



ISSN (E): 2277-7695
 ISSN (P): 2349-8242
 NAAS Rating: 5.23
 TPI 2023; 12(3): 982-986
 © 2023 TPI
www.thepharmajournal.com

Received: 26-01-2023
 Accepted: 28-02-2023

Shailendra Sagar Prajapati
 Ph.D., Scholar, Department of
 Plant Breeding and Genetics,
 Jawaharlal Nehru Krishi
 Vishwavidyalaya, Jabalpur,
 Madhya Pradesh, India

Sanjay Kumar Singh
 Senior Scientist, Department of
 Plant Breeding and Genetics,
 Jawaharlal Nehru Krishi
 Vishwavidyalaya, Jabalpur,
 Madhya Pradesh, India

MK Shrivastava
 Principal Scientist, AICRP on
 Soybean, Jawaharlal Nehru
 Krishi Vishwavidyalaya,
 Jabalpur, Madhya Pradesh,
 India

Manoranjan Biswal
 Ph.D., Scholar, Department of
 Plant Breeding and Genetics,
 Jawaharlal Nehru Krishi
 Vishwavidyalaya, Jabalpur,
 Madhya Pradesh, India

Pratik Kumar
 Ph.D., Scholar, Department of
 Plant Breeding and Genetics,
 Jawaharlal Nehru Krishi
 Vishwavidyalaya, Jabalpur,
 Madhya Pradesh, India

Shivangi Rahangdale
 Ph.D., Scholar, Department of
 Plant Breeding and Genetics,
 Jawaharlal Nehru Krishi
 Vishwavidyalaya, Jabalpur,
 Madhya Pradesh, India

Karishma Behera
 Ph.D., Scholar, Department of
 Plant Breeding and Genetics,
 Jawaharlal Nehru Krishi
 Vishwavidyalaya, Jabalpur,
 Madhya Pradesh, India

Corresponding Author:
Shailendra Sagar Prajapati
 Ph.D., Scholar, Department of
 Plant Breeding and Genetics,
 Jawaharlal Nehru Krishi
 Vishwavidyalaya, Jabalpur,
 Madhya Pradesh, India

Evaluation of genetic parameters for yield and yield related traits in mungbean [*Vigna radiata* (L.) Wilczek]

Shailendra Sagar Prajapati, Sanjay Kumar Singh, MK Shrivastava, Manoranjan Biswal, Pratik Kumar, Shivangi Rahangdale and Karishma Behera

Abstract

Mungbean is India's most important leguminous crop. Since, there is not a lot of genetic diversity, India needs to focus more on research to develop better cultivars to increase productivity. During Late *kharif* 2020-21, a trial was done on 39 Mungbean genotypes to look at their genetic parameters for yield and the traits that go along with them. All of the genotypes were planted three times using a Randomised Block Design (RBD). Quantitative traits were recorded, and various genetic parameters such as PCV, GCV, heritability_(bs), and genetic advance were calculated, based on the observations made. ANOVA analysis indicated that most of the genotypes exhibited significant variations for every trait. The highest GCV and PCV was found to be biological yield plant⁻¹ (gm), number of effective pods plant⁻¹, total number of pods plant⁻¹ and number of pods cluster⁻¹, number of primary branches plant⁻¹ as well as pod length (cm). The heritability was recorded high for total number of pods plant⁻¹, number of pods cluster⁻¹, harvest index (%), number of effective pods plant⁻¹, pod length (cm), biological yield plant⁻¹ (gm), number of seeds pod⁻¹, days to pod initiation, 100-seed weight (gm), seed yield plant⁻¹ (gm), number of primary branches plant⁻¹, number of clusters plant⁻¹, plant height (cm) and days to 50% flowering. The character's days to maturity as well as days to flower initiation revealed medium genetic advance. The traits such as biological yield plant⁻¹ (gm), number of effective pods plant⁻¹, total number of pods plant⁻¹, number of pods cluster⁻¹, number of primary branches plant⁻¹, pod length (cm), harvest index (%), number of seeds pod⁻¹, seed yield per plant (gm), number of clusters plant⁻¹ and 100-seed weight (gm) showed high heritability_(bs) and a significant genetic advance as a percentage of the mean.

