Journal of Pharmacognosy and Phytochemistry

Available online at www.phytojournal.com

Pavan K
1) Department of Agriculture, Mandsaur University, Mandsaur, Madhya Pradesh, India
2) School of Agriculture Lovely Professional University, Phagwara, Punjab, India

Reddy P
1) Department of Agriculture, Mandsaur University, Mandsaur, Madhya Pradesh, India
2) School of Agriculture Lovely Professional University, Phagwara, Punjab, India

Chandra Mohan Mehta
School of Agriculture Lovely Professional University, Phagwara, Punjab, India

Estimation of variability through genetic parameters and identification of superior pure lines for yield attributing traits in green gram [*Vigna radiata* (L.)]

Pavan K, Reddy P and Chandra Mohan Mehta

Abstract
The entire paper attempts to estimate the variability through genetic parameters and identification of superior pure lines for yield attributing traits in green gram [*Vignaradiata* (L.)] This analysis of data revealed that, existence of highly significant difference among the pure lines for all the traits. The phenotypic coefficient of variation and genotypic coefficient of variation were comparatively high for seed yield per plant, harvest index, pods per plant, cluster per plant, pods per cluster, seeds per pod, pod length and secondary branches. Heritability and genetic advance as per mean estimates were higher for harvest index followed by pods per plant, seed yield per plant, plant height and number of productive branches per plant. The heritability estimates accompanied with genetic advance indicated the predominance of additive gene action. With respect to findings of the experimental work, pure lines viz., HUM-16, Kopergan, Pusa Vishal and LM-05 were identified as superior with respect to yield attributing traits.

Keywords: Genetic Variability, Heritability, Genetic advance, Coefficient of Variation and ANOVA.

Introduction

India is the primary producer of green gram contributes about 75 percent of the world production. In India, mung bean is cultivated as the third major pulse crop after chick pea and red gram. The states, viz, Andhra Pradesh, Maharashtra, Gujarat, Orissa and Tamil Nadu are major producers of green gram. In green gram the low yield is due to many reasons like cultivation in rain fed areas, in unfertile land, low application of fertilizers and lack of superior varieties or hybrids. Yield component characters play important role in the genetic variability. Amount of variability is high in green gram for different characters like flowering, number of days to maturity, plant height, harvest index, number of pods per plant, number of clusters per plant, etc. all this characters were utilized in breeding programs to release good number varieties in green gram. On the other hand these varieties cannot be used for many years due to genetic erosion and susceptibility to pest and diseases. This makes to put forth replacement of old varieties with new developed ones. Main aim of this research is to check genetic variability between the genotypes. Considering the above mentioned information, the present study has been initiated to obtain the precise information on the extent of natural variability in respect of various Attributing Traits in Pure Lines of Green gram.

Genetic Variability

The tendency of individual genetic characteristics in a population is to vary from one another. This is useful in detection of variation between the genotypes of working population. There are so many studies been conducted to evaluate the genetic variability among different genotypes of green gram More than fifty genotypes of green gram for genetic variability was analyzed by, Logan than *et al.* (2001b). High phenotypic coefficient of variability indicated the favorable effect of environment for number of clusters per plant and seed yield per plant and high genotypic coefficient of variability, suggested substantial amount of genetic variability

Correspondence
Pavan K
1) Department of Agriculture, Mandsaur University, Mandsaur, Madhya Pradesh, India
2) School of Agriculture Lovely Professional University, Phagwara, Punjab, India

for number of pods per plant and seed yield per plant. Similarly another study of Venkateswarlu, (2001) [11] reports that seed yield expressed, high genotypic coefficient of variation coupled with high heritability and genetic advance. While, comparing variability parameters of green gram, a large differences between phenotypic and genotypic coefficients of variability, were observed for root length, number of secondary roots per plant and root shoot ratio, indicating that these characters are influenced by environment, Chakrabarty et al. (2001).

Even thoughthe genotypes differed significantly for all characters studied. Higher genotypic coefficient of variation and phenotypic coefficient of variation, was observed for harvest index followed by biological yield per plant, Gadakh SS et al. (2013) [3]. Phenotypic coefficient of variation was slightly higher in magnitude than the genotypic coefficient of variation, Kumar et al. (2013). But dominant variance, were more pronounced except, for the traits like plant height, pod cluster per plants, pods per plant, 100 seed weight and yield per plant indicating the importance of dominant gene effects for those traits. Partial, dominance was observed for plant height, number of pods per plant and yield, per plant, P.S. Bainade et al. (2014) [1].

