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Genetic Variability, Heritability and Genetic advance for Yield and Yield contributing Traits of Greengram

ANUHYA JAYAPRADA*, ROOPA LAVANYA, RAM BABU, CH NAGA, SAI KRISHNA AND T SUDHEER REDDY

ABSTRACT

Greengram is an important short duration pulse crop grown extensively throughout India. The productivity is very less when compared to other pulse crops in India and in Uttar Pradesh. Hence, the experiment was conducted with the aim of identifying different genotypes and characters that will be useful in improving its productivity. The present investigation was intended to study the extent of variation, heritability and genetic advance among different characters of greengram in sandy loam soils of Uttar Pradesh in a set of 20 genotypes including check Samrat in randomized block design with three replications during the Kharif, 2017. Observations were recorded for 13 quantitative characters. The genotypes KM11 584, KM11 583, RMG 1030, MH 934, NAVYA and SHARIF were identified as desirable genotypes. Harvest index, biological yield per plant, number of clusters per plant, number of seeds per pod exhibited high GCV, PCV, heritability and genetic advance as percent of mean. Thus priority should be given to these characters during selection in breeding programme for greengram yield improvement.

KEYWORDS

Greengram, variability, heritability and genetic advance

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INTRODUCTION

Greengram (Vigna radiata (L.) Wilczek) is a self-pollinating diploid legume with the chromosome number 2n=2x=22 (Karpechenko, 1925) and originated in India (Candolle (1959)) or the Indo-Burma region (Vavilov, 1951). It is also known as mungbean or moong is an important pulse crop grown extensively in both tropical and subtropical regions of the world. It is a short duration grain legume with wide adaptability (Singh et al., 2013b). Due to their short duration, photo insensitivity and dense canopy, they have a special significance in crop intensification, diversification and sustainable production system (Singh and Bhatt (2013)). Since greengram matures in about 60 to 70 days after sowing, it is an excellent crop for rotation in different cropping systems. It contains 24-25% protein and hence is consumed widely in India (Singh *et al* (2013)).

In India food grains occupy 65% of total gross cropped area comprising cereals in 50% and pulses in about 15% (Singh *et al*, 2015). Within pulses, greengram occupies only 2% of gross cropped area. Under individual crop category greengram contributes only 14% and 8% in terms of area (42.57 lakh ha) and production (20.09 lakh tons) share to total pulses, while its productivity is 472 (kg/ha) only during 2017-18 in India. The area, production and productivity under greengram was very low in Uttar Pradesh [0.90 lakh ha (2.60%), 0.48 lakh tons (2.98%) and 533 kg/ha respectively] (Anonymous (2018)). Hence the present study was undertaken in order to find suitable character that are to be used in the breeding programme for improvement of greengram yield.

For developing suitable selection strategy, the knowledge of genetic variability present in the available germplasm for yield and its associated characters is essential (Srivastava and Singh, 2012). Grain yield in greengram, as in other crops, is a complex character and is influenced both by genetic and environmental factors. It is considered as quantitative character as it is contributed by continuous variation and governed by polygenes. Thus the phenotypic variance of yield or a yield associated character is a resultant of genetic and environmental components and their interactions. The proportion of phenotypic variance of a character due to genetic component determines the heritability for that character.

Heritability of a character is a parameter of particular significance to the breeder as it measures the degree of resemblance between the parents and the off-springs and its magnitude indicates the efficacy with which a genotype can be identified by its phenotypic expression, while genetic advance aids in exercising the necessary selection pressure. If calculated from the total genetic component it is referred to as broad sense heritability, whereas, if only the additive proportion of the genetic component is utilized in the calculation, the heritability is known as narrow sense. Genetic improvement by selection largely depends on an additive gene action component. A particular heritability estimate is specific only for that population and the environment in which the population was grown.

