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Interpreting genotype × environment interaction in greengram (*Vigna radiata* L. Wilczek) using Eberhart and Russell Model

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Abstract
Fifty four genotypes of greengram were investigated under four different environments in a randomised block design with three replications during the year 2021. Eberhart and Russell's model was carried out which revealed significant G × E interaction for all the traits, indicating the differential response of genotypes to changing environments. The linear and non-linear G × E components were significant for majority of the characters, suggesting the presence of both predictable and non-predictable components. The genotypes *viz*., VMG-66, VMG-39, VMG-79, VMG-97 and GM 6 were found to be stable and high yielding across the environments. These genotypes were also found stable for two or three other yield contributing component traits. It can be inferred from the stability analysis that none of the genotype was noticed to be ideal with greater adaptability for all the characters.

Keywords: Stability, Greengram, Environment, G × E interaction

INTRODUCTION

India with an alarming increasing population has become self-sufficient in food production through the green revolution. In India, however, the issue of protein and calorie malnutrition persists. The primary sources of protein for India's largely vegetarian population are pulse crops, which provide 14% of the total protein in a typical Indian diet. In recognition of the multiple health benefits of pulses, the United Nations proclaimed 2016 the "International Year of Pulses." The yield of pulses is much below what is necessary to even meet the very minimal level of per capita consumption. To meet the country's growing population's demand for protein, agricultural scientists must develop a strategy to increase the production of pulses. Chickpeas, pigeon peas, green gram, black gram, lentils, *etc*. are some of the major pulses cultivated in India.

Self-pollinated leguminous greengram (*Vigna radiata* L. Wilczek), 2n=22, is cultivated in India and is said to have originated here. Following the chickpea and pigeonpea, it is the third most significant pulse crop. It is a short-lived crop that performs well in rotation and mixed farming systems, is well adapted to a wide range of soil types, has a low water requirement, making it an excellent choice for drought-tolerant crops and also enhancing soil fertility and physical properties through biological nitrogen fixation with the help of Rhizobium bacteria in nodules. It contains a quantity of minerals (4%), vitamins (3%), and carbohydrates (55–66%). It is also a good source of protein (24 to 26 %). It is cultivated in Gujarat over a total area of 1.54 lakh hectares, producing 1.10 lakh tonnes annually with average productivity of 712 kg per ha during the year 2020 (Anonymous, 2022).

One of the most sensitive sectors to climate change is agriculture. In any breeding program, it is necessary to screen and identify phenotypically stable genotypes which could perform more or less uniformly under different environmental conditions (Saleem *et al*., 2015). Evaluation of genotypes for yield performance typically reveals interactions between genotype and environment (GE) that make choosing or recommending cultivars more difficult. One of the genetic factors thought to be responsible of phenotypic stability and adaptation is GE interaction. The evaluation of GE interactions gives an idea of the buffering capacity of the population. These investigations are equally crucial to crop enhancement. Greengram has traditionally been grown in a variety of climatic environments. The findings of this experiment may be helpful to breeders as well as farmers to select suitable genotypes for sustainable greengram production. Thus, in order to evaluate and carry out breeding programmes and predict the stable genotypes, it is required to investigate the interaction between genotype and environment in greengram genotypes sown at different times.

MATERIALS AND METHODS

In the current study, a group of 54 genotypes of greengram were assessed in four distinct environments produced by two different sowing dates in the summer (18-2-2021 and 18-3-2021) and *kharif* (16-7-21 and 28-8-2021) seasons at Regional Research Station (RRS), Anand Agricultural University, Anand (22° 35' N, 72° 55' E), Gujarat, India during the year 2021. The trials were set up in a randomized complete block design with three replications having single row plots of 4 m in length with a row spacing of 45 cm and plant to plant spacing of 10 cm. Every experiment had a border row around it to prevent damage and border effects. By implementing the essential agronomic and plant protection measures, the crop was successfully cultivated. Five competitive plants were observed for eleven morphological characteristics, including days to 50% flowering, days to maturity, plant height, branches per plant, clusters per plant, pods per plant, pod length, seeds per pod, seed yield per plant, test weight and protein content on five plants randomly chosen from each entry in all environments. The data were analyzed for stability parameters following Eberhart and Russsell (1966) model. The model is defined as follows:

$$Y_{ij} = \mu_i + \beta_i I_j + \delta_{ij}$$

Where,

Y_{ij} = Mean performance of ith genotype in jth environment.

μ_i = Mean performance of ith genotype over all environments.

β_i = Regression coefficient that measures the response of ith genotype to varying environments.

I_j = Environment index, as the deviation of the mean of all genotypes in the jth environment from grand mean.

δ_{ij} = The deviation from regression of the ith genotype in jth environment.

i = Number of genotypes (1, 2…i)

j = Number of environments (1, 2…j)

RESULTS AND DISCUSSION

In the present study, a pooled analysis of variance for stability analysis across four different environments was performed on 54 genotypes of greengram (**Table 1**). The combined analysis of variance results showed that the mean squares due to genotypes were significant for all the traits, with the exception of clusters per plant, indicating that the material assessed for yield and its component traits had a sufficient level of variability. Plant breeders can choose superior and desirable genotypes for further crop improvement programmes because of the broad spectrum of diversity. All the environments considerably varied, indicating that each of the environments was unique. For all characters, the pooled analysis also revealed significant genotype × environment interactions, indicating that the genes were dependent on environmental factors. This also suggests differential response of genotypes to changing environments. The findings were in conformity with Singh and Sharma *et al*. (2014), Rita *et al*. (2016) and Desai *et al.* (2020), who found genotype × environment interaction significant for most of the traits.