Heritability and Genetic advance
High heritability, coupled with high genetic advance was observed in pods per plant, plant height and test weight indicating the importance, of additive gene effect for expression of these characters Makeen et al., (2007) [8]. The magnitude of phenotypic coefficients of variation was higher than genotypic coefficients of variation for all the traits showing greater influence of environment, on these traits with the finding of by, Siddique et al. (2006) [14] and Makeen et al. (2007) [8] who also reported similar effects of environment. Jagadeesan et al. (2008) [5] and Tah, (2009) [16] who reported high heritability and partial agree, with, Neha et al. (2005) [9] and Veeramani et al. (2005) [17] and also the heritability estimates for different characters in green gram were in broad agreement with reports of Idress et al. (2006) [4]; Tabasum et al.,(2010) [15]; Rahim et al.(2010) [10]; Reddy et al.(2011) [11]; Makeen et al.(2007) [8]; Roychowdhury et al.(2012) [12]. High heritability, associated with high expected genetic advance, observed for harvest index, pods per plant, seed yield per plant, plant height, and number of productive branches per plant revealed preponderance of these traits.
Heritability in conjunction with genetic advance, is more useful than heritability alone in the prediction of resultant effect of selecting the best individual, Johnson et al. (1955) [6] and Singh et al.(2010).On the basis of genetic variability study only 100 seed weight exhibited, high heritability estimates (narrow sense) coupled with high genetic advance, indicating the preponderance of additive gene action, Kumar et al.(2013). High heritability and genetic advance, was observed in biological yield per plant, harvest index and number of pods per plant indicating the impact of additive, gene affecting expression of three characters, Gadakh. S.S et al. (2013) [3]. High heritability, coupled with high expected genetic advance was observed in seed yield per plant indicating the impact of additive gene expression, Sheetal Patel, (2014) [13].

Materials and Methods
The experimental research on green gram titled 'Estimation of Variability through Genetic Parameters and Identification of Superior Pure Lines for Yield Attributing Traits in Green Gram [*Vigna Radiata* (L.)]' was conducted during the *Summer* season of 2016-2017, in main experimental form of Lovely Professional University, Phagwara, Kapurthala (district), Punjab at the latitude and longitude range of 31.2554° N and 75.7058° E respectively, following detailed plan of work. Each genotype was space planted in row plot of 5m length, having spacing of 40 cm × 10 cm, following row method in replication, to keep the plant population at optimum level. The experimental area occupied was quite uniform in respect of topography and fertility with sandy loam soil. Recommended agronomic practices were followed to have a good crop. The particulars of materials and methods used during these experimental trail and the statistical procedures followed were listed below.

Experimental Materials
The material used for the experiment consists of 13 genetically diverse genotypes which are obtained from the source Banaras Hindu University, Varanasi and from Punjab Agricultural University, Ludhiana. The list of genotypes and their source is listed below.

Genotypes and their source
Genotypes: Pusa Vishal, HUM 12, HUM 8, Kopergan, HUM 16, ML 720, LM 5, LG 420, IPM 2, PUSA 4061, HUM 1 from BHU, Varanasi and Moongi, Gold from PAU, Ludhiana.

Experimental methods
Summer season, 2016-17
Totally, 13 genotypes are considered for the experiment. These genotypes were sown in a single day in all three replications. Standard agronomic practices were followed to raise the crop. The seeds of each genotype were harvested separately from each replication to analyze the genetic variability, correlation and path analysis.

Harvest Index
Harvest index was calculated by,

$$\text{Economic yield} = \frac{\text{Harvest index}}{\text{Biological yield}} \times 100$$

1000 grain weight (g)
One thousand threshed grains will be take randomly after sun drying at 12% moisture level and weighted in gram with the help of electric balance.

Statistical Analysis
The mean values of five randomly selected observational plants for ten different characters were used for statistical analysis. The following statistical parameters were calculated for presentation of data on different quantitative attributes.

Analysis of variance (ANOVA)
The analysis of variance (ANOVA) was calculated as proposed by Sukhatme and Panse (1985) in the following format:

Table 1: ANOVA

Sr No.	Source of variation	Degrees of freedom	Expected mean sum of squares
1	Replication	r-1	$\sigma^2 e + t\sigma^2 r$
2	Treatment	t-1	$\sigma^2 e + r\sigma^2 t$
3	Error	(r-1) (t-1)	$\sigma^2 e$
4	Total	(rt-1)	

Whereas, r = number of replications t = number of treatments

Genotypic coefficient of variation (GCV)
The gcv was estimated by the formula proposed by Burton (1952).

$$GCV = \sqrt{\sigma^2 g} \,/\, 8 \; X \; 100$$

Where $\sigma^2 g$ = Vg = genotypic variance
8 = general mean of the character

Phenotypic Coefficient of Variation (PCV)

$$PCV = \sqrt{\sigma^2 p} \,/\, 8 \; X \; 100$$

$\sigma^2 p$ =Vp = phenotypic variance
8 = general mean of the character.

