

Genotype × Environment Interaction and Stability Analysis in Mungbean

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Abstract: Mungbean is an important grain legume widely grown in India. Thirty genotypes of mungbean developed through mutation breeding from three parents namely B1, B105 and SML32 were evaluated on seven environments of West Bengal, India. Stability parameters were computed to know genotype x environment interaction and genotypic performance for yield per plant and its components. Wide range of variation was observed for seed yield and components across environments. Genotypes were grown best in sandy-loam textured soil coupled with low pH (5.7), indicating acidity and moderate water holding capacity, accompanied with higher proportion of available nitrogen percentage, moderate P₂O₅ and organic C. The analysis of variance showed highly significant variance for genotypes, environments and genotype x environment interaction. The significance of genotype x environment interaction accentuated the implication of stability analysis in crop improvement programme. The analysis of variance exhibited comparatively higher magnitudes of linear components than the non linear components and thus the characters were predictable in nature. Identification of stable genotypes over environments was done by stability analysis following model of Eberhart and Russell. Sustainability index was also estimated for searching the stable genotypes. In most of the cases, the stability for yield components was concomitant with stability for seed yield per plant. Four mutant genotypes namely CUM1, CUM4, CUM10 and CUM13 registered average stability coupled with high mean performance for seed yield per plant and components consistently, based on regression parameters and sustainability index.

Keywords: Genotype x environment interaction, Mungbean, Stability, Sustainability index

I. Introduction

Mungbean (*Vigna radiata* L. Wilczek), a short duration grain legume, is one of the most important pulse crops grown all over India. Mungbean ranks third among pulse crops of India covering approximately 3 million hectares, with the production of about 1 million tonnes accounting for 12% of the total pulse acreage. The earlier research works were more focused to improve the crop largely through simple procedures of selection with or without hybridization from local collections. The existing genetic variability of mungbean is a great concern for which conventional selection may not be effective.

Mutation breeding is already an established technology. Ionizing radiation such as X-rays, γ -rays, neutrons have already been used in mungbean for inducing variations (Nilan and Konzak, 1961; Matsumura *et al.*, 1963; Juran *et al.*, 1986; Klu *et al.*, 1997). In other crops also successful reports are available like in wheat (Giroux, 1998), rice (Chakraborty, 1995), sweet corn and maize (Hannah *et al.*, 1993) and pea (Macleod, 1994).

Yield, a complex quantitative character, depends upon interactions of multiple component characters. Undesirable linkage among yield components sometimes deters the overall improvement of yield (Webb *et al.*, 1968). Mutagenic treatments can cause alterations in negative association of characters (Hensz, 1991; Lapade *et al.*, 1995) which were originally undesirable from the production point of view. On the contrary, it is true that only few mutants in general, turn out to be useful or desirable when any mutagen is exercised for improvement. Nevertheless, the resultant mutants seemed to be very precious which otherwise may not be possible to achieve.

An ideal variety always combines high yield with stability of performance (Eberhart and Russell, 1966). The genotype × environment is the main bottleneck which can vitiate entire efforts of a plant breeder for boosting higher yield. Thus, breeding for climate or environment resilient varieties is crucial (Allard and Bradshaw, 1964). Several methods of simultaneous selection for yield and stability and relations among them were discussed by Kang and Pham (1991) and Kang (1998).

The phenotype has been confidently defined as a linear function of genotype, environment and interaction between two (Lu *et al.*, 1986; Scheiner, 1993). The works of various scientists viz., Immer and Power (1934), Salmon (1951), Horner and Frey (1957) and Sandison and Barlett (1958) reflected that variety × season interactions were basic estimates of adaptability. Yates and Cochran (1938) subdivided the genotype × environment interactions into linear and nonlinear partitions. Eberhart and Russell (1966) developed a model based on the regression technique for measuring the stability of populations grown from single and three-way crosses of maize. Numerous statistics, parametric as well as non-parametric have been proposed for the measurement of yield stability (Wricke, 1962; Finlay and Wilkinson, 1963; Eberhart and Russell, 1966; Perkins

and Jinks, 1968; Hanson, 1970; Tai, 1971 and Nassar and Huhn, 1987). Depending upon the final goal of the breeder and the character under consideration, two concepts of stability were of great importance for biological and agronomic concept (Backer, 1981). The concept of genotype-environment interactions leads to measure the agronomic stability of the genotype. Under the biological concept stable genotype is one, whose phenotype shows little deviation from the expected character level when performance of genotype is tested over a number of environments.

