www.ThePharmaJournal.com

The Pharma Innovation

ISSN (E): 2277- 7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2021; SP-10(8): 854-860

www.thepharmajournal.com
Received: 01-06-2021
Accepted: 03-07-2021

RS Wankhade
Assistant Professor, (Horticulture), Agriculture Research Station, Dr. P.D.K.V., Anjangaon Road, Achalpur, Maharashtra, India

VS Kale
Associate Professor, University Department of Vegetable Science, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola, Maharashtra, India

HH Dikey
Assistant Professor, Regional Research Centre, Dr. P.D.K.V., Amravati, Maharashtra, India

YD Charjan
Associate Professor, Agriculture Research Station, Dr. P.D.K.V., Achalpur, Maharashtra, India

Corresponding Author
RS Wankhade
Assistant Professor, (Horticulture), Agriculture Research Station, Dr. P.D.K.V., Anjangaon Road, Achalpur, Maharashtra, India

Stability studies with special emphasis on phenotypic character in cluster bean

RS Wankhade, VS Kale, HH Dikey and YD Charjan

Abstract
Stability was studied for seed yield and their component characters in fifty five genotypes of cluster bean under four environmental conditions during Summer and *Kharif* 2014 at two locations (Akola and Amravati). The variance due to genotype × environment (linear) was found to be highly significant against pooled deviation for six traits *viz*., internodal length, number of dry pod cluster^{-1}, days to first picking of dry pod, length of dry pod, width of dry pod and seed to husk ratio and the non linear component (pooled deviation) was also highly significant for all the traits except internodal length, length of dry pod and width of dry pod. The environment + (genotypes X environment) was highly significant for all the characters except plant spread and number of dry pods cluster plant^{-1} against pooled deviation indicating distinct nature of environments and the effects due to environments (linear) was highly significant for all the characters. Based on stability parameters and over all mean, six genotypes *viz*., IC-421839, IC-324032, IC-329036, IC-421816, IC-421815 and IC-421834 were stable in performance for dry pod yield hectare^{-1} and the genotypes namely IC-421834, IC-421839, IC-421815, IC-324032 and IC-421798 were stable in performance for seed yield plot^{-1} (20 plants).

Keywords: deviation from regression, genotypes, GXE interactions, regression coefficient

Introduction
Cluster bean [*Cyamopsis tetragonoloba* (L.) Taub] [2n=14] is one of the most important and potential vegetable cum industrial crop grown for its tender pods for vegetable purpose and endospermic gum [30-35%]. The endosperm fraction of cluster bean seed is rich in galactomannan (16.80 to 30.90%), while the germ and hull portion termed as guar meal obtained after the extraction of gum is rich in protein (28.90–46.00%) and used as animal and poultry feed.
In India, cluster bean for seed production (Guar seed) occupies an area of 42.15 lakh hectares with a production of 18.96 lakh tones (Baldodiya and Awasthi, 2018) [1]. In Indian states like Rajasthan, Haryana, Gujarat and Punjab, guar is mainly cultivated for guar gum production and for forage.
Considering the importance of cluster bean gum for industrial and medical purpose, there is a prime need for its improvement. Breeding for varieties suited to specific agro-ecological conditions for seed purpose is urgently needed for Western Vidarbha region of Maharashtra state. Hence, evaluation of genotypes study was undertaken to identify the superior genotypes on the basis of phenotypic stability for seed yield in cluster bean genotypes.

Materials and Methods
The experimental material for the present investigation comprised of 55 cluster bean genotypes were grown in a randomized block design with two replications over four different environments at University Department of Horticulture, Dr. PDKV, Akola and Regional Research Centre, Dr. PDKV, Amravati, Maharashtra during summer and *kharif* 2014. Each plot (1.20 m x 1.00 m) consisted of 20 plants in two rows of 1 m length with a spacing of 60 cm X 10 cm. All the recommended package of practices for guar was followed. The experimental season showed different temperature regimes, humidity, rain fall and sunshine hours during the crop durations. Observations were recorded on five competitive plants in respect of 10 characters viz., plant spread cm^2 (90 DAS), internodal length (cm), number of dry pod clusters plant^{-1}, number of dry pod cluster^{-1}, days to first picking of dry pod, length of dry pod, width of dry pod, dry pod yield hectare^{-1} (q), seed yield plot^{-1} (20 plants) and seed to husk ratio. The stability parameters estimated were mean of the trait (X), linear regression (bi) and mean square deviation from the regression (S^2di) line.

As per the Eberhart and Russel model of stability, components S^2di measures the predictability, whereas bi measures the stability. Stability of a genotype can be predicted more precisely if G X E interaction is present but S^2di values is non significant. According to them, a genotype which possess high mean (x), unit regression coefficient (bi=1) with the deviation from regression line approaching zero ($S^2di=0$) is considered to be stable one, i.e., possessing average stability, whereas a variety with regression coefficient lower than one has above average stability and is specially adapted to unfavourable (poor) environments. They hardly express response to improved environmental conditions. A variety with regression coefficient greater than one (bi>1) has below average stability and is suitable for favourable/rich environments. In the present study, the G x E interaction and stability analysis of different genotypes across the four environments were worked out as per the model given by Eberhart and Russel (1966) [5].

Results and Discussion

Pooled analysis of variance for stability

Pooled analysis of variance for stability of all traits across four different environments revealed that there were highly significant differences among the genotypes tested for all the characters studied. Henry and Kackar (2001) [6] and Jain, *et al. (*2012) [7] reported similar result in cluster bean.

The environment in which these experiments were conducted showed highly significant differences in all the observations indicating the validity of conduct of experiment in these environments (Table 1). Chaudhary, *et al.* (2005a) [2], Chaudhary, *et al.* (2005b) [3] and Pathak *et al*. (2010b) [8] reported genotype (G) and environment (E) were significant for all the traits in cluster bean.

