

## Genetic Variability of Mung Bean for Yield and Yield Contributing Traits

Umesh Kumar Singh\* and Lalji Bharti

<sup>1</sup>Assistant Professor, Department of Plant Breeding & Genetics,  
Dr. Rajendra Prasad Central Agricultural University, Pusa, Samastipur (Bihar), India.

<sup>2</sup>M.Sc. Scholar, Department of Plant Breeding & Genetics,  
Dr. Rajendra Prasad Central Agricultural University, Pusa, Samastipur (Bihar), India.

(Corresponding author: Umesh Kumar Singh\*)

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**ABSTRACT:** Production potential of mung bean is greatly reduced due to abiotic stress like drought. The optimum temperatures for germination of this crop is 25 to 30°C. The temperature is of key importance for plant development, influencing the rate of photosynthesis, flowering and even pod setting or grain filling. High temperature stress during germination and flowering and drought and salinity stresses during entire life cycle of crop cause considerable yield losses in mung bean. Global warming is posing a great threat to the modern agriculture. Due to abrupt increase in environmental temperature; production of majority of the crops including mung bean is adversely affected. This is aggravating the problem of farming community increasing their demand for mung bean varieties resistant to various abiotic stresses. Many breeding programmes have been initiated to develop drought tolerant/ resistant varieties in mung bean. This experiment was conducted at Research Farm, Tirhut College of Agriculture, Dholi, Muzaffarpur, Bihar with 24 mung bean genotypes during the summer of 2019 in Randomized Block Design with three replications and 16 characters. The Analysis of variance (ANOVA) was found highly significant variation among the genotypes for all the characters. The higher estimation of PCV and GCV both were found in these characters viz., number of primary branches per plant, number of secondary branches per plant, biological yield per plant (g), and grain yield per plant (g). The indicating lesser influence of environment in expression of the character hence selection for these traits may be effective. The characters viz., number of primary branches per plant, number of secondary branches per plant, grain yield per plant(g), biological yield per plant(g), harvest index(%), number of pods per plant, main shoot length(cm), 100-seed weight(g) and number of clusters per plant observed high heritability with high genetic advance as percent of the mean. The genotypes SML 1825, VGG 17-040, MH 1451, Pusa M 19-42, and VGG 17-015 producing higher grain yield per plant are high yielding and well-performing genotypes.

**Keywords:** Variation, heritability, genotypes.

### INTRODUCTION

Mung bean (*Vigna radiata* L. Wilczek) belongs to the sub-family Papilionaceae of family Fabaceae of the order Leguminales. Mung bean is native to India and central Asia. It is a highly self-pollinated crop having somatic chromosome number  $2n = 2x = 22$  and a genome size of 579 Mb (Shiv *et al.*, 2017). Mung bean is one of the most useful crops in most Asian countries like India, China, and Pakistan and also, most of the sub-tropical and tropical pieces of the world. It is under cultivation throughout the plains and up to 6000 feet elevation on the Himalayas in India.

Mung bean is also called green gram, mung bean, golden gram, mash bean and green soy. Mung bean is a great wellspring easily digestible protein with low flatulence which supplements the staple rice diet in Asia. They are also used cooked (in soups, rice flavoring, and broths) or canned. Mung is also used as a green manure crop. It is widely grown in monoculture in dry and semi-dry regions, as well as being used as an

intercrop throughout much of the country because of its drought tolerance and nitrogen-fixing soil fertilization to improve the yield of the next crop (Wang *et al.*, 2018). The optimum temperatures for germination are 25 to 30°C. Since the temperature is of key importance for plant development, influencing the rate of photosynthesis, flowering and even pod setting or grain filling. High temperature stress during germination and flowering, and drought & salinity stresses during entire life cycle of crop cause considerable yield losses in mung bean (Goswamy and Panwar 2014).