In Eberhart and Russell model, genetic and environmental interactions are divided into linear and non-linear components of variation, which reveal the predictable and unpredictable sources of variation that influence genetic and environmental interactions for all traits. With the exception of pod length, the effect of Environments + (Genotype × Environments) was found to be significant against pooled error for all characters, suggested distinct nature of seasons and genotypes may respond to changing environments differently. For all of the characters, the impact of Environments (linear) was found to be highly significant, which revealed that environments varied greatly across different seasons and considerable additive environmental variance for all of the attributes. The higher magnitude of mean squares for Environments (linear) compared to Genotype× Environments (linear) indicated that the linear response of environment accounted for the major part of the total variation for all the traits. It also indicates adaptation of genotypes in relation to yield and its components.

For traits *viz*., days to maturity, branches per plant, pods per plant, test weight and protein content, the mean squares due to genotype × environments (linear) were found to be significant, indicating that all the

Table 1. Pooled ANOVA for stability analysis as per Eberhart and Russell (1966) for various characters of green gram

Source	df	Days to 50% flowering	Days to maturity	Plant height	Branches per plant	Clusters per plant
Genotypes (G)	53	20.67**	67.15**	60.85**	0.39**	1.38
Environments (E)	3	804.70**	917.71**	1375.47**	2.58**	26.79**
Genotypes × Environments	159	2.58**	6.52**	18.04**	0.12**	1.03**
Environments + (G × E)	162	17.44**	23.39**	43.18**	0.16**	1.50*
Environments (linear)	1	2414.10**	2753.14**	4126.42**	7.74**	80.37**
G × E (linear)	53	1.96	9.42**	15.69	0.19**	0.94
Pooled deviations	108	2.84**	4.97**	18.86**	0.08**	1.05**
Pooled error	424	0.62	0.97	5.19	0.02	0.09

Source	df	Pods per plant	Pod length	Seeds per pod	Seed yield per plant	Test weight	Protein content
Genotypes (G)	53	64.02**	0.93**	0.71**	5.88**	0.86**	4.94**
Environments (E)	3	5728.28**	2.31**	31.00**	157.84**	13.29**	8.86**
Genotypes × Environments	159	29.87**	0.14**	0.42**	3.40**	0.13**	0.50**
Environments + (G × E)	162	135.39**	0.18	0.98**	6.26**	0.38**	0.65**
Environments (linear)	1	17184.84**	6.93**	92.99**	473.51**	39.86**	26.57**
G ×E (linear)	53	53.67**	0.14	0.41	3.89	0.17*	0.89**
Pooled deviations	108	17.63**	0.13**	0.41**	3.09**	0.11**	0.29**
Pooled error	424	1.24	0.09	0.15	0.20	0.02	0.29

*, ** Significant at 5% and 1% level of significance, respectively

regression coefficients are not statistically at par and that the variation in genotype performance was due to regression of genotype and environment interaction and as a result, genotype performance would be predictable. Lahre (2016) and Borude (2017) also reported similar findings for the majority of greengram traits. For all of the traits, the non-linear component of the G × E interaction (pooled deviation) was found to be significant, indicating that the accuracy of the genotype response predictions made using regression analysis for these traits may not be very robust. It also suggested unpredictable portion formed the major part of the G × E interactions. The findings are in conformity with Kuchanur *et al*. (2017) and Sharma *et al*. (2022). On comparing the relative magnitude of genotype × environment (linear) and pooled deviation from linearity (non-linear), it was noted that the linear component was high for days to maturity, seed yield per plant, branches per plant and protein content indicating that linear component contributed more towards the genotype × environment interactions, while a high value of non-linear components was observed in days to 50% flowering, plant height and clusters per plant. In the case of pod length, seeds per pod and test weight both linear and non-linear components were almost equal indicating the importance of both linear and non-linear components in determining genotype × environment interactions for these attributes. The observed preponderance of linear components could aid in precise genotype performance prediction across environments.

The mean performance, regression (b_i) and squared deviation (s^2d_i) for eleven morphological traits are presented in **Table 2**. It's remarkable to note that no single accession exhibited stability for every trait. For 54 genotypes, with desirable mean value and non-significant S^2d_i were classified into the three groups based on regression coefficient value given in **Table 3**. Group I having desirable mean performance ($\overline{x}_i$), regression coefficient close to unity (b_i=1) and deviation from regression approaching to zero (s^2d_i=0) was considered stable. Group II with a desirable mean ($\overline{x}_i$), regression coefficient significantly greater than unity (b_i>1) and non-significant deviation from regression (s^2d_i=0) considered as below average responsive genotypes and suitable for favorable environments. Group III having superior mean ($\overline{x}_i$), regression coefficient significantly less than unity (b_i<1) and non-significant deviation from regression (s^2d_i=0) considered as above average responsive genotypes and suitable for poor or stress environments. The genotypes having significant s^2d_i were treated as unstable.

