Original Research Article

Assessment of Genetic parameters for yield and its associated traits in Greengram [*Vigna radiata* (L.) Wilczek]

Abstract

Greengram is India's most significant legume crop, and because there is relatively little genetic variety, increasing productivity demands increased attention in research for the development of superior cultivars. During *Kharif* 2020-21, an experiment was conducted to the evaluation of the genetic parameters for yield and their associated attributes for thirty-nine Mungbean genotypes. Using a Randomised Block Design (RBD), all genotypes were sown in three replications. The observations on various quantitative characters were recorded, and the genetic parameters, PCV, GCV, heritability$_{(bs)}$, and genetic advance, along with the analysis of variances, were estimated. According to ANOVA, almost all genotypes exhibited significant variances for all characters. The highest GCV and PCV was found to be pod length (cm), number of pods cluster^{-1}, number of primary branches plant^{-1}, biological yield plant^{-1} as well as seed yield plant^{-1}. The heritability was recorded high for pod length (cm) followed by number of primary branches plant^{-1}, number of pods cluster^{-1}, days to pod initiation, number of seeds pod^{-1}, days to 50% flowering, seed yield plant^{-1}, biological yield plant^{-1}, number of effective pods plant^{-1}. The character's days to flower initiation, total number of pods plant^{-1}, harvest index and number of clusters plant^{-1} revealed medium genetic advance. High heritability$_{(bs)}$ coupled high genetic advance as percent of mean was observed for pod length (cm), number of branches plant^{-1}, number of pods cluster^{-1}, days to pod initiation, number of seeds pod^{-1}, days to 50% flowering, seed yield plant^{-1}, biological yield plant^{-1} and number of effective pods plant^{-1}.

Keywords: Greengram, ANOVA, Variability, Heritability, Genetic advance

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INTRODUCTION

An Indian or Indo-Burmese native, Mungbean ("*Vigna radiata* (L.) Wilczek") ($2n = 22$) ranks 3rd in importance among short-duration grain legumes after chickpea and pigeonpea in terms of self-pollination and productivity. Mungbean genetic diversity is thought to be concentrated in Central Asia (Kumar and Kumar, 2014). In comparison to other plants, the mung bean has a tiny (579 megabyte) genome (Parida *et al*., 1990 and Kang *et al*., 2014). It is similarly named as green bean and green soy, in addition to greengram as well as goldengram (Markam *et* *al*., 2018). Greengram is primarily consumed as porridge or dhal in South Asia and as sprouts or noodles in rest of Asia. Pulse sprouts have historically been regarded as a crucial continuous component in Asian and vegan diets (Ebert *et al*., 2017). In healthcare, various combinations of mungbean sprouts are exploited as a nutritional supplement (Gan *et al*., 2017). Greengram is a good source of protein. Moong is consumed in households as whole grains, sprouted form, and dhal in a variety of forms. It's also a green manure crop. Moong may be used as cow feed. The husk of the seed can also be soaked in water and used as cattle feed. These crops are grown in India throughout three distinct seasons: *kharif*, *rabi*, and *summer*. Protein deficiency is a major problem in developing nations, and mung bean is a significant and inexpensive protein-rich food source throughout Asia, especially for the poor (Selvi *et al*., 2006). High quality protein (20-24%), low flatulence (40–70 ppm), and high iron content (40–70 ppm) this allows for a well-balanced diet (Selvi *et al*., 2006 and Vairam *et al*., 2016). As a source of vitamin C and folate, as well as fodder, feed, and hay for livestock, it is a popular ingredient in Asian cuisine. China, India, Bangladesh, Thailand, Myanmar, Vietnam, Sri Lanka, Australia, Pakistan, Indonesia, and the Philippines are among the countries that grow a lot of mung beans (Alam *et al*., 2014b). With a total area under mung bean cultivation of 40.20 Mha with a production of 1.42 Mt in 2019–20, India is the largest mungbean producer in the worldwide (Anonymous, 2019–20). In India *Summer* cultivation of moongbean is increasing day by day due climatic adversity in the main growing season.