Keywords: Greengram, ANOVA, variability, heritability, genetic advance

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, [14]. In comparison to other plants, the mung bean has a tiny (579 megabyte) genome (Parida *et al.*, [2] and Kang *et al.*,)" [3]. It is similarly named as green bean and green soy, in addition to greengram as well as goldengram (Markam *et al.*, 2018) [4]. 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.*,) [5]. In healthcare, various combinations of mungbean sprouts are exploited as a nutritional supplement (Gan *et al.*,) [6]. 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: *late 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.*,) [7]. 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.*, and Vairam *et al.*, 2016) [7-8]. 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.*, b) [9]. 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) [10].

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 *late kharif* (2020–21) using a randomised 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 [11]. Heritability and genetic advance estimates were estimated using heritability formula given by Hanson *et al.*, [12] and Johnson *et al.*, [13], respectively”.

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 harvest index (%) (162.86) followed by total number of pods plant⁻¹ (86.762) and plant height (cm) (76.884) and minimum variation present in 100-seed weight (0.973) 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 (28.00-36.00), days to 50% flowering (31.00-43.00), days to pod initiation (37.33-51.00), days to maturity (56.00-72.00), plant height (cm) (29.42-51.47), number of primary branches plant⁻¹ (2.00-4.00), total number of pods plant⁻¹ (11.33-31.00), number of effective pods plant⁻¹ (7.00-22.33), pod length (cm) (4.50-9.34), number of clusters plant⁻¹ (3.10-7.50), number of pods cluster⁻¹ (2.30-6.55), 100-seed weight (gm) (3.32-6.06), number of seeds pod⁻¹ (5.96-12.24), seed yield plant⁻¹ (gm) (4.18-8.23), biological yield plant⁻¹ (gm) (9.89 -30.40) and harvest index (%) (23.07-51.35) (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) and phenotypic coefficient of variation (PCV) exhibited in value from low (<10%), moderate (10-20%) and high (>20%) were proposed via Sivasubramanian and Menon (14). The high values of genotypic coefficient of variation (GCV) was noted for biological yield plant⁻¹ (gm) (30.59%), number of effective pods plant⁻¹ (28.19), total number of pods plant⁻¹ (27.01%) and number of pods cluster⁻¹ (25.73%), number of primary branches plant⁻¹ (24.56%) and pod length (cm) (21.26%) and the high value of phenotypic coefficient of variation (PCV) was recorded for biological yield plant⁻¹ (gm) (33.39%), number of effective pods plant⁻¹ (30.44), total number of primary branches plant⁻¹ (28.33), total number of pods plant⁻¹ (28.32%) and number of pods cluster⁻¹ (27.04%) and pod length (cm) (22.95%). In conformity with the present findings by Kumar and Katiyar [15] for seed yield plant⁻¹, pods plant⁻¹, 100-seed

weight, number of seeds pod⁻¹ and number of branches plant⁻¹, for pods plant⁻¹, days to 50% flowering, days to maturity, plant height, 100-seed weight and yield plant⁻¹, Malli *et al.* [16] for harvest index, primary branches plant⁻¹, seed yield plant⁻¹ and pods plant⁻¹, Kumar *et al.*, [17] for seed yield and yield components and Garg *et al.*, [18] 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.*, [13]. Heritability_(bs) percent ranged from days to flower initiation (45.00%) to total number of pods plant⁻¹ (91.00%). In the current study, highest heritability_(bs) was recorded for total number of pods plant⁻¹ (91.00%), number of pods cluster⁻¹ (90.60%), harvest index (%) (89.80%), number of effective pods plant⁻¹ (85.80%), pod length (cm) (85.80%), biological yield plant⁻¹ (gm) (83.90%), number of seeds pod⁻¹ (81.00%), days to pod initiation (78.60%), 100-seed weight (gm) (77.70%), seed yield plant⁻¹ (gm) (76.60%), number of primary branches plant⁻¹ (75.20%), number of clusters plant⁻¹ (72.50%), plant height (cm) (69.70%) and days to 50% flowering (67.60%). The moderate heritability was recorded for days to maturity (59.70%) and days to flower initiation (45.00%) 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.*, [19], Kumar and Katiyar [15], Perera *et al.*, [20]. Ahmad *et al.*, [21], Anand *et al.*, [22] for number of pods plant⁻¹. Degefa *et al.*, [23] 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.* [13]. 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.

