



## Genetic Variability and Stability Analysis in Greengram [*Vigna radiata* (L.) Wilczek]

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### Abstract

Pooled analysis of variance showed significant amount of variability for all traits under study. High GCV and PCV were observed for harvest index and number of pods per plant. High heritability was observed for seed yield per plant followed by biological yield per plant harvest index, test weight, plant height, number of pods per cluster, number of pods per plant, pod length, days to maturity, number of clusters per plant, days to 50% flowering and number of seeds per pod. High heritability coupled with high genetic advance was recorded in plant height, indicating that this character is controlled by additive gene effects and simple selection for this trait may be useful. The stability analysis revealed significant differences for genotypes, sowing conditions and their interactions for almost traits including seed yield per plant. The orthogonal partitioning of components also significant in this stability model. Considering all traits and conditions under study none of the test genotypes were found stable for all the traits. However seven genotypes namely; Pusa 371, HUM 12, Pusa 672, Pusa Baisakhi, ML 1451, WGG 37 and BDRY 1 were found to be stable for maximum traits while rest genotypes may be suitable for favorable and other conditions in present study.

**Key Words:** *Greengram, Environment, Variation, Selection, Genotypes, Stability*

### INTRODUCTION

Greengram [*Vigna radiata* (L.) Wilczek] is an important annual legume belonging to family fabaceae, sub-family papilionoideae, genus *Vigna*. The genus *Vigna* has been divided to include about 170 species, 120 from Africa, 22 from Asia, and a few from other parts of the world (Ghafoor *et al.*, 2001). Seven species of *Vigna* are cultivated as pulse crops specially in Asia, Africa and some parts of America (Anishetty & Moss, 1988). It is well suited to dry areas, mainly under irrigated conditions. It is self-pollinated diploid species with chromosome number  $2n = 22$  with an estimated genome size of 543 mega bases (Mb) (Kang *et al.*, 2014). It is the native of Indo-Burma region of Hindustan centre (Vavilov, 1926). Green gram crop is widely cultivated throughout South Asia including India, Pakistan, Bangladesh, Sri Lanka, Thailand, Cambodia, Vietnam, Indonesia, Malaysia and South China. In India, it is the third most important pulse crop after chickpea and pigeon pea (Rajendra Prasad, 2011) and cultivated in Rajasthan, Maharashtra, Andhra Pradesh, Madhya Pradesh and Bihar. Andhra Pradesh ranks 6th in greengram production with 0.83 lakh tones under an area of 1.13 lakh ha with productivity of 735 kg/ha according to third advance estimates of 2020-21. On account of its short duration, photo-insensitivity and dense crop canopy, it assumes special significance in crop intensification, diversification, and conservation of natural resources as well as sustainability of the production system.

Plant Breeders aim is for identify the genotypes that are both genetic variable and stable to environment (s) before releasing the as varieties, allowing for fast genetic improvement (Showemimo *et al.*, 2000, Mustfa *et al.*, 2001, Yan and Kang 2003). To understand, G x E interaction sound biometrical or statistical methods must be used. The analysis of variance aids in determining the existence, significant and degree of the GxE interaction, but it does not explain its significance or ramifications. As a consequence, biometrical models were advocated to characterize the degree of G x E interactions, their patterns and plant breeding implications. When tested in separate environments, there are many approaches for deterring stable performance of genotypes. The number of environments available, the significance level required and the type of information required all plays a vital role in deciding which analysis to use for experimental observations. In general, the evaluation process should be dependable, simple to comprehend, including minimal statistics and be relevant to both small and big groups of environments (Schmid *et al.*, 2011).

Yates and Cochran (1938) provided one of the most simple and simplest ways of stability evaluation, which was later modified by Finlay and Wilkinson (1963) and Eberhart and Russell (1966) and is now a widely used method. According to this model the stability analysis technique partitions the genotypes x environment interaction components of variance of each genotype into two parts. Therefore, each genotypes is characterized by three parameters viz.; (1) mean yield ( $\bar{x}$ ) over all environments, (2) a linear regression coefficient ( $b_i$ ) in relation to environment index and (3) the deviation from linear regression ( $S^2_{di}=0$  or not). Since, the average slope for the environmental index is 1.0, regression coefficient for each genotype may be 1.0 or greater or lesser than 1.0, the genotype with regression value of 1.0 is considered to have an average adaptability, whereas the value less than 1.0 or higher than 1.0 would mean below average and above average adaptability respectively. Another stability parameters ( $S^2_{di} = 0$  or not) is considered to be stable as suggested by Singh and Chaudhary (1985). A genotype with a regression deviation variance of zero has a highly predictable response, whereas a genotype with a regression deviation greater than zero has a less predictable response (Scapin *et al.*, 2010). Earlier, many stability analyses have been worked out for mungbean yield in India (e.g. Mahalingam *et al.*, 2018,

Anandi *et. al.*, 2019 and Nath *et. al.*, 2013). However, there is a scarcity of information on mungbean cultivar stability. Therefore, the objective of the present investigation is to wide range of variable and more stable genotypes in mungbean with high and stable yield suitable for diverse environment or a wide range of locations.