Materials and Methods

Thirty-nine greengram genotypes were sourced from the Department of Plant Breeding and Genetics, College of Agriculture, JNKVV, Jabalpur (M.P.), India. The field experiment was carried out throughout *Kharif* (2020–21) using a randomised full block design that was replicated three times. Genotypes were raised in four rows of three metres each, with a row-row spacing of 30 cm and a plant-plant distance of 10 cm between them. Sixteen characters were recorded from 5 randomly selected plants in each: days to flower initiation, days to 50% flowering, days to pod initiation, days to maturity, plant height (cm), branches plant^{-1}, total pods plant^{-1}, effective pods plant^{-1}, pod length (cm), clusters plant^{-1}, pods cluster^{-1}, 100-seed weight (gm), number of seeds pod^{-1}, seed yield plant^{-1} (gm), biological yield plant^{-1} (gm), and harvest index (%). The analysis of variance was performed in accordance with Burton (1952). Heritability and genetic advance estimates were estimated using heritability formula given by Hanson *et al*., (1956) and Johnson *et al*., (1955), respectively.

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RESULTS AND DISCUSSION

Mean sum of squares related to genotypes was significant for sixteen quantitative traits, indicating that genotypes were genetically differ and that there was a significant degree of variability among all genotypes. Maximum variation present among the genotypes in biological yield plant^{-1} (50.698 gm) followed by days to pod initiation (40.028) and total number of pod plant^{-1} (34.524) and minimum variation present in 100-seed weight (1.001 gm) according to mean sum of squares of various traits (Table 1). Mean performance revealed various range of variations for the traits studied *i.e*. days to flower initiation (30.00-39.00), days to 50% flowering (35.00-47.00), days to pod initiation (40.00-55.33), days to maturity (60.00-75.00), plant height (cm) (38.00-48.00), number of primary branches plant^{-1} (2.70-7.83), total number of pods plant^{-1} (11.72-23.19), number of effective pods plant^{-1} (8.50-17.63), pod length (cm) (5.47-12.45), number of clusters plant^{-1} (3.87-6.88), number of pods cluster^{-1} (2.41-7.00), 100-seed weight (gm) (4.10-6.65), number of seeds pod^{-1} (7.23-11.96), seed yield plant^{-1} (gm) (2.92-6.37), biological yield plant^{-1} (gm) (13.80-29.50) and harvest index (%) (16.06-26.81) (Table-2).

For all of the traits, assessments of the PCV were greater than the associated GCV, showing that the environment had impact on the traits under investigation.

Genotypic coefficient of variation (GCV) exhibited in value from low (<10 %), moderate (10-20%) and high (>20 %) were proposed via Sivasubhramanian and Menon (1973). The high values of GCV was noted for pod length (cm) (26.18), number of pod cluster^{-1} (25.80), number of primary branches plant^{-1} (25.08), biological yield/plant (20.58) and seed yield/plant (20.44) and the high value of PCV was recorded for number of pods cluster^{-1} (28.27), pod length (cm) (28.09), number of primary branches plant^{-1} (27.29), total number of pods plant^{-1} (24.57), biological yield plant^{-1} (24.37 gm), seed yield plant^{-1} (24.15 gm) and number of effective pods plant^{-1} (22.61). In conformity with the present findings by Kumar and Katiyar (2015) for seed yield/plant, pods plant^{-1}, 100-seed weight, number of seeds pod^{-1} and number of branches plant^{-1}, Bhanu *et al*., (2016) for pods plant^{-1}, days to 50% flowering, days to maturity, plant height, 100-seed weight and yield plant^{-1}, Malli *et al*. (2018) for harvest index, primary branches plant^{-1}, seed yield plant^{-1} and pods plant^{-1}, Kumar *et al*., (2019) for seed yield and yield components and Garg *et al*., (2017) for all the traits studied in the present investigation.

Heritability$_{(bs)}$ assists as decent index for transfer of traits as of parents to their offspring also supports breeders as a tool for choosing best genotypes from diverse genetic population. It gives a precise knowledge of heritable portion of variability. Heritability percent showed from low (<30%); moderate (30-60%); and high (>60) were categorized by Johnson *et al*., (1955).