Plant improvement involves jointly the manipulation of genetic characteristics to optimize productivity in relation to the limitations of the environmental factors. However, lack of intensive systematic research efforts on mungbean stands as a barrier to its improvement, which needs a comprehensive and diversified approach. Elite or promising varieties with advantageous yield contributing characters adaptable for West Bengal, India as a whole still are of in need. The present study, aimed at identifying stable elite and promising mutant lines, especially for agro-climatic situations of West Bengal, India.

II. Materials and Methods

The elite mutant lines chosen in the investigation were (Table 1) developed from three parents namely B1, B105 and SML32 at Agricultural Experimental Farm of Calcutta University, Baruipur, South 24-Parganas, West Bengal, India (Latitude: 22.3497N, Longitude: 88.4392E, Altitude: 29”). The lines along with their parents (checks) were grown in different agro-ecological locations over seasons following normal cultural practices. Lines were grown in three replications in RBD design and spacing of 45 cm was maintained between family rows and 10 cm between plants in a row of 3m long. Ten randomly selected plants of each genotype from each replication excluding the border plants were chosen and tagged for recording observation. Altogether experiments were conducted at different locations and seasons which constituted seven environments and were referred as E1, E2, E3, E4, E5, E6, and E7.

II.I Observations recorded

Ten plants from each replication were selected for data recording and finally averaged. The data of each mutant included yield and yield components namely 1) Number of pods per plant; 2) Number of pods per cluster; 3) Pod length (cm); 4) Number of seeds per pod; 5) Number of seeds per plant; 6) 100-seeds weight (g); 7) Seed yield per plant (g).

II.II Stability Analysis

The stability analysis was done according to the models of Eberhart and Russell (1966). The model is defined as follows :

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

Where, Y_{ij} = mean of the i^{th} genotype at the j^{th} environment, ($i=1,2,\dots,v$; $j=1,2,\dots,n$)

μ_i = mean of the i^{th} genotype over all environments,

b_i = regression coefficient that measures the response of the i^{th} genotype to varying environments,

δ_{ij} = deviation from regression of the i^{th} genotype at the j^{th} environment and

I_j = environmental index obtained as the mean of all the genotypes at the j^{th} environment minus the grand mean

$$= (\sum Y_{ij}/v) - (\sum \sum Y_{ij} / vn) \quad \sum I_j = 0$$

II.III Stability Parameters

In the present study an overview of the parametric stability measures and their underlying stability concepts are presented in Table 2.

II.IV Measurement of two parameters by Eberhart and Russell (1966) method

The first stability parameter is a regression coefficient and was estimated as follows :

$$\begin{aligned} b_i &= \sum_j Y_{ij} I_j / \sum I_j^2 \\ &= \sum_j (Y_{ij} - \bar{Y}_i) (\bar{Y}_j - \bar{Y}_.) / \sum_j (\bar{Y}_j - \bar{Y}_.)^2 \\ &= 1 + [\sum_j (Y_{ij} - \bar{Y}_i - \bar{Y}_j + \bar{Y}_.) (\bar{Y}_j - \bar{Y}_.) / \sum_j (\bar{Y}_j - \bar{Y}_.)^2] \end{aligned}$$

The estimated value of b_i for each genotype was tested by the following formula and against table value of t at pooled error d.f. :

$$t = \frac{b_i - 1}{SE(b_i)}$$

where $SE(b_i) = \sqrt{MS \text{ due to pooled deviation of the } i^{\text{th}} \text{ variety} / \sum_j I_j^2}$

As a second measure, they considered the deviation from regression as follows:

$$s^2 d = [\sum_j \delta_{ij}^2 / (s - 2)] s_e^2 / r$$

Where, $\delta_{ij}^2 = [\sum_j (Y_{ij} - \bar{Y}_i - \bar{Y}_j - \bar{Y}_{..})^2 - (b_i - 1)^2 \sum_j (\bar{Y}_j - \bar{Y}_{..})^2]$
 $= W_i - (b_i - 1)^2 \sum e_j^2$ and

s_e^2 / r = estimate of the pooled error (or the variance of a genotype mean of the j^{th} environment).