Heritability percentage
Heritability percentage in broad sense calculated as suggested by Burton (1952).
h² (bs) = heritability percentage in broad sense

$$h^2 (BS) \% = \frac{\sigma^2 g}{\sigma^2 p} \; x \; 100$$

Whereas, $\sigma^2 p$ = phenotypic variance; $\sigma^2 g$ = genotypic variance

Genetic advance
Genetic advance was calculated by the formula proposed by Johnson et al (1955) [6].

$$G\,A = k \; x \; (\sigma^2 g \,/\, \sigma^2 p) \; x \; \sigma p \quad Or \quad G\,A = k \; x \; h^2 \; x \; \sigma p$$

Where, K = selection differential which is 2.06 at 5 percent selection intensity

$\sigma^2 g$ = Vg = Genotypic variance; $\sigma^2 p$ = Vp = Phenotypic variance

Experimental Results
The current experiment on green gram [*Vignaradiata* (L.)Wilzeck] with 13 genotypes were done to understand the genetic variability, correlation and path analysis in *summer* season 2017. Several parameters were considered and the results obtained from observations were represented in this section.

Analysis of Variance
The 13 characters which were included in this experimental work showed highly significant differences through analysis of variance were shown in the table 2.

Table 2: Analysis of variance - green gram in 13 different characters.

Sl no.	Characters	Mean sum of squares		
		Replications (R)	Treatment (T)	Error (E)
1	Days to 50% flowering	11.0833	21.7564**	4.4583
2	Days to maturity	15.6987	19.3974	7.5320
3	Pri, branches per plant	0.1116	0.1965	0.0754
4	Sec. branches per plant	0.7033	2.1485	0.7627
5	Clusters per plant	0.2471	3.8502**	0.6271
6	Pods per cluster	0.1323	1.0085**	0.1567
7	Plant height (cm)	0.9155	12.4818	4.2030
8	Pod length (cm)	0.4430	1.9564	0.6569
9	Pods per plant	19.9017	174.700**	10.5501
10	Seeds per pod	2.0392	3.9778*	0.9903
11	Test weight	0.1187	0.3797**	0.0534
12	Seed yield per plant	3.2215	41.5776**	2.7790
13	Harvest index	227.821*	882.954**	60.7774

'*' and '**' denotes significance at 5% and 1% level of probability respectively.

Days to 50% flowering
This character had a population mean of 67.17and Kopergan (62.33), LM-5 (62.33) were the genotypes in which flowering was early, followed by HUM-16 (65.33), Pusa Vishal (65.66), HUM-12, IPM-2 and HUM-08. Some required very less time to 50% flowering compared to mean of population they are Kopergan (62.33), LM-05(62.33), HUM-16 (65.33), Pusa Vishal (65.66) and HUM-12 (66.66). The genotypes LG-420 (70.33), HUM-01 (70.33) followed by Pusa-460(69.66), ML-720 (69.66), IPM-02(67.33) and HUM-08(67.66) were the

one to flower late when compared with mean.

Days to maturity
The character had a population mean of 99.25. The first matured genotype was LM-05 (95.00) followed by Kopergan (96.33), HUM-16 (97.00), Gold (97.33), IPM-02 (97.66) and Moongi (98.33). There are some genotypes which had early maturity than population mean LM-05 (95.00), Kopergan (96.33), HUM-16 (97.00), Gold (97.33), IPM-02 (97.66) and Moongi (98.33). The genotypes which were lately matured

were listed as LG-420 (102.66), Pusa-460 (102.33), ML-720 (102.00) followed by HUM-08 (101.66), HUM-01 (101.33), HUM-12 (99.33) and Pusa Vishal (99.33).

Plant height (cm)
In this character out of 13 genotypes, the mean population was evaluated as 30.83. The maximum plat height was recorded by a genotype Pusa-460 (34.33), followed byLM-05 (33.97), HUM-08 and Pusa Vishal. The dwarf genotype was HUM-12 (27.53). Along with this some plants had recorded less than the populations mean, they are HUM-01 (28.70), Moongi (29.33), LG-420 (29.73), HUM-16 (29.83), Kopergan (30.00), Gold (30.66) and ML-720 (30.68).