## MATERIAL AND METHODS:

### 1. Experimental Material

In the present study, three experiments were conducted with twenty five diverse genotypes of mungbean namely; Pusa Vishal, Pusa-371, HUM-12, Pusa-672, MH-218, Pusa Baisakhi, Pusa-9531, MH-2-15, TM 96-25, RMG-991, RMG-975, IPM 02-19, IPM 99-125, ML-1451, WGG-37, MH-0891, MH-521, RMG-90, PDM 96-262, AKM-9904, BDRY-1, Pusa-16, NDM-6, COGG-912 and Pusa-1431 at Agricultural Research Farm Brahamanand P.G. College, Rath in in a Randomized Block Design (RBD) *Kharif* 2019 with three replications and sown on different dates of sowing as early (01-08-19), medium (11-08-19) and late (21-08-19). All recommended package of practice has been followed to retain a good crop.

### 2. Observation Recording

Five competitive plants were randomly selected from each replication and tagged for recording the observations on days to 50% flowering, days to maturity, plant height, number of pods per plant, number of clusters per plant, pod length, number of pods per cluster, number of seeds per pod, test weight, biological yield per plant, harvest index and seed yield per plant.

### 3. Statistical Analysis

Windostat software was applied to analyze all recorded observations with environments treated as random effects and cultivars treated as fixed effects. Analysis of Variance was calculated by formula of Panse and Sukhatme (1969), GCV and PCV as per given formula by Burton and Devane (1952), Heritability and Genetic advance by suggested method of Allard, (1960), Johnson *et al.* (1955) and stability analysis was done as per the stability model suggested by Eberhart and Russell (1966). The statistical formulas for the model are explained in literature (Eberhart and Russell 1966, Singh and Chaudhary 1985 and Lin *et. al.*, 1986).

## RESULT AND DISCUSSION:

### 1. Analysis of Variance:

The analysis of variance (Table-1) showed significance differences for twelve characters namely; days to 50% flowering (19.48\*\*), days to maturity (65.45\*\*), plant height (450.85\*\*), number of pods per plant (123.66\*\*), number of clusters per plant (1.88\*\*), pod length (1.20\*\*), number of pods per cluster (0.77\*\*), number of seeds per pod (1.98\*\*), test weight (1.97\*\*), biological yield per plant (72.56\*\*), harvest index (189.89\*\*) and seed yield per plant (10.33\*\*) among the genotypes and the mean performance of different genotypes had a wide range of variation for the characters.

### 2. Genetic Parameters:

In Table-2, the high percent of genotypic coefficient of variation (GCV) was recorded for harvest index( 29.79) and number of pods per plant (26.43) and phenotypic coefficient of variation (PCV) were also showed by harvest index( 26.43) and number of pods per plant (26.69). Moderate genotypic co-efficient of variation was observed for seed yield per plant ((24.61) followed by plant height (21.44), biological yield per plant (16.89), test weight (16.87), number of pods per cluster (13.38) and number of clusters per plant (13.18). However, Moderate phenotypic co-efficient of variation was also observed for seed yield per plant ((24.61) followed by plant height (21.59), biological yield per plant (16.90), test weight (16.95), number of pods per cluster (13.50) and number of clusters per plant (13.50). Further, the present finding showed that estimates of PCV were generally higher than their corresponding GCV for all the characters studied indicated that these traits influence by environmental factors. High heritability was recorded for seed yield per plant (99.95) followed by biological yield per plant (99.87), harvest index (99.82), test weight (99.14), plant height (98.54), number of pods per cluster (98.16), number of pods per plant (98.04), pod length (97.82), days to maturity(97.15), number of clusters per plant (95.37) and days to 50% flowering (91.77). Maximum genetic advance as percent of mean was showed by harvest index (61.32), number of pods per plant (53.91), seed yield per plant (50.67) and plant height (43.84). While the rest the traits showed moderate to low genetic advance as percent of mean thereby, suggesting average response for selection based on per se performance. Similar findings were also found by Similar the finding of Garge *et.al* (2017), Krishanan *et.al* (2018), Muthuswamy *et.al* (2019) Mariyammal *et.al.* (2019), Mohammed *et al.* 2020 and Khatik,*et.al.*, 2022).

### 3. Stability parameters of Eberhart and Russell's model

Analysis of variance (Table-3,4 and 5 ) indicated highly significant differences among the test genotypes in respect of all traits under study under environments-1, 2 and 3, which showed a wide range of variation under early, timely and late sown conditions respectively.

