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Research article

Stability analysis for yield and yield attributing characters of cluster bean [*Cyamopsis tetragonoloba* (L.) Taub.] elite genotypes

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Abstract

Cluster bean is an important rainy season legume for arid and semi-arid areas of India. Due to its vast industrial application, its gum serves as a valuable export commodity for India. To understand G X E interaction and stability analysis, the present study was conducted using twenty-five genotypes of cluster bean, evaluated over eight environments. The genotypes, environments, and G X E interaction showed highly significant differences for all the characters, revealing that both genotypes and environments were significantly different and there was differential behavior of genotypes in changing environments with respect to cluster bean yield along with its attributing characters. Genotype RGC 1066 was found stable under all environments for seed yield per plot and harvest index. Other genotypes stable over the environments for different traits were identified for use in future improvement programmes.

Keywords: Cluster bean, G X E interaction, Regression coefficient, Stability analysis

Introduction

Cluster bean (*Cyamopsis tetragonoloba* L. Taub.) also known as 'Guar' is an important multipurpose crop of arid and semi-arid regions primarily grown for its seed. It's a diploid (2n=14), self-pollinated, erect herb with papilionaceous flowers arranged in axillary raceme with 10 stamens in diadelphous arrangement and head shaped stigma. Cluster bean has become an industrial crop from poor man's crop due to vast industrial applications of gum (guar gum) present in the endosperm of its seeds. This gum is a galactomannan polysaccharide, a natural thickener, and forms a gel in water (Priti *et al.*, 2022). The derivatives of guar gum are extensively used in industries like oil and gas drilling, textile, paper, confectionaries, food processing industries, cosmetics, water treatment, mining, pharmaceuticals, *etc*. (Mudgil *et al.*, 2014). India is the leading cluster bean producing country accounting for more than 80% of its production in the world. Apart from India it is also grown in the arid and semi-arid areas of Pakistan, USA, Italy, Morocco, Germany and Spain (Jukanti *et al.*, 2015; Kumari *et al.*, 2020). India is a major exporter of various derivatives of Guar gum to many countries including, U.S.A., Germany, Russia, Norway and Netherlands. The country has exported 406513.53 MT guar gum to the world, worth about rupees 4944.60 crores/617.14 Millions USD during the year 2022-23 (APEDA, 2023). In India, it is grown in Rajasthan, Gujarat, Haryana, Punjab, Uttar Pradesh and Madhya Pradesh in the areas with light to medium textured soils, no water logging, rainfall range of 250-450 mm with 3-4 spells and temperature ranging from 25 to 40°C (Panchta *et al.*, 2017; Kumar *et al.*, 2019). Rajasthan is occupying about 82% cluster bean producing area of the country (Meena and Nagar, 2017).

Yield is a polygenic character highly influenced by the environment. The stable genotypes are desirable in any crop. The Genotype X Environment (G X E) interaction studies are required to be conducted while planning and executing the selection of genotypes in a crop (Rajora *et al.*, 2017).The ultimate aim of multi-environment studies is to identify genotypes which are superior in terms of yield than the commercial check and to have insights on stability and adaptability over a range of varying environments (Yathish *et al.*, 2024).. Therefore, present study was carried out to assess the stability of elite cluster bean genotypes for their yield and yield components using Eberhart and Russell, 1966 model.

Materials and Methods

***Experimental material*:** A set of 25 diverse cluster bean genotypes (Table 1), were evaluated in the field experiments conducted during *Summer* 2019 ad 2020, and *Kharif* 2019 and 2020 at two locations in Haryana *i.e.,* Dry land research area, CCS Haryana Agricultural University, Hisar (29°08′45.2″N 75°39′38.7″E) and Research area, Regional Research Station, Bawal (28°04′43.5″N 76°35′41.5″E), Chaudhary Charan Singh Haryana Agricultural University, Hisar, representing two agro-climatic zones of Haryana (Table 2). The experiment was conducted in randomized block design (RBD) with three replications. Four rows of 4 m length of each genotype were grown in a plot of 1.8 m X 4 m with 45 cm row to row spacing.