Number of primary branches
The character got the mean population as 4.97. The variation of primary branches ranged as 4.33 to 5.40.Pusa Vishal (5.40), ML-720 (5.23), LG-420 (5.13), Pusa-460 (5.00), LM-05 (5.00), HUM-16 (5.00) and HUM-08 (5.00) weregenotypes given rise to more number of primary branches than the mean. Out of 13 genotypes, 4wereshown profuse branching than the population mean. The genotype type with less primary branches was Moongi (4.33)

Number of secondary branches:
The population mean of this character was 6.51. The variation of secondary branches ranged as 4.53 to 7.80. The genotype Moongi (7.80) recorded highest number of secondary branches which was followed by HUM-16 (7.46), ML-720 (7.40), Pusa-460 (6.86), LG-420 (6.80), Gold (6.66) and HUM-01 (6.60). Out of 13 genotypes, 4 genotypes given rise to more secondary branches compared to mean.

Length of Pod
This character recorded population mean as 7.21. The range of variation among the genotypes was 5.32 to 8.62. The genotypesHUM-16(8.62) showed the highest pod length which was followed by genotypes HUM-01(8.20), LM-05(7.97), Pusa Vishal (7.46), LG-420(7.33) and Moongi (7.24). The genotype HUM-12(5.32) recorded smallest pod length, which were also followed by HUM-08(6.73), Gold (6.74), Pusa-460(6.91), IPM-02(6.95) recorded less pod length then mean.

Number of pods per plant
More number of pods were harvested from the genotype Kopergan (44.20), followed by LM-05(37.60), Pusa Vishal (36.06), HUM-16(32.66). The population means of this character was 27.73. Some genotypes had recorded lowest number of pods harvested from them compared to population mean they are HUM-12(16.66), HUM-01(21.23), IPM-02(23.60), HUM-08(23.80), ML-720(24.53), LG-420(24.66), Pusa-460(25.13), Moongi (25.20), Gold (25.20). Out of 13 genotypes, 5 genotypes were recorded lowest number of pods harvested from them.

Number of seeds per pod
Out of 13 genotypes, 4 genotypes such as HUM-16 (10.18), HUM-01 (9.33), IPM-02 (8.73) and ML-720 recorded more number of seeds per pod than population mean. The population mean for this character was 8.08. The genotype HUM-12 recorded with least number of seeds per pod.

Number of pods per cluster
The population mean of this character was 3.84. The inbreed lines like LM-05(4.73), HUM-16(4.53), HUM-08(4.53), Pusa Vishal (4.46) and Kopergan (4.46) recorded more number of pods. Among 13 genotypes only 5 produced more number of pods than the population mean. The inbreed line HUM-01(3.00) had very least number of pods per cluster.

Number of clusters per plant
The population mean of this character was7.23. The inbreed line Kopergan (9.00) showed maximum number of clusters per plant, followed by Pusa-460(8.40), Moongi (8.13), LM-05(8.06), Pusa Vishal(7.80), Gold(7.26), LG-420(7.26) and HUM-16(7.26). Among 13 inbreed lines only 4had more number of clusters per plant compared to population mean. The genotype HUM-12(5.33) had very least number of clusters per plant.

Yield per plant
Out of 13 genotypes only 4 had recorded high yield per plant than the population mean. The population mean of this character was 11.62. The inbreed line HUM-16(18.03) showed highest yield per plant, followed by Kopergan (17.31), Pusa Vishal (15.36), LM-05(12.88). The range of variation among the inbreed lines was 3.95 to 18.03.

100 Seed Test weight (gm)
The mean of population was 5.06. Out of 13 genotypes, 10 genotypes were shown highest test weight than the population mean. The genotype Pusa Vishal (5.41) shown test weight higher, followed by HUM-16(5.39), Gold (5.37), LG-420(5.33), Pusa-460(5.27), ML-720(5.23), Kopergan (5.20), IPM-02(5.11) and HUM-01(5.16). Minimum test weight was recorded by the genotype LM-05(4.37).

