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Research Article

Stability analysis in common bean (P*haseolus vulgaris* L.) genotypes of Kashmir

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Abstract:
In the present study 17 local genotypes were evaluated in three diverse locations during 2008-09 with observations recorded on maturity, morphological and yield parameters. Analysis of variance revealed that the genotypes exhibited highly significant genetic variability for all the traits viz., day to 50 per cent flowering, days to maturity, number of branches plant^{-1}, number of pods plant^{-1}, pod length, number of seed pod^{-1}, 100-seed weight, seed yield plant^{-1} and protein content. The mean squares due to environments were also significant for all the traits indicating the environments selected were random and were different in agro-climatic conditions. Interaction of genotypes with the environment (G x E) were observed to be significant for all the traits except number of branches plant^{-1} and protein content. Based on the stability parameter of Eberhart and Russel model, SAUAR 28 was considered as stable and average responsive to the environments for yield and most of the component traits.

Key words: Common bean, Stability, Eberhart and Russel model, G X E Interaction.

Introduction:

Rajmash or common bean is regarded as “Grain of hope” as it is an important component of subsistence agriculture. Globally, with 21 million tones produced from about 26 Mha, it accounts for about half of the total pulse production. In India common bean is grown over an area of about 6 Mha with a production of about 2.5 million tonnes (FOA, 2010). Beans also offer an alternative for diversification of agricultural system but poor yield renders them poor competitors of cereals, oilseeds and other cash crops. Therefore, there is an urgent need to enhance the yielding ability of bean cultivars to make pulse cultivation a profitable venture.

Although there are many stability parameters, Eberhart and Russel (1966) modle’s parameter S^2di appeared to be very important. Since the variance of S^2di is a function of number of environments hence several environments with minimum replications per environment are advocated to be necessary to obtain reliable estimates of S^2di. To identify the stable genotypes having adaptability over a wide range of agro-climatic conditions is of major significance in crop improvement. With the statistical techniques developed to estimate stability parameters (Finlay and Wilkinson, 1963; Eberhart and Russel, 1966) it is possible to detect genotypic differences for wide adaptability in crop improvement. In the present investigation, an attempt has been made to study the stability of 17 genotypes over three environments in common bean.

Material and methods

The present study was undertaken during kharif 2008-2009 at three diverse locations representing diverse agro-ecological regimes. The random locations were: Pulse Research Sub-Station Naseembag Habak, Srinagar (E-I), Regional Research Station and Faculty of Agriculture, Wadura, Sopore, Baramullah (E-II) and Krishi Vigyan Kendra, Pombay, Kulgam (E-III). Seventeen diverse genotypes of common bean including two checks i.e, Shalimar Rajmash-1 and Canadian Red were evaluated for maturity, morphological and yield components and quality in three environments in a completer Randomised Block Design with three replications at each location. The experimental plot consisted of three rows each of 3 m length. The materials were provided the cropping geometry of 30 cm between the rows and plant to plant spacing of 10 cm. The experimental fields were well prepared and standard recommended package of practices were followed to raise a good crop.

Analysis of variance for stability

The phenotypic stability of seventeen genotypes studied in three different environmental conditions was worked out following the linear model proposed by Eberhart and Russel (1966). The parameters are defined by the following model. The estimated parameters were mean of the trait ($\overline{X}$), linear regression (b_i) and mean square deviation from regression (S^2d_i), where $\overline{X}$ provides a measure of the performance of a variety as compared to other entries, the b_i and S^2d_i values are the measure of the G x E interaction. In general, if G x E interactions are non-significant or where this G x E interaction is either linear or predominantly linear as compared to its non-linear component, the prediction of stability of a genotype over environments becomes more reliable.