[1] Deptt. of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Allahabad-211007, Uttar Pradesh, India
*Corresponding author email: anuhyajayapradat@gmail.com

Therefore, the present study was undertaken with an objective to study genetic variability, heritability and genetic advance in respect to various desirable characters in 20 genotypes including check, which will help in identifying promising lines for use in future hybridization programme of greengram.

MATERIALS AND METHODS

The present investigation was conducted at the Field Experimentation Centre, Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Allahabad, U.P. during Kharif, 2017. Allahabad is situated at an elevation of 98 meters above the sea level; 25.87°N latitude and 81.5°E latitude. Climate is subtropical. During summer, the temperature reaches up-to 46-48°C, while during winter season especially in the month of December and January; temperature drops down to as low as 1°C - 20°C. The average rainfall in this area is around 1013.4 mm, mostly a few occasions light showers and drizzles have seen in the winter also. The soil type of the experimental site was sandy loam, low in organic carbon.

The experimental materials comprised of 20 genotypes [KMII 584, KMII 583, KMII 585, KMII 582, KMII 551, KMII 587, KMII 564, SHARIF 1, NAVYA, RMG 344, RMG 1042, RMG 1091, RMG 1030, RMG 975, RMG 1092, RMG 1004, RMG 492, RMG 1014, MH 934 and SAMRAT (CHECK)] and were conducted in Randomized Block Design with three replications during kharif 2017. The genotypes are previously available in the institute. All the standard package of practices were followed in raising the crop. Random sampling technique was adopted for recording various quantitative characters of greengram. Five plants in each treatment from each replication were taken at random at the time of recording the data on various characters. Data of five plants were averaged replication wise and mean data was used for statistical analysis.

Observations viz., plant height (cm), number of primary branches per plant, days to 50% flowering, number of clusters per plant, number of pods per plant, days to maturity, number of seeds per pod, pod length (cm), seed index (g) by weighing samples of 100 randomly taken seeds from each plant, biological yield per plant (g), harvest index (%), protein content (%) (Macrokjeldahl Method-AOAC 1975) and seed yield per plant (g) were recorded on each genotype. Mean value of each character was worked out by dividing the totals by the corresponding number of observations. Range was taken as the difference between the highest and lowest mean value for each character. The recorded observations were subjected to different statistical analysis viz., analysis of variance (Fisher, 1936); Genotypic variance, Phenotypic variance, Environmental or error variance, Standard error of mean (SEM), Critical differences (CD) and Coefficient of variation (phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) and environmental/error coefficient of variation (ECV) (Burton, 1952); Heritability (h^2) (Lush (1949) and Gw and Devane (1953)) and genetic advance (Johnson *et al*, 1955) were predicted (Johnson *et al*, 1955).

RESULTS AND DISCUSSION

The Analysis of Variance (ANOVA) revealed that there is a significant difference among all the 13 characters studied in the 20 genotypes including check (Table 1), indicating the presence of sufficient variation in the genotypes studied and it provides an opportunity for further analysis and estimation of genetic parameters. Similar results were also obtained by Biradar *et al* (2007), wherein the genotypes differed significantly in analysis of variance among themselves for all the characters indicating the presence of adequate variability in greengram.