In Table 6, the significant differences were recorded among the genotypes on based analysis of combined over three environments for all the traits studied. When compared to the pooled error and pooled deviation, the joint ANOVA indicated sufficient significant differences in seed yield between genotypes. The differences in seed yield between the environments were also exhibited to be highly significant. When evaluated against pooled error and pooled deviation, there was significant G x E as well as G x E (linear) interactions for all traits, indicating that genotypes showed may even be cultivars with specific adaptability.

### 4. Gene x Environment Interaction

Stability parameters namely; population mean ( $\bar{x}$ ), deviation from regression ( $S^2_{di}$ ) and regression coefficient ( $b_i$ ) were analyzed as per the model suggested by Eberhart and Russell's model presented in table- 7., the lower mean values than population mean, negative regression coefficient ( $b_i$ ) < 1.00 or near to unity and negative non- significant  $S^2_{di}$  as desirable in both traits and exhibited by the four genotypes *viz*, Pusa Baisakhi (Mean 34.33,  $b_i$  -0.95 and  $S^2_{di}$ -0.46), Pusa 371 (Mean 34.67,  $b_i$  -0.93 and  $S^2_{di}$ -0.24), TM96-25 (Mean 36.22,  $b_i$  -0.36 and  $S^2_{di}$ -0.24) and HUM 12 (Mean 36.22,  $b_i$  -0.80 and  $S^2_{di}$ -0.40) which shows their adaptability for short days to 50% flowering and the six genotypes Pusa 371 (Mean 70.11,  $b_i$  -0.96 and  $S^2_{di}$ -1.10), IPM02-19 (Mean 69.78,  $b_i$  -0.15 and  $S^2_{di}$ -0.27), Pusa 9531 (Mean 70.78,  $b_i$  -0.92 and  $S^2_{di}$ -0.31), MH218 (Mean 68.00,  $b_i$  -0.83 and  $S^2_{di}$ -0.47), COGG912 (Mean 69.11,  $b_i$  -0.72 and  $S^2_{di}$ -0.57) and HUM 12 (Mean 72.11,  $b_i$  -0.91 and  $S^2_{di}$ -0.18) had their stable performance for short days to maturity under all sowing conditions. Remaining genotypes showed there suitable performance for favorable environment or early sown condition for these trait in present study. While the considering higher mean values than population mean and regression coefficient ( $b_i$ ) < 1.00 or near to unity and non- significant  $S^2_{di}$  for rest characters. The three genotypes *viz*; Pusa Baisakhi (Mean 61.14,  $b_i$  0.83 and  $S^2_{di}$  1.94) and BRDY 1 (Mean 60.29,  $b_i$  0.87 and  $S^2_{di}$  1.69) were indicated their grater suitability for plant height to all sowing conditions and rest genotypes may be suitable for other conditions. The

genotypes viz; Pusa Vishal (Mean 24.78, bi 0.94 and  $S^2di$  1.55), Pusa 692 (Mean 24.69, bi 0.95 and  $S^2di$  1.18) and BRDY 1 (Mean 28.69, bi 0.93 and  $S^2di$ ) had their most stable performance for number of pods per plant to all dates of sowing and remaining genotypes which showed their stable performance other favorable sowing conditions. Genotypes namely; Pusa Baisakhi (Mean 6.51, bi 0.91 and  $S^2di$  0.05), RMG 90 (Mean 6.50, bi 0.90 and  $S^2di$  0.01) and HUM 12 (Mean 6.87, bi 0.82 and  $S^2di$  0.07) showed their most stable performance for number of clusters per plant under all dates of sowing and remaining genotypes which showed their adaptable nature other favorable sowing conditions. The Genotypes namely; RMG991 (Mean 7.22, bi 0.27 and  $S^2di$  0.01) had stable for pod length under all dates of sowing and remaining genotypes may be suitable for other favorable sowing conditions. The Genotypes namely; RGM90 (Mean 6.50, bi 0.90 and  $S^2di$  0.01) and HUM12 (Mean 6.87, bi 0.82 and  $S^2di$  0.07) were found stable for number of pods per cluster under all dates of sowing and rest genotypes which showed their stable performance for other favorable sowing conditions. The Genotypes namely; RGM975 (Mean 11.72, bi 0.05 and  $S^2di$  0.11) had their stable for number of seeds per pod under all dates of sowing and rest twenty four genotypes which showed their stable performance for other sowing conditions. The Genotypes namely; Pusa 371 (Mean 5.25, bi 0.99 and  $S^2di$  0.00) expressed their stable for test weight under all dates of sowing and others genotypes which showed their stable performance other favorable sowing conditions. The Genotypes namely; COGG (Mean 32.04, bi 0.94 and  $S^2di$  0.03) showed their stable for biological yield per plant under all dates of sowing and rest genotypes which showed their stable performance for other favorable sowing conditions. The Genotypes namely; IPM99-125 (34.27, bi 0.92 and  $S^2di$  0.81), WGG 37 (27.29, bi 0.94 and  $S^2di$  0.86) and MH521 (29.90, bi 0.96 and  $S^2di$  0.03) indicating their stable for harvest index under all dates of sowing and remaining genotypes which showed their stable performance for other favorable sowing conditions. The six genotypes namely; Pusa vishal (10.69, bi 0.89 and  $S^2di$  0.15), Pusa 371 (7.99, bi 0.98 and  $S^2di$  0.02), IPM99-125 (7.96, bi 0.85 and  $S^2di$  0.02), Pusa 672 (9.18, bi 0.97 and  $S^2di$  0.06), MH521 (8.88, bi 0.93 and  $S^2di$  0.03) and MH 0891 (7.84, bi 0.92 and  $S^2di$  0.01) showed their stable for seed yield per plant under all dates of sowing and remaining genotypes which showed their stable performance other favorable sowing conditions.

