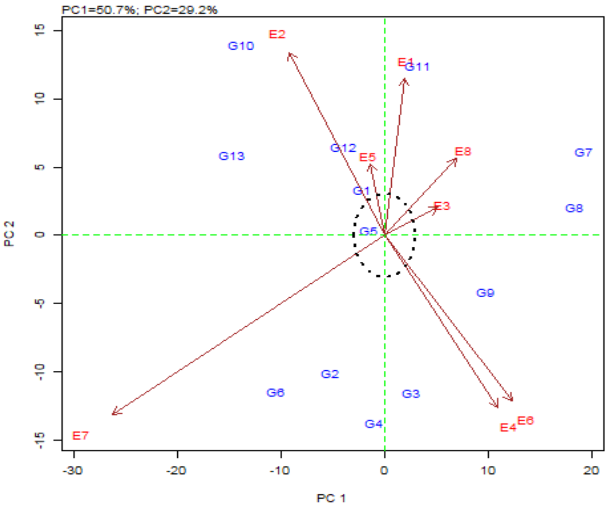

Fig 2: AMMI biplot 2 for seed yield.

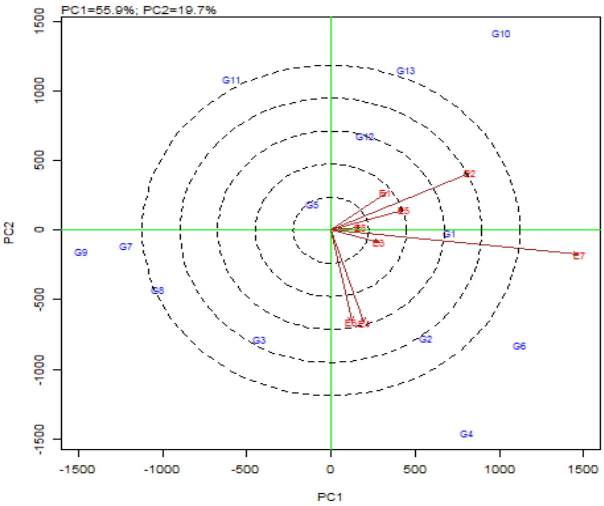

Fig 3: Relationship among environments.

environment. Therefore E7 (VIJ)) can be considered as the best test environment having high discriminative ability and representativeness for selecting generally adapted genotypes. Further E1 (SKN) and E6 (DEV) are discriminating but non-representative test environments indicating the usefulness of these environments in selecting specifically adapted genotypes.

Genotype evaluation based on GGE biplot

Performance of the genotypes in specific environments

From Fig 5 the performance of each genotype in each environment can be visualised. None of the genotype performed above average when considered all the environments together though specific to each environment genotypes performed exceptionally well. Genotypes, G2 ,G6 and G4 performance were above average while genotypes G3, G7, G8 and G9 were below average in the most discriminating and representative E7 (VIJ) environment.

Mean performance and the stability of the genotypes

Genotypes were evaluated on both mean performances and stability across environments (Fig 6). The AEA line points to higher mean yield across environments. Thus, G8 had the highest mean yield, followed by G4 and G2 while G9 and G7 had the lowest mean yield. The double-arrowed line is the AEC cordinate pointing towards greater variability (poorer stability) in either direction. Thus, G10 and G13 were highly unstable whereas G8 was highly stable. The genotypes *viz*., G8, G4, G2 and G5 were with high mean and less variation over environments whereas other genotypes exhibited greater variation with the environment. Jain and Patel (2012) also reported stable genotypes across environments.

Which-won-where

One of the most attractive features of a GGE biplot is its ability to show the which-won-where pattern of a genotype by environment dataset as it addresses important concepts such as crossover GE, mega-environment differentiation and specific adaptation, *etc*. (Yan and Tinker, 2005). In Fig 7, a polygon is drawn on genotypes that are furthest from the biplot origin so that all other genotypes are contained within the polygon. Then perpendicular lines to each side of the polygon are drawn, starting from the biplot origin. The genotype on the vertices of the polygon indicates that they are either best or poorest performers in one or more environments. Accordingly, the genotype G6 performed best in E7 (VIJ)) and E3 (KOT) environment while genotype G4 performed best in E4 (DER) and E6 (DEV) environments while genotype G10 was best performer for all other test environments. This pattern suggests that the target environments may consist of three mega environments and different genotypes should be selected and deployed for each. Further G3 and G8 are located on the line that connects G4 and G9 which means that the rank G4>G3>G8>G9 holds true in all the environments.