The observations made on various yield and its attributing characters were presented on Table 2 . Wide ranges of values were observed for all the characters. Plant height varied from 36.66 (MH 934) to 54.73 (KM11 584), number of primary branches varied from 2.00 (KM11 585, RMG 1092) to 2.53 (NAVYA), days to 50% flowering varied from 40.66 (RMG 1004) to 46.66 (RMG 975, NAVYA), number of clusters per plant varied from 6.53 (KM11 551) to 11.40 (KM11 583), number of pods per plant varied from 16.00 (SAMRAT) to 27.46 (KM11 584), days to maturity varied from 65.33 (KM11 587) to 72.66 (KM11 564), number of seeds per pod varied from 9.70 (RMG 975) to 11.70 (KM11 584), pod length varied from 6.04 (RMG 975) to 7.28 (NAVYA), seed index varied from 2.81 (RMG 975) to 3.49 (NAVYA), biological yield per plant varied from 17.07 (KM11 587) to 29.56 (KM11 584), harvest index varied from 22.81 (KM11 585) to 39.51 (KM11 583), protein content varied from 21.70 (RMG 1030) to 23.46 (RMG 1042) and seed yield per plant varied from 4.03 (RMG 1091) to 8.95 (KM11 584). Higher single plant yield was recorded for the genotype KM11 584 (8.95) followed by KM11 583 (8.32), RMG 1030 (7.53), MH 934 (7.33), NAVYA (7.11). Based on these results, the genotypes KM11 584, KM11 583, RMG 1030, MH 934, NAVYA and SHARIF could be utilized as parents for enriching yield and yield attributing characters.

Phenotypic and Genotypic variances:

Wide ranges of phenotypic and genotypic variances were observed for all the characters studied (Table 3 & Figure 1). The highest variance (phenotypic and genotypic) was recorded for the plant height (33.96 and 31.28) followed by harvest index (24.40 and 20.44) and biological yield per plant (11.59 and 9.53). The difference between phenotypic variance and genotypic variance is more in days to maturity (5.13) followed by harvest index (3.95), days to 50% flowering (3.23) and plant height (2.68). For meaningful comparison among characters for variability, the variance is standardized with respective mean values and is explained below as phenotypic coefficient of variation and genotypic coefficient of variation.

Phenotypic and Genotypic Coefficient of Variation (PCV & GCV):

It was observed that the estimates of PCV were higher than the corresponding GCV in all the characters studied (Table 3 & Figure 1). This indicates that the apparent variation is

Table 1: Analysis of Variance in green gram genotypes

Characters	Mean sum of squares		
	Replications (d.f.=2)	Treatments (d.f.=19)	Error (d.f.=38)
Plant Height	1.140	96.510**	2.684
Number of Primary Branches per Plant	0.015	0.090*	0.035
Days to 50% Flowering	9.266	9.610*	3.231
Number of Clusters per Plant	1.222	5.615**	0.449
Number of Pods per Plant	5.622	23.293**	2.030
Days to Maturity	2.0166	14.894*	5.139
Number of Seeds per Pod	0.174	0.653**	0.152
Pod length	0.044	0.308**	0.043
Seed index	0.008	0.086**	0.011
Biological Yield per Plant	3.671	30.650**	2.053
Harvest index	3.489	65.291**	3.956
Protein content	0.171	0.668**	0.162
Seed Yield per Plant	0.064	5.738**	0.059