In this investigation, high genetic advance was exhibited for characters *viz.*, biological yield plant⁻¹ (gm) (57.72), number of effective pods plant⁻¹ (53.78), total number of pods plant⁻¹ (53.07), number of pods cluster⁻¹ (50.44), number of primary branches plant⁻¹ (43.86), pod length (cm) (40.57), harvest index (%) (36.25), number of seeds pod⁻¹ (31.29), seed yield plant⁻¹ (gm) (29.87), number of clusters plant⁻¹ (28.27) and 100-seed weight (gm) (21.36). Medium genetic advance was showed by plant height (cm) (19.33), days to pod initiation (14.31) and days to 50% flowering (11.24), while remaining two characters like, days to flower initiation (6.49) as well as days to maturity (5.35) revealed lower genetic advance.

High heritability_(bs) coupled high genetic advance as% of mean was exhibited for biological yield plant⁻¹ (gm) (83.90, 57.72), number of effective pods plant⁻¹ (85.80, 53.78), total number of pods plant⁻¹ (91.00, 53.07), number of pods cluster⁻¹ (90.60, 50.44), number of primary branches plant⁻¹ (75.20, 43.86), pod length (cm) (85.80, 40.57), harvest index (%) (89.80, 36.25), number of seeds pod⁻¹ (81.00, 31.29), seed yield plant⁻¹ (gm) (76.60, 29.87), number of clusters plant⁻¹ (72.50, 28.27) and

100-seed weight (gm) (77.70, 21.36) (Kumar *et al.*)^[17] also as% of mean for number of clusters plant⁻¹. stated highest heritability_(bs) coupled with high genetic advance

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	2.829	9.399**	2.724
2	Days to 50% flowering	3.111	21.820**	3.006
3	Days to pod initiation	2.214	37.635**	3.135
4	Days to maturity	2.989	16.366**	3.101
5	Plant height (cm)	8.308	76.884**	9.729
6	Number of primary branches plant ⁻¹	0.123	1.243**	0.123
7	Total number of pods plant ⁻¹	3.546	86.762**	2.780
8	Number of effective pods plant ⁻¹	3.546	52.997**	2.780
9	Pod length (cm)	0.019	6.065**	0.317
10	Number of clusters plant ⁻¹	0.006	2.830**	0.317
11	Number of pods cluster ⁻¹	0.123	3.672**	0.123
12	100-seed weight (gm)	0.470	0.973**	0.085
13	Number of seeds pod ⁻¹	1.003	7.143**	0.518
14	Seed yield plant ⁻¹ (gm)	1.081	3.177**	0.294
15	Biological yield plant ⁻¹ (gm)	0.962	76.876**	4.618
16	Harvest index (%)	0.914	162.864**	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	31.75	28.00	36.00	4.70	7.01	45.00	2.06	6.49
2	Days to 50% flowering	37.75	31.00	43.00	6.63	8.07	67.60	4.24	11.24
3	Days to pod initiation	43.26	37.33	51.00	7.84	8.84	78.60	6.19	14.31
4	Days to maturity	62.83	56.00	72.00	3.36	4.35	59.70	3.36	5.35
5	Plant height (cm)	42.11	29.42	51.47	11.24	13.46	69.70	8.14	19.33
6	Number of primary branches plant ⁻¹	2.49	2.00	4.00	24.56	28.33	75.20	1.09	43.86
7	Total number of pods plant ⁻¹	19.59	11.33	31.00	27.01	28.32	91.00	10.40	53.07
8	Number of effective pods plant ⁻¹	14.51	7.00	22.33	28.19	30.44	85.80	7.81	53.78
9	Pod length (cm)	6.51	4.50	9.34	21.26	22.95	85.80	2.64	40.57
10	Number of clusters plant ⁻¹	5.68	3.10	7.50	16.11	18.92	72.50	1.61	28.27
11	Number of pods cluster ⁻¹	4.23	2.30	6.55	25.73	27.04	90.60	2.13	50.44
12	100-seed weight (gm)	4.63	3.32	6.06	11.76	13.34	77.70	0.99	21.36
13	Number of seeds pod ⁻¹	8.81	5.96	12.24	16.87	18.75	81.00	2.76	31.29
14	Seed yield plant ⁻¹ (gm)	5.92	4.18	8.23	16.57	18.94	76.60	1.77	29.87
15	Biological yield plant ⁻¹ (gm)	16.05	9.89	30.40	30.59	33.39	83.90	9.26	57.72
16	Harvest index (%)	38.95	23.07	51.35	18.57	19.60	89.80	14.12	36.25

