

## Stability analysis in bush type Rajmash (*Phaseolus vulgaris* L.) under temperate Kashmir conditions

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### Abstract

Present investigation was undertaken during 2012-2014 to generate information through evaluation of a set of material at the farmers' field along with the farmers' variety as a check through stability using Eberhart and Russel model. The yield and yield attributing traits of all genotypes was recorded on ten competitive plants of both grandmother and mother trial. The genotypes were evaluated for stability analysis and revealed divergence across locations. The mean squares of all the traits were significant reflecting that the material was genetically divergent. The pooled deviation was significant and the variance due to variety  $\times$  environment was significant for various traits indicating that the variation in the performance of the genotypes is both unpredictable and predictable. Most of the genotypes were having higher mean than the average,  $b_i$  less than unity indicating that the varieties were more specifically adapted to the unfavorable environments than favourable ones. Some of the genotypes having higher mean yield,  $b_i > 1$  and  $S_{di}^2$  tending to zero were specifically adapted to favourable environments. On the basis of stability parameters genotypes WB-185, WB-195, WB-966 and Shalimar *Rajmash*-1 were identified as the most stable genotypes for seed yield per plot across all locations on the basis of high mean performance and non-significant estimates of  $b_i$  and  $S_{di}^2$  from unit and zero respectively, however latter genotype showed sensitivity to better environments for biological yield on the basis of significant  $b_i$  estimates. Similarly these genotypes were identified as consistent for early flowering for all the locations.

### Highlights

- Mean squares due to genotypes were highly significant for all the yield attributing traits, hence proving that genotypes were genetically divergent.
- Bush type bean genotypes WB-185, WB-195, WB-966 and Shalimar *Rajmash*-1 were identified as the most stable genotypes for seed yield per plot across all locations.
- Similarly these genotypes were identified as consistent for early flowering for all the locations.

**Keywords:** Common bean, *Rajmash*, mother trial, stability, Eberhart and Russel model, adaptation

*Rajmash* or dry common bean (*Phaseolus vulgaris* L.) is the most important pulse crop of the world and accounts for about half of the global pulse acreage. Like other legumes, they are rich in proteins, carbohydrates, vitamins and minerals. It is potential pulse crop in India and is grown in a number of states for grains as well as for vegetable (Singh and Singh, 2015). In terms of use category

*Rajmash* is classified as dry or pulse type and snap or vegetable types. Snap beans are also called as French beans, String beans, Green beans or Squeaky beans. Despite being called as "Grain of Hope" and "Poor man's Meat", this pulse crop has not received the just attention from breeders, farmers' and policy makers alike due to inherently low yield of pulses, relegation to harsh environments, lack



of major technological breakthrough and the lack of encouraging market and price support from the government. The UN General Assembly announced that 2016 will be the “International Year of Pulses”. This will probably attract much needed attention to a commodity group which has, despite its many substantial qualities, proven quite undervalued. One of the major challenges for improving food security in rural resource poor communities is to develop varieties that are bred for specific environments. While, varieties are typically developed at a national or international centre and incorporate a number of genetically useful traits, it is a major challenge for scientists with limited resources to test the full range of genetic diversity generated by a breeding program under all possible environments. Use of diverse cultivars with high yielding ability, high protein content and early maturity would enable farmers to achieve higher production.

Besides, yield potential and early maturity, the variety should also possess stability in its performance over a range of environments. Knowledge on the interaction and stability is foremost in breeding varieties for wider adaptation in diverse agro-climatic conditions. Genotype-environment interactions are of major importance to the plant breeder in developing improved cultivars (Kang, 1990). An ideal variety is the one that combines high yield with stability of performance (Eberhart and Russell, 1966). Such a genotype is acceptable over a wide range of environmental conditions (Allard and Bradshaw, 1964). The foremost dilemma of the bean improvement program in Kashmir has been the lack of genotypes that consistently perform well across different bean growing environments. Hence, the development of high yielding genotypes and information on multilocation stable performance are of paramount importance in our The objective of this study was to generate information through evaluation of a set of bush type bean genotypes at the farmers’ field along with the farmers’ variety as a check through stability using Eberhart and Russel (1996) model.