The deviation from regression for each genotype was tested by the following formula:

$$F = \sum \delta_{ij}^2 / (s - 2) / \text{pooled error}$$

Eberhart and Russell (1966) defined desirable criteria for stability as $b_i \approx 1$ and $s^2 d_i \approx 0$ while genotypes with $b_i < 1.0$ usually had below average stability.

II.V Measurement of Sustainability Index (S.I.)

Sustainability index was estimated by following the formula used by other workers (Singh and Agarwal, 2003; Gangwar *et al.*, 2004 and Tuteja, 2006, Atta *et al.*, 2009).

$$\text{Sustainability Index (S.I.)} = \frac{Y - \sigma_n}{Y_M} \times 100$$

Where Y = Average performance of a genotype, σ_n = Standard deviation and Y_M = Best performance of a genotype in a year.

The values of sustainability index were divided arbitrarily into 5 groups viz. very low (upto 20%), low (21 - 40%), moderate (41 - 60%), high (61-80%) and very high (above 80%).

III. Results and Discussion

Inconsistency of seed yield often experienced in mungbean, is due to its differential response of genotypes to various growing season or conditions. In general, productivity of a plant is influenced by several factors such as climate, soil type, photoperiodic response and micro-environments (Hamblin *et al.*, 1978). Thus, the significance of genotype x environment interaction for obvious reason deserves high priority in any crop improvement program. Promising genotypes need to be evaluated in multi-environmental test over several years for identification of the stable and widely adapted genotypes. The present study was undertaken to assess genotype x environment interaction for seed yield/plant and its component character for identifying stable and superior genotypes over varied environments.

The environmental influence disguised expression of the characters and varied genotypic responses were observed over seven environments in different seasons. The tested genotypes when averaged over all environments exhibited a wide range of variation for yield and yield components. The range of variation between environments was almost double for some characters like pods / plant and seeds / plant. For other characters also, quite high range of variation was observed (Table 3). This confirmed considerable genetic variability of genotypes.

The environment six (E6) was found to be more favourable environment for better expression of characters for almost all the traits including yield (Table 3).

III.I Stability analysis

The importance of genotype x environment interaction has been widely discussed by Comstock and Mall (1963) for quantitative characters. The importance of genotype x environment interactions is well recognized well and these are known to be heritable (Jinks and Mather, 1955). The significance of linear regression analysis of genotype x environment interaction has not been understood earlier in crop breeding program. So, nature and extent of genotype x environment interaction turn up to be of momentous importance, especially, when the issue of stability analysis comes into focus. The present study dealt with analyzing performance of 30 genotypes over different environments adopting the approach of regression analyses of Eberhart and Russell (1966).

The analysis of variance indicated that highly significant differences were present among genotypes and environment for seven characters (Table 4). The linear component of environments registered highly significant variation for the characters like number of pods per plant, pod length, number of seeds per pod, number of seeds per plant and seed yield per plant (Table 4). The significance of genotype x environment interactions and its linear components for pods per plant, seeds per plant and seed yield per plant indicated that the genotypes responded differently in varying environments. Similar observation was also reported by Singh and Nanda (1997) and Manivannan *et al.* (1998) in mungbean.

The analysis of variance revealed that though the magnitudes of non linear [environment + (genotype x environment)] components were significant, but were lower in comparison to linear genotype x environment for all the characters except pod length. Thus, the performance of genotypes on different environments can be predicted for the trait like seed yield per plant, being insignificant non-linear component or higher ratio of linear component compared to non-linear component. A significant g X e interaction may be either crossover, in which a significant change in rank occurs from one environment to others, or a non-crossover g X e interaction, in which the ranking of genotypes remains constant across environments and the interaction was significant because of change in the magnitude of response (Baker, 1988; Blum, 1983; Matus *et al.*, 1997). In present study, the significant g X e interaction seems to be of a crossover nature.