The differences due to G × E interactions were found to be highly significant for all the characters except width of dry pod against pooled error indicating considerable amount of interaction between the genotypes and environments. The G × E interactions differed significantly high for the traits *viz* internodal length, number of dry pod cluster^{-1}, days to first picking of dry pod, length of dry pod, width of dry pod and seed to husk ratio. The results obtained are in agreement with the findings of earlier workers Chaudhary, *et al.* (2005b) [3], Chaudhary, *et al.* (2005a) [2], Pathak, *et al*. (2010b) [8], Pathak, *et al*. (2011) [9] and Jain, *et al.*(2012) [7] in cluster bean.

The environment + (genotypes X environment) were also highly significant for all the characters except plant spread and number of dry pods cluster plant^{-1} against pooled deviation (Table 1). Similar result reported by Chaudhary *et al.* (2005b) [3] found significant E+ (G+E) for all traits in cluster bean.

The effects due to environments (linear) were highly significant for all the characters indicating that environmental effects are additive (Table 1). Chaudhary *et al.* (2005a) [2], Chaudhary *et al.* (2005b) [3] and Jain *et al.*(2012) [7] observed significant environment (linear) interaction in cluster bean.

The variance due to G × E (linear) was found to be highly significant against pooled deviation for traits viz., internodal length, number of dry pod cluster^{-1}, days to first picking of dry pod, length of dry pod, width of dry pod and seed to husk ratio (Table 1) revealing that the behavior of genotypes could be predicted over the environments more precisely and accurately as G x E interaction was the outcome of the linear function of the environmental components. Similar result reported by Chaudhary *et al.* (2005b) [3] that G×E (linear) interaction was significant for all the traits except days to maturity in cluster bean.

The G x E (linear) was found to be non-significant for four traits *viz*., plant spread, number of dry pods clusters plant^{-1}, dry pod yield hectare^{-1} against pooled deviation, indicating that the differential response of genotypes to the changing environments was not controlled genetically and pointed to the difficulty in prediction of performance of the genotypes across the environment. Similar results reported by Chaudhary *et al.* (2005a) [2].

The mean sum of squares due to pooled deviation was also found highly significant for all the characters except internodal length, length of dry pod and width of dry pod which indicates the non linear or unpredictable portion of G × E interaction was predominant when tested against pooled error. Chaudhary *et al.* (2005a) [2] reported highly significant mean squares due to pooled deviations for all traits except days to maturity, plant height and pod length in cluster bean.

Stability analysis for different characters

The results pertaining to these stability parameters are discussed character-wise as suggested by Eberhart and Russell (1966) [5].

a) Plant spread cm^2 (90DAS)

The genotypes *viz*., IC-415157(04) had high mean values for plant spread with nearer to unity regression value and non significant deviation from regression line. This suggested that this genotype is well adapted to all the environment for this trait. The genotypes *viz*., IC-415160 (05), IC-421797 (08) IC-329639(31), IC-248087(33), PLG-354 (35), IC-329036 (39), IC-373427 (41) and RGC-936 (45) had high mean values for plant spread with more than regression coefficient and non significant deviation from regression line. This suggested that these genotypes are adapted to favourable environment for this trait. The genotypes IC-415102 (03), IC-370478 (36) and HG-3-100 (54) well adopted to unfavourable environment (Table 2).

b) Internodal length (cm)

The genotypes IC-415157 (04) and AVT-GR-11(55) were well adapted to all the environment as far as internodal length is concerned, as indicated by stability parameters considered as stable genotype as it had high mean value with regression coefficient near to unity and non significant deviation from regression line. Since the genotypes IC-298638 (01), IC-415102 (03), IC-415165 (07), IC-421797(08), IC-421801(09), IC-421806 (11), IC-421826(18), IC-421831 (21), IC-421839 (25), IC-369789 (30), IC-329639(31), IC-325811(40), IC-311441 (43), RGC-1031(46) and IC-421812 (50) showed the high mean, regression coefficient more than one and non significant deviation from regression line, these genotypes were suitable for favourable environment. While genotypes *viz.*, IC-370742 (02), IC-421803 (10), IC-421811(12), IC-421816 (13), IC-421820(14), IC-421825 (17), IC-421828(19), IC-421830(20), IC-421834(23), IC-421837(24), IC421842(28) and IC-421815(32) were adapted to unfavourable environment as these genotypes exhibited mean values high, regression coefficient less than one and non significant deviation from regression line (Table 2).

c) Number of dry pod clusters plant^{-1}

The genotype PLG-85 (38) recorded higher number of dry pod clusters plant^{-1} and regression coefficient around unity

with non significant deviation from regression line indicating its average stability i.e. well adapted to all environments (stable). The five genotypes IC-421825 (17), IC-421830 (20), IC-421839 (25), IC-248087(33) and IC-329036 (39) expressed high number of dry pod clusters plant^{-1}, regression coefficient greater than unity and non significant S^2di, thus indicating below average stability for favourable environmental situations. The four genotypes IC-421831 (21), IC-421834 (23), IC-421837 (24) and IC-324032 (34) recorded more number of dry pod clusters plant^{-1} and bi value less than one with non significant S^2di, explaining its suitability in unfavourable environments thus indicating above average stability (Table 2).

d) Number of dry pod cluster^{-1}

According to Eberhart and Russell model (1966) [5], the genotype IC-325811 (40) had high mean (6.75), regression value (1.00) and non significant deviation from regression line (0.00) considered as most stable expressed for number of dry pod cluster^{-1}. While the genotype IC415163 (06) recorded higher number of dry pod cluster^{-1} and regression coefficient around unity with non significant deviation from regression line indicating its average stability. The genotype IC-415102 (03), IC-415160(05), IC-421803(10), IC-415109 (37) and IC-311441(43) recorded more number of dry pod cluster^{-1} and bi value more than one with non significant S^2di, explaining its suitability in favourable environments (below stability).The genotype IC-298638(01), IC-415165 (07), IC-421830 (20), IC-329639 (31), IC-415159 (42), RGC-936 (45) and IC-373480 (48) recorded more number of dry pod cluster^{-1} and bi value less than one with non significant S^2di, explaining its suitability in poor environments (unfavourable) with predictable performance (Table 2).

e) Days to first picking of dry pod

Considering the three parameters together of Eberhart and Russell model high mean, regression value nearer to unity and non significant deviation from regression line exhibited by the genotype IC-421821 (15), IC-421830 (20), IC-421840 (26), IC-370478 (36), IC-329036 (39), IC-325811 (40), IC-373427 (41) IC-415159 (42) considered as stable genotype expressed for days to first picking of dry pods over the environments.