***Observations recorded*:** Observations were recorded on five randomly selected competitive plants per genotype per replication under all the environments. Data were recorded for the number of branches per plant, number of pods per cluster, pod length (cm), harvest index (%), number of clusters per plant and seed yield per plot (kg) at maturity. In the present investigation, the G X E interaction and stability analysis of different cluster bean genotypes over the eight environments were worked out as per the model given by Eberhart and Russel (1966). When deviations from regression line (S^2di) are non-significant, the conclusions may be drawn by joint consideration of mean yield and regression coefficient values (bi) (Eberhart and Russell, 1966). A Genotype with high mean value, unit regression coefficient (bi=1) and deviation not significantly differing from zero ($S^2di=0$) was taken as stable genotype *i.e.,* possessing average stability. The genotype with regression coefficient (bi<1) and deviation not significantly differing from zero ($S^2di=0$) has above average stability and is specifically adapted to unfavourable (poor) environments. They are generally unresponsive to the favourable (rich) environments. The genotype with regression coefficient (bi>1) and deviation not significantly differing from zero ($S^2di=0$) has below average stability and is specifically adapted to favourable (rich) environments.

Results and Discussion

***Analysis of variance and characters*:** Pooled analysis of variance was executed on yield and component characters for stability as per Eberhart and Russell (1966). The genotypes showed significant differences for all the characters when tested against pooled deviation indicating that the selected genotypes are rich in variation for various characters and may not be showing uniform performance in different environments (Table 3). Environments showed highly significant differences for all the characters under study when tested against pooled deviation indicating that the environments were different from each other. The G x E interaction components showed significant differences for all the characters when tested against pooled deviation, indicating wide differential behaviour of genotypes in changing environments. Mean sum of squares due to environments + (genotypes x environments) were highly significant for all the characters studied, depicting the distinct nature of environments and genotype x environment interaction on phenotype expression. Significance of the environment (linear) component for all the characters when tested against pooled deviation indicated that the genotypes responded linearly for all the characters under study. Highly significant mean

Table 1. List of cluster bean genotypes along with their source/origin

S. No.	Genotype	Source/origin	S. No.	Genotype	Source/origin
1	HG 2-20	CCSHAU, Hisar	14	GG 2	SDAU Gujarat
2	HG 884	CCSHAU, Hisar	15	RGC 1017	RARI, Durgapura
3	HG 870	CCSHAU, Hisar	16	RGC 1038	RARI, Durgapura
4	HG 563	CCSHAU, Hisar	17	RGC 936	RARI, Durgapura
5	HG 365	CCSHAU, Hisar	18	RGC 1055	RARI, Durgapura
6	HG 3-52	CCSHAU, Hisar	19	RGC 1002	RARI, Durgapura
7	HG 6	CCSHAU, Hisar	20	RGC 1003	RARI, Durgapura
8	HVG 2-30	CCSHAU, Hisar	21	RGC 1066	RARI, Durgapura
9	HG 100	CCSHAU, Hisar	22	RGS 3	RARI, Durgapura
10	FS 277	CCSHAU, Hisar	23	M 83	RARI, Durgapura
11	X 10	Shaktivardhak seeds	24	HG 75	CCSHAU, Hisar
12	PNB	IARI, New Delhi	25	RGC 1033	RARI, Durgapura
13	GG 1	SDAU, Gujarat			

Table 2. Details of environments and code used for different environments

Season/year	Location	Code	Season/year	Location	Code
Summer 2019	Hisar	HS 19	Summer 2020	Hisar	HS 20
Kharif 2019		HK 19	*Kharif* 2020		HK 20
Summer 2019	Bawal	BS 19	Summer 2020	Bawal	BS 20
Kharif 2019		BK 19	*Kharif* 2020		BK 20

Table 3. Pooled ANOVA over eight environments for different characters in cluster bean (Eberhart and Russell, 1966 model)