The identification of the varieties for adaptation can also be accomplished by the graphical procedure. A graphical procedure of identifying stable/adaptable varieties has also been proposed by Tai (1971). The regression coefficient (b_i) was plotted against their corresponding mean for seed yield per plant is presented in **Fig.1**. The generally adapted genotypes are those falling in the

Table 2. Stability parameters for morphological traits across environments

S.No.	Genotypes	Days to 50% flowering			Days to maturity			Plant height (cm)			Branches per plant			Clusters per plant		
		Mean	b_i	S^2d_i	Mean	b_i	S^2d_i	Mean	b_i	S^2d_i	Mean	b_i	S^2d_i	Mean	b_i	S^2d_i
1	AM-15-1-1	38.92	0.85	1.94*	61.92	0.06**	1.41	40.65	0.50	14.35*	2.58	1.46	0.07*	4.45	-0.24*	0.27*
2	AM-15-3-2	46.25	0.55*	1.54*	70.17	0.58	29.41**	51.53	0.90	5.17	3.57	2.48	0.32**	4.98	0.94	0.16
3	AM-15-18-1	40.25	1.25*	0.03	61.17	0.82	6.75**	45.63	0.68	11.96*	3.28	3.82	0.30**	5.47	2.83*	1.10**
4	AM-15-19-2	40.67	0.84	1.41*	60.08	0.88	1.45	45.73	0.81**	-5.06	2.71	0.17	0.01	5.53	0.12	3.25**
5	AM-15-25-1	41.58	1.16**	-0.61	61.00	0.94	9.17**	46.03	1.09	12.06*	3.32	3.26	0.18**	4.98	0.39	1.54**
6	AM-15-41-1	42.25	0.81	5.79**	67.25	1.39*	0.65	47.67	0.12	26.73**	2.99	2.70**	0.03	6.28	0.60	2.81**
7	AM-15-47-2	41.92	0.70**	-0.51	68.08	0.99	6.57**	46.68	0.39	13.46*	2.27	1.23	0.02	4.61	0.46**	-0.04
8	AM-15-51-1	41.58	1.03	4.59**	65.42	1.02	7.64**	46.80	1.34	0.75	2.52	0.53**	-0.02	5.27	-0.10	0.49**
9	AM-15-53-1	40.25	1.11	0.23	62.42	1.03	0.00	42.03	0.54**	-3.68	2.85	0.65	0.13**	5.41	1.51	0.64**
10	AM-K 18-2	42.92	0.84	0.10	68.75	1.24**	-0.95	46.22	0.98	4.58	2.37	-1.01**	0.02	5.22	0.70	2.08**
11	AM-K-18-5	46.33	1.09	12.60**	72.75	1.50**	-0.46	51.17	1.78**	-1.63	3.15	1.85**	-0.02	5.77	1.16	-0.01
12	AM-K-18-8	48.83	0.98	6.80**	77.25	0.65**	-0.90	52.67	1.13	10.85*	3.15	0.02**	-0.02	6.58	0.17	0.34**
13	ANDGG-12-2	41.25	1.06	-0.40	65.25	1.06	0.23	46.57	0.77**	-4.84	2.85	2.98**	0.04	4.83	2.24	0.65**
14	ANDGG 13-01	47.58	1.09	14.48**	75.08	1.41**	-0.91	53.07	1.17	59.72**	2.72	1.60*	-0.01	5.80	0.50	0.57**
15	BHU-16	42.17	0.77**	-0.35	64.67	0.71	6.17**	49.95	1.22	22.50**	2.65	1.78	0.00	5.40	1.88	0.86**
16	GJM 1714	40.67	0.74	0.43	71.25	1.91*	6.24**	44.25	1.01	69.02**	2.57	-0.92**	-0.01	5.62	0.86	0.58**
17	GM-4	39.67	1.07	0.42	61.75	0.85	8.04**	43.83	0.86	13.33*	2.68	1.33	-0.01	4.23	1.76	1.25**
18	GAM-5	39.58	0.74	0.83	61.17	0.23*	4.15**	45.10	1.20	-0.21	2.56	0.16	0.02	5.42	0.26	0.48**
19	GM-6	40.92	0.97	-0.15	60.75	0.64**	-0.03	43.38	1.26	11.76*	2.37	0.25**	-0.02	5.28	0.08	1.09**
20	GM-7	41.08	0.86	-0.20	63.67	0.69**	-0.81	43.08	0.37*	0.98	2.64	0.29**	-0.02	4.98	1.20	0.87**
21	Jabugam SP	40.33	0.88	1.40*	64.17	1.18*	-0.68	45.10	0.84	5.79	2.72	1.58	0.03	5.57	0.65	1.19**
22	Meha	43.08	0.59**	0.11	68.92	0.47**	-0.41	50.27	1.05	37.26**	2.78	0.30	0.12**	5.00	-0.09	0.83**
23	VBN-3	45.42	0.62*	0.73	71.50	0.62	5.03**	56.25	1.17	-4.12	2.48	0.39	0.01	5.57	1.65**	-0.01
24	VGG-15-030	44.83	1.04	1.20	75.33	1.21	18.14**	53.17	2.16*	19.75**	3.25	0.64	0.08*	6.35	1.71	1.50**
25	VGG-16-55	42.92	1.03	2.25*	64.50	0.36	16.97**	50.68	2.22**	3.74	2.88	0.66	0.12**	5.23	1.70	1.04**
26	VGG-17-048	45.42	1.23	3.34**	71.25	0.60	6.98**	52.45	2.26	80.31**	2.63	0.91	-0.01	5.98	0.86	1.15**
27	Vijapur selection	47.17	1.30	10.73**	70.08	1.09	36.29**	49.57	1.36	-1.29	3.08	1.39	0.02	5.62	0.38	2.38**
28	VMG 10	42.92	1.41	10.49**	68.00	1.96**	0.38	42.12	0.32**	-2.27	2.66	0.03	0.10**	4.93	0.67	1.21**
29	VMG-12	42.58	1.20	2.12*	62.75	0.64**	-0.94	48.97	0.96	-1.41	3.08	2.06*	0.01	6.02	0.92	0.49**
30	VMG-15	44.50	1.37*	0.81	65.08	0.27**	2.52*	50.00	1.23	16.13*	2.82	1.67	0.16**	5.23	1.97**	0.05
31	VMG-19	41.92	1.11	-0.25	67.00	0.78	2.29*	45.48	1.02	-4.44	2.54	0.55	0.00	4.95	1.23	1.21**
32	VMG-25	43.08	1.16	0.37	71.92	1.16	2.25*	51.03	1.19	5.89	2.58	1.97*	0.01	5.21	1.90	0.98**
33	VMG-30	40.50	1.13	1.80*	60.33	1.04	-0.70	46.45	0.56**	-3.22	2.50	0.51	0.00	6.63	1.30	5.19**
34	VMG-32	44.75	0.93	0.69	71.25	1.08	17.81**	53.38	0.94	25.55**	2.79	0.51	0.00	5.45	1.63	1.00**
35	VMG-37	43.00	0.71	0.62	65.08	0.72	1.04	47.55	0.98	-4.16	3.05	1.69	0.00	5.72	1.05	0.24*
36	VMG-39	42.92	1.27**	-0.25	65.50	1.09	0.24	47.13	0.62	36.54**	2.57	0.11**	-0.02	5.80	0.59	0.31*
37	VMG-47	46.17	1.06	2.00*	72.33	1.37	4.54**	54.38	0.80	8.05	3.62	3.85**	0.13**	6.97	2.51	1.11**
38	VMG-58	44.00	1.03	5.31**	68.58	0.73	3.32*	50.23	1.79**	1.57	2.93	1.43	0.05*	6.37	2.23*	0.44**
39	VMG-62	42.92	1.08	-0.16	65.58	0.81**	-0.78	46.18	0.77	8.46	2.90	-0.28**	0.00	5.38	0.17	0.53**
40	VMG-66	39.83	0.90	0.71	63.17	1.12	-0.23	42.90	0.92	-4.12	2.68	0.68	0.16**	5.33	2.21*	0.34**
41	VMG-69	39.75	1.04	0.56	67.42	1.68**	-0.18	43.55	0.84	8.86	2.55	0.78	0.01	5.60	0.64	0.85**
42	VMG-71	40.50	0.95	0.80	67.92	1.81**	-0.76	43.23	0.88	1.87	2.55	-0.18	0.08*	4.88	0.42	0.66**
43	VMG-75	43.50	1.27*	0.10	65.50	0.63**	-0.54	45.25	1.04	-4.77	2.82	2.64**	0.03	5.73	1.55*	-0.01