The genotypes *viz*., IC-421837(24), IC-421839 (25), IC-421841(27), IC-415140 (44), IC-373480 (48), IC-369861(49), IC-421812 (50), IC-369868 (52) and RGC-986 (53) recorded high mean, regression value grater than unity and non significant deviation from regression line. This suggests that these genotypes were well adapted to favourable environments indicated below average stability. The genotype IC-415165 (07), IC-421806 (11), IC-421811(12), IC-421816 (13), IC-421834 (23), IC-421815 (32) and PLG-85 (38) showed high mean, regression value less than unity and non significant deviation from regression line indicating above average stability suitable for unfavourable environment (Table 2).

f) Length of dry pod (cm)

As per Eberhart and Russell model of stability no one genotype exhibited stable trend. The genotypes viz., IC-370742 (02), IC-415160 (05), IC-421801(09), IC-421816 (13), IC-421821(15), IC-421837(24), IC-329639 (31), IC-415109(37), IC-329036 (39), IC-373427 (41), IC-311441 (43) and IC-369868 (52) recorded high mean, regression value greater than unity and non significant deviation from regression line indication these genotypes were well adapted to favourable environments indicating below average stability. The genotype IC-298638(01), IC-415102(03), IC-415163 (06), IC-421803(10), IC-421843(29), RGC-936 (45), RGC-1031(46), IC-373480 (48), IC-369861 (49) RGC-986 (53), HG-3-100 (54) and AVT-GR-11(55) showed high mean, regression value less than unity and non significant deviation from regression line indicating above average stability suitable for unfavourable environment (Table 3).

g) Width of dry pod (cm)

Considering the three parameters together of high mean, regression value nearer to unity and non significant deviation from regression line, four genotypes IC-421801 (09), IC-329639 (31), IC-324032 (34) and IC-369866 (52). exhibited this trend. The genotypes IC-298638 (01), IC-415102 (03), IC-421816 (13), IC-421828 (19), IC-421842(28), IC-421843 (29) and IC-373480 (48) recorded below stability due to more width of dry pods and bi value more than one with non significant S^2di, explaining its suitability in favourable environments. The genotype IC-370742 (02), IC-415160(05), IC-415163 (06), IC-415165 (07), IC-421797 (08), IC-421803 (10), IC-421806 (11), IC-421811(12), IC-421820 (14), IC-421831 (21), IC-421834 (23), IC-421841 (27), IC-329036 (39) and IC-421798 (51) recorded above average stability due to more width of dry pod and bi value less than one with non significant S^2di, explaining its suitability in poor environments (unfavourable) (Table 3).

h) Dry pod yield hectare^{-1} (q)

Three genotypes namely IC-421839 (25), IC-324032 (34), IC-329036 (39) IC-421816 (13), IC-421815 (32) and IC-421834 (23) recorded average stability as it had higher dry pod yield hectare^{-1} with regression coefficient near to unity and non significant deviation from regression line with predictable performance across the environments for this yield component trait i.e. stable genotypes. Seven genotypes recorded below average stability viz. IC-298638 (01), IC-421797 (08), IC-421830 (20), IC-248087 (33), IC-370478 (36), IC-373480 (48) and IC-369861 (49) had recorded higher dry pod yield hectare^{-1} with bi value greater than one with non significant S^2di indicating suitability of these genotypes under favourable environmental situations with predictable performance.The genotypes viz. IC-421831 (21), IC-421837 (24) and IC-421798 (51) recorded above average stability as it had more dry pod yield hectare^{-1} and bi value less than one with non significant S^2di, explaining its suitability in poor environments (unfavourable) with predictable performance whereas dry pod yield hectare^{-1} observed additional stable genotypes namely IC-421834 (23) & IC-421815 (32), IC-421834 (23) and IC-421816 (13) & IC-421815 (32) respectively (Table 1).

i) Seed yield plot^{-1} (20 plants) (g)

The genotypes namely IC-421834 (23), IC-421839 (25), IC-421815 (32), IC-324032 (34) and IC-421798 (51) recorded higher seed yield plot^{-1} with regression coefficient near to unity and non significant deviation from regression line indicating its average stability with predictable performance across the environments for this yield component trait i.e. stable genotypes. The genotypes viz. IC-298638 (01), IC-415163 (06), IC-421797 (08), IC-248087 (33), IC-370478 (36), IC-329036 (39), RGC-1031 (46), IC-373480 (48) and IC-369861 (49) had recorded higher seed yield plot^{-1} with bi

value greater than one with non significant S^2di indicating suitability of these genotypes under favourable environmental situations with predictable performance with below average stability. Three genotypes *viz.*IC-421816 (13), IC-421831 (21) and IC-421837 (24) recorded more seed yield plot^{-1} and bi value less than one with non significant S^2di, explaining its suitability in poor environments (unfavourable) with predictable performance with above average stability (Table 3).