Source of variation	DF	BPP	PPC	PL	H.I.	CPP	SYPP
Genotype	24	344.801**	63.682**	11.958**	0.053**	2770.734**	0.715**
Environment	7	36.612**	19.728**	4.214**	0.071**	1438.409**	1.326**
Gen. X Envion	168	2.259*	1.195*	0.103*	0.003**	77.881**	0.023**
Env+Gen X Env	175	3.633**	1.936**	0.268**	0.006**	132.303**	0.075**
Env (Linear)	1	256.284**	138.099**	29.496**	0.498**	10068.861**	9.282**
Env X Gen(Lin)	24	5.179**	2.997**	0.27**	0.008**	273.513**	0.062**
Pooled deviation	150	1.701**	0.859**	0.072**	0.002**	43.465**	0.016**
Pooled error	384	1.13	0.272	0.034	0.001	3.884	0.004
Total	199	44.779**	9.383**	1.678**	0.011**	450.505**	0.153**

BPP: Number of branches per plant; PPC: Number of pods per cluster; PL: Pod length (cm); HI: Harvest index (%); CPP: Number of clusters per plant; SYPP: Seed yield per plot (kg)

squares for genotype x environments (linear) indicate that the variation in the performance of genotype is due to the regression of genotypes on environments and the performance is predictable in nature. High and significant, pooled deviations were found for most of the characters, revealing the presence of significant fluctuations in the performance from the respective linear path response to the environment.These result corroborates with the findings of Kumar *et al.* (2016), Arunkumar *et al.* (2017), Wankhade *et al.* (2017) and Teja *et al.* (2022) in cluster bean for different components of analysis of variance and characters.

***Stability parameters of yield and its components*:** Seed yield per plant was positively and significantly associated with branches per plant, pods per cluster, pod length, harvest index, cluster per plant, indicating simultaneous selection based on these characters would be effective for seed yield (Table 4-5). Therefore, the genotypes exhibiting higher mean value than the overall mean for above mentioned characters are desirable. These results have supported either one or more than one character indicated as earlier reported by Kumar *et al.* (2017), Panchta *et al.* (2017), Patel *et al.* (2018), Reddy *et al.* (2018), Kumar *et al.* (2019), Sharma *et al.* (2021) and Sushmita *et al.* (2024).

On the basis of mean performance across the environments, the number of branches per plant ranged from 0.91 (RGC 1066) to 11.51 (RGC 1038) with an overall mean of 8.61 branches per plant (Table 4). Out of 25 genotypes evaluated, 18 genotypes showed the number of branches per plant more than the overall mean. The genotypes *viz.*, HG 884, HG 870, HG 563, HG 365, GG-1, RGC 1038, RGC 936, RGC 1055, RGC 1002 and RGC 1033 were recorded with high mean value, regression coefficient significantly equal to unity and non-significant deviation from regression. These genotypes were found suitable for all the environments with average stability. The genotypes *viz.*, HG 2-20, X-10, GG-2 and RGS 3 recorded high mean value than overall mean, significant regression coefficient more than unity and non-significant deviation from regression, adjudged as suitable genotypes for better environment with below average stability. In cluster bean, Wankhade *et al.* (2017) suggested genotypes with specific adaptability for poor and rich environments and with general adaptability for high number of branches per plant.

For harvest index (%), eight genotypes out of 25 evaluated, showed more harvest index than over all mean *i.e.*, 30.33% (Table 5). The mean value of the harvest index ranged from 15.06% (FS 277) to 36.00% (RGC 936). The genotypes *viz.*, HG 884, HG 870, HG 3-52, HG 6, RGC 1017, RGC 1038 and, RGC 1066 were found suitable for all tested environment with average stability as they recorded high mean value, regression coefficient significantly equal to unity and non-significant deviation from regression.