## Materials and Methods

The present investigation was undertaken during the years 2012 to 2014 in three districts of Kashmir valley namely Baramulla 34.15° N Latitude, 74.35° E Longitude, Bandipora 34.50° N Latitude, 74.68°

E Longitude and Kupwara 34.43° N Latitude, 74.12° E Longitude which are potential areas for *rajmash* cultivation. All the three environments fall in temperate zone and experience almost same temperature with slight differences. The selection of sites was done in consultation with KVK’s of respective districts and line (agriculture) departments. All the three districts were selected on the basis of their strategic importance. Twenty three diverse genotypes of *Rajmash* (*Phaseolus vilgaris* L.) viz., WB-22, WB-147, WB-195, WB-185, WB-209, WB-223, WB-249, WB-191, WB-192, WB-634, WB-462, WB-490, WB-1031, WB -569, WB-330, SR-1, WB-479, WB 54, WB-489, WB-487, WB-852, WB-966, WB-885 were evaluated for yield and yield contributing characters.

### *Laying of grandmother and mother trials*

Grandmother trial is a modified form of mother trial laid on the research station under researcher management to allow optimal trait expression. The trials were laid in replicated design to provide for computation of various components of variation. The mother trials are used to compare all the entries together in a farmer’s field. They are researcher designed but farmer-managed trial at their own field. The mother trial should be usually selected at a central place of the desired location. The quantitative data related to the various traits is being recorded by the researcher himself. Each trial is a single replicate as it has only one plot of each variety. Mother trials consist of preliminary evaluation of a fairly large number of entries (mostly released varieties/pipeline material/advanced breeding lines) in a researcher designed and farmer managed trials.

Four mother trials of bush type and farmer’s variety as check were planted at four different locations. The trials were laid at Longate Kupwara, Rohama Tangmarg, Malangam Bandipora and Regional Research Station Wadura Sopore. The experiment consisting of 23 genotypes were laid in a replicated design with three replications in RCBD for each genotype represented by 2 metre bed with six rows spaced by 50 cm between plots to allow for farm walk. The close spacing was used at all locations including research station trial in order to bring homogeneity to plant responses to spacing, as an attempt to replicate farmers conditions at research

station. The farmers' own variety was used as check. At each individual location the trials were designed by scientists but exclusively managed by farmers' to provide for real situation assessment of performances of different genotypes. The genotypes that were selected for these villages, was done on the basis of participatory rural appraisal, topography and cropping pattern of these villages.

### Observation of Data

The data for various traits viz. morphological (days to 50% flowering, days to maturity, plant height) yield components (pods plant<sup>-1</sup>, pod length, number of seeds pod<sup>-1</sup>, 100-seed weight) and yield (pod yield plant<sup>-1</sup>, seed yield plot<sup>-1</sup>) was recorded from ten competitive plants from each replication for various morphological, agronomical, yield and yield attributing traits to study their stability performance over four random environments. Each selected plant were taken at random from each experimental plot in a replication and tagged for recording biometrical observations. Mean value of all characters and median values for days to flowering and days to maturity were worked out. Observations were recorded at the appropriate developmental stages of the plant growth as per the descriptors for *Rajmash*.

## Results and Discussion

The present investigation was carried out for evaluation of released varieties, pre-released materials, advanced breeding lines, landraces or germplasm accessions on farmers' fields under his management practices. Twenty three (23) genotypes were evaluated to identify genotypes suitable for specific niche areas. Besides the genotypes were assessed for the stability in their performance to characterize the nature of genotype × location interaction for various yield and yield related traits at different environments, the genotypes were

evaluated in a Randomized Complete Block Design (RCBD) with three replications across four random environments separately.

### Analysis of variance of mother trial

The analysis of variance of genotypes of grandmother trial (Table 1) revealed that mean squares due to genotypes were highly significant for almost all of the traits indicating existence of genetic difference among Rajmash genotypes. There was substantial variability among genotypes, and the variability was studied for all traits except number of pods per plant (Table 1 and 2).