Table 3: Mean performance of green gram genotypes for 13 different characters
P = name of the pure lines

Sl no	P1	P2	P3	P4	P5	P6	P7	P8	P9	P10	P11	P12	P13
Kopergan	62.33	96.33	4.86	6.43	9.00	4.46	7.50	30.06	7.06	44.20	17.31	5.20	73.26
PusaVishal	65.66	99.33	5.40	6.26	7.80	4.46	7.70	32.08	7.46	36.06	15.36	5.41	74.00
LM-05	62.33	95.00	5.00	5.93	8.06	4.73	7.97	33.97	7.7	37.60	12.88	4.37	60.96
HUM-16	65.33	97.00	5.00	7.46	7.26	4.53	10.18	29.83	8.62	32.66	18.03	5.39	88.70
HUM-12	66.66	99.33	4.80	4.53	5.00	3.60	5.33	27.53	5.32	16.66	3.95	4.60	33.43
HUM-08	67.66	101.66	5.00	5.86	5.33	4.53	7.70	33.20	6.73	23.80	10.25	4.62	72.80
ML-720	69.66	102.00	5.23	7.40	6.0	3.66	8.60	30.68	7.27	24.53	10.98	5.23	46.36
LG-420	70.33	102.66	5.3	6.80	7.26	3.53	7.46	29.73	7.33	24.66	9.92	5.33	35.96
IPM-02	67.33	97.66	5.13	6.00	6.73	3.46	8.73	30.73	6.95	23.60	10.82	5.11	70.66
Pusa-460	69.66	102.33	5.00	6.86	8.40	3.20	8.43	34.33	6.1	25.13	11.14	5.27	48.36
HUM-01	70.33	101.33	4.93	6.60	7.00	3.00	9.33	28.70	8.20	21.23	10.75	5.16	67.43
Gold	68.33	97.33	4.80	6.66	7.26	3.53	8.56	30.66	6.74	25.20	11.52	5.37	54.33

Moongi	67.66	98.33	4.33	7.80	8.13	3.26	7.53	29.33	7.24	25.20	8.21	4.69	40.53
Mean	67.17	99.25	4.97	6.51	7.23	3.84	8.08	30.83	7.2	27.73	11.62	5.06	58.98
S.E±	1.21	1.58	0.15	0.50	0.45	0.22	0.57	1.18	0.46	1.87	0.96	0.13	4.50
C.D 5%	3.55	4.62	0.46	1.47	1.33	0.66	1.67	3.45	1.36	5.47	2.80	0.38	13.13
C.D 1%	4.82	6.26	0.62	1.99	1.80	0.90	2.27	4.68	1.85	7.41	3.95	4.37	33.43

Whereas, P1 =days to 50% flowering, P2 =days to maturity, P3 =primary branches per plant, P4 =secondary branches per plant, P5 =clusters per plant, P6 =pods per cluster, P7 =seeds per pod, P8 =plant height (cm), P9 =pod length (cm), P10 =pods per plant, P11 =seed yield per plant, P12 =test weight and P13 =harvest index (%) S.E= standard error;C.D 5% and 1% = critical difference

Harvest Index

The population mean of this character was 58.98. The range of variation among this genotypes was 33.43 to 88.70. Compared to mean, out of 13 genotypes only 4 genotypes were recorded highest harvest index. The genotypes such as HUM-16(88.70), Pusa Vishal (74.00), Kopergan (73.26), HUM-08(72.80), IPM-02(70.66), HUM-01(67.43) and LM-05(60.96) showed highest harvest index.

Parameters of genetic variability

Table 4: Traits showing Genetic Parameters of Variability 2017:

Sl.no	Characters	Range	G.M	GCV	PCV	Heritability (bs) (%)	G.A	G.A as 5% of mean
1.	D T F 50%	62.33–70.33	67.17	3.57	4.76	56.4	3.71	5.53
2.	D T M	95.00–102.66	99.25	2.00	3.41	34.4	2.40	2.42
3.	Pri. branches/ plant	4.33-5.40	4.97	4.04	6.84	34.8	0.24	4.9
4.	Sec. branches/ plant	4.53-7.80	6.51	10.44	16.99	37.7	0.86	13.20
5.	Clusters/ plant	5.00-9.00	7.23	14.32	18.02	63.1	1.69	23.44
6.	Pods per cluster	3.00-4.73	3.84	14.58	17.85	66.8	0.94	24.54
7.	Seeds / pod	5.33-10.18	8.08	12.34	17.43	50.1	1.45	18.01
8.	Plant height (cm)	27.53-34.33	30.83	5.38	8.55	39.6	2.154	6.98
9.	Pod length (cm)	5.32-8.62	7.21	9.11	14.46	39.7	0.85	11.83
10.	Pods / plant	16.66-44.20	27.73	26.67	29.12	83.8	13.95	50.30
11.	Seed yield / plant	3.95-8.03	11.62	30.92	34.09	82.3	6.72	57.80
12.	100 seed wt (gm)	4.37-5.41	5.06	6.51	7.95	67.1	0.55	10.99
13.	Harvest index (%)	33.43-88.70	58.98	28.06	31.02	81.8	30.85	52.30

G.M= general mean; GCV= genotypic coefficient of variation; PCV= phenotypic coefficient variation; bs = broad sense; G.A= genetic advance.