The present data indicated that the identification of stable genotypes in respect to each of these characters would be effective following stability model of Eberhart and Russell (1966). The environmental index, as suggested by Eberhart and Russell (1966), was also carried out (Table 5). Environment 6 (E6) exhibited highest environmental index for all the characters. On the contrary, E1 showed highly negative value for all the traits. In spite of many objections to this environmental index (Tai, 1971; Hardwick and Wood, 1972), it has been shown that, generally interpretation of a set of data dependent little on whether independent or dependent values were used for the index in calculating the regression slopes (Perkins and Jinks, 1973; Fripp and Caten, 1973).

III.II Identification of stable genotypes by stability analysis

In the present study, an attempt has been made to identify stable genotypes on the basis of seed yield per plant and other yield components from 30 genotypes following the approach of stability analysis viz. regression coefficient (b_i) and deviation mean square (s^2_{di}) (Eberhart and Russell, 1966). Usefulness of the parameter S^2_{di} as was questioned sometimes its importance was not considered (Lin. *et al.*, 1986). The relative performance of the genotypes for individual yield and its component traits were discussed below.

The genotypes, which were found to be stable on the basis of the approach of stability analysis for all or most of the characters, were considered to be highly stable. This kind of treatment was considered because the genotypes with complete agreement with all the characters discussed here would likely to express high level of stability over environments but no such genotype was found to be considered as highly stable.

The relative stability performance of individual genotype for yield and its important components viz. number of pods per plant, number of pods per cluster, pod length, number of seeds per pod, number of seeds per plant, 100 seed weight and seed yield per plant were considered here to identify stable genotypes.

Seed yield : Horizontal line passing through $b_i=1.0$ and vertical line passing through population mean of 16.51, for average seed yield/plant (gm) were two reference lines against which comparison was done. The proportion of genotype showing predictable behavior across the environments was 66.35%. The performance of seed yield was found best in E6 in all the genotypes. The genotypes recorded to be average stable were CUM2, CUM4, CUM10, CUM19, CUM26 and CUM30 having b_i values close to 1 and seed yield per plant more than the population mean (Table 3, Table 6, Figure1).

Out of these stable genotypes CUM2, CUM4 and CUM10 also showed deviation from regression close to 1. All three mutants were gamma irradiated materials from parent B105. So, these three genotypes were considered as most desirable stable mutant among 30 genotypes.

Pods per plant: The average number of pods per plant over all the genotypes and environments were found to be 34.65 (Table 6). Total 19 genotypes surpassed population mean and in 9 out of 19 genotypes namely CUM1, CUM4, CUM13, CUM14, CUM15, CUM16, CUM17, CUM18 and CUM23 b_i values were close to 1.

Pods per cluster: The mutant CUM1 exhibited highest mean followed by genotypes CUM12 and CUM11. Out of 18 genotypes showing high mean performance higher than general mean, 8 genotypes namely CUM1, CUM4, CUM10, CUM13, CUM20, CUM25, CUM26 and CUM27 also exhibited b_i value close to 1.

Pod length: The pod lengths of eighteen genotypes were higher than the general mean (6.55) across environments. 36% genotype turned out to be predictable across the environments. Seven genotype namely, CUM1, CUM4, CUM5, CUM10, CUM24, CUM28 and CUM30 were adapted to all environments, having high mean value and b_i value close to 1 (Table 6).

Seeds per pod : Among twenty two genotypes which surpassed general mean across environments, seven genotypes namely CUM1, CUM4, CUM10, CUM13, CUM17, CUM22 and CUM28 were recorded to exhibit average stability having b_i value, close to 1 (Table 6). Performance of genotypes was predictable as their linear components were significant, and the proportion of genotypes showing predictability was 62.39%.

Seeds per plant : Environment six (E6) emerged as the best environment due to high mean (Table 3). It is interesting to note that almost all the linear and nonlinear components were highly significant (Table 4) for seeds/ plant. Among the twenty one genotypes that showed higher mean performance over the general mean, only ten namely CUM1, CUM2, CUM4, CUM8, CUM10, CUM21, CUM22, CUM26, CUM29 and CUM30 were specifically adapted to all environments having high mean value and b_i value close to 1 (Table 6).

100 seed weight: Twenty nine genotypes albeit, showed mean values higher than the general mean, but ten were widely adapted to all environments having b_i value close to 1.