** Significant at 1% level of significance
* Significant at 5%level of significance

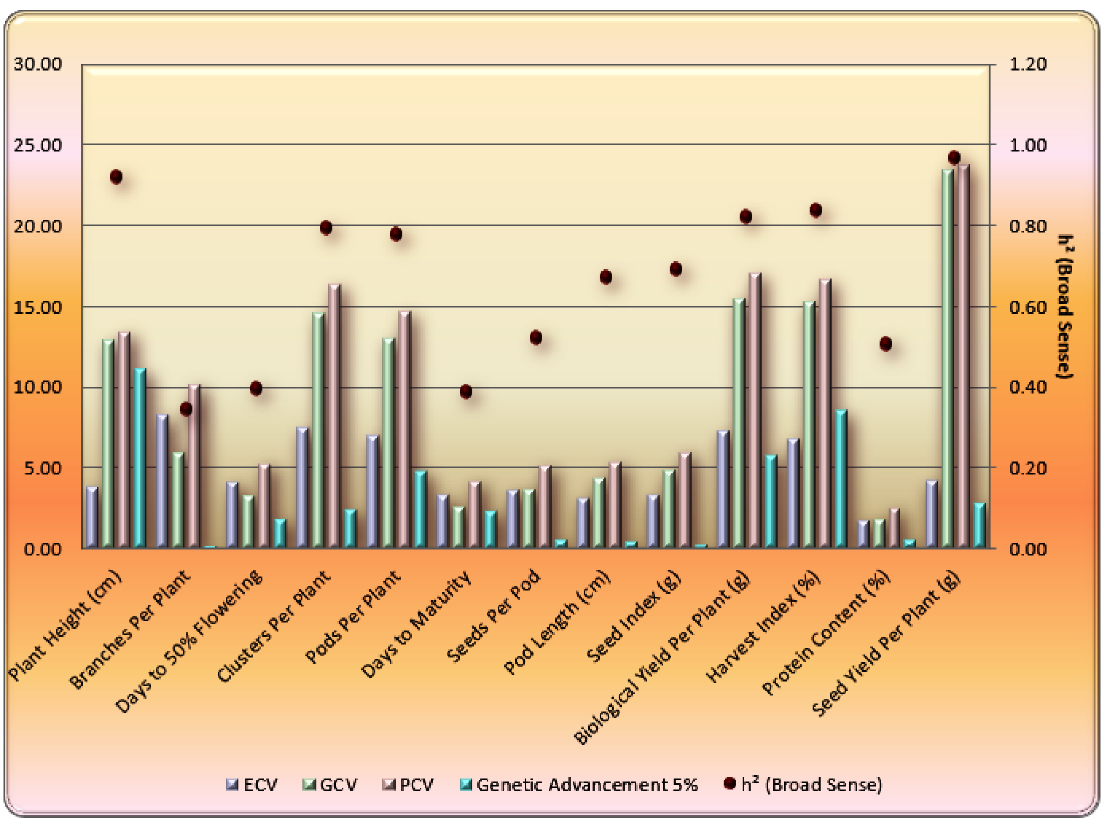

Fig. 1: Genetic parameters in greengram genotypes

Table 2: Mean performance for greengram genotypes for 13 different seed yield characters