Table 4. Estimates of stability parameters for number of branches per plant, number of pods per cluster and pod length of cluster bean genotypes tested across the eight environments

S. No.	Genotypes	Number of branches per plant			Number of pods per cluster			Pod length (cm)		
		Mean	**bi**	**S^2di**	**Mean**	**bi**	**S^2di**	**Mean**	**bi**	**S^2di**
1	HG 2-20	11.23	1.876**	0.121	4.93	0.348**	-0.042	5.69	1.02	-0.007
2	HG 884	10.84	1.305	-0.222	4.73	0.239**	-0.041	5.49	0.839	-0.001
3	HG 870	10.71	0.928	-0.217	4.88	0.920	0.010	5.86	1.658**	0.006
4	HG 563	10.19	0.451	-0.062	5.28	0.647	-0.032	5.57	0.672	0.002
5	HG 365	10.6	0.957	0.209	4.48	0.067**	0.110*	5.53	0.758	-0.001
6	HG 3-52	10.67	2.003**	0.436*	4.66	0.943	-0.0.13	5.55	0.735	-0.003
7	HG 6	4.76	0.219*	0.047	4.63	0.660	0.013	5.38	0.922	0.062**
8	HVG 2-30	2.2	0.365	-0.14	5.26	0.999	0.133*	7.14	2.232**	0.024*
9	HG 100	10.89	1.557	0.654*	5.10	1.255	0.052	5.46	0.779	-0.007
10	FS 277	1.21	-0.115**	-0.182	11.07	2.791**	0.480**	5.67	1.675**	-0.002
11	X-10	10.62	2.025**	0.282	5.05	0.535*	-0.065	5.54	0.862	0.024**
12	PNB	1.02	-0.279**	-0.277	9.73	0.331**	1.316**	8.51	0.851	0.068**
13	GG-1	11.07	1.395	0.412	4.30	1.505*	0.456**	5.43	0.756	-0.009
14	GG-2	10.73	1.666*	0.06	4.26	0.200**	0.138*	5.35	0.385**	-0.002
15	RGC 1017	11.13	1.656*	0.656*	5.17	1.089	0.161*	5.66	1.305	0.001
16	RGC 1038	11.51	0.753	-0.051	5.21	1.408	0.025	5.65	1.440**	0.019*
17	RGC 936	10.74	1.45	0.147	4.22	0.796	-0.042	5.5	0.752	0.038**
18	RGC 1055	10.42	0.666	-0.211	4.84	0.647	0.010	5.71	1.504**	0.002
19	RGC 1002	10.82	1.066	0.325	5.67	2.216**	0.263**	5.58	0.829	0.029**
20	RGC 1003	11.2	1.519	0.501*	5.52	2.403**	0.136*	5.36	0.177**	0.011
21	RGC 1066	0.91	0.012**	-0.221	7.25	1.526*	0.708**	5.93	1.003	-0.007
22	RGS 3	10.87	1.666*	0.055	4.59	0.733	-0.062	5.47	0.833	0.010
23	M-83	4.32	-0.259**	0.266	6.09	2.003**	0.320**	6.83	1.803**	0.027**
24	RGC 1033	10.72	1.111	0.139	5.08	0.621	0.308**	5.59	0.556**	0.007
25	HG 75	5.75	1.008	2.035*	4.55	0.118**	0.552**	5.37	0.652*	0.02*
	Over all mean	8.61			5.46			**5.79**		

Table 5. Estimates of stability parameters for harvest index, number of clusters per plant and seed yield per plot of cluster bean genotypes tested across the eight environments