Sustainability index was estimated to identify the stable genotypes on the basis of seed yield (Table 7). Genotypes namely, CUM1, CUM6, CUM7, CUM9, CUM16, CUM20, CUM21, CUM25, CUM26, CUM27, CUM28 and CUM29 showed very high sustainability index (%). On the contrary, some genotypes namely, CUM2, CUM4, CUM5, CUM8, CUM10, CUM12, CUM13, CUM15, CUM17, CUM18, CUM19, CUM22, CUM23, CUM24, and CUM30 were found high sustainability index (%) was estimated indicating these genotypes were stable across the environments which were characterized with wide adaptability and high mean.

The comparative study between the two stability models revealed that the genotypes CUM1, CUM4, CUM10 and CUM13 which were characterized with wide adaptability for some traits including seed yield as per Eberhart and Russell (1966) model, also corroborates with high sustainability index (%). So, any of the techniques can be considered for identifying wide adaptable genotypes.

In general, genotypes did not show wide adaptability uniformly for all characters. However, four genotypes namely CUM1, CUM4, CUM10 and CUM13 registered average stability coupled with high mean performance for seed yield per plant and some yield components consistently. Out of these 4 mutant lines, three genotypes namely CUM1, CUM4 and CUM10 were developed from variety B105. On the contrary, the genotype CUM13 was selection from irradiated population of variety B1. Both B1 and B105 were widely adapted varieties to different environments and same adaptability pattern existed in mutant lines evolved from these two varieties. The four genotypes CUM1, CUM4, CUM10 and CUM13, therefore, could be considered to be outstanding for cultivation in all environments having average stability and high yield.

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Table 1: List of the elite mutant lines

Line	Developed from	Treatment dosage	Line	Developed from	Treatment dosage
CUM 1	B 105	45 KR γ ray	CUM 16	B 1	60 KR γ ray
CUM 2	B 105	15 KR γ ray	CUM 17	B 1	1.50% EMS
CUM 3	B 105	1.50% EMS	CUM 18	B 1	45 KR γ ray
CUM 4	B 105	30 KR γ ray	CUM 19	B 1	1.00% EMS
CUM 5	B 105	60 KR γ ray	CUM 20	B 1	60KR γ ray
CUM 6	B 105	30 KR γ ray	CUM 21	SML 32	15 KR γ ray
CUM 7	B 105	1.50% EMS	CUM 22	SML 32	30 KR γ ray
CUM 8	B 105	0.50% EMS	CUM 23	SML 32	0.50% EMS
CUM 9	B 105	15 KR γ ray	CUM 24	SML 32	45 KR γ ray
CUM 10	B 105	1.00% EMS	CUM 25	SML 32	0.50% EMS
CUM 11	B 1	30 KR γ ray	CUM 26	SML 32	15 KR γ ray
CUM 12	B 1	45 KR γ ray	CUM 27	SML 32	45 KR γ ray
CUM 13	B 1	15 KR γ ray	CUM 28	SML 32	15 KR γ ray
CUM 14	B 1	0.50% EMS	CUM 29	SML 32	30 KR γ ray
CUM 15	B 1	30 KR γ ray	CUM 30	SML 32	15 KR γ ray

Table 2: Stability parameters and their underlying stability concepts

Stability parameters	Symbol	Stability concept involved
Regression coefficient Deviation mean square	b_i s^2d	Biological/ Agronomic Agronomic

Table 3: Summary of yield and its components over the seven environments for the genotypes of mungbean

	Pods / plant	Pods / cluster	Pod length	Seeds /pod	Seeds / plant	100 seed weight	Seed yield
Average value	34.65	6.14	6.55	11.41	538.58	4.22	16.51
Range	28.73 – 53.17	5.99 – 6.38	6.21 – 7.29	10.61 – 12.76	435.04 – 857.28	4.08 – 4.31	15.20 – 18.93
Environment with							
Highest Mean	E6	E7	E6	E6	E6	E6	E6
Lowest Mean	E3	E3	E3	E3	E1	E3	E1

Table 4: Analysis of variance (mean square) for yield and yield components (Eberhart And Russell, 1966)