### Genotypes

The pooled analysis of variance for stability of genotypes for nine quantitative traits over four environments (Table 1 and 2) revealed that mean squares due to genotypes and environments were significant for all the traits studied. The interaction of component genotype' environment was significant for all traits. Recently similar results were also revealed in chickpea (Desai *et al.*, 2016)

### Estimation of stability parameters and identification of stable bean genotypes

In the present investigation, estimation of stability parameters for bush type of genotypes including farmer's variety as checks were estimated to identify the most suitable genotypes across a range of environments and for suitable environments. Estimation of stability parameters for different traits viz. morphological (days to 50% flowering, days to maturity, plant height) yield components (pods plant<sup>-1</sup>, pod length, number of seeds pod<sup>-1</sup>, 100-seed weight) and yield (pod yield plant<sup>-1</sup>, seed yield plot<sup>-1</sup>) across four random environments are presented in the Table 2. The stability parameters

**Table 1:** Analysis of variance of mother trial for bush type bean genotypes

Source of variation	d.f.	Mean sum of squares								
		Days to 50 % flowering	Days to maturity	Plant height (cm)	Number of pods plant <sup>-1</sup>	Pod length (cm)	Pod yield plant <sup>-1</sup> (g)	Seeds pod <sup>-1</sup>	Seed yield plot <sup>-1</sup> (g)	100-seed weight (g)
Genotype	22	66.7**	75.8**	2032.3**	47.94	9.3**	2095.2**	3.6**	417361.1**	73.5**
Replication	2	11.9**	79.8**	40.4**	7.07	6.5**	177.0**	0.9**	17151.2**	11.9**
Error	176	16.7**	24.3**	330**	26.59	2.6**	306.8**	0.9**	74877.4**	34.3**

**Table 2:** Analysis of variance for stability of different traits in bush type bean genotypes across four environments

Source of variation	d.f.	Days to 50% flowering	Days to Maturity	Plant height	No. of pods plant <sup>-1</sup>	Pod length	Pod yield/ plant	Seeds/ pod	100 seed weight (g)	Seed yield/plot
Replication With In Environments	8	0.2	0.9	0.4	0.4	0.2	3.1	0.1	0.2	441.4
Varieties	22	109.2**	122.6**	1661.7**	130.6**	12.1**	1642.5**	1.5**	151.6**	39611**
Environment + (Varieties × Environment)	69	4.0**	1.8**	7.5	21.8**	0.7*	928.2*	0.6	37.1*	22399*
Environments	3	11.7**	16.3**	7.4**	37.9*	8.2**	2363.9	0.8*	8.7**	34482**
Varieties × Environment	66	3.6**	1.2**	7.5*	21.0**	0.7*	862.9**	0.6*	38.4**	21850**
Environment (Linear)	1	35.6**	49.1**	22.4	113.9**	24.7**	7091.9**	2.5*	26.3	10348*
Varieties × Environment (Linear)	22	7.4***	2.4**	5.8	43.7**	0.4**	810.2*	0.9*	73.4**	24864*
Pooled Deviation (Non Linear)	46	1.6**	0.6**	8.0*	9.3**	0.4**	850.6**	0.4**	20.0**	19458**
Pooled Error	176	0.4	0.4	0.5	0.2	0.1	4.5	0.08	0.2	432.3
Total	91	29.4	31.0	407.4	48.1	3.5	1100.9	0.8	64.8	205606

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

estimated were mean of the trait ( $\bar{X}$ ), linear regression ( $b_i$ ) mean square deviation from regression ( $S_{di}^2$ ), where  $\bar{X}$  provides a measure of the performance of a variety as compared to other entries, the  $b_i$  and  $S_{di}^2$  values are the measure of the G' E interaction. The components  $S_{di}^2$  measures predictability and the component  $b_i$  measure the stability. In general, if G' E is non-significant or where this G' 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. As per the Eberhart and Russel's model of stability, the component  $S_{di}^2$  measures predictability and  $b_i$  the stability. Stability of a genotype can be predicted more precisely if G × E interaction and  $S_{di}^2$  value are non-significant.

