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Identification of guar [*Cyamopsis tetragonoloba* (L.) Taub.] genotypes with wider adaptability to rainfed environments through stability analysis

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Abstract

The stability and yield of guar genotypes are important factors for the long-term development of this gum-producing industrial crop. A study was undertaken to assess the impact of the G × E interaction on yield stability in guar genotypes at seven distinct sites. Yield and its component traits such as the total number of pods per plant, pod length and seeds per pod were evaluated in the kharif season of 2020-21 and 2021-22 resulting in 14 environments. Stability tests for multivariate stability parameters were performed based on analyses of variance. For all the traits, the pooled analysis of variance revealed highly significant (p < 0.01) variations which provided sound evidence for the validity of the experiments. Genotypes KGG 6 and KGG 5 had desirable stability parameters for the number of pods per plant and pod length respectively. KGG 12 and KGG 3 were stable under all environments for number of seeds per pod. In the case of yield per hectare, the genotype KGG 6 recorded highest yield followed by KGG 4 and KGG 1. Among the tested genotypes, KGG 1 and KGG 2 were highly stable with average yield performance. AMMI biplots identified genotypes KGG 11 and KGG 12 as stable ones but these genotypes exhibited low-yield. The high-yielding stable genotypes identified in the present study could be recommended for commercial production in guar-growing areas of arid and semi-arid regions. Aside from these, the genotypes KGG 6 and KGG 4 were suited for exploiting better environmental conditions and genotype KGG 7 recorded more pod yield per plant and bi value less than one, explaining its suitability in poor environments. However, these genotypes could be incorporated into breeding strategy for yield enhancement in targeted environments.

Keywords: Guar, Genotypes, Environments, G×E interaction, Stability.

INTRODUCTION

Guar (*Cyamopsis tetragonoloba* (L.) Taub) is an annual legume that can withstand heat and drought. It is cultivated primarily in India and to a smaller extent, in Pakistan and the United States. Despite its significant impact in the industrial sector, it remains a niche crop (Gresta *et al.*, 2017). Clusterbean, chavlikayi, guari, and kutti are other common names for guar (Kumar and Rodge 2012). Hymowitz (1972) proposed the theory of trans-domestication for the origin of this crop. This theory explains how drought-tolerant wild African species *C. senegalensis* evolved into the domesticated guar plant, *C*.

tetragonoloba,. But still there is no universal agreement on this theory. As mature guar seeds contain beany flavour and other anti-nutritional compounds, they are consumed in lower quantities than other pulse crops (Couch *et al.*, 1966). Guar seeds contain nutrients that are essential for human health. According to Sharma *et al.* (2017), there were roughly 26%, 3%, 10%, 5%, and 54% of protein, fat, fibre, ash, and carbs in 100 g of dry guar seed, respectively. Guar has historically been used as food, fodder, and green manure, but its real significance comes from its galactomannans, also known as gum. These are

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made up of branching galactose units that split off of a mannose unit core in a 2:1 ratio, and the water-soluble gum found in the endosperm of guar seeds is used as an emulsifier, thickener, and stabiliser in a variety of food products (Gresta et al., 2017). Despite the worldwide importance of guar and its products, the productivity of this crop is very low and huge fluctuations in productivity are observed (Adams et al., 2020, Ravelombola et al., 2021). The development of varieties in self-pollinated crops is mostly dependent on hybridization through different mating strategies followed by selection in segregating generations. Next, to ascertain the subsequent advanced generations' appropriateness as breeding material, the yield and associated attributes are assessed (Patel et al., 2021, Sharma et al., 2022, and Gandhi et al., 2024). Once the best genotypes are developed, next step is minimising agricultural yield reduction caused by environmental influences by identifying genotypes with high yield potential that are more adaptable, and steady in performance over diverse locations and years. In order to identify genotypes with predicted performance that are responsive to environmental variables, it is necessary to analyse each genotype's adaptability and stability in order to lessen the effects of the GE interaction (Oladosu et al., 2017). The selection of cultivars with greater adaptability is influenced by the G×E interaction (GEI), which is the genotype's varying response to various environments (Patel et al., 2018 and Sharma et al., 2022). Obtaining information on the degree of genotype x environment interaction for yield and its component traits is essential to breeding a stable variety (Patel et al., 2021). In order to understand the significance of the GEI, an attempt has been made in the current work to evaluate different guar genotypes across locations and to apply stability analysis to explore the stability of genotypes for multiple attributes in addition to seed yield.