Sources of variation	d. f.	Pods / plant	Pods / cluster	Pod length	Seeds /pod	Seeds / plant	100 seed weight	Seed yield
Genotypes	32	71.72**+	0.59	0.43	1.59**	45408.87**+	1.37*	36.59*+
Environments	6	2396.60*	0.57	4.05**+	14.75*	788685.25**	0.31	61.42**+
Genotype × Environment	192	12.88**+	0.23	0.15	0.50	3618.39***+	0.05	4.20**
Environment +(Genotype × Environment)	198	85.11**+ +	0.23	0.27	0.93	27408.29**+ +	0.06	5.93***+
Environments (linear)	1	14379.66	3.44	24.32**	88.49*	473213.40**	1.85	368.55**
Genotype × Environment (linear)	32	19.14**+ +	0.42	0.09	0.73	10603.92**+ +	0.07	6.96***+
Pooled deviation	165	11.27**	0.18	0.16	0.44	2153.83**	0.05	3.53**
Pooled error	224	5.01	0.06	0.04	0.12	720.32	0.03	2.60
Linear component (%)		62.94	70.00	36.00	62.39	83.12	58.33	66.35
Non-linear component (%)		37.06	30.00	64.00	37.61	16.88	41.67	33.65

Significant against pooled error at 5% is denoted by * Significant against pooled error at 1% is denoted by** Significant against pooled deviation at 5% is denoted by + Significant against pooled deviation at 1% is denoted by ++

Table 5: Estimates of environmental additive effects (I_e) for seven environments for seed yield and its component of mungbean

Location	Seed yield	Pods / plant	Pods / cluster	Pod length	Seeds /pod	Seeds / plant	100 seed weight
E1	-1.31	-4.30	-0.07	-0.08	-0.11	-103.49	-0.01
E2	-1.29	-1.75	0.05	0.02	0.06	-65.70	0.06
E3	-0.14	-5.92	-0.15	-0.30	-0.79	-89.58	-0.13
E4	0.04	-3.35	-0.11	-0.16	-0.44	-96.97	-0.04
E5	1.13	1.54	-0.02	-0.02	-0.07	92.11	0.05
E6	2.42	18.52	0.04	0.78	1.36	318.75	0.10
E7	-1.30	-4.74	0.24	0.03	0.05	-54.79	0.06

Table 6: Estimates of stability parameters according to Eberhart And Russell (1966) model for yield and yield components of mungbean

Line	Seed yield		Pods per plant		Pods per cluster		Pod length	
	μ_i	b_i	μ_i	b_i	μ_i	b_i	μ_i	b_i
CUM1	16.73	0.52	35.53	1.04	6.74	1.03	7.03	0.98
CUM2	16.52	0.88	35.53	1.24	6.31	-2.03	6.36	1.69
CUM3	17.95	1.87	33.13	1.16	6.12	-0.12	6.28	1.40
CUM4	16.32	0.93	36.20	1.15	6.43	1.32	6.81	1.03
CUM5	16.50	0.64	33.12	1.18	6.08	0.42	6.60	1.13
CUM6	15.53	0.43	33.77	1.04	6.41	-0.71	6.54	0.75
CUM7	15.77	0.30	34.76	1.20	6.07	0.16	6.23	1.69
CUM8	16.03	0.79	36.13	1.25	6.10	0.17	6.34	1.43
CUM9	16.11	0.44	36.05	1.20	6.37	0.27	6.78	0.90
CUM10	16.60	1.10	34.82	1.24	6.14	0.90	6.57	1.36
B105	10.50	0.01	24.96	0.44	5.70	0.82	6.34	0.18
CUM11	19.14	3.19	40.80	1.28	6.56	0.72	6.63	0.88
CUM12	20.00	2.38	38.88	1.04	6.74	1.54	6.77	0.42
CUM13	19.22	1.22	36.03	1.02	6.15	1.10	6.44	1.30
CUM14	19.16	3.23	34.91	1.10	5.93	2.66	6.54	1.08
CUM15	17.43	1.35	35.71	1.12	6.04	1.95	6.60	0.78
CUM16	16.84	0.37	34.93	1.05	6.29	2.55	6.55	0.73
CUM17	17.41	1.72	35.03	1.14	6.23	3.65	6.39	0.41
CUM18	17.57	1.37	35.07	1.11	6.24	2.43	6.46	1.41
CUM19	17.15	1.17	34.10	1.07	6.09	1.85	6.60	1.41
CUM20	17.08	0.71	38.90	1.10	6.19	1.03	6.48	1.42
B1	10.75	-0.02	27.33	0.49	5.52	-0.11	6.09	0.57
CUM21	15.73	0.28	35.59	0.89	6.19	0.50	6.72	0.92
CUM22	16.39	0.79	36.16	0.88	5.97	-0.17	6.95	0.68
CUM23	16.51	0.96	34.93	1.00	5.79	-0.35	6.58	0.75
CUM24	17.36	1.64	35.20	0.84	5.84	-1.80	6.68	1.01
CUM25	15.92	0.59	34.38	0.85	6.22	1.07	6.55	0.86
CUM26	17.01	0.86	35.33	0.90	6.17	1.15	6.81	0.70
CUM27	17.32	0.86	35.26	0.71	6.31	0.91	6.54	1.11
CUM28	16.59	0.57	35.84	0.86	6.06	-1.95	6.77	1.23
CUM29	16.58	0.62	37.38	0.86	6.20	0.39	6.46	1.05
CUM30	16.58	1.27	35.12	0.84	6.17	-0.42	6.66	0.98
SML32	10.47	-0.02	26.48	0.70	5.39	-0.44	5.75	1.05
Grand mean	16.51	-	34.65	-	6.14	-	6.55	-