The main object of selection in breeding scheme is to develop a population that has a mean value greater than the average mean value of all the genotypes tested. This difference should be due to differences in genotypes and not to the environment (House, 1985). Analysis of variance from the present investigation stated that genotypes showed significant differences in all traits including yield per plant over the environments, demonstrating that the observed differences in all traits performances had genetic causes and thereby, offered the possibility of selection and genetic improvement for all traits under study. The magnitude of variation due to environment (linear) was higher than Gx E (linear) for seed yield per plant, which indicated that most of the total variation was contributed by environment only. Significant pooled deviation indicates that genotypic performance varies in response to the environment. The predominance of linear components would be aid in predicting genotype performance under all environments. Similar results were also reported for significance levels, interaction effects and G X E (linear) on greengram seed yield and other traits by Garge *et al* 2017, Krishnan *et al* 2018, Muthuswamy *et al* 2019, Mariyammal, *et al.* 2019, Mohammed *et al.* 2020, Sridhar *et al.*, 2022 and Khatik, *et al.*, 2022).

#### Conclusion:

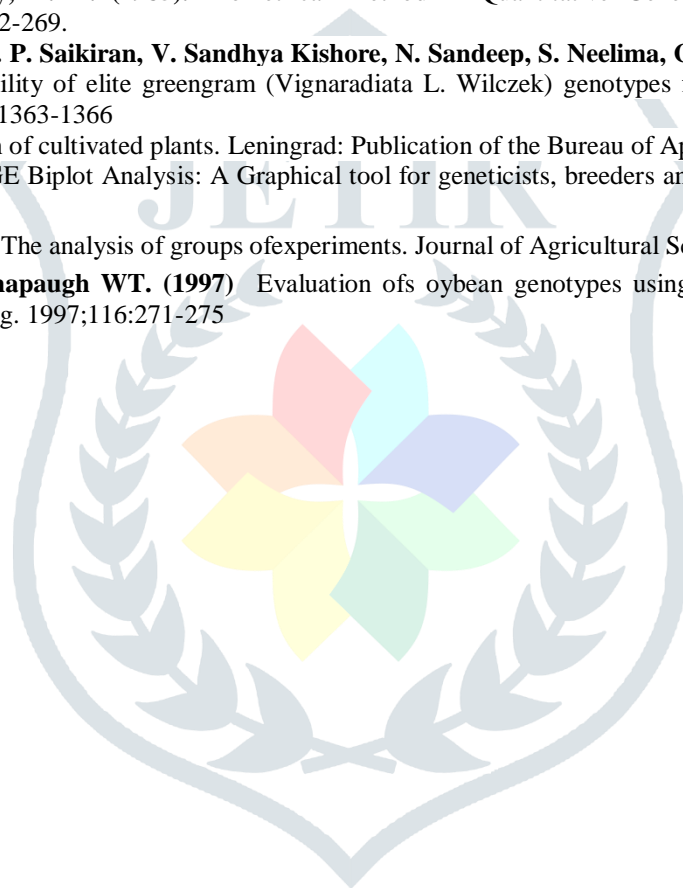
Based on the foregoing discussion it has concluded that the genetic variability showed average response for selection based on per se performance might be effective for high heritable traits and as per stability parameters none of the test genotypes were found stable for all the traits under study only seven genotypes Pusa 371, Hum 12, Pusa 672, Pusa Baisakhi, ML 1451, WGG 37 and BRDY 1 were found stable for maximum traits under all environments in present study. Hence, these genotypes could be utilized in breeding programme for the development of stable genotypes of greengram.