Heritability$_{(bs)}$ percent ranged from 100-seed weight (23.00) to pod length (86.90). In the current study, highest heritability$_{(bs)}$ was recorded for pod length (cm) (86.90 cm) followed by number of primary branches plant^{-1} (84.40), number of pods cluster^{-1} (83.30), days to pod initiation (80.90), seeds pod^{-1} (75.50), days to 50% flowering (74.90), seed yield plant^{-1} (71.70), biological yield plant^{-1} (71.30), number of effective of pods plant^{-1} (70.70). The moderate heritability was recorded for days to flower initiation (59.10), total number of pods plant^{-1} (54.90), harvest index (44.00) and number of cluster plant^{-1} (30.60) signifying that selection of these traits are in a condition to accumulates more additive gene leading to further improvement of their performance (Table 2). Similar findings were reported for seed yield plant^{-1} by Raturi *et al*., (2014), Kumar and Katiyar (2015), Payasi (2015), Keerthiga *et al*., (2017), Perera *et al*., (2017). Ahmad *et al*., (2014), Anand *et al*., (2016) for number of pods plant^{-1}. Degefa *et al*., (2014) for number of primary branches plant^{-1}, number of seeds plant^{-1}, number of pods plant^{-1} & 100-seed weight (gm) were in agreement with the present findings.

Genetic advance regulates the genetic gain under selection. Genetic advance expressed as percent exhibited in value from lower (<10%), moderate (10-20%) and high (>20%) were suggested by Johnson et al. (1955). Genetic advance as percentage of mean is additional consistent index for accepting the effectiveness of selection in enhancing the characters since its assessed value is derived by contribution of heritability, phenotypic standard deviation and intensity of selection.

Table 1: ANOVA for various quantitative traits of Greengram

S. No.	Characters	Mean sum of squares		
		Replication	**Treatments**	**Error**
	Df	**2**	**38**	**76**
1	**Days to flower initiation**	0.077	15.291**	2.866
2	**Days to 50% flowering**	1.923	29.097**	2.923
3	**Days to pod initiation**	2.043	40.028**	3.023
4	**Days to maturity**	9.47	16.567**	8.567
5	**Plant height (cm)**	3.103	20.603**	10.576
6	**Number of primary branches plant^{-1}**	0.465	2.717**	0.157
7	**Total nsumber of pods plant^{-1}**	1.389	34.524**	7.418
8	**Number of effective pods plant^{-1}**	7.365	18.896**	2.296
9	**Pod length (cm)**	1.09	12.844**	1.007
10	**Number of clusters plant^{-1}**	1.05	1.434**	0.617
11	**Number of pods cluster^{-1}**	0.396	4.350**	0.272
12	**100-seed weight (gm)**	0.591	1.001**	0.528

13	**Number of seeds pod^{-1}**	1.05	5.309**	0.518
14	**Seed yield plant^{-1} (gm)**	1.19	2.525**	0.294
15	**Biological yield plant^{-1} (gm)**	0.504	50.698**	5.993
16	**Harvest index (%)**	0.714	19.956**	5.944

Table 2: Grand mean, range, variability, heritability (broad sense), genetic advance and genetic advance as per cent of mean for different quantitative traits of Greengram