MATERIALS AND METHODS

Genetic materials: The research included twelve guar genotypes/lines (**Table 1**) that were developed at the Pulses Research Station, Sardarkrushinagar Dantiwada Agricultural University in Gujarat, India. The pedigree method of selection was used to select pure lines after hybridization. The advanced strains were selected with an emphasis on the quality of grains, resilience to diseases and pests, earliness, production and architectural design of the plants. The locations were Sardarkrushinagar (SKN), Bachau (BCHU), Radhanpur (RAD), Vijapur (VIJ), Derol (DER), Devgadhbariya (DVG) and Deesa (DEE) regions of Gujarat representing various agro-ecological zones.

Experiment design and cultural practices: The trial was conducted in a randomized complete block design having three replications in each of the seven locations during the *kharif* seasons of 2020–2021 and 2021–2022. Eight rows of 4 m each with 10 cm spacing between plant and a 45 cm between rows comprised the experimental units. To record the observations on the number of pods per plant (NPP), pod length (PL), number of seeds per pod (NSP), five competitive plants from each replication were randomly chosen in each plot. To record seed yield (SY) at harvest, the outer rows were not used and six middle rows (net plots) were harvested, in order to control border effects and to minimize experimental error.

Statistical analysis: The stability parameters were calculated using the model set forth by Eberhart and Russell (1966) and a two-way analysis of variance was carried out. The determination of this kind of stability is based on the regression coefficient (bi), average values, and departure from the regression line. A genotype is thought to have average stability if bi equals unity, meaning it performs the same in all environments. If bi is larger than one, it is thought to have less than average stability, meaning it performs well in favourable environments, allowing it to use resources more extensively than those of stable ones. Accordingly, a stable variety is defined by this model as having a minimum departure from the regression line (s²d=0) and a regression coefficient of unity (bi=1). Further, the GEI for seed yield was studied as per the AMMI model given by Zobel et al. (1988).

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

S.No	Code	Genotype	Parentage					
1	G1 KGG 201		RGC 1092 x GG 1					
2	G2	KGG 202	GAUG 0005 x RGC 2021					
3	G3	KGG 203	HG -2-30 x GG 1					
4	G4	KGG 204	Mutant of Kutch 8					
5	G5	KGG 205	GG 2 x HG 365					
6	G6	KGG 206	HG -2-4 x GG 1					
7	G7	KGG 207	PNB x GG 2					
8	G8	KGG 208	GG 2 x GAUG 0522					
9	G9	KGG 209	PRT 15 x GG 1					
10	G10	KGG 210	HG 365 x GAUG 0003					
11	G11	KGG 211	GG 2 x GAUG 0513					
12	G12	KGG 212	Mutant of HG 75	Mutant of HG 75				

Stability Anova								
	DF	Pods per plant	Pod length (cm)	Seeds per pod	Yield (t/ ha)			
Rep within Env.	28	423.97	0.08	0.14	0.02			
Varieties	11	428.66	0.15 *	0.39 *	0.13 **			
Env.+ (Var.x Env.)	156	3256.59 **	0.28 **	0.45 **	0.31 **			
Environments	13	34606.49 **	2.52 **	3.12 **	3.21 **			
Var. x Env.	143	406.60**	0.08*	0.20**	0.10*			
Environments (Lin.)	1	449884.40 **	32.73 **	40.57 **	41.73 **			
Var. x Env.(Lin.) 11		816.64 **	0.13 *	0.21	0.13 **			
Pooled Deviation 144 341.393		341.393 **	0.064 **	0.19 **	0.04 **			
Pooled Error 308 107.35		107.35	0.04	0.12	0.01			

Table 2. Pooled analysis of variance for seed yield and its attributes in guar

DF = Degree of freedom; G = Genotypes; E = Environment; Significance codes: '**' = 0.01, '*' = 0.05

RESULTS AND DISCUSSION

Guar is produced on marginal soils with limited resources, which leads to erratic yield levels. Data from multiple locations that were pooled throughout the years were subjected to a combined analysis of variance. Pooled analysis of variance (table 2) showed that for all the characters under study, the mean sum of squares attributed to genotypes (G) and environments (E) were significant. This suggests that the material selected for the study had a sufficient degree of variability and that the environments differed from one another, providing strong evidence for the validity of the experiments. For each trait, the non-linear component of the $G \times E$ interaction (pooled deviations) was shown to be significant when compared to the pooled error, indicating the influence of the unpredictable components of the environments on these traits. The results obtained in the present study are in agreement with the findings of El-Shaieny et al. (2015) in cowpea and Patel et al. (2021) in pigeonpea. In order to confirm the presence of variance resulting from components of the genotype × environment interaction, stability analysis was conducted following the Eberhart and Russell (1966) model. This model involves the estimation of three stability parameters, namely, mean (x), regression coefficient (bi), and deviation from regression (S²di).