Results and discussion

Analysis of variance: Analysis of variance revealed that the genotypes possessed highly significant genetic variability for all the traits viz., day to 50 per cent flowering, days to maturity, number of branches plant^{-1}, number of pods plant^{-1}, pod length, number of seeds pod^{-1}, 100-seed weight, seed yield plant^{-1} and protein content. The mean squares due to environments were also significant for all the traits indicating the environments selected were random and were different in agro-climatic conditions. Interaction of genotypes with the environment (G x E) were observed to be significant for all the traits except number of branches plant^{-1} and protein content, thereby revealing that genotypes performed differently for traits under study at different locations (Table 1). Partitioning of environment + (G x E) interaction into Environment (linear), G x E (linear) and pooled deviation revealed that mean square due to environment (linear) was significant for all traits, which confirmed that significant differences existed between environments and had shown considerable influence on expression of traits under study. Similarly, G x E (linear) was observed to be significant for all traits except for number of seeds pod^{-1} revealing that the behaviour of the genotypes for these traits is predictable over environments and this has resulted from the linear function of the environmental component. The mean squares due to pooled deviation (non-linear) were significant for all the traits except days to 50 per cent flowering, days to maturity and protein content, revealing that the non-liner component was important for these traits which contributed to total G x E interaction. Thus the genotypes differed considerably for stability for the traits under investigation over the environments.

Significant mean squares have been reported for most the traits in common bean genotypes over environments by Corte *et al.* (2002). For genotype-environment interaction significant mean squares have been reported by Rafi *et al.* (2004), Dar *et al.* (2009) and Mwale *et al.* (2009). The variance due to genotypes x environments (linear) was found significant for various traits by Singh *et al.* (2007).

Stability analysis: In the present investigation genotypes such as SKUA-R-19, SKUA-R-28 and PBG-37 displayed significant deviation from regression for days to maturity. Similarly some genotypes which had significant deviation from regression for other traits namely, SKUA-R-11, SKUA-R-25 and PBG-29 for number of branches plant^{-1}; SKUA-R-12, SKUA-R-15 and SKUA-R-16 for number of pods plant^{-1}; SKUA-R-12, SKUA-R-16, SKUA-R-25, PBG-24 and Canadian Red for pod length; SKUA-R-21, PBG-24, Shalimar Rajmash-1 and Canadian Red for number of seed pod^{-1}; all the genotypes except SKUA-R-05, SKUA-R-11, SKUA-R-19, SKUA-R-25 and PBG-30 for 100-seed weight and SKUA-R-05 and PBG-37 for protein content. Contrarily, mean square deviation from regression was non-significant for day to 50 per cent flowering for all the seventeen genotypes. The genotypes showing non-significant mean square deviation (S^2di) from the regression indicated that non-linear component (heterogeneity from regression) was equal to zero.

The significant deviation from unity for linear regression was recorded in various traits with respect to genotypes such as SKUA-R-28, PBG-32, Shalimar Rajmah-1 and Canadian Red (days to 50 % flowering); PBG-24 and PBG-29 (days to maturity); PBG-32, Shalimar Rajmash-1 (number of branches plant^{-1}); PBG-32, Shalimar Rajmash-1 and Canadian Red (number of pods plant^{-1}); SKUA-R-16 and SKUA-R-26 (100-seed weight) and Canadian Red (protein content). The genotypes not deviating significantly from unit regression for a particular trait revealed that they were average in response to the environments. In case of days to 50 per cent flowering the genotypes showing average stability and high mean performance i.e., well adapted to the environment, were SKUA-R-05, SKUA-R-11, SKUA-R-21, SKUA-R-26, PBG-30 and PBG-37. In case of days to maturity the genotypes showing average stability and high mean performance were SKUA-R-5, SKUA-R-11, PBG-30, Shalimar Rajmah-1 and Canadian Red; for number of branches plant^{-1} the genotypes with average stability and high mean performance were SKUA-R-16, SKUA-R-19, SKUA-R-21, SKUA-R-28, PBG-24, PBG-30, PBG-32 and PBG-37; for number of pods plant^{-1} the genotypes revealing average stability with high mean performance were SKUA-R-11, SKUA-R-26, SKUA-R-28, PBG-29, PBG-30 and PBG-37; for pod length the genotypes with average stability and high mean performance were SKUA-R-19, SKUA-R-28, PBG-29, PBG-32 and Shalimar Rajmah-1; for number of seed pod^{-1} genotypes showing average stability and high mean performance were SKUA-R-28, PBG-29, PBG-30 and PBG-37; for 100-seed weight the genotypes were SKUA-R-17, SKUA-R-16, SKUA-R-19, SKUA-R-21, PBG-24 and PBG-32.