Mung bean is a major pulse crop of India, which can be grown from arid to humid tropic, and semi-arid locations. India contributes around 45 percent of the total world mung bean production among pulse crops. Mung bean occupied area, production, productivity 4.30 (mha), 2.46(mt), 572(kg/ha) in India; 0.169(mha), 0.118(mt), 700(kg/ha) in Bihar; and 0.023(mha), 0.017(mt), 750(kg/ha) in Muzaffarpur (Bihar) respectively (DES 2018-19). In recent years, there has

been a sharp decline in the production of pulses in India. The major limiting factor for pulses production and productivity in our country is the non-availability of high-yielding varieties that can tolerate environmental fluctuations to a great extent and other limiting factors are poor management practices, lack of disease and pest resistant varieties etc. Hence, it is the need of the hour to breed HYV of various pulse crops including mung bean which are tolerant to abiotic stresses especially to drought condition. Considering the above fact, the present investigation was undertaken with the objective to determine the genetic variability of mung bean for yield and yield contributing traits.

## MATERIAL AND METHODS

The experiment was conducted at the "Research Farm of Tirhut College of Agriculture, Dholi, Muzaffarpur, Bihar" during the summer of 2019. The experimental materials comprised of 23 genotypes viz. OBGG 102, IPM 604-1, VGG 17-045, Pusa BM-8, Samrat, VGG 17-040, HUM 12, IPM 610-2, SML 1831, OBGG 101, IPM 02-3, VGG 17-038, TRCRM-147, VGG 17-015, WBSM 48-5, MH 1344, Pusa M 19-42, MH 1451, IPM 205-7, SKNM-1608, SML 1825, IPM 701-4, and Pusa M 19-41 along with one national check HUM-16 (Malaviya Jankalyani) were grown on 13<sup>th</sup> March 2019 in a "Randomized Block Design" with three replications. Each genotype in each replication has sown the seeds in 6 rows per plot of 3.0 m length, adopting a spacing of 30 cm between rows and 10 cm between the plants. Two non-experimental border rows were sown on each side of the block. Thinning of seedlings was carried out after 10 days of sowing by keeping one seedling per hill. The recommended

cultural practices were adopted in respect of irrigation, weeding and fertilization. The field selected for the experiment is uniform with typical medium soil having medium fertility. Geographically "Research Farm of Tirhut College of Agriculture, Dholi" is located at between latitude of 25.980°N and longitude of 85.670°E at 51.8 m above mean sea level.

The observation days to first flowering, days to 50% flowering and days to maturity were recorded on a plot basis and the rest of the observations like Plant height (cm), Main shoot length (cm), Number of primary branches per plant, Number of secondary branches per plant, Number of cluster per plant, Number of pods per cluster, Number of pods per plant, Pod length (cm), Biological yield per plant (g), Number of grains per pod, 100 -seed weight (g), Harvest- index (%), and Grain yield per plant (g) recorded on five competitive plants from each plot were randomly selected.

The mean value is measured by dividing the totals by the corresponding number of observations of each character. Analysis of variance was estimated by following the standard procedures. The PCV and GCV were calculated as per the method suggested by Burton (1952), whereas Heritability and expected genetic advance were estimated according to Johnson *et al.* (1955); Allard (1960). Heritability in broad sense ( $h^2 b$ ) was calculated as per Burton and Vane (1953).

## RESULTS AND DISCUSSION

All the characters are found highly significant mean sum of squares due to genotype, indicating the presence of sufficient genetic variability among the genotypes in the experiment.

**Table 1: Analysis of variance (ANOVA) for all the morphological characters of 24.**

	Character	Replications (df = 2)	Genotypes (df = 23)	Error (df = 46)
1.	Days to First flowering	0.54	8.31**	0.59
2.	Days to 50% flowering	0.87	9.80**	0.61
3.	Days to maturity	0.79	8.12**	0.92
4.	Plant height (cm)	3.96	51.98**	3.54
5.	Main shoot length (cm)	0.43	58.74**	3.23
6.	Number of primary branches per plant	0.02	2.84**	0.14
7.	Number of secondary branches per plant	0.01	1.08**	0.05
8.	Number of cluster per plant	0.32	1.36**	0.19
9.	Number of pods per cluster	0.53	0.33**	0.13
10.	Number of pods per plant	1.25	29.82**	3.55
11.	Pod length (cm)	0.63	1.07**	0.21
12.	Biological yield per plant (g)	17.46	223.46**	12.29
13.	Number of grains per pod	0.91	2.73**	0.44
14.	100 -seed weight (g)	0.01	1.29**	0.04
15.	Harvest- index (%)	2.55	72.51**	3.99
16.	Grain yield per plant(g)	0.41	11.29**	0.83