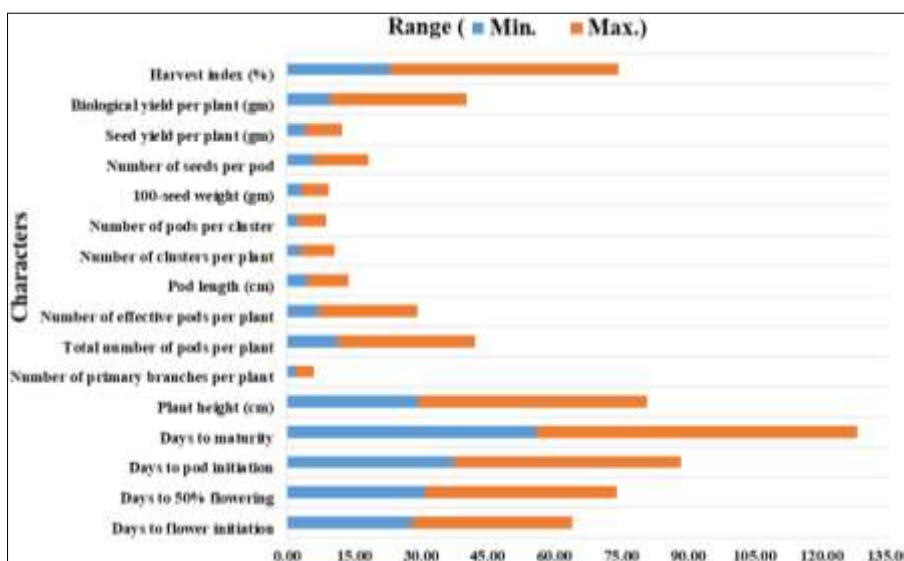


Fig 1: Range (Min.- minimum and Max.- maximum) for different quantitative traits of Greengram