S. No.	Genotypes	Harvest index (%)			Number of cluster per plant			Seed yield per plant (kg)		
		Mean	bi	S^2di	Mean	bi	S^2di	Mean	bi	S^2di
1	HG 2-20	32.57	1.319	0.0003*	52.78	1.829**	-0.683	0.98	1.347**	0.0008
2	HG 884	31.95	1.139	0.0001	47.64	1.513**	0.826	0.88	1.109	0.0042**
3	HG 870	31.29	0.787	0.0001	46.86	0.938	10.849**	0.89	1.109	0.0019*
4	HG 563	32.66	1.104	0.0006**	50.57	2.218**	-0.542	0.93	1.469**	0.0021*
5	HG 365	32.57	0.779	0.0003*	46.06	1.510**	3.332**	0.85	1.337**	0.0044**
6	HG 3-52	33.26	1.502**	0.0000	38.38	1.285**	2.85**	0.75	1.313**	0.0021*
7	HG 6	35.11	1.702**	0.0002	34.82	0.973	-0.307	0.63	0.458**	0.0067**
8	HVG 2-30	27.05	0.104**	0.0003*	20.65	0.143**	8.227**	0.47	0.512**	0.0041**
9	HG 100	31.87	0.846	0.0006**	37.79	1.508**	22.486**	0.74	1.007	0.0027**
10	FS 277	15.06	-0.130**	0.0003*	13.41	-0.292**	23.165**	0.42	0.305**	0.0028**
11	X-10	31.49	1.124	0.0003*	47.87	1.419**	11.774**	0.93	1.417**	0.0014*
12	PNB	24.95	1.023	0.0020**	15.37	-0.419**	43.956**	0.39	0.411**	0.0068**
13	GG-1	29.09	0.056**	0.0004**	27.21	-0.780**	28.506**	0.56	0.447**	0.0031**
14	GG-2	29.93	0.864	0.0002	34.88	1.335**	14.23**	0.67	1.059	0.0021*
15	RGC 1017	32.50	0.979	0.0002	43.95	2.471**	16.909**	0.78	1.655**	0.0065**
16	RGC 1038	32.31	0.917	0.0000	41.37	11.080	7.328**	0.77	1.172	0.0016*
17	RGC 936	23.59	-0.360**	0.0003*	26.88	1.472**	14.833**	0.52	1.158	0.0062**
18	RGC 1055	36.00	2.081**	0.0008**	40.25	1.510**	2.827**	0.76	1.482**	0.0009
19	RGC 1002	32.61	1.348*	0.0004**	33.74	1.392**	11.321**	0.64	1.331**	0.0014*
20	RGC 1003	33.54	2.360**	0.0009**	35.06	1.536**	2.126*	0.64	1.291**	0.0025**
21	RGC 1066	34.45	0.983	0.0002	32.61	0.023**	55.11**	0.84	1.171	0.0006
22	RGS 3	30.12	0.822	0.0003**	36.42	0.739**	14.647**	0.69	0.733**	0.0064**
23	M-83	21.75	1.419*	0.0009**	20.91	0.211**	4.413**	0.44	0.492**	0.0168**
24	RGC 1033	32.27	0.842	0.0006**	42.8	0.776*	13.193**	0.77	0.705**	0.0025**
25	HG 75	32.00	1.393*	0.0004**	29.97	0.871	18.467**	0.53	0.509**	0.0164**
	Over all mean	30.33			35.93			0.70		

No genotypes recorded higher mean value than the overall mean, regression coefficient significantly more than or less than unity and non-significant deviation from regression. Therefore, none of the genotypes was found suitable for a better environment and for a poor environment.

Mean value for pod length ranged from 5.35 cm (GG-2) to 8.51 cm (PNB) with an overall mean of 5.79 cm (Table 4). Among the genotypes tested, 20 genotypes showed pod length more than overall mean. Considering short pods as desirable phenotypes, the genotypes *viz.* HG 2-20, HG 884, HG 563, HG 365, HG 3-52, HG 100, GG-1, RGC 1017, RGC 1066 and RGS 3 recorded low mean value than the overall mean, regression coefficient significantly equal to unity and non-significant deviation from regression. These genotypes were found suitable for all the environments with average stability. The genotypes *viz.*, HG 870 and RGC 1055 were found suitable for better environments with below average stability, as they recorded low mean value than the overall mean, significant regression coefficient more than unity and non-significant deviation from regression. The genotypes namely GG-2, RGC 1003 and RGC 1033 with low mean value than overall mean than the general mean, regression coefficient significantly less than unity and non-significant deviation from regression were identified as suitable genotypes for poor environment with above average stability.Using Eberhart and Russell's model, Teja *et al.* (2022) reported genotypes, in cluster bean and El-Shainey *et al.* (2015) in cowpea with general adaptation for pod length.