\*\* Significant of P = 0.01

The existence of genetic variation is a basic necessity for the evolution of any species. The information on the amount of genetic variability present in the genotype with respect to important traits is considered a priority for direct improvement in the concerned species. The variability for yield and its components that we can see, measure and study is the ultimate result of the

variability in the genetic constitution of the individuals. The selection program depends primarily upon the magnitude of the heritable portion of variability. Heritability estimate provides information on the transmission of character from the parent to progeny and are used to predict genetic advance under selection so that breeders are used to predict genetic gain and

able to anticipate improvement for different types which, in turn, intensifies selection of various genotypes. This is further substantiated by Johnson et al. (1955) who found that heritability estimates in association with genetic advance are much useful for selection than heritability alone.

The above result of the present study, corroborates with earlier results of Muthuswamy *et al.* (2019); Kumar *et al.* (2019); Mehandi *et al.* (2018); Ghimire *et al.* (2018); Sushmitharaj *et al.* (2018); Azam *et al.* (2018); Govardhan *et al.* (2018); Baisakh *et al.* (2016); Jeberson *et al.* (2017) indicating the presence of sufficient variability among the evaluated genotype for the traits under consideration.

The SML 1825 genotype produced higher grain yield per plant(g) followed by VGG 17- 040, MH 1451, Pusa M 19-42, and VGG 17-015 the remaining genotypes producing lesser grain yield in respect of these genotypes. In this regard, the most desirable genotypes were HUM 12, Samrat, and VGG 17-038, for early first flowering; for early 50% flowering VGG 17-038, VGG 17-015, Samrat, HUM 12, and TRCRM-147; for plant height Pusa BM-8, Pusa M 19-42, and SML 1825, have longer stature. For longer main shoot length Pusa BM-8, WBSM 48-5, SKNM- 1608, Pusa M 19-42, and Pusa

M 19-41; For maximum number of primary branches per plant VGG 17-040, OBGG 101, SML 1831, IPM 02-3, and Pusa BM-8; For maximum number of secondary branches per plant OBGG 101, Pusa BM-8, IPM 02-3, Pusa M 19-41, and VGG 17- 045; For maximum number of clusters per plant SML 1825, OBGG 101, SML 1831, IPM 701-4, and VGG 17-040; For maximum number of pods per cluster WBSM 48-5, OBGG 101, SKNM- 1608, and IPM 610-2; For maximum number of pods per plant SML 1825, OBGG 101, IPM 02- 3, WBSM 48-5, and IPM 701-4; For larger pod length SML 1825, and TRCRM-147; For maximum biological yield per plant(g) SML 1825, VGG 17-040, Pusa M 19-42, WBSM 48-5, and VGG 17-015; For number of grains per pod WBSM 48-5, MH 1451, VGG 17-045, Pusa M 19-42, and MH 1344; For 100- seed weight(g) TRCRM-147, VGG 17-015, HUM 12, Pusa BM-8, and OBGG 101; For harvest index in percent MH 1344, Samrat.

The genotypes SML 1825, VGG 17-040, MH 1451, Pusa M 19-42, and VGG 17-015.

Producing higher grain yield per plant are more suitable and well performing genotypes. That can be cultivated as a variety of this environment during summer season.