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S.No.	Genotypes	Days to 50% flowering			Days to maturity			Plant height (cm)			Branches per plant			Clusters per plant		
		Mean	b_i	S^2d_i	Mean	b_i	S^2d_i	Mean	b_i	S^2d_i	Mean	b_i	S^2d_i	Mean	b_i	S^2d_i
44	VMG-79	40.50	1.36	3.40**	63.25	1.52**	-0.50	45.52	0.95	29.54**	2.83	2.45	0.14**	6.30	1.66	1.52**
45	VMG-83	42.83	0.95	2.17*	65.33	1.05	4.13**	43.90	0.36	49.90**	2.36	0.65	0.05*	4.38	0.96	0.24*
46	VMG-85	43.17	1.09	6.44**	65.50	0.81	2.73*	42.72	0.58	11.31*	2.48	-0.19	0.16**	5.23	1.24	0.39**
47	VMG-88	40.42	1.06	0.38	64.33	1.28	3.36*	44.25	0.67	2.13	2.12	-0.25	0.06*	5.55	0.37	3.18**
48	VMG-90	42.00	0.95	-0.20	68.08	1.49**	-0.50	50.70	1.34	70.29**	2.53	0.06**	-0.02	5.90	0.28**	-0.03
49	VMG-92	41.08	0.63	3.48**	65.25	1.32	9.20**	47.43	1.05	5.95	2.95	2.21**	-0.02	5.23	1.42	1.62**
50	VMG-93	41.08	0.73	0.28	61.17	0.50**	-0.60	36.88	0.46	21.62**	2.39	0.77	0.20**	4.65	-0.95*	1.34**
51	VMG-95	41.08	0.90	0.08	69.50	1.53	4.10**	47.85	1.23	-0.27	2.65	0.65	0.23**	5.18	0.54	0.66**
52	VMG-97	40.08	1.14	1.30*	64.75	1.72**	-0.91	43.08	0.79	-3.65	2.48	-0.40	0.19**	5.70	-0.01	0.62**
53	VMG-100	44.33	1.18	6.43**	66.58	0.97	-0.81	47.38	1.44	9.55	2.46	0.13	0.03	4.33	1.30	0.55**
54	VMG 103	43.42	1.22	1.41*	66.42	0.79	-0.32	49.33	1.11	50.14**	2.89	-0.58	0.11**	5.60	1.99*	0.22*
-	Mean	42.53	-	-	66.54	-	-	47.16	-	-	2.75	-	-	5.44	-	-