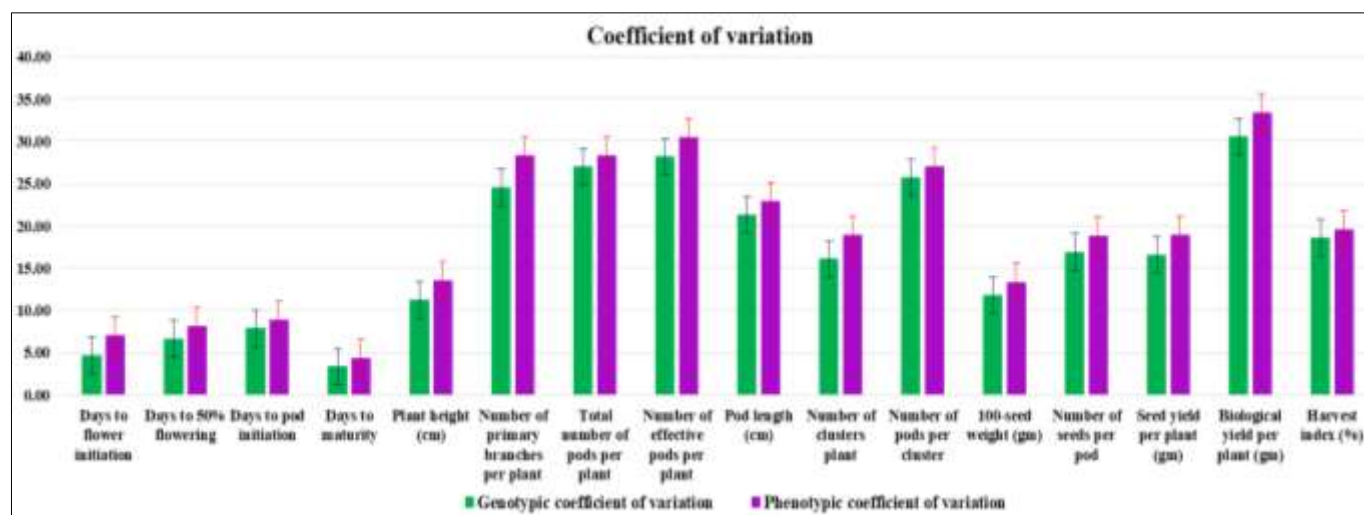


Fig 2: Genotypic coefficient of variation and phenotypic coefficient of variation for different quantitative traits of Greengram

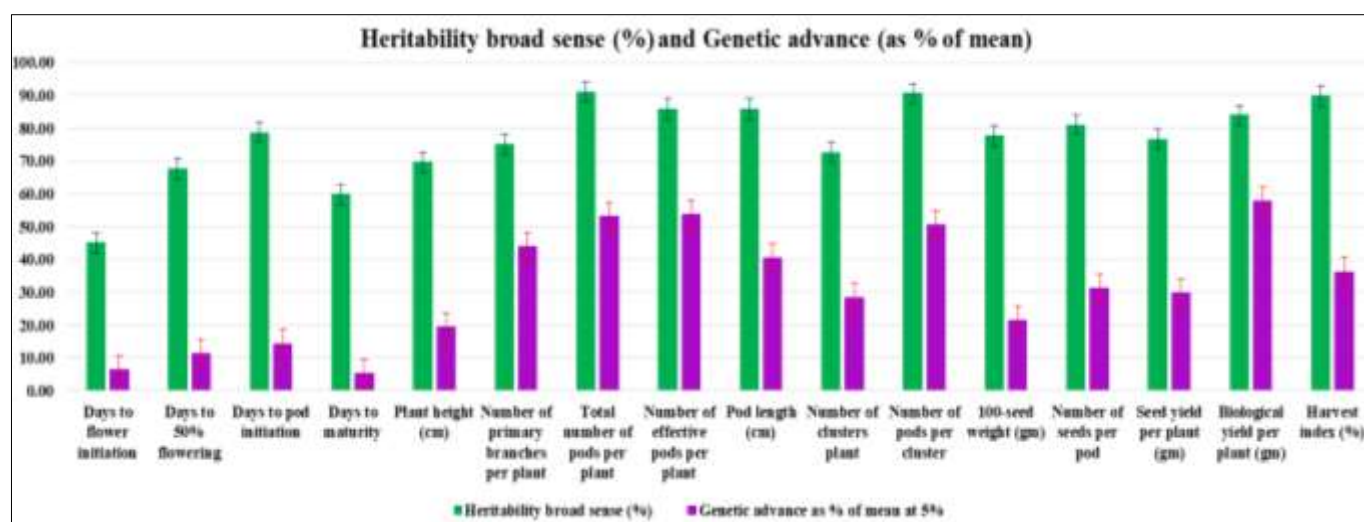


Fig 3: Heritability broad sense (%) and Genetic advance (as% of mean) for different quantitative traits of Greengram

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.

Acknowledgement

The authors are very much thankful to the Bhabha Atomic Research Institute, Trombay, Mumbai (India) for providing valuable materials for this research experiment.

References

1. Kumar S, Kumar R. Genetic improvement in mungbean for yield, nutrition and resistance to stresses: A review.

International Journal of Tropical Agriculture. 2014;32:3-4.