S. No.	**Characters**	**Grand mean**	**Range**		**Coefficient of Variation**		**Heritability broad sense (%)**	**Genetic advance at 5%**	**Genetic advance as % of mean at 5%**
			Min.	**Max.**	**GCV**	**PCV**			
1	**Days to flower initiation**	34.79	30.00	39.00	5.85	7.61	59.10	3.22	9.26
2	**Days to 50% flowering**	41.05	35.00	47.00	7.20	8.31	74.90	5.27	12.83
3	**Days to pod initiation**	45.46	40.00	55.33	7.74	8.60	80.90	6.52	14.33
4	**Days to maturity**	65.11	60.00	75.00	2.51	5.15	23.70	1.64	2.52
5	**Plant height (cm)**	43.64	38.00	48.00	4.19	8.55	24.00	1.85	4.23
6	**Number of primary branches plant^{-1}**	3.68	2.70	7.83	25.08	27.29	84.40	1.75	47.47
7	**Total number of pods plant^{-1}**	16.51	11.72	23.19	18.21	24.57	54.90	4.59	27.79
8	**Number of effective pods plant^{-1}**	12.38	8.50	17.63	19.00	22.61	70.70	4.07	32.91
9	**Pod length (cm)**	7.71	5.47	12.45	26.18	28.09	86.90	3.88	50.26
10	**Number of clusters plant^{-1}**	5.17	3.87	6.88	10.10	18.25	30.60	0.60	11.52
11	**Number of pods cluster^{-1}**	4.52	2.41	7.00	25.80	28.27	83.30	2.19	48.51
12	**100-seed weight (gm)**	5.10	4.10	6.65	7.79	16.24	23.00	0.39	7.70
13	**Number of seeds pod^{-1}**	9.40	7.23	11.96	13.44	15.47	75.50	2.26	24.06
14	**Seed yield plant^{-1} (gm)**	4.22	2.92	6.37	20.44	24.15	71.70	1.50	35.65
15	**Biological yield plant^{-1} (gm)**	18.76	13.80	29.50	20.58	24.37	71.30	6.72	35.80
16	**Harvest index (%)**	22.87	16.06	26.81	9.45	14.25	44.00	2.95	12.91

In this investigation, high genetic advance was exhibited for characters *viz*., pod length (cm) (50.26), number of pods cluster^{-1} (48.51), number of primary branches plant^{-1} (47.47), biological yield plant^{-1} (gm) (35.80), seed yield plant^{-1} (gm) (35.65), number of effective pods plant^{-1} (32.91), total number of pods plant^{-1} (27.79) and number of seeds pod^{-1} (24.06). Medium genetic advance was showed by days to pod initiation (14.33), harvest Index (12.91),

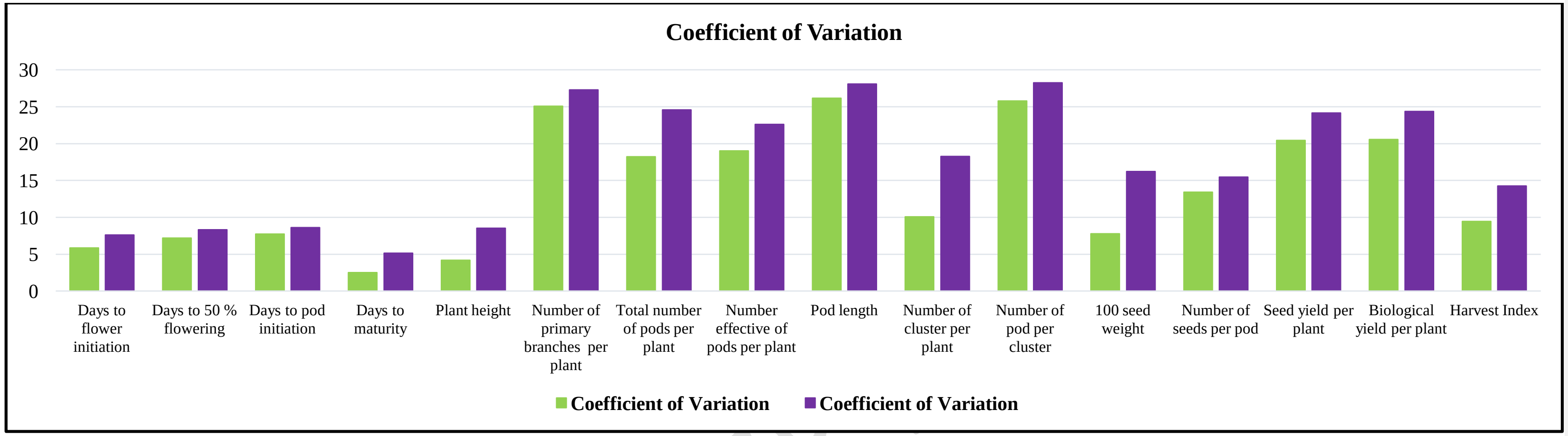

Figure 1: **Genotypic coefficient of variation and phenotypic coefficient of variation for different quantitative traits of Greengram**