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**List of tables****Table-1. Pooled analysis of variance for seed yield and its components characters in Greengram [*Vigna radiata* (L.) Wilczek]**

Source of variation	d.f.	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of pods per plant	Number of clusters per plant	Pod length (cm)	Number of pods per cluster	Number of seeds per pod	Test weight (g)	Biological yield per plant (g)	Harvest index (%)	Seed yield per plant (g)
Replication	2	2.60	1.78	1.56	1.70	0.27	0.01	0.22	0.09	0.03	0.22	0.03	0.17
Treatment	24	19.48**	65.45**	450.85**	123.66*	1.88**	1.20**	0.77**	1.98**	1.97**	72.56**	189.89**	10.33*
Error	48	0.57	0.64	2.21	0.82	0.03	0.01	0.05	0.06	0.01	0.03	0.11	0.02

\*, \*\* significant at 5% and 1% level, respectively

**Table-2. Pooled estimates of variability parameters for twelve characters in Greengram [*Vigna radiata* (L.) Wilczek]**

Characters	PCV (%)	GCV (%)	Heritability(%)	G.A.	G.A. as % mean
Days to 50% flowering	6.96	6.67	91.77	4.96	13.15
Days to maturity	6.52	6.43	97.15	9.44	13.05
Plant Height (cm)	21.59	21.44	98.54	25.01	43.84
Number of pods per plant	26.69	26.43	98.04	13.05	53.91
Number of clusters per plant	13.50	13.18	95.37	1.58	26.52
Pod length (cm)	8.95	8.85	97.82	1.29	18.03
Number of pod per cluster	13.50	13.38	98.16	1.03	27.30
Number of seeds per pod	5.98	5.36	80.29	1.12	9.89
Test weight (g)	16.95	16.87	99.14	1.67	34.61
Biological yield per plant (g)	16.90	16.89	99.87	10.12	34.77
Harvest index (%)	29.82	29.79	99.82	16.37	61.32
Seed yield per plant (g)	24.61	24.61	99.95	3.82	50.67

**Table- 3. Analysis of variance for seed yield and its components in Greengram [*Vigna radiata* (L.) Wilczek] over Environment-1 (E<sub>1</sub>)**

Source of variation	d.f.	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of pods per plant	Number of clusters per plant	Pod length (cm)	Number of pods per cluster	Number of seeds per pod	Test weight (g)	Biological yield per plant (g)	Harvest index (%)	Seed yield per plant (g)
Replication	2	0.33	1.77	10.39	0.79	0.89	0.58	0.36	7.56	0.00	0.33	0.15	0.00
Treatment	24	22.58*	76.26*	445.88**	128.31**	1.94*	1.24**	0.82*	1.86*	1.98**	72.93**	159.92**	8.60**
Error	48	1.46	1.93	12.69	3.28	0.19	0.08	0.03	0.97	0.00	0.13	0.31	0.01

\*, \*\* significant at 5% and 1% level, respectively

**Table- 4. Analysis of variance for seed yield and its components in Greengram [*Vigna radiata* (L.) Wilczek] over Environment-2 (E<sub>2</sub>)**

Source of variation	d.f.	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of pods per plant	Number of clusters per plant	Pod length (cm)	Number of pods per cluster	Number of seeds per pod	Test weight (g)	Biological yield per plant (g)	Harvest index (%)	Seed yield per plant (g)
Replication	2	1.44	9.37	1.47	7.02	0.44	0.21	0.18	0.66	0.01	0.14	0.22	0.04
Treatment	24	18.49*	63.85**	486.51**	116.31**	1.96*	1.14**	0.63*	0.89*	2.31**	74.81**	223.82**	12.62**
Error	48	1.25	1.19	1.31	4.37	0.11	0.03	0.04	0.30	0.04	0.14	0.35	0.01

\*, \*\* significant at 5% and 1% level, respectively

**Table- 5 Analysis of variance for seed yield and its components in Greengram [*Vigna radiata* (L.) Wilczek] over Environment-3 (E<sub>3</sub>)**

Source of variation	d. f.	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of pods per plant	Number of clusters per plant	Pod length (cm)	Number of pods per cluster	Number of seeds per pod	Test weight (g)	Biological yield per plant (g)	Harvest index (%)	Seed yield per plant (g)
Replication	2	0.05	0.01	0.21	0.20	1.43	0.04	0.14	0.12	0.00	0.22	0.01	0.02
Treatment	24	21.78*	59.34**	430.86**	134.21**	2.02*	1.30**	0.92*	1.68*	2.03**	71.41**	195.13**	10.27**
Error	48	1.43	2.03	1.19	0.82	0.11	0.03	0.02	0.17	0.04	0.14	0.34	0.01

\*, \*\* significant at 5% and 1% level, respectively

**Table- 6 ANOVA for stability parameters for yield and its components in 25 genotypes of Greengram [*Vigna radiata* (L.) Wilczek] as per Eberhart and Russell's Model, 1966**