For the number of pods per cluster, out of 25 genotypes evaluated, 20 genotypes showed pods per cluster less than overall mean *i.e.*, 5.46 pods per cluster (Table 4). Mean values for pods per cluster were ranged from 4.22 (RGC 936) to 11.07 (FS 277). Considering less pod per cluster as desirable feature, the genotypes *viz.*, HG 870, HG 563, HG 3-52, HG 6, HG 100, RGC 1038, RGC 936, RGS 3 and RGC 1055 recorded low mean value than overall mean, significant regression coefficient more equal to unity and non-significant deviation from regression. These genotypes were found well adapted to all environments with average stability. No genotype recorded a low mean value than overall mean, regression coefficient significantly more than unity and non-significant deviation from regression. Hence, no genotype was found suitable for a better environment. The genotypes namely HG 2-20, HG 884 and X-10 with low mean value than overall mean, regression coefficient significantly less than unity and non-significant deviation from regression. These genotypes were identified as suitable genotypes for a poor environment with above average stability. On the basis of mean performance across the environments, the number of clusters per plant ranged from 13.41 (FS 277) to 52.78 (HG 2-20) with an overall mean of 35.93 clusters per plant. Out of 25 genotypes evaluated, 13 genotypes showed the number of clusters per plant more than the overall mean. Three genotypes namely, HG 2-20, HG 884 and HG 563 recorded higher mean value than overall mean, regression coefficient significantly more than unity and non-significant deviation from regression. These genotypes were found suitable for a better environment with below average stability. The genotype, HG 6 was found with mean value higher than overall mean, regression coefficient significantly equal to one and non-significant deviation from regression and hence, it was found suitable for all the tested environments with average stability. None of the genotypes was found suitable genotypes for poor environment. Singh *et al.* (2020) reported genotype, in cowpea with specific adaptability for favourable and unfavourable environments with high mean for number of clusters per plant.

Mean value for seed yield per plot ranged from 0.39kg (PNB) to 0.98kg (HG 2-20) with an overall mean of 0.70 kg (Table 5).18 genotypes out of 25 genotypes showed seed yield per plot more than overall mean. The genotype RGC 1066 was found suitable for all tested environments with average stability as it recorded higher mean value than overall mean, regression coefficient significantly equal to unity and non-significant deviation from regression. Two genotypes namely, HG 2-20 and RGC 1055 recorded higher mean value than overall mean, regression coefficient significantly more than unity and non-significant deviation from regression. These genotypes were found suitable for better environment with below average stability. No genotype was identified as suitable for poor environment. Using Eberhart and Russell's model, Arunkumar *et al.* (2017), Wankhade *et al.* (2017) and Wankhade *et al.* (2021) suggested genotypes, specifically adapted to rich and poor environments, and with general adaptability in cluster bean for seed yield.

Conclusion

On the basis of stability analysis over eight environments, the genotype RGC 1066 was identified as high yielding and stable for harvest index and seed yield per plot. Similarly, nine genotypes, for number of pods per cluster (HG 870, HG 563, HG 3-52, HG 6, HG 100, RGC 1038, RGC 936, RGS 3 and RGC 1055), one for number of clusters per plant (HG 6) and ten each for pod length (HG 2-20, HG 884, HG 563, HG 365, HG 3-52, HG 100, GG-1, RGC 1017, RGC 1066 and RGS 3) and number of branches per plant (HG 884, HG 870, HG 563, HG 365, GG-1, RGC 1038, RGC 936, RGC 1055, RGC 1002 and RGC 1033) were considered as desirable and stable over the tested environments. These stable genotypes may be used as parents for the development of high yielding and stable cluster bean varieties.

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