μ_i = mean

b_i = regression coefficient

Continued

Table 6: Estimates of stability parameters according to Eberhart And Russell (1966) model for yield and yield components of mungbean

Line	Seeds per pod		Seeds per plant		100 seed weight	
	μ_i	b_i	μ_i	b_i	μ_i	b_i
CUM1	11.57	1.28	539.95	1.23	4.30	0.95
CUM2	11.32	1.40	541.96	1.20	4.30	1.09
CUM3	11.42	0.90	542.85	1.43	4.38	1.66
CUM4	11.41	0.98	549.40	1.05	4.34	0.83
CUM5	11.82	1.43	519.12	1.17	4.36	0.89
CUM6	11.22	0.98	505.15	1.24	4.27	1.08
CUM7	11.18	1.89	523.21	1.27	4.30	1.87
CUM8	11.57	1.77	537.65	1.14	4.44	2.34
CUM9	11.75	0.31	574.68	0.40	4.48	0.08
CUM10	11.72	1.19	541.91	1.22	4.35	0.65
B105	10.26	0.28	297.17	0.75	2.50	1.54
CUM11	11.82	0.27	627.47	0.85	4.47	1.30
CUM12	12.43	1.05	610.33	0.86	4.83	0.66
CUM13	11.44	1.22	636.81	0.54	4.40	1.18
CUM14	11.30	1.43	636.25	0.71	4.33	1.19
CUM15	11.10	1.59	591.84	0.58	4.27	2.45
CUM16	11.34	1.27	567.10	0.67	4.35	3.63
CUM17	11.41	0.99	588.30	0.61	4.23	1.85
CUM18	11.64	1.50	615.46	0.60	4.32	1.64
CUM19	11.51	1.68	592.47	0.62	4.31	2.03
CUM20	11.91	1.38	552.23	0.64	4.28	1.50
B1	10.24	0.70	306.76	0.79	3.14	1.36
CUM21	11.18	0.24	537.55	1.11	4.31	0.81
CUM22	11.51	0.98	579.99	1.10	4.21	0.02
CUM23	11.68	0.54	526.76	1.24	4.30	0.34
CUM24	11.52	0.89	576.37	1.33	4.23	0.31
CUM25	11.79	0.37	521.69	1.27	4.28	-0.05
CUM26	11.41	0.34	571.48	1.19	4.40	-0.56
CUM27	11.60	-0.11	534.14	1.29	4.37	-0.40
CUM28	11.56	0.97	553.30	1.11	4.28	0.21
CUM29	11.73	0.30	551.68	1.18	4.33	0.14
CUM30	12.11	0.80	537.23	1.25	4.38	-3.15
SML32	10.21	0.47	342.67	0.74	3.08	1.59
Grand mean	11.41	-	538.58	-	4.22	-

μ_i = mean

b_i = regression coefficient

Table 7: Estimates of sustainability index for seed yield in 33 genotypes of mungbean