Source of Variation	d.f.	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of pods per plant	Number of clusters per plant	Pod length (cm)	Number of pods per cluster	Number of seeds per pod	Test weight (g)	Biological yield per plant (g)	Harvest index (%)	Seed yield per plant (g)
Variety	24	19.49*	65.46**	450.81**	123.66**	1.88*	1.20**	0.77*	1.19*	1.98**	72.57**	189.84**	10.33**
Environment	2	2.41*	11.35**	5.05*	1.72	0.04	0.24**	0.22*	1.92*	0.17**	2.15**	6.78**	1.18*
Var. X Environ.	48	0.73*	0.51	1.80	1.31	0.05*	0.01*	0.01*	0.15*	0.06*	0.24*	1.56**	0.08*
Env. +Var. X Env.	50	0.80	0.95	1.93	1.33	0.05*	0.02*	0.03*	0.48*	0.04**	0.13	0.33	0.01*
Env. (Linear)	1	4.86**	22.64**	10.10*	3.45*	0.08*	0.49**	0.02*	0.22	0.07**	0.32*	1.77	0.13*
Env. X Var. (Linear)	24	0.85*	0.43	0.91	0.81	0.07*	0.02*	0.44*	3.85*	0.33**	4.32**	13.57*	2.35*
Pooled Deviation	25	19.49*	65.46**	450.81**	123.66**	1.88*	1.20**	0.02*	0.17*	0.06	0.23	1.89*	0.13*
Pooled Error	144	2.41*	11.35**	5.05*	1.72	0.04	0.24**	0.00	0.12	0.07	0.24	1.18	0.03

\*, \*\* significant at 5% and 1% level, respectively

**Table-7 Estimates of stability parameters for seed yield and its components in Greengram as per Eberhart and Russell's (1966)**

S.L.	Genotype	Days to 50% flowering			Days to maturity			Plant height (cm)			Number of pods per plant		
		Mean	bi	S <sup>2</sup> di	Mean	bi	S <sup>2</sup> di	Mean	Bi	S <sup>2</sup> di	Mean	bi	S <sup>2</sup> di
1	Pusa Baisakhi	34.33	-0.95	-0.46	71.11	0.33	0.09	61.14	0.83	3.47	18.29	-1.29	-0.94
2	Pusa Vishal	35.44	0.23	-0.46	71.56	0.30	0.02	41.78	0.56	0.39	24.78	0.94	1.55
3	Pusa 371	34.67	-0.93	-0.24	70.11	-0.96	1.10	57.36	1.06	0.74	22.16	-2.01	0.67
4	RMG 991	33.67	5.46	-0.36	69.44	0.49	0.28	54.98	-1.30	0.82	19.42	-0.17	-0.68
5	RMG 975	39.44	-0.71	-0.40	68.00	0.52	0.23	59.11	1.01	1.68	21.84	4.42	1.68
6	Pusa 1431	40.00	-2.79	1.59*	72.56	0.30	0.02	53.27	-1.67	1.27	20.13	0.99	-0.84
7	ML 1451	41.00	2.70	-0.45	76.00	1.25	0.51	52.11	1.48	0.23	22.38	-1.85	0.22
8	IPM 99-125	38.56	1.49	-0.25	70.44	0.49	0.28	61.84	-0.18	0.61	28.73	-3.47	0.42

9	IPM 02 - 19	35.78	0.23	-0.46	69.78	-0.15	0.27	66.82	1.46	- 1.38	25.89	-0.40	-0.86
10	Pusa 672	36.89	-3.18	-0.42	71.78	1.43	0.51	71.80	1.63	1.66	24.69	0.95	1.18
11	TM 96 - 25	36.22	0.36	-0.24	66.67	0.21	0.34	70.78	0.89	1.69	21.20	4.17	7.16*
12	MH 02 - 15	36.56	-0.43	0.44	71.00	-1.05	0.54	75.29	2.92	- 1.63	15.38	-0.74	-0.22
13	Pusa 9531	41.44	2.06	-0.20	70.78	-0.92	0.31	61.51	1.50	- 0.65	16.96	4.23	-0.60
14	WGG 37	38.22	-1.26	0.94	65.00	-1.01	0.83	69.53	1.02	2.43	21.07	2.79	0.87
15	Pusa 16	39.89	1.39	1.61*	82.00	-0.42	0.20	56.00	-1.73	- 0.99	19.02	0.05	-0.51
16	PDM 96 - 262	40.22	-0.37	-0.24	81.44	0.06	1.59	46.87	-4.34	- 1.66	20.47	-2.14	0.03
17	BDRY 1	36.78	-0.93	-0.05	80.33	-0.32	0.57	60.29	0.87	1.69	28.69	0.93	0.52
18	MH 218	36.00	-1.94	-0.41	68.00	-0.83	0.47	61.96	0.17	- 1.65	19.87	1.67	-0.39
19	AKM 9904	41.22	0.53	-0.39	79.33	-0.53	0.55	50.18	-0.96	1.12	26.62	1.02	0.62
20	COGG 912	33.56	-2.28	0.41	69.11	-0.72	0.57	61.42	0.97	1.94	20.67	2.12	-0.08
21	RMG 90	38.78	2.13	0.38	71.89	0.03	0.57	47.91	-0.79	3.26	36.60	1.04	0.93
22	MH 521	34.67	-3.77	-0.40	67.67	0.41	0.38	36.02	-0.73	- 1.67	43.87	0.95	-0.91
23	NDM 6	41.00	2.65	0.50	77.89	-0.70	0.13	33.51	-0.55	- 1.59	32.60	0.89	-0.21
24	HUM 12	36.22	-0.80	-0.40	72.11	-0.91	0.18	35.09	-0.61	- 1.57	25.56	-3.50	-0.93
25	MH 0891	38.44	0.32	3.05*	74.33	-0.16	0.54	79.60	0.28	- 1.60	28.42	0.27	-0.57
	Population mean	37.68			72.33			57.05			24.21		
	Se (mean)	0.542			0.533			1.136			0.932		
	SE (b)		0.730	1.30		0.792	1.72		1.530	5.07		0.355	2.82