Stability parameters such as mean ( $\bar{X}$ ), regression coefficient ( $b_i$ ) and deviation from regression ( $S_{di}^2$ ), as suggested by Eberhart and Russell (1966) were considered to explain and discuss the stability of different genotypes for various characters under consideration. Analysis of variance for stability in the performance of different genotypes across four random environments revealed that the mean squares due to genotypes were highly significant

for all the traits viz., days to 50 per cent flowering, days to maturity, plant height, number of pods plant<sup>-1</sup>, pod length (cm), number of seeds pod<sup>-1</sup>, pod yield plant<sup>-1</sup>, seed yield plot<sup>-1</sup> and 100 seed weight. The material selected were thus divergent and possessed significant genetic variation for all traits. Environments selected revealed significant differences for the expression of days to 50 per cent flowering, days to maturity, plant height, pods plant<sup>-1</sup>, pod length, number of seeds pod<sup>-1</sup>, pod yield plant<sup>-1</sup>, seed yield plot<sup>-1</sup> and 100 seed weight, confirming that the environments selected were variable and random and influenced the expression of most of the traits selected for the stability studies. Mean squares arising due to genotype × Environment (G×E) interaction revealed that variance ratio was significant for all the traits indicating thereby that the genotypes were having, by and large, significant differential response to the changing environments. The environment + (genotype × environment) mean were significant for all the traits.

However, partitioning this variance into components like environments, environments (linear), genotype × environment (linear) and pooled deviation



Table 3 : Stability parameters for yield and yield attributes in bush type beans evaluated across four random environments

Genotypes	Days to 50 % flowering			Days to Maturity			Plant height (cm)			No. of pods per plant			Pod length(cm)			Pod yield (g)		
	Mean ( $\bar{X}$ )	$b_i$	$S^2d_i$	Mean ( $\bar{X}$ )	$b_i$	$S^2d_i$	Mean ( $\bar{X}$ )	$b_i$	$S^2d_i$	Mean ( $\bar{X}$ )	$b_i$	$S^2d_i$	Mean ( $\bar{X}$ )	$b_i$	$S^2d_i$	Mean ( $\bar{X}$ )	$b_i$	$S^2d_i$
WB-22	40.1	-1.6	0.5	94.3	2.1	-0.3	32.0	-1.5	9.7	17.6	3.9	6.3	9.5	0.3	0.2	80.6	1.5	1.3
WB-147	45.0	1.2	0.2	97.0	1.7	0.8	45.8	-3.5	11.6	21.2	0.6	-0.07	11.5	1.3	0.04	84.5	0.9	0.3
WB-195	46.8	1.3	0.3	95.5	-1.0	0.02	55.9	1.2	0.2	25.4	1.0	0.03	9.6	0.7	-0.1	87.3	1.1	0.9
WB-185	42.3	-3.0	0.7	93.0	0.7	-0.4	<b>53.7</b>	<b>-0.8</b>	<b>0.01</b>	14.7	-3.4	6.0	10.1	1.1	1.4	84.4	1.8	4.4
WB-209	42.7	2.3	-0.2	89.4	2.9	0.1	37.4	-1.7	11.8	12.7	3.7	4.2	12.9	1.5	-0.1	66.5	0.8	0.05
WB-223	42.9	1.9	-0.7	94.1	1.4	-0.1	45.1	1.7	0.5	<b>28.8</b>	<b>0.6</b>	<b>0.5</b>	<b>13.3</b>	<b>-0.07</b>	<b>0.7</b>	<b>126.7</b>	<b>-0.4</b>	<b>0.6</b>
WB-249	44.5	1.6	-0.1	93.0	1.6	0.1	55.5	1.8	-0.3	13.5	1.3	0.4	12.1	0.7	-0.1	86.4	4.3	2.2
WB-191	43.2	0.2	1.8	96.7	0.2	-0.1	81.1	1.4	4.7	9.0	0.6	4.9	10.4	0.9	0.7	40.0	1.9	1.4
WB-192	44.0	1.0	3.5	96.8	0.6	-0.3	37.5	-3.0	3.9	12.4	1.4	-0.01	6.2	2.4	-0.1	55.2	3.9	2.1
WB-634	46.3	0.3	1.0	84.1	-0.06	0.04	83.3	7.8	6.5	<b>29.6</b>	<b>0.6</b>	0.7	8.1	0.8	-0.1	135.8	0.01	0.2
WB-462	41.9	1.8	2.2	84.0	1.3	-0.1	76	2.2	3.1	11.8	-2.2	12.1	9.2	1.2	2.1	91.1	5.7	4.6
WB-490	55.5	-2.9	1.1	86.9	1.8	0.4	88.4	3.1	8.8	12.5	1.3	0.3	12.6	0.9	-0.04	63.3	1.2	2.01
WB-1031	51.9	2.0	-0.2	83.5	0.9	-0.4	74.5	1.4	-0.02	15.9	2.1	1.1	11.0	1.3	0.9	68.5	0.1	3.4
WB-569	55.0	1.4	1.7	82.0	-0.2	0.9	69.3	3.4	-0.3	12.1	-1.4	7.3	10.3	1.2	-0.1	70.8	1.9	3.2
WB-330	44.0	-4.5	1.5	82.9	0.09	-0.4	42.4	1.5	2.1	14.4	1.4	3.7	9.5	1.1	3.7	73.2	3.5	2.7
SR-1	46.8	1.4	0.7	86.1	0.06	0.3	67.1	1.0	-0.4	17.8	1.0	0.2	13.5	1.0	-0.1	96.2	-0.3	0.5
WB-479	52.6	2.5	2.8	83.4	2.2	0.2	62.2	0.8	1.6	8.7	-3.4	15.0	8.6	0.9	-0.05	74.7	2.05	2.5
WB-54	42	2.0	2.6	91.6	1.6	-0.2	45.6	3.0	0.3	11.7	-1.1	4.2	9.4	0.4	-0.1	70.0	-0.6	3.7
WB-489	45.0	1.9	2.4	82.4	4.6	-0.03	94.1	-1.5	4.7	13.7	-1.0	5.6	9.8	1.5	-0.1	81.1	0.5	2.5
WB-487	51.8	1.4	-0.2	82.5	2.4	-0.1	75.2	2.5	0.8	20.3	2.0	3.1	11.1	1.2	-0.04	96.4	0.9	2.5
WB-852	53.4	1.4	2.9	85.2	2.9	3.5	84.7	2.4	-0.1	11.0	1.3	0.1	10.3	1.5	0.1	71.6	1.5	0.7
WB-966	47.1	1.4	0.8	83.1	0.6	-0.3	93	1.2	0.9	16.0	-0.8	0.4	10.4	0.5	-0.01	89.0	-0.3	0.8
WB-885	42.5	2.5	-0.06	84.6	1.4	1.02	96.6	0.7	1.5	16.3	1.9	0.4	9.4	1.5	0.04	85.7	1.1	0.8
Population mean		47.1			83.3		65.4			15.8			10.3			80.9		
SE(m)		0.7			0.4		1.6			1.7			0.3			16.8		
SE(b <sub>i</sub> )		1.0			0.5		2.8			1.3			0.6			1.6		