Variation coefficient

The estimates of GCV (genotypic coefficient of variation) were lower than the PCV (phenotypic coefficient of variation) in the experiment for all the characters for all characters. The highest GCV was recorded for yield per plant (30.92), followed by harvest index (28.06), pods per plant (26.66)., pods per cluster (14.58), cluster per plant (14.32), seeds per pod (12.34), sec. branches per plant (10.43), pod length in cm (9.11), 100 seed weight (6.51), plant height in cm (5.38), primary branches per plant (4.04), days to 50 percent flowering (3.57) and days to maturity(2.00). The maximum PCV was shown by the characters pods per plant (29.12), clusters per plant (18.02), pods per cluster (17.85) seeds per pod (17.43), secondary branches per plant (16.99), pod length in cm (14.46) and plant height in cm (8.55).

The highest magnitudinal differences among the GCV and PCV were shown to the character secondary branches per plant(10.44 and 16.99 respectively) followed by pod length, seeds per pod, clusters per plant, pods per cluster and plant height in cm. The character days to 50% flowering had the minimal differences between the GCV and PCV.

Heritability Percentage (broad sense)

The estimates of heritability varied as 34.4 (days to maturity) and 83.8 (pods per plant). The character pods per plant (83.8) had the highest heritability which was followed by yield per plant (82.3), harvest index (81.8), test weight (67.1) and pods per cluster (66.8). The character days to maturity (34.4) had recorded lowest heritability which was followed by primary branches per plant (34.8), secondary branches per plant (37.7), plant height (39.6), pod length (39.7) and seeds per pod (50.1).

Genetic advance as 5% of mean

The highest Genetic advance as percent of mean 5% was shown in the character yield per plant(57.80), harvest index(52.30), pods per plant(50.30), pods per cluster(24.54) and clusters per plant(23.44).The character days to maturity(2.42) exhibited lowest genetic advance as mean of 5%. However yield per plant (57.80) and harvest index (52.30) recorded high genetic advance as mean of 5% accompanied with higher genetic variability's.

High values of genetic advance were observed in the characters harvest index (30.85), pods per plant (13.95) and yield per plant (6.72). Whereas primary branches per plant (0.24), test weight (0.55), pod length (0.85), secondary branches per plant (0.86) and pods per cluster (0.94) recorded lowest genetic advance.

Discussion of Results

Any experimental work related with plant breeding success depends on selection of exclusive genotypes and also knowledge of genetic diversity and variability of the germplasm which is selected. For a particular character, GCV and PCV measure the extent of variation present in a population. Transmission of character from parents to their off springs will be indicated by heritability and it is also very important to determine the phenotypic characters in the off springs were transferred from the parents or due to environmental effect. Best selection is possible when heritability combines with genetic advance.

Variability

During experimental work considerable variation was

observed in all the 13 characters evaluated. The variability range of yield per plant ranged between 3.95 g to 18.03 with a mean of 11.62. As well as other yield related characters had also shown considerable variability such as days to 50 percent flowering(62.33 to 70.33),days to maturity(95.00 to 102.66), plant height in cm (27.53 cm to 34.33), number of primary branches(4.33 to 5.40), number of secondary branches(4.53 to 7.80), number of clusters (5.00 to 9.00), number of pods per cluster (3.00 to 4.73), number of pods per plant (16.66 to 44.20), pod length (5.32 to 8.62), seeds per pod (5.33 to 10.18), 100 seed weight (4.37 to 5.41) and harvest index (33.43 to 88.70).This range of variability is similar with the characters days to 50% flowering, days to maturity, plant height (cm), number of productive, branches per plant, number of productive pods per plant, number of seeds per pod, harvest index and seeds per plant (g), plant height, pods per plant, total plant weight and seed yield,, Aqsa Tab sum, (2010) [15]. Within the 13 genotypes of green gram for the character days to 50 percent flowering- HUM-01, character days to maturity- LG-420, number of primary branches- Pusa Vishal, number of secondary branches- Moongi, number of clusters per plant- Kopergan, number of pods per cluster- LM-05, number of pods per plant- Kopergan, pod length in cm- HUM-16, seeds per pod- HUM-16, 100 seed weight in gm- HUM-16, harvest index% -HUM-16 recorded highest per se performance for respective characters. The estimates of PCV were magnitudinally higher than the estimates of GCV for all the characters indicating the environmental influence factor on these traits.