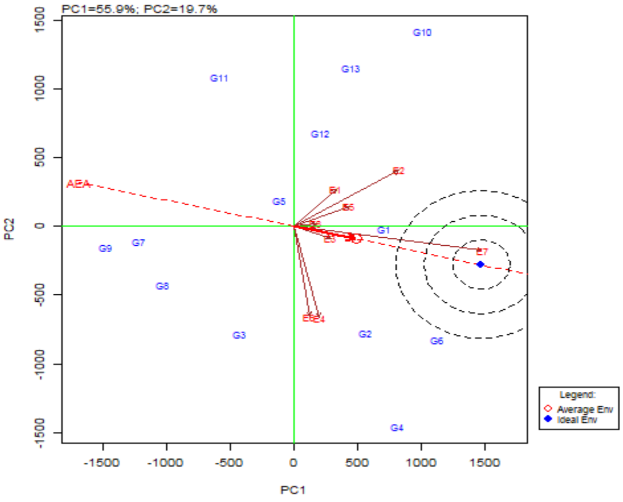

Fig 4: Discriminating ability and representativeness of test environments.

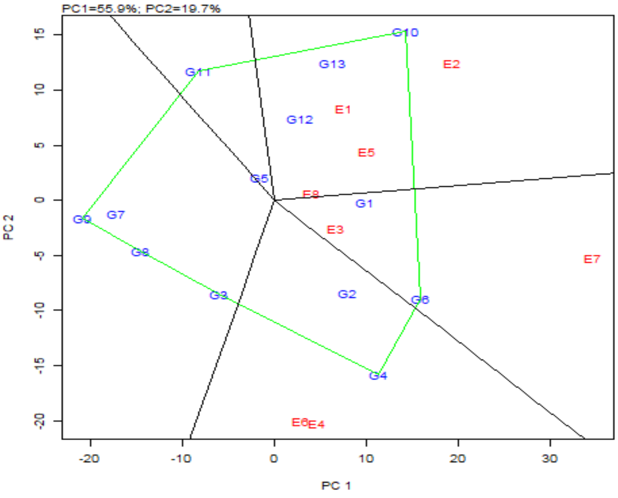

Fig 7: Which-won-where biplot for seed yield.

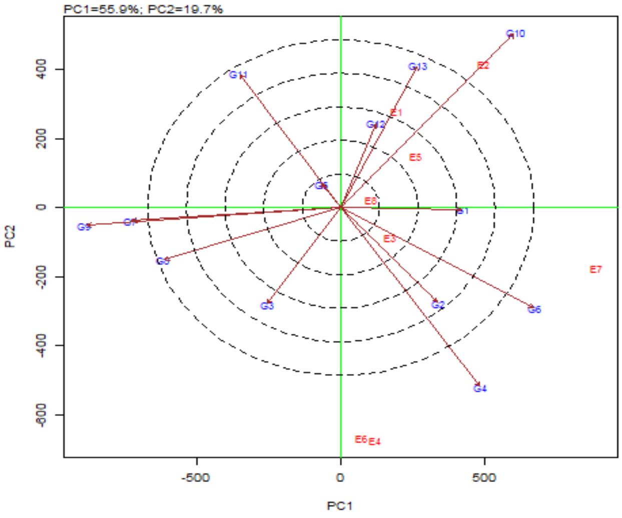

Fig 5: Performance of genotytpes in each environment.

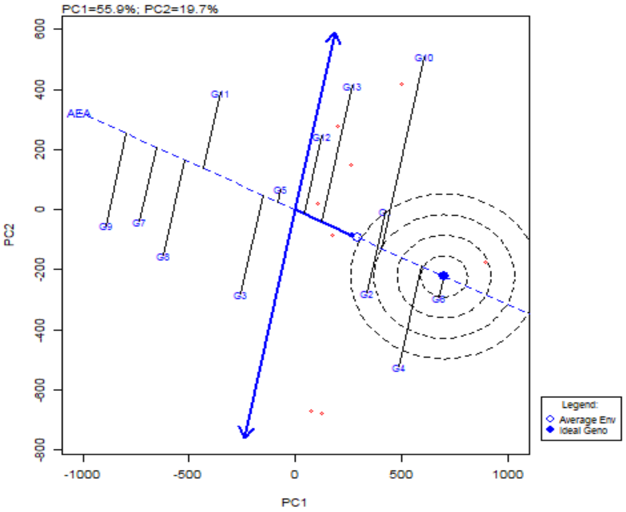

Fig 6: Mean performance and stability of genotypes.

CONCLUSION

Genotypes cultivated under different environmental conditions will not respond similarly due to fluctuations in seasons, locational heterogeneity and their complex interactions. AMMI and GGE Biplot analysis not only provide for easy evaluation of genotypes but also comprehensive understanding of test environments. Environment E7 (VIJ)) was the best test environment having high discriminative ability and representativeness for selecting generally adapted genotypes. The genotype G8 (GAUG 1507), having high mean values and less variation over environments was the most stable genotype, hence it can be recommended for cultivation across locations for stable performance. Genotype G10 (GG 1806) was specifically adapated to E7 (VIJ) environment while G4 (GG 1) for E4 (DER) and E6 (DEV) environments inferring that these genotypes can be considered for cultivation in specific environments only.

Conflict of interest: None.

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