Table 2 Cont.…

S. No.	Genotypes	Pods per plant			Pod length (cm)			Seeds per pod			Seed yield per plant (g)			Test weight (g)			Protein content (%)		
		Mean	b_i	S^2d_i	Mean	b_i	S^2d_i	Mean	b_i	S^2d_i	Mean	b_i	S^2d_i	Mean	b_i	S^2d_i	Mean	b_i	S^2d_i
1	AM-15-1-1	11.30	0.41*	16.19**	9.06	2.71	0.02	10.82	1.07	-0.12	4.83	0.48	6.10**	5.49	2.12**	0.10**	24.79	-0.19	0.35
2	AM-15-3-2	21.62	1.63	96.57**	7.55	-0.98	0.25*	11.25	-0.80**	0.26	6.68	2.95	21.39**	3.48	0.64**	-0.02	24.44	1.55	-0.14
3	AM-15-18-1	17.55	0.92	7.13**	8.64	2.16	0.24*	11.15	0.99	0.34*	6.03	1.06	5.10**	4.38	1.17	0.39**	25.85	2.52	0.24
4	AM-15-19-2	16.85	0.32**	2.97*	7.73	-0.52	0.04	10.42	0.88	-0.08	5.78	0.14**	-0.08	4.05	1.03	0.04*	24.30	2.08**	-0.26
5	AM-15-25-1	18.38	0.87	23.83**	8.03	2.44	-0.01	9.95	1.85	1.66**	5.58	0.98	0.99**	4.06	1.26	0.12**	23.69	-0.29	0.62*
6	AM-15-41-1	25.22	1.13	24.76**	7.53	-0.25	0.00	11.10	0.39*	0.01	6.92	1.50	2.65**	3.40	0.81	0.17**	23.68	0.47	-0.19
7	AM-15-47-2	17.42	0.81	25.92**	7.52	0.95	-0.07	10.98	1.25	0.64**	5.10	0.97	2.67**	4.10	1.94**	-0.02	25.74	0.93	-0.14
8	AM-15-51-1	16.08	0.61**	4.68**	7.79	1.17	0.16	10.47	1.74	0.58**	4.97	0.20**	-0.01	3.67	0.85	-0.01	25.23	2.30**	-0.27
9	AM-15-53-1	16.43	0.83	41.18**	8.16	2.59	0.26*	10.60	1.77**	-0.02	5.17	0.87	0.95**	4.48	1.34	0.20**	22.67	0.96	-0.03
10	AM-K 18-2	19.63	1.14	0.81	7.84	1.24	0.13	10.78	0.56**	-0.15	8.60	2.98	17.30**	3.95	0.64*	0.00	24.43	1.73	-0.21
11	AM-K-18-5	19.83	1.23	43.14**	8.11	1.06	-0.07	10.93	0.52	0.05	6.63	1.36	2.00**	4.02	0.38	0.30**	23.37	2.14	-0.07
12	AM-K-18-8	24.30	1.83	70.75**	7.47	0.07	-0.04	10.85	0.57	-0.03	6.64	1.90	10.60**	3.53	0.12	0.18**	23.34	1.40*	-0.27
13	ANDGG-12-2	18.75	1.13	12.38**	8.16	0.56	0.14	11.27	0.60	0.54*	5.83	1.52	1.34**	3.71	0.70	0.05*	23.97	-1.46**	-0.24
14	ANDGG 13-01	25.22	1.83**	4.06*	7.29	0.38	-0.04	10.53	0.28*	0.01	6.42	2.01	13.82**	3.99	0.75	0.17**	22.63	-0.80	1.07**
15	BHU-16	18.35	1.00	1.55	8.15	1.29	0.13	11.07	0.82	0.52*	7.02	1.37	0.55*	4.70	2.16*	0.22**	25.17	-0.84**	-0.15
16	GJM 1714	22.48	1.19	15.46**	7.63	0.50**	-0.09	11.05	0.89	-0.11	7.27	1.36	0.56*	4.50	1.48	0.09**	24.58	2.39	0.10
17	GM-4	15.00	0.82	1.64	7.85	1.93*	-0.06	10.83	1.00	-0.11	4.33	0.14**	-0.16	4.13	0.98	0.24**	25.75	2.28*	-0.11
18	GAM-5	18.95	0.90*	-0.65	7.83	0.81	0.08	10.62	0.95	0.24	6.30	0.69	0.53*	4.19	1.09	0.26**	26.00	1.63	0.12
19	GM-6	15.88	0.48**	10.97**	9.01	4.01**	-0.07	11.10	1.32	-0.01	5.50	0.42	2.04**	4.84	1.42**	-0.01	25.00	1.09	-0.18
20	GM-7	15.17	0.56	21.62**	8.65	0.97	-0.04	11.67	1.23*	-0.14	5.38	0.55	2.10**	4.66	1.44*	0.01	26.21	-0.90*	-0.01
21	Jabugam SP	16.68	0.58	18.76**	7.90	1.47	0.12	10.80	1.45	0.23	5.47	0.68**	-0.19	4.09	1.13	0.25**	23.18	0.11**	-0.28
22	Meha	19.27	0.99	2.71*	7.12	-0.08	0.50**	10.42	0.98	0.46*	6.72	0.10	3.47**	3.13	0.65	0.06*	25.11	2.51*	-0.08
23	VBN-3	21.27	1.06	40.44**	7.91	-0.24	0.08	10.63	0.93	0.08	8.92	0.40	5.62**	3.91	0.63	0.01	25.02	0.43	-0.22
24	VGG-15-030	33.27	2.33**	62.58**	7.01	0.21	0.08	10.58	0.70**	-0.13	9.82	0.63	0.58*	3.33	0.65	0.01	23.66	-1.26**	-0.15
25	VGG-16-55	26.97	1.48*	12.96**	7.43	-0.52*	-0.03	10.70	0.84	-0.04	7.53	1.64	2.87**	3.71	0.55**	0.00	23.73	2.30	0.46
26	VGG-17-048	23.68	1.38	12.98**	8.11	-0.06	0.19*	10.82	0.63	-0.05	8.73	0.38	6.71**	3.84	0.90	0.06*	25.15	2.14	0.00
27	Vijapur selection	22.20	1.46*	15.97**	7.47	1.34	-0.07	10.37	1.29	0.57**	5.40	1.69	3.28**	3.65	0.61**	-0.01	23.09	1.46	-0.03
28	VMG 10	14.17	0.38**	1.68	7.32	1.90	0.17	10.12	1.30	0.49*	4.23	0.32**	-0.01	4.08	1.21	0.19**	22.78	1.48*	-0.27