Numerous previous studies (Sharma and Sridevi 2016, Sandhiya and Shanmugavel 2018 etc.) have demonstrated a strong correlation between yield and its contributing traits, such as the number of pods per plant, pod length, and seeds per pod. For this reason, these traits were taken into consideration for the current study in addition to yield. **Table 3 and Fig. 1** show the stability characteristics for number of pods per plant. KGG 8 had the most number of pods when averaged in all fourteen environments, followed by KGG 10 and KGG 9. KGG 3 showed the least divergence from regression, whereas KGG 6, KGG 11, and KGG 12 exhibited regression coefficients close to unity. Similar results were reported

by Jain and Patel (2012). The genotypes KGG 10 and KGG 2 demonstrated above average stability and can be explored for rich environments. However, genotype KGG 5 was adapted to low performance environments (**Fig. 1**). Based on high mean and bi (linear response) value of about 1.0 with minimal deviation from regression, genotype KGG 6 was determined to be suitable for a broad recommendation under all environmental conditions for this trait.

Pod length is one of the most crucial characteristics that, coupled with the quantity of pods per plant, contribute to a high yield. Table 3 shows the stability parameters for this feature. Of the genotypes that were evaluated, five showed pods that were longer than the population mean (5.44), with genotype KGG 6 showing the longest pod, followed by KGG 5. KGG 1 and KGG 5 had regression coefficients (bi) that were almost equal to unity, whereas KGG 8 and KGG 3 had the least amount of divergence from regression (S²di). Better stability and adaption to high-performance conditions were shown by the KGG 6 and KGG 12 genotypes. However, the genotype KGG 8 exhibited above-average stability and adaptation to poor environment (Fig. 2). Sharma et al. (2022b) also obtained similar results regarding pod length in cowpea.

The stability parameters for number of seeds per pod of the individual genotypes are illustrated in **Table 4 and Fig 3**. KGG 5 and KGG 3 had the most number of seeds per pod across environments. Regression coefficients for the genotypes KGG 12, KGG 3, and KGG 2 were close to unity, although KGG 6 and KGG 12 showed the least amount of divergence from regression. Jain and Patel (2012) as well as Vishwnatha *et al.* (2017) found similar outcomes for different guar yield-related variables. **Fig. 3** show that, whilst genotypes KGG 4 and KGG 8 were adapted to low performance environments, KGG 5 exhibited above average stability and might be investigated for rich environments.

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Genotypes		Pods	s per plant	:			Pod	length (cm	ı)	
	Gen.µ	S ² Di	Rank	ßi	Rank	Gen.µ	S ² Di	Rank	ßi	Rank
KGG 1	97.34	21.71	2	0.89	7	5.36	0.01	4	0.94	1
KGG 2	99.95	47.67	4	0.91	5	5.33	0.04	11	0.71	11
KGG 3	100.11	10.69	1	1.10	6	5.40	0.00	2	1.16	7
KGG 4	91.62	711.05	12	0.76	12	5.32	0.05	12	0.75	9
KGG 5	87.14	58.14	5	0.84	9	5.57	-0.02	5	0.92	2
KGG 6	97.90	419.46	10	0.99	1	5.58	0.04	10	0.58	12
KGG 7	96.63	159.64	8	0.92	4	5.42	0.02	6	1.13	4
KGG 8	103.29	114.78	7	1.19	10	5.40	0.00	1	1.14	5
KGG 9	100.29	490.33	11	1.16	8	5.55	0.04	9	1.17	8
KGG 10	102.45	41.05	3	1.24	11	5.47	0.01	3	1.26	10
KGG 11	91.48	97.88	6	0.98	2	5.31	0.03	8	1.10	3
KGG 12	87.72	319.49	9	1.03	3	5.55	0.03	7	1.15	6
Population Mean	96.32					5.44				

Table 3. Mean and stability parameters for pods per plant and pod length in guar.