Table-7.Cont.....

S.L.	Genotype	Number of clusters per plant			Pod length (cm)			Number of pods per cluster			Number of seeds per pod		
		Mean	Bi	S <sup>2</sup> di	Mean	bi	S <sup>2</sup> di	Mean	Bi	S <sup>2</sup> di	Mean	bi	S <sup>2</sup> di
1	Pusa Baisakhi	6.51	0.91	0.05	6.72	-1.17	-0.01	3.81	0.14	-0.01	12.04	1.02	-
2	Pusa Vishal	5.30	7.66	-0.04	7.69	1.09	0.02*	4.61	0.14	-0.01	10.83	0.26	-
3	Pusa 371	5.56	-2.94	-0.04	7.61	0.80	-0.01	3.28	0.74	-0.01	10.87	1.58	-
4	RMG 991	5.87	5.01	-0.02	7.22	0.27	0.01	4.26	-0.21	-0.01	10.68	0.73	-
5	RMG 975	7.12	4.03	-0.03	6.82	0.11	0.00	4.09	0.01	-0.01	11.72	1.05	-
6	Pusa 1431	6.39	-1.86	-0.02	6.62	-0.82	-0.01	4.39	1.00	-0.01	11.37	0.94	-
7	ML 1451	7.04	2.52	-0.04	7.23	0.92	-0.01	3.99	0.88	-0.01	11.37	1.04	-
8	IPM 99-125	7.83	-0.39	0.01	6.75	-0.12	-0.01	3.97	-0.18	0.00	11.97	0.26	-
9	IPM 02 - 19	5.82	-5.57	-0.03	7.46	-0.54	-0.02	4.27	-1.66	-0.01	10.71	0.49	-
10	Pusa 672	4.90	2.70	-0.04	8.57	-1.84	-0.02	3.70	0.65	0.00	12.18	-1.07	-
11	TM 96 - 25	6.33	2.79	-0.03	6.70	0.49	-0.01	4.17	-1.93	-0.01	11.68	-1.18	-
12	MH 02 -	4.87	1.74	-0.04	8.22	-0.10	-0.01	3.32	-0.98	0.00	10.94	1.15	-

	15												0.13
13	Pusa 9531	4.38	-0.86	-0.04	7.31	1.80	0.01	3.83	0.54	-0.01	10.47	0.73	
14	WGG 37	6.04	2.52	-0.04	6.84	-1.10	-0.02	4.43	1.03	-0.01	10.58	0.31	0.14
15	Pusa 16	5.77	-0.68	-0.04	6.94	0.17	-0.01	3.77	0.54	-0.01	10.57	1.64	0.15
16	PDM 96 - 262	5.28	4.18	0.07	8.06	0.90	-0.01	4.01	0.14	-0.01	11.44	1.06	0.16
17	BDRY 1	6.61	0.95	-0.02	6.04	1.38	-0.01	3.28	1.95	-0.01	10.08	-0.29	0.14
18	MH 218	5.63	-0.68	-0.04	6.78	-0.31	-0.01	3.50	-0.01	-0.01	11.17	-0.06	0.09
19	AKM 9904	6.17	3.75	-0.04	6.54	-0.68	-0.01	2.86	1.71	0.00	12.27	0.56	2.45
20	COGG 912	5.54	-4.33	-0.03	7.47	0.83	-0.01	3.66	-0.27	-0.01	12.33	-0.23	0.14
21	RMG 90	6.50	0.90	0.01	6.01	0.77	-0.01	3.73	0.26	-0.01	11.17	-0.16	0.16
22	MH 521	5.76	-10.00	-0.02	6.79	0.57	-0.01	2.86	0.94	-0.01	11.48	-1.24	0.16
23	NDM 6	5.30	-0.04	-0.03	6.64	0.14	0.00	2.83	-0.07	-0.01	11.70	-1.78	0.16
24	HUM 12	6.87	0.82	0.07	7.44	0.82	-0.01	3.46	0.39	-0.01	10.72	-1.42	0.16
25	MH 0891	5.63	-2.37	-0.04	7.69	-1.71	-0.01	4.32	0.80	-0.01	11.86	-0.14	0.12
	Population mean	5.96			7.13	-1.17		3.77			11.28		
	Se (mean)	0.113			0.062			0.031			0.244		
	SE (b)		1.890	0.13		0.628	0.05		0.332	0.00		0.880	0.12

Table-7. Cont....