D'almeida and Tikka (2003) observed genotypes HGS-843, RGC-1022, RGC-1017, GAUG-8832 and GG-1 gave stable performance for seed yield, whereas genotype GAUG-9003 was found to be highly responsive to unfavourable environments in cluster bean. Chaudhary *et al.* (2005a) [2] observed thirty genotypes gave stable performance for seed yield. Average, above average and below average responses were exhibited by 15, 8 and 7 genotypes, respectively, indicating that these will be suitable for across the environments, favourable and less favourable environments, respectively. Genotypes RGC-1038, RGC-1031, HGS-844, RGM-112, RGC-1002, HGS-891, RGM-114 and HGS-365 had above average seed yield, average response (b=1) and deviation to regression ($S^2di=0$), thereby indicating that it will be suitable for wider range of environments in cluster bean. Jain *et al*. (2012) [7] observed the genotypes viz., GAUG-0309 and GAUG-0511 were the most stable under rainfed situation for improvement of seed yield in cluster bean.

j) Seed to husk ratio

No genotypes showed average stability performance for this trait. Seven genotypes viz. IC-415165 (07), IC-421840 (26), IC-421841(27), IC-421815 (32), IC-248087 (33), IC-324032 (34) and IC-415159 (42) recorded higher seed to husk ratio with bi value greater than one with non significant S^2di indicating suitability of these genotypes under favourable environmental situations. The thirteen genotypes viz. IC-421803 (10),IC-421828 (19), IC-421831 (21), IC-421832 (22), IC-421839 (25), IC-329639 (31), IC-415109(37), IC-373427 (41), RGC-936 (45), IC-369861 (49), IC-369868 (52), RGC-986 (53) and HG-3-100 (54), recorded more seed to husk ratio and bi value less than one with non significant S^2di, explaining its suitability in unfavourable environments (Table 3).

Considering overall performance of the genotypes, six genotypes *viz*., IC-421839, IC-324032, IC-329036, IC-421816, IC-421815 and IC-421834 were stable in performance for dry pod yield hectare^{-1} and the genotypes namely IC-421834, IC-421839, IC-421815, IC-324032 and IC-421798 were stable in performance for seed yield plot^{-1} (20 plants). Considering above facts there is better chances of utilizing these genotypes in breeding programme to develop superior genotypes having stable performance than existing ones.

Table 1: Analysis of variance for stability of different characters over four environment (two *summer* and two *kharif*, 2014)

Sr. No.	Source of variation	d.f.	Mean sum of square				
			Plant spread cm² (90 DAS)	Internodal length (cm)	Number of dry pod clusters plant^{-1}	Number of dry pod cluster^{-1}	Days to first picking of dry pod.
1	Rep within Env.	4	4.72	0.14	0.83	0.04	1.49
2	Genotypes	54	857.67**++	0.69**++	31.70**++	1.82**++	8.59**++
3	Environments	3	314.19**++	5.15**++	70.57**++	78.21**++	5283.17**++
4	Genotype x Environment	162	38.36++	0.22**++	8.28++	0.82**++	7.01**++
5	Total	219	244.16	0.40	14.91	2.12	79.68
6	Pooled error	216	3.27	0.10	1.09	0.03	2.55
7	Environment +(Genotype x Environment)	165	43.38++	0.31**++	9.41++	2.23**++	102.94**++
8	Environment (Linear)	1	942.57**++	15.45**++	211.70**++	234.61**++	15849.51**++
9	Genotype x Environment (Linear)	54	33.56++	0.41**++	6.59++	2.18**++	11.82**++
10	Pooled deviation	110	40.02++	0.12	8.96++	0.14++	4.52++
Sr. No.	**Source of variation**	**d.f.**	**Length of dry pod (cm)**	**Width of dry pod (cm)**	**Dry Pod yield hectare^{-1} (q)**	**Seed yield plot-1 (g) (20 plant)**	**Seed to husk ratio**
1	Rep within Env.	4	0.01	0.00	1.22	149.85	0.0003
2	Genotypes	54	0.34**++	0.01**++	149.48**++	7454.85**++	0.101**++
3	Environments	3	5.58**++	0.19**++	2006.20**++	122491.11**++	0.28**++
4	Genotype x Environment	162	0.09**++	0.002**	34.43++	1842.14++	0.02**++
5	Total	219	0.22	0.01	89.81	4878.82	0.04
6	Pooled error	216	0.01	0.0015	7.1800	401.51	0.0003
7	Environment+(Genotype x environment)	165	0.19**++	0.01**++	70.28**++	4035.75**++	0.02**++
8	Environment (Linear)	1	16.73**++	0.56**++	9018.90**++	367473.31**++	0.82**++
9	Genotype x Environment (Linear)	54	0.24**++	0.0031**++	38.09++	2276.4++	0.05**++
10	Pooled deviation	110	0.01	0.0011	32.01++	1595.46++	0.0012++

* Significant at 5% level against pooled deviation, + significant at 5% level against pooled error, ** Significant at 1% level against pooled deviation and ++ Significant at 1% level against pooled error

Table 2: Estimates of stability parameters for plant spread, intermodal length, No. of dry pod clusters plant^{-1}, No. of dry pod cluster^{-1} and days to first picking of dry pod in cluster bean genotypes