**Table 2: Mean performance of 24 genotypes of mung bean for sixteen different morphological characters.**

Sr. No.	Genotypes	DFE	DPF	DM	PH	MSL	NPB	NSB	NCP	NPC	NPP	PL	BYP	NGP	SW	HI	GY
1.	OBGG 102	40.00	45.00	63.33	42.57	35.13	2.80	2.20	5.20	3.90	18.62	5.81	32.14	7.73	5.20	22.52	7.18
2.	IPM 604-1	40.33	44.67	64.67	29.53	23.20	1.80	1.47	5.27	3.40	16.73	5.35	21.75	8.67	5.17	33.19	7.21
3.	VGG 17-045	38.67	43.00	62.67	35.00	26.73	2.73	2.30	4.20	3.73	14.60	6.53	22.54	10.20	5.07	33.83	7.54
4.	Pusa BM-8	37.33	42.33	63.67	45.97	38.30	3.40	2.83	5.27	3.27	17.17	6.24	30.60	9.13	5.60	27.72	8.44
5.	Samrat	36.00	41.67	61.33	34.23	26.87	2.57	2.20	4.20	3.50	14.45	5.87	13.19	7.33	4.30	34.56	4.55
6.	VGG 17-040	38.00	43.67	66.00	40.90	32.87	4.67	2.27	5.40	3.60	18.65	6.00	38.69	8.80	5.27	28.33	10.96
7.	HUM 12	35.33	41.67	61.67	38.67	29.27	1.57	1.37	4.73	4.00	16.75	7.07	25.80	7.80	6.07	29.57	7.64
8.	IPM 610-2	38.00	43.00	64.00	33.97	26.47	2.17	1.53	4.20	4.20	17.64	5.98	21.16	8.53	4.10	26.17	5.51
9.	SML 1831	39.00	44.33	66.33	40.10	31.57	3.67	1.97	5.47	3.60	19.08	6.31	33.44	7.27	5.03	17.87	5.99
10.	OBGG 101	37.33	42.33	61.00	39.13	31.70	4.47	3.27	6.13	4.27	22.72	6.11	27.91	8.13	5.60	30.38	8.44
11.	IPM 02-3	38.67	43.00	63.33	36.83	29.37	3.63	2.60	5.33	3.87	20.71	6.83	28.53	7.67	5.33	29.79	8.47
12.	VGG 17-038	36.00	41.33	62.00	32.50	25.00	1.60	1.27	4.27	3.53	13.00	6.66	13.80	7.47	4.83	33.98	4.71
13.	TRCRM-147	37.00	42.00	63.67	35.10	25.67	1.80	1.40	5.00	3.20	15.67	7.69	26.84	7.93	6.73	28.79	7.66
14.	VGG 17-015	37.67	41.33	62.67	39.57	30.10	2.40	1.47	4.93	3.93	17.75	7.08	33.69	8.67	6.23	26.51	8.92
15.	WBSM 48-5	41.33	47.67	67.00	42.37	37.43	1.67	1.27	5.00	4.47	20.68	6.75	35.84	10.47	3.83	22.33	7.93
16.	MH 1344	37.00	42.33	64.00	34.50	27.23	1.93	1.57	4.47	3.53	14.39	6.64	16.07	9.53	5.40	40.95	6.51
17.	Pusa M 19-42	38.00	42.67	63.67	43.27	36.07	1.73	1.37	5.00	4.03	18.89	7.27	36.29	9.93	5.50	28.49	10.30
18.	MH 1451	38.00	42.33	63.33	37.23	29.13	1.07	1.04	4.47	4.10	16.93	7.27	32.81	10.33	5.60	31.90	10.44
19.	IPM 205-7	38.67	43.33	63.67	33.20	26.43	1.77	1.17	3.80	3.73	12.83	6.42	18.51	8.93	5.17	34.06	6.28
20.	SKNM-1608	38.00	42.67	64.00	42.67	37.13	1.93	1.27	5.13	4.27	19.84	6.93	24.27	8.20	4.57	29.32	7.10
21.	SML 1825	42.67	48.67	67.00	43.17	35.13	2.53	2.00	6.47	3.87	25.08	7.82	46.89	9.13	5.23	25.61	12.02
22.	IPM 701-4	39.00	43.67	63.67	38.97	32.27	1.07	1.03	5.40	3.93	20.15	6.71	25.82	9.27	4.53	32.77	8.41
23.	Pusa M 19-41	37.00	42.00	62.33	34.60	36.07	1.80	2.33	3.93	3.47	12.97	6.85	16.79	8.87	5.03	34.35	5.78
24.	HUM-16 (NC)	38.00	43.33	62.00	39.60	31.93	2.70	1.73	4.13	3.53	14.49	6.83	16.81	8.00	4.77	32.82	5.51
	<b>Mean</b>	<b>38.21</b>	<b>43.25</b>	<b>63.63</b>	<b>38.07</b>	<b>30.88</b>	<b>2.39</b>	<b>1.79</b>	<b>4.89</b>	<b>3.79</b>	<b>17.49</b>	<b>6.63</b>	<b>26.67</b>	<b>8.67</b>	<b>5.17</b>	<b>29.82</b>	<b>7.65</b>
	S.E.±	0.45	0.45	0.55	1.09	1.04	0.22	0.13	0.25	0.21	1.09	0.27	2.02	0.38	0.12	1.15	0.53
	C.D. (5%)	1.27	1.29	1.58	3.10	2.95	0.62	0.37	0.72	0.59	3.10	0.77	5.76	1.09	0.34	3.28	1.50
	C.V.(%)	2.03	1.81	1.51	4.95	5.82	15.67	12.65	9.01	9.55	10.78	7.07	13.15	7.66	3.98	6.70	11.95