29	VMG-12	17.20	0.72**	0.96	8.01	1.49	0.17	11.25	1.50**	-0.11	5.55	0.72*	-0.04	4.26	0.87	0.19**	24.52	0.58*	-0.27
30	VMG-15	18.60	0.85**	-0.88	7.72	0.67	0.02	11.63	1.25	0.31*	6.80	0.32*	0.62*	3.83	1.12	0.10**	23.99	1.99**	-0.27
31	VMG-19	17.68	1.09	2.26	7.52	0.54	-0.07	10.62	1.21	-0.09	4.88	1.03	0.70*	3.98	0.56**	-0.02	25.12	1.87	0.66*
32	VMG-25	17.38	0.95	2.10	7.60	1.57	-0.08	10.07	1.47	1.02**	6.03	1.16	2.92**	3.87	0.91	-0.01	24.35	-0.28	0.21
33	VMG-30	11.88	0.36**	3.36*	8.70	3.07	0.16	10.13	2.01	1.43**	4.32	0.09**	0.04	5.19	2.56**	0.00	26.20	1.48*	-0.27
34	VMG-32	19.50	0.96	8.37**	7.45	-0.20	0.08	11.32	0.58	0.12	6.08	1.05	6.06**	3.58	0.54	0.11**	22.23	-0.03	0.03
35	VMG-37	22.87	1.08	8.94**	7.51	2.82	0.57**	10.83	0.79	0.40*	6.22	0.63	0.67*	3.33	0.74	0.33**	24.79	2.87*	0.03
36	VMG-39	16.68	0.77*	1.49	7.43	0.46	0.07	10.17	1.46	0.05	6.50	1.05	0.00	4.08	1.31	0.06*	25.90	2.68	0.53
37	VMG-47	25.83	1.43	55.49**	7.95	0.21	0.00	11.37	1.00	0.56**	8.68	1.35	8.31**	3.63	0.49**	0.00	23.42	-0.08	1.39**
38	VMG-58	25.02	1.92**	36.45**	7.30	0.80	-0.08	10.50	0.66	-0.08	6.70	2.24*	3.32**	4.06	1.79**	0.01	24.75	1.22	-0.28
39	VMG-62	16.80	0.80**	-0.37	7.78	1.17	-0.05	10.82	1.04	0.34*	6.48	1.11	4.85**	3.79	0.60	0.03	23.26	1.07	-0.18
40	VMG-66	23.28	1.30	14.75**	7.20	1.10	0.00	10.40	1.11	0.19	6.53	1.21	-0.02	3.61	0.66	0.10**	24.36	1.62	-0.02
41	VMG-69	17.88	0.92	12.40**	8.36	-0.36	-0.02	10.90	0.48**	-0.10	6.13	1.13	-0.05	4.68	1.26	0.22**	25.26	1.44	-0.16
42	VMG-71	18.78	0.86	2.54*	7.62	1.52	0.00	10.45	1.37	0.30	5.62	0.99	1.73**	4.09	0.71	0.04	24.52	2.45	0.06
43	VMG-75	20.30	1.23	3.59*	7.24	0.69	-0.06	10.28	0.48	0.64**	4.98	1.25**	-0.19	3.48	1.02	-0.02	24.06	-0.68**	-0.21
44	VMG-79	18.88	0.89	22.05**	8.42	1.74	0.03	10.73	0.91	0.02	6.43	1.18	-0.06	4.46	0.88	0.02	25.33	1.61	0.03
45	VMG-83	16.45	0.79*	1.05	8.02	1.73	-0.06	10.83	1.49	0.51*	6.27	1.32	3.57**	4.48	1.35**	-0.02	25.60	0.35	-0.16
46	VMG-85	19.22	1.16*	0.89	7.67	0.32	0.04	10.62	1.10	0.05	5.30	1.58	0.62*	3.80	1.05	0.01	24.90	-0.15	0.35
47	VMG-88	19.58	0.81	45.66**	7.39	-0.15	-0.04	10.77	1.16	1.71**	4.73	0.59	3.46**	3.73	0.60*	0.00	24.97	2.83**	-0.12
48	VMG-90	21.90	0.45**	1.10	7.98	1.03	-0.04	10.77	1.54	0.15	6.57	-0.34**	1.05**	3.90	0.72	0.17**	24.92	2.64**	-0.26
49	VMG-92	23.42	1.05	3.37*	7.02	1.61**	-0.09	9.77	1.25	-0.09	6.47	1.17	0.57*	3.75	1.46	0.10**	26.62	0.67	-0.27
50	VMG-93	15.03	0.48**	6.04**	7.06	3.08**	-0.01	10.15	1.40	0.54*	3.97	0.33	2.23**	3.59	0.55	0.06*	22.01	-1.52*	0.36
51	VMG-95	21.82	0.96	4.09*	7.70	0.56	0.02	10.77	0.70	0.18	7.18	0.28*	0.76**	3.59	1.13	0.01	22.76	1.15	-0.11
52	VMG-97	24.23	0.97	2.20	7.40	0.47	-0.02	10.25	1.40*	-0.09	6.35	0.92	0.32	3.74	0.78	0.00	23.13	-3.42**	0.02
53	VMG-100	16.77	0.82	11.80**	7.87	0.02**	-0.07	11.43	0.65	0.25	6.02	1.25	0.57*	3.86	0.54	0.13**	25.43	1.81**	-0.26
54	VMG 103	21.90	1.08	42.64**	7.15	0.94	0.01	10.30	0.01*	0.15	5.60	1.10	1.59**	3.72	1.16	0.47**	25.36	1.68**	-0.28
-	Mean	19.64	-	-	7.76	-	-	10.72	-	-	6.19	-	-		-	-	24.45	-	-