Sr. No.	Genotype	Plant spread cm^2 (90 DAS)			Internodal length (cm)			Number of dry pod clusters plant^{-1}			Number of dry pod cluster^{-1}			Days to first picking of dry pod.		
		Mean	bi	S^{2}di	Mean	bi	S^{2}di	Mean	bi	S^{2}di	Mean	bi	S^{2}di	Mean	bi	S^{2}di
1	IC-298638	21.94	0.41	57.54**	4.86	1.50	-0.09	14.08	5.15	18.61**	7.13	-0.33**	0.00	70.88	1.22	0.86
2	IC-370742	22.38	0.69	1.48	4.76	-0.24	0.00	12.30	0.66	3.23*	5.41	1.01	0.00	72.93	0.93	2.86
3	IC-415102	38.18	0.83	-1.09	4.73	1.32**	-0.10	12.90	1.34	2.49*	6.43	1.27	0.01	73.38	1.26	10.16**
4	IC-415157	39.75	0.89	-2.09	4.54	1.05	-0.04	11.51	1.28	4.97**	6.25	0.35	0.22**	73.56	1.07	-1.83
5	IC-415160	64.09	1.56	-0.28	5.11	2.23	0.20*	10.49	0.48	11.77**	7.01	1.14*	-0.03	74.21	0.98	0.50
6	IC-415163	52.35	1.57	29.96**	4.33	1.47	-0.02	11.86	2.95	12.90**	6.85	0.91*	-0.03	74.01	0.58	31.25**
7	IC-415165	26.83	0.78	-1.93	4.73	1.20	-0.06	11.33	1.92	7.06**	6.54	0.74	0.00	75.46	0.70	4.40
8	IC-421797	57.93	2.61	3.27	5.41	4.10	0.06	13.89	2.19	5.23**	6.08	1.18	0.12**	75.05	0.77	13.33**
9	IC-421801	21.76	-1.27	37.18**	4.80	1.76	-0.03	10.65	1.30	5.42**	5.74	0.46	0.21**	73.01	0.77	-1.15
10	IC-421803	21.81	1.60	-1.52	4.81	0.74	-0.07	7.35	0.46	2.19	7.06	1.52*	-0.02	73.48	0.62	0.23
11	IC-421806	20.36	-0.06*	-3.04	4.81	1.81	0.00	12.71	2.10	9.65**	6.74	0.27	0.13**	75.54	0.77	-1.44
12	IC-421811	19.08	0.17	-0.36	4.63	0.76	-0.09	11.60	1.15	10.40**	5.86	0.20**	-0.01	75.15	0.81	-0.03
13	IC-421816	24.20	0.98	-3.05	4.42	0.20	-0.04	11.81	2.31	3.80*	6.51	0.64	0.13**	76.24	0.68	-0.41
14	IC-421820	19.89	1.85	-1.97	5.06	0.52*	-0.09	11.21	1.97	28.10**	5.75	0.88	-0.02	77.66	0.97	11.71**
15	IC-421821	14.24	-0.91**	-2.92	4.67	-0.79	0.79**	11.56	-0.12	26.55**	7.48	2.09*	0.16**	75.58	0.93	3.81
16	IC-421822	14.96	0.75	-0.61	3.92	1.09	-0.04	11.92	2.76	7.51**	6.11	0.34*	0.03	74.15	1.02	-1.15
17	IC-421825	41.51	3.68	120.36**	4.44	0.01*	-0.09	13.36	1.42	1.20	7.07	0.02	0.89**	74.38	0.85	2.46
18	IC-421826	16.13	0.45	-1.95	4.13	2.72	0.13	14.22	1.54	4.68**	6.89	1.11	0.10*	73.19	0.86	-0.60
19	IC-421828	49.75	5.86	662.56**	4.39	0.46	-0.08	13.00	1.42	10.29**	6.16	0.65	0.03	73.55	1.01	-0.10
20	IC-421830	19.29	1.09	-1.54	4.44	0.10	-0.08	13.09	3.11*	-0.82	6.47	0.78*	-0.02	77.96	1.00	2.69
21	IC-421831	26.50	0.65	0.62	4.54	1.30	-0.09	13.27	0.21	1.46	6.16	0.77	0.36**	74.30	0.57**	-2.14
22	IC-421832	14.97	-0.84	0.16	5.56	6.71	1.56**	12.74	0.96	5.37**	6.24	0.35	0.14**	73.25	0.91	-1.38
23	IC-421834	17.12	-0.44	-1.10	4.48	0.87	-0.01	18.32	0.53	-0.57	5.87	0.81	0.22**	76.64	0.84*	-2.40
24	IC-421837	17.33	0.56	-3.09	4.52	0.26*	-0.09	15.40	-0.79	1.15	5.47	0.98	-0.01	75.01	1.07	-1.72
25	IC-421839	52.69	1.11	42.87**	4.53	1.20	-0.06	14.39	1.48	0.87	5.53	1.08	0.19**	77.48	1.39	3.90
26	IC-421840	30.20	-0.30**	-3.18	3.70	0.09	-0.08	13.09	-1.64	23.46**	7.64	3.79*	0.77**	76.31	1.04	3.08
27	IC-421841	27.78	0.81	-1.69	4.07	0.54*	-0.10	10.54	0.59	0.09	5.77	0.33*	-0.01	77.03	1.13	2.79