Note : DFF = Days to First flowering, DPF = Days to 50% flowering, DM = Days to maturity, PH = Plant height (cm), MSL = Main shoot length (cm), NPB = Number of primary branches per plant, NSB = Number of secondary branches per plant , NCP = Number of cluster per plant, NPC = Number of pods per cluster, NPP = Number of pods per plant, PL= Pod length (cm), BYP= Biological yield per plant (g), NGP = Number of grains per pod, SW = 100 -seed weight (g), HI = Harvest- index (%), GY = Grain yield per plant(g).

The number of primary branches per plant (42.61%) are highest estimated for PCV followed by number of secondary branches per plant, biological yield per plant (g), grain yield per plant (g) and number of pods per plant are found higher estimation (>20%) of PCV. The number of primary branches per plant (39.62%) are highest estimated for GCV followed by number of secondary branches per plant, biological yield per plant (g) and grain yield per plant (g) are found higher estimation (>20%) of GCV.

Plant breeding is the application of the genetic variability available in the breeding material for various characters to change the genetic architecture of plants in order to develop improved germplasm possessing a higher economic yield and value than the existing one. Genetic variability is the raw material on which selection acts to bring out improvement in the genetic architecture of the plant.

The PCV were higher than the GCV indication of the lesser influence of environmental effect over these characters and the effectiveness of selection based on phenotypic value for grain yield and yield contributing traits. Similar results were observed by Muthuswamy *et al.* (2019); Sushmitharaj *et al.* (2018); Govardhan *et al.* (2018); Aher *et al.* (2018); Ghimire *et al.* (2018); Azam *et al.* (2018).

The characters 100-seed weight (g) (90.80%) estimation of highest heritability in broad sense followed by number of secondary branches per plant, number of primary branches per plant, main shoot length(cm), biological yield per plant (g), harvest index (%), days to 50% flowering, plant height (cm), days to first flowering, grain yield per plant (g), days to maturity, number of pods per plant, number of clusters per plant, and number of grains per pod were estimated

high heritability(> 60%). The characters number of primary branches per plant, number of secondary branches per plant, biological yield per plant (g), grain yield per plant (g), harvest index (%), number of pods per plant, main shoot length (cm), 100-seed weight (g) and number of clusters per plant exhibiting high estimates (>20%) of genetic advance as percent of the mean.

Heritability estimates in broad sense alone are not a true indicator of the effectiveness of selection. Heritability is used to predict genetic advance under selection so that breeders are used to predict genetic gain and able to anticipate improvement for different types and intensities of selection. Heritability estimate provides information on the transmission of character from the parent to the progeny. Heritability ( $h^2_{(bs)}$ ) and genetic advance in percent of mean as direct selection parameters provide an index of transmissibility of traits. Such estimates facilitate evaluation of hereditary and environmental effects in phenotypic variation and thus aid in selection.

The characters number of primary branches per plant, number of secondary branches per plant, grain yield per plant(g), biological yield per plant(g), harvest index(%), number of pods per plant, main shoot length(cm), 100-seed weight(g) and number of clusters per plant, was recorded high estimate of heritability coupled with high genetic advance are indicating may be presence of additive gene effect and similar results were observed by Kumar *et al.* (2019); Muthuswamy *et al.* (2019); Mehandi *et al.* (2018); Govardhan *et al.* (2018); Sushmitharaj *et al.* (2018); Azam *et al.* (2018); Chandra *et al.* (2017); Payasi (2015); Rahim *et al.* (2010); Raturi *et al.* (2015).