*, ** Significant at 5% and 1% level of significance, respectively

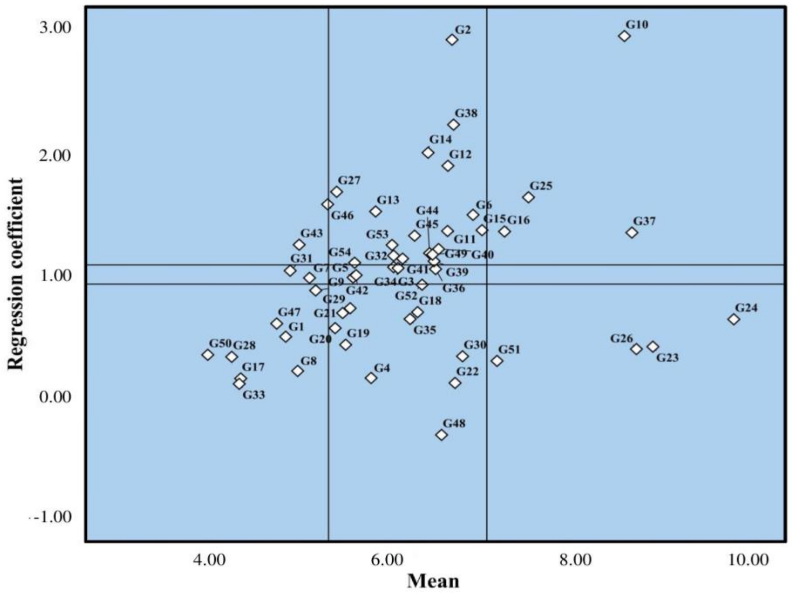

Fig. 1. Scatter plot of mean against regression coefficient (b_i) for seed yield per plant

Table 3. Grouping of genotypes based on stability parameters

S.No.	Characters	Group I (b_i=1)	Group II (b_i>1)	Group III (b_i<1)
1.	Days to 50% flowering	GAM-5, GM-4, VMG-69, VMG-66, AM-15-53-1, GM-6,VMG-88, VMG-71, GJM 1714, GM-7, VMG-90,VMG-93, VMG-95, ANDGG-12-2, VMG-19	AM-15-18-1, AM-15-25-1	AM-15-47-2, BHU-16
2.	Days to maturity	AM-15-19-2, VMG-30, AM-15-53-1, VMG-66, VMG-37, ANDGG-12-2, VMG 103, VMG-39	VMG-79, VMG-97 Jabugam SP	GM-6, VMG-93, VMG-12, GM-7, VMG-75, VMG-62
3.	Plant height	AM-15-3-2, VMG-25, VMG-12, VMG-100 VMG-95, VMG-37, VBN-3, Vijapur selection, VMG-92	AM-K-18-5, VGG-16-55, VMG-58	-
4.	Branches per plant	Vijapur selection, VMG-37	AM-K-18-5, VMG-12, AM-15-41-1, VMG-92, ANDGG-12-2, VMG-75	-
5.	Clusters per plant	AM-K-18-5	VMG-75, VBN-3	-
6.	Pods per plant	VMG-97	-	VMG-90
7.	Pod length	AM-15-1-1, VMG-30, AM-K-18-5, AM-15-25-1, VMG-83, VMG-62	GM-4, GM-6	-
8.	Seeds per pod	GM-6, GJM 1714, VMG-79, AM-K-18-8, AM-15-1-1, GM-4, VGG-17-048, Jabugam SP, VMG-90	GM-7, VMG-12	VMG-69, AM-K 18-2
9.	Seed yield per plant	VMG-66, VMG-39, VMG-79, VMG-97	-	-
10.	Test weight	VMG-71, VMG-79	VMG-30, GM-6, GM-7, VMG-83, AM-15-47-2, VMG-58	-
12.	Protein content	VMG-92, VMG-39, VMG-71, AM-15-18-1, VGG-17-048, VMG-79, VMG-69, GM-6, VMG-58, GJM 1714	VMG-30, VMG-100, VMG 103, Meha, GM-4, AM-15-51-1, VMG-88, VMG-90, VMG-37	VMG-12