28	IC-421842	19.87	-0.11	98.24**	4.55	0.37	-0.07	18.87	2.13	20.03**	5.59	0.98	0.00	72.73	0.97	-2.05
29	IC-421843	29.41	-0.12**	-3.25	3.99	1.47	-0.07	12.51	3.66	8.02**	6.13	0.22**	-0.02	74.53	0.83	4.01
30	IC-369789	31.89	1.07	-1.63	4.57	1.26	-0.09	12.04	0.61	3.50*	6.17	0.86*	-0.03	73.56	1.07	-1.86
31	IC-329639	62.83	1.49	-0.94	4.63	1.65	-0.02	16.26	1.17	34.33**	6.29	0.82	-0.02	76.96	1.29	5.58*
32	IC-421815	43.52	2.10	39.97**	4.43	0.03	-0.01	12.79	-0.47	1.83	6.69	2.26*	0.15**	74.91	0.79	-1.02
33	IC-248087	58.47	1.78*	-3.08	4.19	0.04	0.06	13.78	1.53	0.72	6.11	0.79*	-0.02	72.66	0.96	1.60
34	IC-324032	33.06	3.90	10.90*	4.19	0.63	-0.06	14.62	0.52	2.20	5.43	1.16	-0.01	73.65	1.02	-0.71
35	PLG-354	58.30	1.63	-2.10	4.35	1.66	-0.05	18.83	1.63	2.83*	5.62	1.77**	-0.01	74.32	0.98	-1.16
36	IC-370478	47.39	-0.23	-1.44	4.31	0.31	-0.06	17.08	0.28	27.08**	5.59	1.39	0.03	75.44	0.94	-0.06
37	IC-415109	27.85	0.41	-2.75	4.00	-0.98	0.23*	12.17	-0.58	0.12	6.71	2.16**	-0.02	73.80	1.04	-0.78
38	PLG-85	19.39	2.07*	-2.89	4.23	0.70	-0.02	13.49	0.92	0.71	5.90	0.86	0.02	75.95	0.88	-2.10
39	IC-329036	43.76	2.68	2.31	3.79	1.40	0.00	14.79	1.42	-0.62	5.93	1.00	0.00	75.52	0.92	-0.80
40	IC-325811	48.54	-0.37	144.67**	4.41	1.67*	-0.09	19.91	0.79	39.34**	6.75	1.00	0.00	75.53	1.00	-2.49
41	IC-373427	38.48	1.10	0.12	3.79	0.97	-0.07	9.99	0.33	1.53	5.09	0.99	0.01	74.93	1.02	2.53
42	IC-415159	21.94	2.43	-0.14	3.98	0.22	-0.04	10.13	0.11	0.76	7.06	0.81**	-0.03	74.98	0.97	-2.10
43	IC-311441	51.31	0.11	51.94**	4.18	2.59	0.13	12.35	-0.18	6.46**	6.49	1.69*	0.03	74.68	0.93*	-2.52
44	IC-415140	15.64	1.10	-2.38	4.05	0.77	0.16	10.26	0.69	0.17	6.09	0.73*	-0.03	75.37	1.10	-2.02
45	RGC-936	52.34	1.43	-0.96	4.24	1.02	-0.06	8.10	-0.41	1.89	6.32	0.80	0.00	72.85	1.17	11.94**
46	RGC-1031	44.09	3.00	107.25**	4.02	1.39	-0.05	17.28	1.98	24.98**	5.19	1.17	0.03	73.51	1.18	1.54
47	IC-402296	37.89	-1.23	351.54**	3.76	0.55	0.01	10.07	-0.26	6.88**	5.98	0.95	0.09*	73.94	1.08	1.68
48	IC-373480	27.43	2.79*	-0.68	3.91	0.11	0.02	10.19	2.42	-0.39	8.32	-0.29**	0.01	75.03	1.21	2.60
49	IC-369861	30.15	1.73	4.89	3.58	1.71	-0.08	16.54	1.95	2.67*	6.04	0.89	0.02	75.38	1.19	1.66
50	IC-421812	51.86	2.26	93.34**	4.13	1.34	-0.04	14.89	0.38	7.41**	5.37	1.04	0.42**	75.15	1.20	-1.19
51	IC-421798	16.86	0.63	-1.90	4.00	0.97	-0.04	17.53	-0.50	19.09**	5.09	1.37	0.06*	75.31	1.21	15.86**
52	IC-369868	42.89	-2.00	220.42**	4.06	0.52	-0.08	13.60	0.33	13.05**	5.54	1.26	0.03	76.49	1.17	4.78
53	RGC-986	18.94	1.03	-2.81	3.82	-1.00	0.02	10.06	-2.19*	-0.65	5.89	2.80	1.13**	75.90	1.28	1.30
54	HG-3-100	44.31	0.09	-1.53	4.00	-0.32	0.24*	9.79	-1.24	0.60	6.00	1.97	0.31**	73.90	1.52**	-2.08
55	AVT-GR-11	34.10	-0.78*	-2.03	4.46	0.99	0.04	7.55	1.28	1.36	7.23	0.23*	0.09*	71.93	1.35**	-2.28
	Mean	33.56			4.36			12.98			6.23			74.70		
	SE (m)±	2.14	1.53		0.19	0.66		1.02	1.53		0.30	0.18		1.06	0.13	
	CD 5%	5.95			0.54			2.84			0.84			2.94		