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Genotypes	Seeds per pod			100 seed weight (g)			Seed yield per pod (g)		
	Mean ( $\bar{X}$ )	$b_i$	$S^2d_i$	Mean ( $\bar{X}$ )	$b_i$	$S^2d_i$	Mean ( $\bar{X}$ )	$b_i$	$S^2d_i$
WB-22	4.7	-0.4	-0.01	42.8	11.4	1.3	1135.8	2.2	1.5
WB-147	4.0	0.1	0.1	31.1	1.6	51.1	1214.8	-0.2	3.7
WB-195	4.0	0.2	0.5	30.8	-1.3	0.5	1371.7	0.3	0.5
WB-185	4.0	-4.1	0.3	41.0	-1.4	7.8	1299.6	0.8	2.2
WB-209	4.6	1.6	-0.03	38.2	1.5	0.07	968.2	1.0	0.6
WB-223	5.4	0.8	0.03	36.3	2.6	0.8	2540.1	-0.8	0.2
WB-249	4.9	2.6	0.1	28.5	10.0	4.1	1243.5	6.3	1.1
WB-191	4.1	6.1	0.6	28.4	0.7	7.2	501.8	1.9	1.0
WB-192	3.4	3.0	2.1	42.9	-15.3	0.4	796.0	-0.5	2.2
WB-634	5.1	-0.4	0.2	38.4	0.6	0.5	2011.2	-0.8	0.1
WB-462	4.5	2.6	0.2	29.8	2.2	3.9	1314.5	8.1	5.9
WB-490	5.9	-5.0	2.4	28.3	2.5	2.9	843.4	-1.05	7.2
WB-1031	5.2	3.1	0.1	27.8	-1.2	9.8	900.2	-0.2	3.9
WB-569	5.1	1.1	-0.04	31.3	2.4	3.4	952.1	2.5	3.6
WB-330	5.7	-1.1	-0.02	31.1	5.0	1.6	1053.3	-0.8	1.8
SR-1	4.7	-1.8	0.4	39.2	-7.7	2.8	1227.8	-0.8	1.6
WB-479	5.6	-1.7	0.9	36.8	2.4	3.9	1010.7	2.3	8.9
WB-54	4.3	3.3	0.7	50.6	-18.7	1.4	964.4	-1.3	1.3
WB-489	4.8	-1.3	0.5	40.3	0.8	0.2	1549.8	0.1	0.2
WB-487	5.0	1.1	-0.07	29.6	1.3	0.6	1337.2	1.3	0.7
WB-852	4.6	3.3	0.03	29.9	0.8	10.8	975.5	2.9	2.6
WB-966	5.1	0.2	0.2	30.2	0.5	0.3	1138.5	0.8	0.1
WB-885	4.7	2.9	0.01	31.3	-1.8	5.3	1215.1	1.4	0.3
Population mean		4.8		34.4			1142.8		
SE(m)		0.3		2.5			64.7		
SE( $b_i$ )		2.0		4.1			2.1		