The estimates of GCV and PCV were of high magnitude for seed yield per plant, harvest index and number of pods per plant indicating fine scope for improvement through selection. These confirmed on the findingfor seed yield per plant and pods per plant. The characters like seed yield per plant, harvest index and number of pods per plant had high estimates of PCV, while for the characters like seed yield per plant, harvest index and pods per plant, pods per cluster, clusters per plant and seed per pod had high estimates of GCV. Whereas, the estimates of GCV and PCV were, moderate in pod length in cm and number of secondary branches per plant. The PCV estimates were high for the characters seed yield per plant, harvest index and number of pods per plant. The GCV estimates were higher in the characters like seed yield per plant, harvest index and pods per plant. These results are opposite to the finding of Kumar et al. (2013). In yield per plant character, the magnitude of GCV was lower than that of PCV. The magnitude of phenotypic coefficients of variation was higher than genotypic coefficients of variation for all the traits showing greater influence of environment, on these traits with the finding of by, Siddique et al. (2006) [14] and Makeen et al. (2007) [8] who also reported similar effects of environment. But on the characters like secondary branches per plant, seeds per pod, pod length, clusters per plant and seed yield per plant had high magnitudinal difference which was shown that environment played major role in the expression of these characters. While, for other characters like days to maturity and days to 50% flowering, 100 seed weight and harvest index the magnitudinaldifference is low for genotypic coefficient of variation and phenotypic coefficient of variation which shows that less influence of environment on genotypes for the expression of phenotype, during selection only phenotype can be taken into consideration.

Heritability and genetic advance
The effectiveness of selection based on phenotype performance which will estimate high heritability. But that doesn't mean high genetic gain for that trait. Panse, 1957 reported that the characters with high genetic gain may be attributed to the additive gene effects which can be easily improved by selection. On the other side low genetic advance with high heritability endorsed to non-additive genetic action and such characters may be improved through hybridization. In the present investigation the heritability coupled with genetic advance estimates were high, indicating less influence of environment and major role of genotype on the characters pods per plant(83.8), seed yield per plant (82.3), harvest index(81.8) and 100 seed weight (67.1). For the characters like days to maturity (34.4), primary branches per plant (34.8), secondary branches per plant (37.7), plant height (39.6) and pod length (39.0) heritability was comparatively low. This results were similar with the findings Gadakh et al. (2013) [3]. This results are in broad agreement with the high heritability estimates of Idress et al. (2006); Tabasum et al, (2010) [15]; Rahim et al. (2010) [10]; Reddy et al. (2011) [11]; Makeen et al. (2007) [8] and Roychowdhury et al. (2012) [12]. According to Johnson et al. (1955) [6] that the genetic gain will be low when there is no additive gene interaction, whereas genetic advance would be high when there is additive gene interaction. While in the present experimental work high heritability for pods per plant (83.8), seed yield per plant (82.3) and harvest index (81.8) which was accompanied with high genetic advance which shows that high heritability is due to additive gene interaction and for improving such traits simple selection is practiced. This shows that heritability coupled with genetic advance gives best result instead of heterosis alone Johnson et al. (1955) [6] and Singh et al. (2010). This are similar with the finding of Sheetal Patel, (2014) [13], high heritability, coupled with high expected genetic advance was observed in seed yield per plant indicating the impact of additive gene expression and for the character pods per plant also similar with Chakraborty et al. (2001), but were opposite to the findings of Loganathan et al. (2001b) [7].

Summary and Conclusion
Thirteen genotypes were collected from Banaras Hindu University, Varanasi as well as from Punjab Agricultural University, Ludhiana. The experimental plot was laid out in the experimental farm with three replications in *summer* season, 2017. All these genotypes are evaluated under 13 yield attributing characters viz., days to 50 percent flowering, days to maturity, number of primary branches, number of secondary branches, number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod, plant height (cm), pod length (cm), seed yield per plant (gm), test weight (gm) and harvest index in percent.

Significant treatment squares of mean for all characters revealed that the characters which were studied has considerable amount of variability in the evaluated genotypes. The magnitude of PCV and GCV were high for seed yield per plant, pods per plant, clusters per plant, pods per cluster, seeds per pod, secondary branches per plant and pod length indicating presence of good amount of variability per plant. Whereas, average amount of PCV and GCV was obtained to the characters pod length, plant height and 100 seed weight. But for the characters days to maturity, days to 50% flowering and primary branches per planthad shown very less GCV and

PCV. Whereas, for the characters secondary branches per plant, number of seeds per pod, pod length and clusters per plant had recorded high magnitudinal difference between PCV and GCV. High magnitude of heritability was recorded for the character pods per plant followed by seed yield per plant, pods per cluster and clusters per plant test weight. High heritability coupled with high genetic advance was observed for the character pods per plant and seed yield per plant, suggest the role of additive gene effect and possibility of achieving high genetic progress through selection. With respect to findings of the present experimental work, pure lines viz., HUM-16, Kopergan, Pusa Vishal and LM-05, were identified as superior recombinant pure lines with respect to yield attributing traits.