	CD 1%	7.83			0.70						3.74			3.87		

*,**- significant at 5% and 1% level and b_i= regression coefficient, S^2d_i = deviation from regression line

Table 3: Estimates of stability parameters for length of dry pod, width of dry pod, dry pod yield hectare^{-1}, seed yield plot $^{-1}$ and seed to husk ratio in cluster bean genotypes

Sr. No.	Genotype	Length of dry pod (cm)			Width of dry pod (cm)			Dry pod yield hectare^{-1} (q)			Seed yield plot^{-1} (g) (20 plant)			Seed to husk ratio		
		Mean	bi	S^2di	Mean	bi	S^2di	Mean	bi	S^2di	Mean	bi	S^2di	Mean	bi	S^2di
1	IC-298638	5.50	-1.27**	-0.008	0.61	1.18	-0.001	33.29	1.40	-4.40	226.76	1.07	31.09	1.31	-1.50*	0.001*
2	IC-370742	5.56	1.19*	-0.009	0.59	0.84*	-0.001	24.98	1.44	44.56**	181.11	1.53	2637.27**	1.49	3.34*	0.001**
3	IC-415102	6.01	-0.57**	-0.007	0.58	1.53	0.001	30.73	0.47	45.48**	220.88	0.57	1322.00*	1.53	3.06*	0.000
4	IC-415157	5.30	2.26**	-0.004	0.56	0.27**	-0.001	25.12	1.09	33.48**	181.05	1.17	1385.27*	1.53	1.60	0.002**
5	IC-415160	5.40	1.59*	-0.007	0.61	0.80	-0.001	25.27	1.13	26.84**	187.60	1.06	667.09	1.68	-2.11*	0.006**
6	IC-415163	5.48	-0.31*	-0.004	0.59	0.84	-0.001	30.78	2.21	17.04*	224.95	2.18	770.18	1.54	1.45	0.000
7	IC-415165	5.08	2.18*	-0.009	0.62	0.44	0.001	26.98	1.62	26.99**	198.88	1.62	1234.05*	1.58	1.05	0.000
8	IC-421797	5.18	0.47	0.014	0.63	0.15**	-0.001	28.22	1.94	5.80	194.29	1.94	126.61	1.35	2.86*	0.001*
9	IC-421801	5.86	1.44*	-0.008	0.61	0.93	-0.001	23.71	0.77	-6.08	170.00	0.72	-340.61	1.47	0.62	0.000
10	IC-421803	5.76	0.38**	-0.009	0.57	0.36	0.001	14.63	0.68	10.02	113.08	0.71	366.00	1.86	-0.33*	0.000
11	IC-421806	5.34	1.50*	-0.007	0.58	0.26	-0.001	27.92	-0.43	185.89**	200.48	-0.37	7869.65**	1.55	2.45**	0.000
12	IC-421811	5.64	2.39	0.225**	0.60	0.53	0.000	17.78	0.09	7.00	127.18	0.13	88.45	1.50	2.34	0.002**
13	IC-421816	5.59	1.42*	-0.009	0.59	1.37	-0.001	26.90	0.86	-6.68	193.95	0.86	-348.49	1.54	0.46*	0.000
14	IC-421820	5.25	-0.20*	0.002	0.60	0.77	-0.001	15.40	0.69	8.15	108.73	0.65	336.05	1.39	0.18	0.001
15	IC-421821	5.43	1.38	-0.003	0.54	1.16	0.000	29.21	0.25	55.83**	207.25	0.22	2541.38**	1.46	0.80	0.000
16	IC-421822	5.19	1.69*	-0.004	0.52	0.81	-0.001	21.60	1.13	-3.58	155.30	1.08	-318.58	1.52	0.25**	0.000
17	IC-421825	5.36	0.07	0.052**	0.56	1.13	0.001	34.26	0.69	33.81**	253.08	0.61	2284.12**	1.61	-0.36*	0.001*
18	IC-421826	5.23	0.94	-0.008	0.55	1.07	0.001	30.31	0.00	39.57**	223.10	0.16	1592.89**	1.66	3.45**	0.001*
19	IC-421828	5.38	1.32	-0.007	0.59	1.71	0.001	27.24	0.38	50.14**	205.98	0.34	2685.38**	1.69	0.56	0.000
20	IC-421830	5.21	1.53*	-0.006	0.55	0.97	0.001	27.71	1.70	1.89	205.72	1.45	990.38*	1.66	-2.80*	0.003**
21	IC-421831	5.14	1.40	-0.002	0.60	0.83	-0.001	27.69	0.76	-5.17	204.18	0.70	-291.69	1.58	-0.20**	0.000
22	IC-421832	5.16	2.09*	-0.004	0.53	0.64	0.001	24.10	0.22	12.61	180.68	0.20	508.77	1.64	0.69*	0.000
23	IC-421834	5.07	1.15*	-0.009	0.58	0.89	-0.001	34.23	0.90	5.65	240.10	0.96	-169.93	1.40	2.55*	0.000
24	IC-421837	5.42	1.24	-0.008	0.57	0.96	0.005*	28.62	0.58	3.22	204.67	0.44	68.03	1.50	-1.98	0.012**
25	IC-421839	5.20	2.44**	-0.007	0.52	0.97	-0.001	27.46	1.01	0.46	203.10	0.95	377.37	1.64	-0.35**	0.000
26	IC-421840	5.25	0.70*	-0.008	0.54	0.77	-0.001	32.70	0.57	49.50**	242.32	0.61	2340.89**	1.64	1.94*	0.000
27	IC-421841	5.15	0.78	-0.001	0.59	0.76	-0.001	18.31	0.58	7.23	141.98	0.63	523.87	1.80	1.20**	0.000