2. Parida S Raina, Narayan R. Quantitative DNA variation between and within chromosome complements of Vigna species (Fabaceae). *Genetica*. 1990;82:125-133.
3. Kang Y, Kim S, Kim M. Genome sequence of mungbean and insights into evolution within Vigna species. *Nat Commun*. 2014;5:5443.
4. Markam NK, Nair SK, Nanda HC, Lakpale N. Studies on allelic relationship for resistance to mungbean yellow mosaic virus disease in mungbean genotypes. *Int. J Chem. Stud*. 2018;6(2):2401-2403.
5. Ebert W, Chang CH, Yan MR, Yang RY. Nutritional composition of mungbean and soybean sprouts compared to their adult growth stage. *Food Chem*. 2017;237:15-22. doi: 10.1016/j.foodchem.2017.05.073.
6. Gan RY, Lui WY, Wu K, Chan CL, Dai SH, Sui ZQ. Bioactive compounds and bioactivities of germinated edible seeds and sprouts: an updated review. *Trends Food Sci. Technol*. 2017;59:1-14. doi: 10.1016/j.tifs.2016.11.010.
7. Selvi R, Muthiah AR, Manivannan N. Tagging of RAPD marker for MYMV resistance in mungbean (*Vigna radiata* (L.) Wilczek). *Asian J Plant Sci*. 2006;5:277-s280.
8. Vairam N, Lavanya SA, Muthamilan M, Vanniarajan C.

- Screening of M₃ mutants for yellow vein mosaic virus resistance in greengram [*Vigna radiata* (L.) wilczek]. Int. J Plant Sci. 2016;11(2):265-269.
9. Alam AKMM, Somta P, Srinives P. Identification and confirmation of quantitative trait loci controlling resistance to mungbean yellow mosaic disease in mungbean [*Vigna radiata* (L.) Wilczek]. Mol. Breed., B. 2014;34:1497-1506.
 10. Anonymous. 1th Advance Estimates, Agriculture Statistics Division, Directorate of Economics and Statistics, New Delhi; c2019-20.
 11. Burton GW, Devane EM. Estimating heritability in tall fescue (*Festuca circumcliaceae*) from replicated material. Agron. J. 1953;45:478-481.
 12. Hanson GH, Robinson HF, Comstock RE. Biometrical studies on yield in segregating population. Agron. J; c1956. p. 268-272.
 13. Johnson HW, Robinson HF, Comstock HS. Estimation of genetic and environmental variability in soybean. Agron. J. 1955;47:314-318.
 14. Sivasubramanian S, Menon M. Heterosis and inbreeding depression in rice. Madras agric. J. 1973;60:1139-1144.
 15. Kumar S, Katiyar M. Genetic variability, heritability, expected genetic advance and character association in mungbean [*Vigna radiata* (L.) Wilczek]. International Journal of Advance Research. 2015;3(5):1371-1375.
 16. Malli SK, Lavanya GR, Nikhil BSK. Genetic variability, heritability and genetic advance in mungbean [*Vigna radiata* (L.) Wilczek] genotypes. Green farming. 2018;9(2):235-238.
 17. Kumar T, Krishna G, Kumar A, Kumar RR, Kishore C, Kumar J, *et al.* Genetic variability, heritability and genetic advance in mungbean [*Vigna radiata* (L.) Wilczek]. International Journal of Chemical Studies. 2019;7(6):77-81.
 18. Garg GK, Verma PK, Kesh H. Genetic Variability, Correlation and Path Analysis in Mungbean [*Vigna radiata* (L.) Wilczek]. International Journal of Current Microbiology and Applied Sciences. 2017;6(11):2166-2173.
 19. Raturi S, Singh K, Sharma V, Pathak R. Genetic variability, heritability, genetic advance and path analysis in mungbean [*Vigna radiata* (L.) Wilczek]. Legume Research-An International Journal. 2015;38:157-163.
 20. Perera UIP, Chandika KKJ, Disna R. Genetic variation, character association and evaluation of mungbean genotypes for agronomic and yield components. Journal of the National Science Foundation of Sri Lanka. 2017;45(4):347-353.
 21. Ahmad HB, Rauf S, Rafiq CM, Mohsin AU, Shahbaz U, Sajjad M. Genetic variability for yield contributing traits in mung bean (*Vigna radiata* L.). Journal of Global Innovations in Agricultural and Social Sciences. 2014;2(2):52-54.
 22. Anand G, Anandhi K, Paulpandi VK. Genetic variability, correlation and path analysis for yield and yield components in F₆ families of Greengram (*Vigna radiata* (L.) Wilczek) under rainfed condition. Electronic Journal of Plant Breeding. 2016;7(2):434-437.
 23. Degefa I, Petros Y, Andargie M. Genetic variability, heritability and genetic advance in Mung bean [*Vigna radiata* (L.) Wilczek] accessions. Plant Science Today. 2014;1(2):94-98.