middle right regions. In **Fig. 1**, the genotypes present in between two lines drawn perpendicular to the regression axis have average stability. Scatter plot of the regression coefficient (b_i) against deviation from regression (S^2d_i) for seed yield per plant is presented in **Fig.2**. The genotypes which fall near deviation from the regression line (s^2d_i=0) are considered for stability. In **Fig. 2**, genotypes with higher mean values, falling in the middle region (s^2d_i=0, b_i=1) are considered stable and well adopted across the environments.

The estimation of the stability parameters collectively indicated that four genotypes of group I *viz.,* VMG-66, VMG-39, VMG-79 and VMG-97 exhibited seed yield higher than the population mean coupled with unit regression coefficient (non-significant at b_i=1) and deviation from regression around zero (S^2d_i=0), which suggested that such genotypes were stable and widely adapted over all the environments. Out of these four, VMG-66 was also found stable for days to 50% flowering and days to maturity as it was placed under group I. Therefore, it was identified as the best genotype to grow in across the environments. Similarly VMG-39 was also found stable for days to maturity and protein content. The genotype VMG-79 fall in group I for seeds per pod, test weight and protein content and falls in group II for days to maturity. VMG-97 was found stable for seed yield as well as stable for trait pods per plant. A genotype AM-K-18-5 placed in group I indicating stable for clusters per plant and pod length and fall in group II for plant height and branches per plant indicated well adapted in a favourable environment. Similarly, VMG-71 had stable performance (group I) for days to 50% flowering, test weight and protein content across the environments. Released variety GM-6 (group I) showed stable performance across the environments for days to 50% flowering, seeds per pod and protein content while fall in group II and adopted in a better environment for pod length and test weight and found stable in a poor environment (group III) for days to maturity.

The study of stability analysis revealed that genotypes found stable for seed yield per plant also manifested stability for two or three component traits which indicated that the stability of various component traits must be responsible for the observed stability of genotypes for seed yield. It can therefore be suggested that while making a selection, attention should be paid to the phenotypic stability of the characters associated with seed yield and genotypes having average stability for different characters could be used in developing stable hybrids. The chances for selection of stable hybrids could be strengthened by selection in favour of stability for the individual component. Thus stability for seed yield might be due to the stability of various yield components.

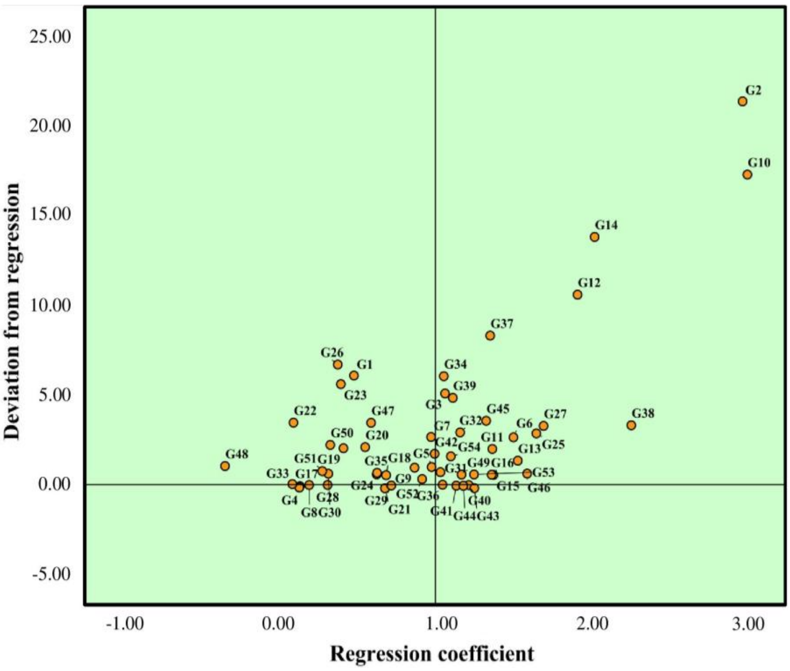

Fig. 2. Scatter plot of regression coefficient (b_i) against deviation from regression (S^2d_i) for seed yield per plant

VMG-66, VMG-39, VMG-79 and VMG-97 were identified as promising with stable performance (group I) and may be employed for general cultivation after taking into account the overall performance. It was discovered that GM 6 was stable in a favorable environment for many traits. It emphasizes the necessity for environment-specific variety because none of the variety was stable in different environments.

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