The genotypes showing above average responsiveness to environment (bi value significant and >1) were SKUA-R-28, Shalimar Rajmash-1 and Canadian Red for days to 50 per cent flowering; SKUA-R-28 for days to maturity; Shalimar Rajmah-1 for number of branches plant^{-1}, Shalimar Rajmash-1 and Canadian Red for number of pods plant^{-1} and SKUA-R-19 for number of seeds pod^{-1}. However, the genotypes having significantly lower bi values than unity (b<1) were PBG-32 and Canadian Red for days to 50 per cent flowering; SKUA-R-19 and PBG-37 for days to maturity; PBG-32 for number of pods plant^{-1}; PBG-030 for pod length, SKUA-R-16 and SKUA-R-25 for 100-seed weight and Canadian Red for protein content. These genotypes are below average in responsive to environment for above mentioned traits and hence adapted to the unfavourable environments.

The genotypes showing significant mean square deviation from regression (pooled deviation) for any trait were not considered, since prediction for stability would not be precise and reliable for these traits. The stability analysis for most important trait i.e., seed yield plant^{-1} in the present study revealed that mean square deviations from the regression were non-significant in case of SKUA-R-05, SKUA-R-11, SKUA-R-12, SKUA-R-16, SKUA-R-25, SKUA-R-28 and PBG-30, thus could be assumed to be equal to zero in these genotypes. Hence, the prediction for stability across the environments for this trait in these genotypes would be precise and reliable. The linear regression coefficient (bi) were significantly higher for SKUA-R-05, SKUA-R-11, SKUA-R-16, SKUA-R-19, SKUA-R-25 and PBG-30, indicating that these genotypes had above average responsive and for favourable environments, while it was non-significant in SKUA-R-12 and SKUA-R-28, where it could be presumed to be equal to unity and hence these genotypes were average in response and well adapted to all the environments. Considering their mean performance and the average stability into consideration, it could be derived that SKUA-R-28 was well adapted to all the environments.

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Table 1: Analysis of variance for morphological, maturity, quality, yield and yield component traits of the common bean (*Phaseolus vulgaris* L) genotypes

Source of variation	d.f.	Days to 50% flowering	Days to maturity	Number of branches Plant^{-1}	No. of pods/plant	Pod length (cm)	Number of seeds pod^{-1}	100 seed weight (g)	Seed yield plant^{-1} (g)	Protein content (%)
Environments	2	348.31**	868.00**	24.10**	27.919**	22.45**	13.988**	28.43**	334.88**	100.43*
Replications	2	117.19**	285.50**	9.25**	10.64**	6.93**	6.93**	8.75*	101.71**	36.97*
Treatment	74	458.53**	3204.47**	8.74**	31.05**	12.16**	5.48**	567.76**	203.21**	28.60**
Environment x treatment	148	5.33**	17.92**	3.61**	4.75**	2.44	1.30**	3.34**	7.53**	4.36**
Error	450	2.03	3.00	2.89	2.16	1.73	0.81	2.04	1.87	1.30

Table.2 : **Stability parameters for different morphological, maturity, quality, yield and yield component traits in the common bean (*Phaseolus vulgaris* L.) genotypes**