References
1. Bainade PS, Manjare MR, Deshmukh SG, Kumbhar SD. Genetic Analysis in Green Gram [*Vignaradiata* (L.)Wilczek] subjected to North Carolina Mating Design-1, Department of Agricultural Botany, MPKV, Rahuri. The Bioscan. 2014; 9(2):875-878.
2. Chakraborty S, Borah B, Borah H,Pathak D, Kalita H, Barman B. Genetic Correlation and Coheritability between F1 and F2 Generations for Quantitative Traits in Crosses of Green Gram [*Vigna radiata* (L.) Wilczek]. Assam Agriculture Research Institute. *Acta Agronomica Hungarica.* 2011, 59(1).
3. Gadakh SS, Dethe AM, Kathale MN, Kahate NS. Genetic diversity for yield and its component traits in green gram [*Vigna radiata* L. Wilczek], Journal of Crop and Weed. 2013; 9(1):106-109.
4. Idress A, Sadiq MS, Hanif M, Abbas G, Haider S. Genetic Analysis and Path Coefficient Analysis in Mutated Generation of Mungbean.[*Vignaradiata* (L.)Wilczek]. Agricultural Research. 2006; 44:181-191.
5. Jagadeesan, Kandasamy SG, Manivannan N, Muralidharan V. Mean and variability studies in M1 and M2 generations of sunflower (*Helianthus annuus* L.). 2008; 31(49):71-78.
6. Johnson HF, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybean. Agronomy Journal. 1995; 47:314-318.
7. Loganathan P, Saravanan PK, Ganeasan J. Genetic variability in green gram [*Vigna radiata* (L.)Wilczek] Research Crops. 2001b; 2(3):396-397.
8. Makeen K, Abrahim G, Jan A, Singh AK. Genetic variability and correlations studies on yield and its components in mungbean (Vignaradiata (L.) Wilczek). J. Agron. 2007; 6(1):216-218.
9. Neha J, Sarvjeet S, Inderjit S. Variability and association studies in lentil. Indian Journal of Pulses Research. 2005; 18:1444-146.
10. Rahim MA, Mia AA, Mahmud F, Zeba N, Afrin KS. Genetic variability, character association and genetic divergence in mungbean (*Vigna radiata* L. Wilczek*).* Plant Omics Journal. 2010; 3:1-6
11. Reddy DKR, Venkateswarlu O, Obaiah MC, Jyothi GLS. Studies on genetic variability, character association and path-coefficient analysis in greengram. Legume Research. 2011; 34(3):202-206.
12. Roychowdhury R, Datta S, Gupta P, Tah J, Analysis of genetic parameters on mutant populations of mungbean[*Vigna radiata* (L.)Wilczek] after ethyl methyl sulphonate treatment, *Notulae Scientia Biologicae*, 2012; 4(1):137-143.
13. Sheetal R, Patel Patel KK, Hitiksha, K Parmar. Genetic Variability, Correlation and Path Analysis for Seed Yield and its Components in Green Gram [*Vignaradiata* (L.)Wilczek].Anand Agricultural University, Anand. The Bioscan. 2014; 9(4):1847-1852.
14. Siddique M, Faisal M, Anwar M, Shahid IA. Genetic divergence, association and performance evaluation of different genotypes of mungbean (*Vigna radiata*). International Journal of Agricultural Biology. 2006; 6:793-795.
15. Tabasum A, Saleem M, Aziz I. Genetic variability, trait association and path analysis of yield and yield components in mungbean [*Vignaradiata* (L.)Wilczek]. Pakistan Journal of Botany. 2010; 42:3915-3924.
16. Tah PR, Saxena S. Induced synchrony in pod maturity in mungbean (*Vigna radiata*). International Journal of Agricultural. Biology. 2009; 11:321–324.
17. Veeramani, Venkatesan NM, Thangavel P, Ganesan J. Genetic variability, heritability and gentic advance analysis in segregating generation of black gram (*Vigna mungo* L. Hepper). Legume research. 2005; 28(1):49-51.