**Table 3: Genotypic ( $\sigma^2_g$ ) and phenotypic variance ( $\sigma^2_p$ ) and other genetic parameters for all the morphological character in mung bean.**

Sr. No.	Character	Genotypic Variance ( $\sigma^2_g$ )	Phenotypic Variance ( $\sigma^2_p$ )	Genotypic coefficient of Variance (GCV)	Phenotypic coefficient of Variance (PCV)	Heritability Broad Sense ( $h^2$ )	Genetic Advance (G A) at 5%	Genetic advance as per cent of Mean
1.	Days to First flowering	2.57	3.17	4.20	4.66	81.10	2.98	7.79
2.	Days to 50% flowering	3.06	3.68	4.05	4.43	83.30	3.29	7.61
3.	Days to maturity	2.40	3.32	2.44	2.87	72.30	2.71	4.26
4.	Plant height (cm)	16.15	19.69	10.56	11.66	82.00	7.50	19.69
5.	Main shoot length (cm)	18.50	21.74	13.93	15.10	85.10	8.18	26.48
6.	Number of primary branches per plant	0.90	1.04	39.62	42.61	86.50	1.82	75.90
7.	Number of secondary branches per plant	0.34	0.40	32.82	35.17	87.10	1.13	63.08
8.	Number of cluster per plant	0.39	0.58	12.75	15.61	66.70	1.05	21.45
9.	Number of pods per cluster	0.07	0.20	6.92	11.79	34.40	0.32	8.37
10.	Number of pods per plant	8.76	12.31	16.92	20.06	71.10	5.14	29.40
11.	Pod length (cm)	0.29	0.51	8.08	10.74	56.60	0.83	12.52
12.	Biological yield per plant (g)	70.39	82.68	31.45	34.09	85.10	15.95	59.78
13.	Number of grains per pod	0.76	1.21	10.09	12.66	63.40	1.43	16.55
14.	100 -seed weight (g)	0.42	0.46	12.48	13.10	90.80	1.27	24.50
15.	Harvest- index (%)	22.84	26.83	16.03	17.37	85.10	9.08	30.46
16.	Grain yield per plant(g)	3.49	4.32	24.42	27.19	80.70	3.46	45.18

## CONCLUSION

The analysis of variance were highly significant for all the characters under study, indicating the presence of considerable genetic variation in the experimental material.

Wide ranges of variation (phenotypic & genotypic) were observed in the experimental material for all the traits under study. The phenotypic variance was found higher than the corresponding genotypic variances for all the traits under study. This may be due to the non-genetic factor which played an important role in the



manifestation of these characters.

The highest estimated of heritability in broad sense was recorded for characters 100-seed weight(g), number of secondary branches per plant, number of primary branches per plant, main shoot length(cm), biological yield per plant(g), harvest index(%), days to 50% flowering, plant height(cm), days to first flowering, grain yield per plant(g), days to maturity, number of pods per plant, number of clusters per plant and number of grains per pod exhibited high heritability (>60%) was estimated. The moderate heritability (>30 to <60%) was estimated for pod length (cm) (56.60%) and number of pods per cluster (34.40%) while the low heritability (<30%) was not estimated in any character.

The high genetic advance was observed for number of primary branches per plant, number of secondary branches per plant, biological yield per plant(g), grain yield per plant(g), harvest index(%), number of pods per plant, main shoot length(cm), 100-seed weight(g), and number of clusters per plant.

The high heritability coupled with high genetic advance for primary branches per plant, number of secondary branches per plant, biological yield per plant(g), grain yield per plant(g), harvest index(%), number of pods per plant, main shoot length(cm), 100-seed weight(g), and number of clusters per plant indicating may be presence of additive gene effects and selection will be effective for such traits.

In the coming days world will witness more fluctuations in environmental condition will global warming and further aggravating problem in agricultural production. Due to depletion of water table and scanty rainfall during peak water requirement period, major crop growing areas face water scarcity which adversely affects overall crop production creating drought like situation. Hence, future challenges in agricultural production will be to identify heat tolerant varieties for mitigating the abiotic stresses.

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**Conflict of Interest.** None.

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