Genotype	Days to 50% flowering			Days to maturity			Number of branches Plant^{-1}			No. of pods/plant			Pod length (cm)			Number of seeds pod^{-1}		
	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**
SKUA-R-05	**55.56**	0.98	-0.12	**9.47**	0.73	0.05	**8.83**	0.77	0.00	**4.22**	0.71	-0.01	**106.93**	1.00	-0.14	**9.98**	0.66	0.00
SKUA-R-11	**48.30**	0.96	0.10	**12.09**	0.84	0.02	**10.48**	-0.47	0.02	**4.41**	0.24	0.00	**102.30**	1.02	0.33	**8.43**	0.95	0.17**
SKUA-R-12	**44.55**	1.01	0.63	**11.24**	0.62	0.64**	**10.33**	2.51	0.03*	**4.24**	1.22	0.02	**98.43**	0.84	0.09	**10.27**	1.19	0.00
SKUA-R-15	**43.99**	0.50	0.46	**10.09**	0.85	0.08*	**10.56**	-0.02	0.01	**4.68**	1.29	-0.01	**98.92**	0.83	-0.26	**9.44**	0.77	0.02
SKUA-R-16	**43.23**	1.00	-0.07	**11.96**	0.30	0.35**	**10.31**	-0.31	0.05*	**5.12**	1.11	0.00	**96.73**	1.22	0.01	**11.72**	1.21	0.00
SKUA-R-19	**46.32**	1.07	0.32	**9.99**	1.21	-0.01	**10.98**	1.12	-0.01	**5.73**	3.09*	-0.01	**101.06**	0.85*	-0.31	**10.67**	0.71	0.00
SKUA-R-21	**53.27**	1.06	-0.23	**11.67**	1.06	0.08*	**10.35**	0.29	0.00	**5.29**	1.19	0.10**	**105.26**	0.78	-0.08	**11.27**	1.11	0.03
SKUA-R-25	**45.01**	1.14	-0.15	**11.69**	1.00	0.03	**10.34**	2.02	0.04*	**4.29**	0.49	-0.01	**97.76**	1.13	0.07	**9.88**	1.03	0.10**
SKUA-R-26	**53.93**	1.03	-0.20	**12.11**	1.39	0.03	**9.86**	1.68	-0.01	**4.04**	0.15	-0.01	**106.59**	0.88	0.99*	**11.14**	1.15	0.01
SKUA-R-28	**43.30**	1.15*	-0.32	**13.58**	1.28	0.01	**12.01**	2.32	0.01	**6.01**	2.03	-0.01	**98.23**	1.20*	-0.29	**10.68**	0.99	0.04
PBG-24	**47.44**	1.18	-0.20	**10.82**	0.91	-0.01	**10.15**	1.32	0.12**	**4.86**	0.05	0.07**	**102.23**	1.01	0.82*	**11.24**	1.22	-0.01
PBG-29	**41.27**	0.97	-0.19	**12.24**	1.35	0.04	**13.69**	2.87	0.02	**6.26**	1.24	0.00	**81.21**	1.17	1.28*	**10.23**	0.65	0.15**
PBG-30	**50.93**	0.81	-0.05	**13.63**	1.09	0.01	**10.60**	-1.45*	0.00	**6.25**	0.00	0.01	**103.34**	1.19	0.01	**10.74**	0.83	0.00
PBG-32	**42.45**	0.90*	-0.32	**10.60**	0.70*	-0.03	**11.22**	1.40	-0.01	**4.89**	0.49	0.00	**100.17**	1.16	0.12	**10.51**	0.89	-0.01
PBG-37	**55.20**	1.09	-0.06	**11.94**	1.02	0.00	**10.18**	0.59	-0.01	**7.05**	1.29	0.00	**107.59**	0.77*	-0.36	**10.80**	1.38	0.04
Shalimar Rajmash-1	**52.89**	1.28*	-0.20	**14.53**	1.44*	-0.01	**11.79**	2.25	0.00	**6.46**	1.98	0.10**	**108.02**	1.07	0.18	**11.23**	1.27*	-0.02
Canadian Red	**48.71**	0.87*	-0.31	**12.14**	1.23*	-0.03	**13.04**	0.11	0.04*	**5.09**	0.41	0.08**	**103.04**	0.89	-0.26	**10.36**	0.99	0.03
Mean	**48.02**	**-**	**-**	**11.75**	**-**	**-**	**10.86**	**-**	**-**	**5.23**	**-**	**-**	**101.07**	**-**	**-**	**10.50**	**-**	**-**
SE(m)±	**0.30**	**-**	**-**	**0.18**	**-**	**-**	**0.10**	**-**	**-**	**0.10**	**-**	**-**	**0.40**	**-**	**-**	**0.13**	**-**	**-**
SE(b)±	**-**	**0.09**	**-**	**-**	**0.14**	**-**	**-**	**0.57**	**-**	**-**	**0.73**	**-**	**-**	**0.10**	**-**	**-**	**0.15**	**-**