Genotypes	Mean Yield	Standard Deviation	Best performance of a genotype in any year	Sustainability Index (%)	Stability
CUM1	16.73	1.31	18.72	82.39	Very High
CUM2	16.52	1.80	19.28	76.33	High
CUM3	17.95	3.50	24.46	59.08	Moderate
CUM4	16.32	1.46	18.94	78.46	High
CUM5	16.5	1.78	20.21	72.86	High
CUM6	15.53	0.68	16.86	88.09	Very High
CUM7	15.77	0.52	16.81	90.72	Very High
CUM8	16.03	1.23	18.91	78.27	High
CUM9	16.11	0.80	17.89	85.60	Very High
CUM10	16.6	1.65	20.21	73.98	High
B105	10.5	0.60	11.67	84.83	Very High
CUM11	19.14	4.29	27.86	53.30	Moderate
CUM12	20	3.96	24.72	64.90	High
CUM13	19.22	3.61	22.88	68.24	High
CUM14	19.16	4.14	27.56	54.52	Moderate
CUM15	17.43	2.20	21.85	69.70	High

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Table 7: Estimates of sustainability index for seed yield in 33 genotypes of mungbean

Genotypes	Mean Yield	Standard Deviation	Best performance of a genotype in any year	Sustainability Index (%)	Stability
CUM16	16.84	1.05	19.07	82.80	Very High
CUM17	17.41	2.81	23.21	62.89	High
CUM18	17.57	2.81	23.76	62.11	High
CUM19	17.15	2.32	22.29	66.55	High
CUM20	17.08	1.37	19.42	80.92	Very High
B1	10.75	1.04	12.49	77.70	High
CUM21	15.73	0.63	16.75	90.18	Very High
CUM22	16.39	1.51	18.72	79.51	High
CUM23	16.51	1.77	19.28	76.43	High
CUM24	17.36	3.15	22.32	63.64	High
CUM25	15.92	0.92	17.22	87.11	Very High
CUM26	17.01	1.72	19.07	80.16	Very High
CUM27	17.32	1.49	19.39	81.63	Very High
CUM28	16.59	1.06	18.09	85.83	Very High
CUM29	16.58	1.10	18.29	84.63	Very High
CUM30	16.58	1.75	20.49	72.39	High
SML32	10.47	0.91	12.47	76.68	High

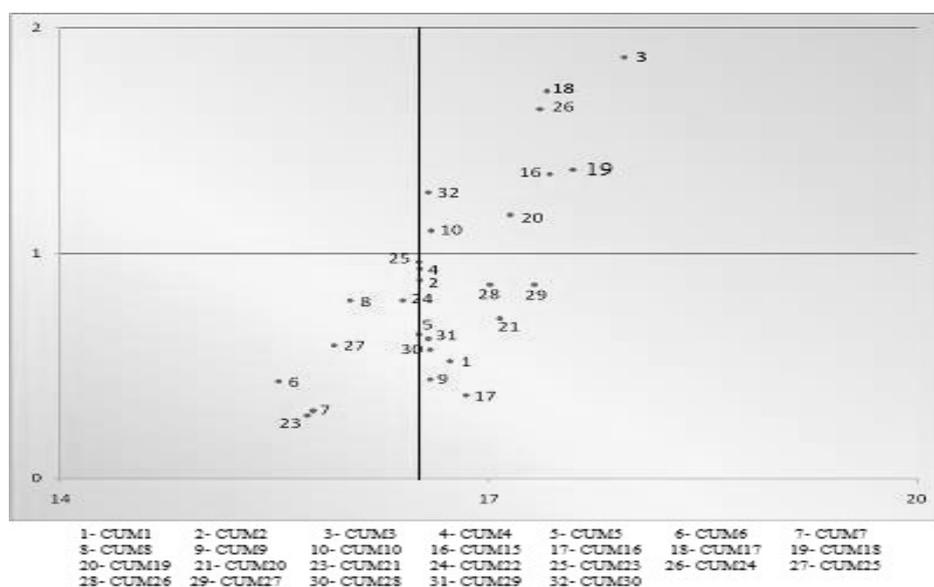


Figure 1 : Relation between seed yield per plant (gm) and stability genotypes plotted graphically with b₁ on x axis and average seed yield per plant (gm) on y axis