Fig. 2. Stability based on regression coefficient and co-efficient of variation for pod length

Table 4. Mean and stability parameters	for seeds per pod and seed yield in guar.
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Genotypes		Seed	ds per pod				Seed	yield (t/ha	a)	
	Gen.µ	S ² Di	Rank	ßi	Rank	Gen.µ	S ² Di	Rank	ßi	Rank
KGG 1	8.01	0.10	7	0.88	5	1.39	0.03	8	1.07	2
KGG 2	8.16	0.10	8	1.09	3	1.38	0.00	2	1.22	9
KGG 3	8.22	-0.02	5	1.07	2	1.31	0.03	6	0.99	1
KGG 4	7.95	0.14	10	1.18	7	1.42	0.03	7	1.17	7
KGG 5	8.56	0.19	12	1.29	9	1.24	0.04	9	0.85	5
KGG 6	8.10	0.00	1	0.71	10	1.43	0.00	1	1.31	12
KGG 7	8.08	0.02	4	1.11	4	1.35	0.06	12	0.73	11
KGG 8	8.17	0.06	6	1.45	12	1.13	0.02	5	0.74	10
KGG 9	8.08	0.11	9	0.86	6	1.17	0.04	10	0.83	8
KGG 10	7.94	-0.01	3	0.58	11	1.34	0.05	11	1.16	6
KGG 11	8.04	0.15	11	0.80	8	1.23	0.01	4	0.88	4
KGG 12	8.21	-0.01	2	0.97	1	1.28	0.01	3	1.07	3
Population Mean	8.13					1.31				

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Fig. 3. Stability based on regression coefficient and co-efficient of variation for seeds per pod

Developing stable genotypes with high yields is the ultimate goal of every plant breeding strategy, especially in light of the constantly shifting climate. Table 4 shows that the mean seed yield (t/ha) varied from 1.13 t/ha in KGG 8 to 1.43 t/ha in KGG 6. Six genotypes produced more seed than the population mean of 1.31 t/ha; genotype KGG 6 had the highest yield, followed by genotype KGG 4. Two genotypes, KGG 12 and KGG 11, were shown to be superior and stable across environments when all stability parameters-a high mean, bi close to one, and S²di close to zero, were taken into account. Additionally, their CV was found to be low (Fig. 4). Two genotypes viz., KGG 6 and KGG 4 were better adapted to take advantage of better environmental conditions since their means were considerably higher than the population means and their regression coefficients were greater than unity. With a bi value of less than one and a higher yield per plant, genotype KGG 7 was more suited for unfavourable situations. Siimilar results were obtained in cowpea by Sharma et al. (2022) and in blackgram by Sridhar et al. (2018).

AMMI analysis was used in order to further analyse the G × E interaction for seed yield. Genotypes that fall almost on a horizontal line have comparable interaction patterns, and those that appear almost on a perpendicular line have similar means, as shown by Yan et al. (2007). Furthermore, interactions are substantial for genotypes with significant IPCA 1 scores in both positive and negative directions, while interactions are small for genotypes with IPCA 1 scores close to zero. Eight of the fourteen environments exhibited below-average main effects and were unfavourable according to the AMMI 1 biplot (Fig. 5). Although not having the highest main effects, environment DEE elevated most genotypes' performance in both years. When it came to genotypes, values near the IPCA1 axis origin indicated that G4 and G11 were the most stable, indicating a lower contribution of G × E interaction. Given its proximity to the origin in the AMMI 2 biplot, the genotype G12 was found (Fig. 6) stable against environmental fluctuations. It showed very little genotype x environment interaction, demonstrating high stability and good yield. Nirmalakumari et al. (2014)

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Fig. 4. Stability based on regression coefficient and co-efficient of variation for seeds yield.



Fig. 5. Stability based on AMMI biplots 1 for seed yield



Fig. 6. Stability based on AMMI biplots 2 for seed yield

and Sharma et al. (2024) similarly identified stable genotypes.

Genotypes cultivated under different environmental conditions will not respond similarly due to fluctuations in seasons, location heterogeneity and their complex interactions. Using G × E analysis, the present study not only identified promising guar genotypes but also provided comprehensive understanding of test environments. Considerable variations in the environment and genotypes for the yield and its component traits indicated the existence of broad variation. Results of this study indicated that we have different stable genotypes for various traits. These genotypes can be directly used in future breeding programs targeting a particular trait for enhancing the cluster bean productivity. Considering all the parameters of the Eberhart and Russell (1966) model and AMMI biplots, the genotypes, KGG 12 and KGG 11 were found to have superior and stable yield across environments, hence these genotypes can be recommended for cultivation under rainfed conditions for stable performance.

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