Contd..

Table 2, contd..

Genotype	100 seed weight (g)			Seed yield plant^{-1} (g)			Protein content (%)		
	Mean	**b_i**	**S^2d_i**	**Mean**	**b_i**	**S^2d_i**	**Mean**	**b_i**	**S^2d_i**
SKUA-R-05	**40.510**	1.19	0.10**	**16.314**	0.68*	0.00	**21.520**	0.78	0.21**
SKUA-R-11	**29.720**	0.56	0.17**	**15.868**	0.44*	0.10	**18.898**	0.95	-0.05
SKUA-R-12	**39.580**	1.37	0.30**	**18.418**	1.15	0.05	**22.638**	0.85	-0.05
SKUA-R-15	**39.853**	0.53	0.02**	**18.905**	0.85	0.24**	**21.583**	0.87	-0.04
SKUA-R-16	**37.755**	0.53*	0.01	**22.048**	0.58*	0.04	**24.035**	1.22	0.08
SKUA-R-19	**40.268**	1.36	0.01*	**23.470**	1.50*	-0.03	**24.225**	0.70	-0.03
SKUA-R-21	**32.748**	0.68	0.12**	**19.947**	0.84	1.35**	**22.603**	0.92	-0.05
SKUA-R-25	**35.020**	0.36*	0.01	**17.618**	0.73*	0.02	**21.575**	0.86	-0.03
SKUA-R-26	**44.380**	1.71*	0.03**	**21.800**	1.14	0.70**	**22.573**	0.79	-0.02
SKUA-R-28	**38.098**	0.98	0.04**	**32.080**	1.07	0.32	**21.288**	1.30	-0.04
PBG-24	**40.098**	1.15	0.01	**21.202**	0.97	1.29**	**23.638**	1.16	-0.03
PBG-29	**28.488**	0.78	0.12**	**22.043**	1.13	0.29**	**20.655**	0.93	-0.01
PBG-30	**23.878**	0.28	0.04**	**20.408**	0.67*	0.08	**20.400**	0.69	-0.01
PBG-32	**45.330**	1.21	0.00	**23.637**	0.88	0.54**	**23.563**	1.35	-0.03
PBG-37	**28.543**	1.47	0.02**	**24.560**	1.17	0.63**	**21.785**	1.94	0.14*
Shalimar Rajmash-1	**32.390**	1.26	0.15**	**28.659**	1.51	2.64**	**20.535**	1.44	-0.03
Canadian Red	**54.480**	1.55	0.08**	**24.410**	1.41	1.71**	**19.923**	0.25*	-0.03
Mean	**37.158**	-	-	**21.582**	-	-	**21.844**	-	-
SE(m)±	**0.15**	-	-	**0.48**	-	-	**0.13**	-	-
SE(b)±	-	**0.23**	-	-	**0.13**	-	-	**0.23**	-

* Significant at p=0.05; ** significant at p=0.01