$b_i$  = linear regression value and  $S^2d_i$  = deviation from linearity



(non-linear) revealed that mean squares due to environment (linear) were highly significant for days to 50% flowering, days to maturity, plant height, pods plant<sup>-1</sup>, pod length, number of seeds pod<sup>-1</sup>, pod yield plant<sup>-1</sup>, seed yield plot<sup>-1</sup> and 100-seed weight. The significant mean squares confirmed that the environment were random and different and they exercised influence on the expression of a trait having significant mean squares and this variation could be attributed to have arisen due to linear response of the expression of the genotypes to the environment.

The mean squares due to G × E (linear) were significant for days to 50% flowering, days to maturity, plant height, pods plant<sup>-1</sup>, pod length, number of seeds pod<sup>-1</sup>, pod yield plant<sup>-1</sup>, seed yield plot<sup>-1</sup> and 100-seed weight, revealing that the behaviour of the genotypes could be predicted for environments more precisely for most of the traits and the G × E interaction was the outcome of the linear function of the environmental components. The non-linear component arising due to heterogeneity, measured as mean squares due to pooled deviation, was significant for days to 50% flowering, days to maturity, plant height, pod length, number of pods plant<sup>-1</sup>, number of seeds pod<sup>-1</sup>, seed yield plot<sup>-1</sup> and 100-seed weight. These significant mean squares revealed presence of non-linear response of the genotypes to the changing environments (stability performance). The significant mean squares for the pooled deviation confirmed contribution of non-linear component total G × E interaction. The analysis of variance of bush type of *rajmash* shows that the genotypes differ significantly across locations. The mean squares of all the characters show significant change.

However there were few genotypes among the bush types which fulfil the criteria of stability as per the condition of Eberhart and Russell (1966) model to be stable across the environments. Genotype-environment interactions are of major importance to the plant breeder in developing improved varieties. When varieties are compared over a series of environments, the relative rankings usually differ. This causes difficulty in demonstrating the significant superiority of any variety (Eberhart and Russell, 1966). Knowledge of the presence and magnitude of genotype' environment interactions (GEI) is very important to plant breeders in making

decisions regarding the development and release of new cultivars (Chakroun *et al.*, 1990). Genotype' environment interaction has been defined as the failure of genotypes to achieve the same relative performance in different environments (Baker, 1988). Moldovan *et al.* (2000) indicated that genotype-environment interactions are of major importance; because they provide information about the effects of different environments on cultivar performance and play a key role for the assessment of performance stability of the breeding materials.