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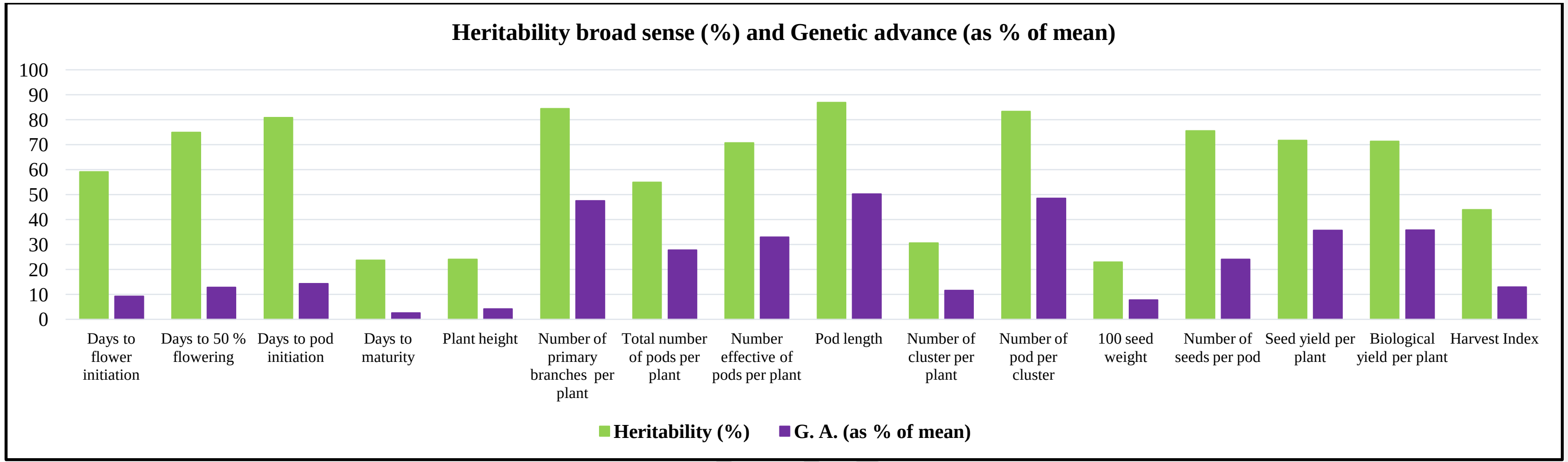

Figure 2: **Heritability broad sense (%) and Genetic advance (as % of mean) for different quantitative traits of Greengram**

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days to 50% flowering (12.83) and number of clusters plant^{-1} (11.52), while remaining characters like, days to flower initiation (9.26), 100-seed weight (gm) (7.70), plant height (cm) (4.23) as well as days to maturity (2.52) revealed lower genetic advance.

High heritability$_{(bs)}$ coupled high genetic advance as % of mean was exhibited for pod length (cm) (86.90, 50.26), primary branches plant^{-1} (84.40, 47.47), pods cluster^{-1} (83.30, 48.51), days to pod initiation (80.90, 14.33), seeds pod^{-1} (75.50, 24.06), days to 50% flowering (74.90, 12.83), seed yield per plant (71.70, 35.65), biological yield per plant (71.30, 35.80) and effective pods plant^{-1} (70.70, 32.91) (Kumar *et al*., 2019) also stated highest heritability$_{(bs)}$ coupled with high genetic advance as % of mean for number of clusters plant^{-1}.

CONCLUSION

Analysis of variance intended for all traits under this investigation was observed to be significant which shows that sufficient genetic variation is present for all the traits. High heritability$_{(bs)}$ coupled with highest genetic advance was recorded for most of the characters. The selection of high yielding breeding traits to increase the crop's genetic yield potential could be based on qualities discovered to have more heritability as well as high genetic advance as a % of mean. Considering qualities with more heritability and high genetic advance as a % of mean for the selection of transgressive segregants in the segregating generations, a systematic hybridization programme may also be established. The segregants will be crucial to boosting the output and productivity of the greengram in the future along with the increased breeding value.

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