Sr. No.	Genotype	Length of dry pod (cm)			Width of dry pod (cm)			Dry Pod yield hectare^{-1} (q)			Seed yield plot^{-1} (g) (20 plant)			Seed to husk ratio		
		Mean	bi	S^2di	Mean	bi	S^2di	Mean	bi	S^2di	Mean	bi	S^2di	Mean	bi	S^2di
28	IC-421842	5.21	0.15**	-0.009	0.57	1.60	0.000	36.37	0.90	120.30**	265.18	0.93	4879.69**	1.55	2.38*	0.000
29	IC-421843	5.80	0.70*	-0.008	0.63	1.08	-0.001	30.08	2.30	24.91*	211.85	2.33	1034.46*	1.39	3.78*	0.002**
30	IC-369789	5.15	1.37*	-0.009	0.56	-0.13*	-0.001	26.11	1.32	16.74*	191.25	1.36	1060.87*	1.53	2.20*	0.000
31	IC-329639	5.40	2.72**	-0.004	0.60	0.92	-0.001	35.08	0.50	57.13**	263.41	0.37	3410.99**	1.64	-0.92**	0.000
32	IC-421815	5.33	1.09	-0.009	0.54	-0.14*	-0.001	28.10	0.85	-6.43	204.35	0.95	-355.90	1.58	2.22*	0.000
33	IC-248087	5.00	2.00*	-0.006	0.52	0.95	-0.001	29.76	1.50	-3.93	218.73	1.57	-241.93	1.58	2.23*	0.000
34	IC-324032	5.14	0.56*	-0.009	0.60	0.98	-0.001	30.47	1.00	-0.99	229.23	1.01	-82.00	1.68	1.30*	0.000
35	PLG-354	4.85	-0.03	0.010	0.55	1.06	0.001	31.82	2.29	16.00*	232.53	2.08	931.26*	1.52	0.35**	0.000
36	IC-370478	4.80	-0.62**	-0.009	0.55	1.90	0.000	29.57	1.20	-0.42	210.99	1.19	-165.93	1.47	0.73	0.000
37	IC-415109	5.43	1.54*	-0.007	0.52	1.33	-0.001	25.52	1.42	0.23	189.09	1.34	-165.17	1.63	-0.58**	0.000
38	PLG-85	5.18	1.76*	-0.007	0.51	3.05*	-0.001	24.94	0.93	34.34**	166.58	1.01	1954.96**	1.24	2.83*	0.000
39	IC-329036	5.77	1.58*	-0.006	0.59	0.78	-0.001	31.08	0.97	1.74	206.48	1.07	-365.31	1.25	3.53*	0.002**
40	IC-325811	4.82	1.95**	-0.008	0.53	1.65	-0.001	39.07	0.30	113.33**	275.78	-0.01	8682.35**	1.43	-3.04*	0.004**
41	IC-373427	5.40	1.80*	-0.004	0.53	1.59*	-0.001	19.21	0.95	-3.58	151.68	0.96	-184.60	1.87	0.41	0.000
42	IC-415159	5.29	1.35*	-0.008	0.50	1.03	-0.001	20.91	0.70	4.62	160.43	0.75	377.13	1.75	1.59	0.000
43	IC-311441	5.56	1.95*	-0.008	0.51	1.18	-0.001	27.04	1.68	33.11**	199.08	1.64	1126.76*	1.59	-0.62*	0.002**
44	IC-415140	5.34	-0.03*	0.004	0.48	0.53	0.001	12.30	0.48	-5.02	85.00	0.43	-278.23	1.31	0.34	0.000
45	RGC-936	5.75	0.35	0.003	0.48	0.53	0.001	17.43	0.70	58.47**	138.53	0.80	3244.30**	1.99	0.06*	0.000
46	RGC-1031	5.68	0.59**	-0.009	0.53	1.59	-0.001	30.18	2.19	23.00*	207.70	2.22	727.05	1.33	4.12*	0.002**
47	IC-402296	5.34	0.03**	-0.008	0.56	2.09*	-0.001	21.89	0.98	32.35**	172.38	1.66	3223.86**	1.47	5.55*	0.004**
48	IC-373480	5.52	0.18	0.013	0.58	1.11	0.000	30.64	1.11	-3.16	231.53	1.22	-362.35	1.69	3.44*	0.001**
49	IC-369861	5.55	0.44*	-0.006	0.53	1.64*	-0.001	35.05	1.48	5.16	262.38	1.38	469.27	1.65	0.05**	0.000
50	IC-421812	5.23	1.96**	-0.008	0.53	1.53*	-0.001	25.93	1.66	70.41**	178.43	1.44	2420.42**	1.35	-1.59*	0.002**
51	IC-421798	5.27	0.89	-0.009	0.60	0.88	-0.001	29.05	0.82	-0.81	197.18	0.99	-389.78	1.33	4.55*	0.002**
52	IC-369868	5.50	1.50*	-0.007	0.57	1.04	-0.001	24.70	1.66	66.44**	184.48	1.68	2434.83**	1.72	-0.99*	0.000
53	RGC-986	5.68	-0.10**	-0.007	0.49	0.76	-0.001	16.58	0.78	31.03**	121.62	0.80	1234.69*	1.60	-0.12*	-0.000
54	HG-3-100	6.29	0.20*	-0.002	0.51	1.25	-0.001	18.72	1.07	43.36**	146.34	1.13	2243.67**	1.85	0.12*	-0.000
55	AVT-GR-11	5.81	-0.06**	-0.008	0.51	0.26	0.007**	12.54	0.52	-1.95	90.50	0.51	-224.03	1.53	-0.14*	0.000
	Mean	5.39			0.56			26.46			192.53			1.56		

	SE (m)+	0.10	0.17		0.02	0.32		2.17	0.54		15.96	0.50		0.05	0.28	
	CD 5%	0.29			0.06			6.04			44.38			0.13		
	CD 1%	0.38			0.07			7.95			58.43			0.16		

*,**- significant at 5% and 1% level and bi= regression coefficient, S2di = deviation from regression line

References

1. Baldodiya Vijay Kumar, Awasthi PK. Guar (*Cyamposis tetragomoloba* L.) seed production status in India. Int. J. Chem. Stu 2018;**6**(6):1436-1440
2. Chaudhary SPS, Saini DD, Singh RV, Khedkar OP, Jaber Singh. Phenotypic Stability for seed yield and yield attributing traits in Clusterbean (*Cyamopsis tetragonoloba* (L.) Taub.). Arid legumes for sustainable agriculture and trade 2005a;1:81-85.
3. Chaudhary SPS, Singh RV, Singh NP, Khedar OP. Stability for seed yield influencing traits in clusterbean [*Cyamopsis tetragonoloba* (L.) Taub.]. Journal of Arid Legumes 2005b;2(1):86-90.
4. D'almeida A, Tikka SBS. Stability of yield and quality traits in guar. Book-Advances in arid legumes research. 2003, 367-371.
5. Eberhart SA, Russell WL. Stability parameters for comparing varieties. Crop Sci 1966;6:36-40.
6. Henry A, Kackar NL. Studies on phenotypic stability in clusterbean under late sown conditions. Current Agriculture. 2001;25(1, 2):103-105.
7. Jain SK, Patel PR. Stability analysis for seed yield and their component traits in breeding lines of guar (*Cyamopsis tetragonoloba* (L.). Legume Res. 2012;35(4):327-331.
8. Pathak R, Singh SK, Singh M, Henry A. Performance and Stability of *Cyamopsis Tetragonoloba* (l.)Taub Genotypes under Rainfed Conditions. Indian J.Dryland Agric. Res. & Dev 2010b;25(2):82-90.
9. Pathak R, Singh M, Henry A. Stability, correlation and path analysis for seed yield and yield-attributing traits in clusterbean (*Cyamopsis tetragonoloba*). Indian Journal of Agricultural Sciences 2011;81(4):309-13.