Stability in performance of a genotype over a wide range of environments is a desirable attribute and depends largely upon magnitude of genotype-environment interaction (Ahmad *et al.*, 1996). Temesgen *et al.* (2008) tested *Rajmash* (*Phaseolus vulgaris* L.) genotypes over locations and years with the objective of identifying high yielding, stable and adaptable varieties for western parts of Ethiopia. The nine *Rajmash* genotypes for yield stability under different sowing dates and watering regimes in three field experiments conducted in the River Nile State-Sudan during 2003 to 2006 were analysed by (Khalifa *et al.*, 2013). Ten test-environments were thus achieved, representing the combined effect of drought and heat stress. Stability analysis (Eberhart and Russell model) was performed to identify the most yield-stable bean lines under limited moisture and temperature stress. Asfaw *et al.* (2014) carried out the stability for grain yield and other traits over test environments and estimates of stability of the varieties for yield and other traits using cultivar superiority measure. Musaana *et al.* (2015) studied the stability of pod yield on fourteen snap bean genotypes introduced or locally bred in Uganda. The study was carried out in three seasons using six agroecological zones.

The wide occurrence of genotype x environment interaction (GEI) is the basic cause of difference between genotypes in their yield stability. Numerous stability parameters have been developed to investigate GEI (Huehn, 1990). Parametric stability statistics obtained by linear regression models (Finlay and Wilkinson, 1963; Eberhart and Russell, 1966; Shukla, 1972) are mathematically simple and biologically interpretable, however, few researchers use statistical measures of yield stability in their breeding programs. Genotypes WB-195, 185, 966, 147, 185 and Shalimar Rajmash-1 were having mean



days to 50% flowering less than the population mean and  $b_i$  and  $S_{di}^2$  equal to 1.3, -3.0, 1.4, 1, 1, 0.6 and 0.3, 0.7, 0.7, 0.8, 0.03, 0.5 respectively. The days taken to maturity also show the mean of Genotypes WB-195, 185, 966, 147, 185 and Shalimar Rajmash-1 less than the average mean.

The characters pods plant<sup>-1</sup>, pod length, number of seeds pod<sup>-1</sup>, 100-seed weight, pod yield plant<sup>-1</sup>, seed yield plot<sup>-1</sup> of the genotypes WB-195, 185, 966, 147, 185 and Shalimar Rajmash-1 are having mean greater than the average mean and the value of  $b_i$  and  $S_{di}^2$  indicate that the varieties are stable across various locations. All the cultivars showing non-significant deviation from regression ( $S_{di}^2$ ) and regression coefficient ( $b_i$ ) were average in stability and poorly or well adapted to the environments. The results were also confirmed through studies carried by Mussana *et al.* 2015. Pod yield stability was studied on fourteen snap bean genotypes in three seasons using six agroecological zones. Variety J12 had the highest yields and the commercial variety Paulista had the lowest. Values of  $b_i$  coefficient indicated that varieties had the highest positive influence on pod yields while location and season had higher negative influence than rust. Variety J12 and SB001 had the most stable and heavy pod yields.

## Conclusion

Analysis of variance revealed the existence of significant differences among the genotypes for all the traits studied indicating the presence of genetic variability in the experimental material under investigation. Mean squares due to environment + (genotype × environment) were significant for most of the traits except days to 50% flowering and days to maturity depicted the distinct nature of environment and genotype × environment interaction on phenotypic expression. Genotype × environment (linear) interaction component showed non-significance only for plant height whereas, all other traits showed high significance indicating location (environment) had a marked influence on the expression among the genotypes and behaviour of the genotypes could be predicted more precisely over environment.

Mean square due to environment (linear) component was found to be non-significant for 100-seed weight, for all the other characters the component was found highly significant except pod length. Pooled

deviation for all the traits was found significant suggested that the performance of different genotypes fluctuated significantly from their respective linear path of response to environments. On the basis of stability parameters genotypes WB-185, WB-195, WB-966 and Shalimar Rajmash-1 were identified as the most stable genotypes for seed yield per plot across all locations on the basis of high mean performance and non-significant estimates of  $b_i$  and  $S_{di}^2$  from unit and zero respectively, however latter genotype showed sensitivity to better environments for biological yield on the basis of significant  $b_i$  estimates. Similarly these genotypes were identified as consistent for early flowering for all the locations.

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