S.L.	Genotype	Test Weight (g)			Biological yield per plant (g)			Harvest index (%)			Seed yield per plant (g)		
		Mean	Bi	S <sup>2</sup> di	Mean	bi	S <sup>2</sup> di	Mean	Bi	S <sup>2</sup> di	Mean	bi	S <sup>2</sup> di
1	Pusa Baisakhi	4.09	-0.34	-0.01	29.53	-2.29	0.35	21.25	-0.33	0.38	6.27	-0.77	0.00
2	Pusa Vishal	6.30	8.04	0.72*	28.36	-0.38	0.41	51.83	7.47	3.80*	10.69	0.89	0.15
3	Pusa 371	5.25	0.99	0.00	30.71	0.27	-0.04	26.02	-1.49	0.33	7.99	0.98	0.02
4	RMG 991	5.19	1.03	0.01	21.03	0.66	0.65	35.37	-0.17	2.68*	7.44	0.46	0.00
5	RMG 975	5.05	-0.18	-0.01	26.98	0.33	0.61	27.00	-1.89	0.90	7.28	-0.91	0.00
6	Pusa 1431	4.17	1.26	-0.01	31.37	-1.38	0.25	19.88	1.57	-0.10	6.24	0.87	0.03
7	ML 1451	3.79	1.27	-0.01	35.08	0.92	-0.03	21.15	-0.03	-0.11	7.42	0.64	0.00
8	IPM 99-125	5.44	-3.36	0.30	23.24	0.50	-0.01	34.27	0.92	0.81	7.96	0.85	0.02
9	IPM 02 - 19	4.78	2.90	0.41*	28.00	1.67	0.41	24.34	-0.68	1.94	6.81	-0.08	0.04
10	Pusa 672	6.07	0.94	0.00	33.02	0.98	0.04	27.80	-0.53	1.00	9.18	0.97	0.06*
11	TM 96 - 25	4.24	-1.01	-0.01	26.74	0.47	-0.04	18.10	-0.50	1.61*	4.84	-0.20	0.12
12	MH 02 - 15	4.49	0.77	-0.01	34.91	-0.36	-0.04	20.31	-1.01	-0.10	7.09	-0.82	0.00
13	Pusa 9531	4.17	-0.18	-0.01	37.00	1.03	-0.03	14.65	-0.46	0.21	5.42	0.02	0.05
14	WGG 37	4.53	-0.21	-0.01	21.28	-1.30	0.12	27.29	0.94	0.86	5.80	-0.13	0.08
15	Pusa 16	4.25	-1.26	-0.01	27.07	-0.71	0.05	25.50	1.13	1.56*	6.90	0.63	0.05*
16	PDM 96 - 262	5.25	-2.48	-0.01	19.04	-0.11	-0.04	33.35	1.02	-0.04	6.35	0.79	0.00
17	BDRY 1	3.46	-1.09	-0.01	32.42	1.97	1.46*	22.65	-1.49	1.63*	7.33	-0.71	0.01
18	MH 218	5.17	-0.37	-0.01	23.06	-0.32	0.62*	37.79	0.20	4.16*	8.71	-0.25	0.03
19	AKM 9904	5.18	0.60	-0.01	26.84	0.63	0.17	34.14	-2.30	1.51*	9.16	1.06	0.01
20	COGG 912	5.26	0.47	-0.01	32.04	0.94	0.03	23.10	-0.68	-0.02	7.40	-0.09	0.00
21	RMG 90	3.69	-0.29	-0.01	35.29	0.79	-0.02	21.39	-0.85	-0.07	7.55	-0.34	0.01



22	MH 521	5.29	-0.59	-0.01	29.70	-2.20	-0.04	29.90	0.96	0.03	8.88	0.93	0.03
23	NDM 6	5.37	-0.65	-0.01	30.38	0.02	-0.04	25.73	-0.39	0.29	7.82	-0.26	0.04*
24	HUM 12	6.27	0.83	0.03	35.88	-0.67	0.05	17.36	-0.70	0.36	6.23	-0.56	0.03
25	MH 0891	3.53	-0.71	-0.01	28.80	-0.98	-0.04	27.22	0.92	-0.01	7.84	0.92	0.01
	Population mean	4.81			29.11			26.7			7.54		
	SE (mean)	0.180			0.345			0.767			0.132		
	SE (b)		1.210	0.07		0.175	0.24		0.470	1.18		0.609	0.03