Genotype	Plant Height (cm)	No. of Branches Per Plant	Days to 50% Flowering	No. of Clusters Per Plant	No. of Pods Per Plant	Days to Maturity	No. of Seeds Per Pod	Pod Length (cm)	Seed Index (g)	Biological Yield Per Plant (g)	Harvest Index (%)	Protein Content (%)	Seed Yield Per Plant (g)
KM11 - 584	54.73	2.06	42.66	10.73	27.46	66.67	11.70	7.04	3.36	29.56	30.52	22.93	8.95
KM11 - 583	51.93	2.13	46.00	11.40	20.73	68.67	11.20	7.11	3.26	21.06	39.51	22.26	8.32
KM11 - 585	40.20	2.00	43.33	9.73	17.60	71.33	10.70	6.92	3.44	19.25	22.81	22.53	4.40
KM11 - 582	51.00	2.26	46.00	8.26	20.60	69.33	10.96	6.92	3.27	22.70	28.14	21.80	6.38
KM11 - 551	42.40	2.35	44.00	6.53	22.40	70.00	11.06	6.86	3.01	19.32	29.94	22.13	5.78
KM11 - 587	50.53	2.20	43.33	9.46	19.13	65.33	11.03	6.71	3.36	17.07	32.51	23.06	5.53
KM11 - 564	38.20	2.26	46.00	8.60	17.80	72.67	10.30	6.59	3.07	17.18	30.57	22.06	5.24
SHARIF - 1	38.73	2.53	42.00	10.33	22.66	66.67	11.13	6.41	3.10	19.29	30.89	22.16	5.95
NAVYA	41.80	2.53	46.66	8.46	22.13	72.00	11.33	7.28	3.49	21.50	33.29	22.66	7.11
RMG - 344	37.66	2.20	46.00	10.73	16.26	66.67	10.36	6.39	3.04	17.16	24.16	22.06	4.18
RMG - 1042	42.03	2.13	43.33	9.33	22.33	69.00	11.10	6.85	3.29	17.10	29.99	23.46	5.12
RMG - 1091	40.93	2.08	41.33	9.73	18.66	67.33	10.86	6.68	3.21	17.49	23.14	22.33	4.03
RMG -1030	50.20	2.20	43.33	9.06	21.40	68.67	10.10	6.58	3.34	26.30	28.77	21.70	7.53
RMG - 975	36.91	2.46	46.66	8.01	20.88	72.00	9.70	6.04	2.81	19.55	26.25	22.73	5.12
RMG -1092	40.66	2.00	43.33	6.60	17.20	68.00	11.06	6.15	3.14	18.15	24.10	22.53	4.35
RMG -1004	40.80	2.46	40.66	9.46	22.33	68.66	10.90	6.66	3.04	17.60	33.61	22.93	5.91
RMG - 492	46.53	2.26	43.33	6.60	18.33	68.00	11.10	6.70	3.06	19.27	28.75	22.86	5.54
RMG -1014	37.18	2.46	43.33	8.66	21.78	66.66	11.03	7.12	3.33	19.31	30.12	22.53	5.81
MH - 934	36.66	2.26	42.66	9.33	22.52	72.33	11.10	6.45	3.09	19.08	38.46	22.06	7.33
SAM-RAT(C)	44.93	2.46	45.33	8.20	16.00	66.66	10.43	6.66	3.25	19.18	23.90	23.10	4.57
	43.20	2.26	43.96	8.96	20.41	68.83	10.86	6.70	3.20	19.86	29.47	22.49	5.86
	3.79	8.25	4.08	7.47	6.98	3.29	3.59	3.10	3.28	7.21	6.74	1.79	4.16
	0.94	0.10	1.03	0.38	0.82	1.30	0.22	0.12	0.06	0.82	1.14	0.23	0.14
	2.70	0.30	2.97	1.10	2.35	3.74	0.64	0.34	0.17	2.36	3.28	0.66	0.40
Min.	36.66	2.00	40.67	6.53	16.00	65.33	9.70	6.04	2.81	17.07	22.81	21.70	4.03
Max.	54.73	2.53	46.67	11.40	27.46	72.66	11.70	7.28	3.49	29.56	39.51	23.46	8.95

not only due to genotype but also due to environment. Similar results were also obtained by Narasimhulu *et al* (2013) in greengram. The magnitude of difference between PCV and GCV were found to be maximum in number of primary branches per plant (4.20) followed by days to 50% flowering (1.94) and number of clusters per plant (1.79). This indicates that these traits are more affected by the environment. Khaimichho *et al* (2014) found high magnitude difference in days to 50% flowering and number of primary branches per plant. The magnitude of difference between PCV and GCV were minimum in seed yield per plant (0.36), plant height (0.54) and protein content (0.73). This indicate that the environmental influence are less and maximum reflection of genotype into phenotype of this trait. The magnitude of PCV was recorded high for seed yield per plant (23.84) followed by biological yield per plant (17.14) and harvest index (16.76). High values of PCV were indicating the presence of high amount of variation in these traits. Similar results were also obtained by Pinchhyo and N (2016) and Shiv *et al* (2017). The magnitude of GCV were recorded high for seed yield per plant (23.48) followed by biological yield per plant (15.55) and harvest index (15.34). Similar results were also obtained by Anand *et al* (2016) and Shiv *et al* (2017).

Heritability:

The heritability estimates (Table 3 & Figure 1) varied from 34.53 (number of primary branches per plant) to 96.95 (seed

Table 3: Genetic parameters in greengram genotypes

Characters	Mean	Variance		Coefficient of variation		Heritability (%) (broad sense)	Genetic advance	Genetic advance as % of mean
		Phenotypic (Vp)	Genotypic (Vg)	Genotypic	Phenotypic			
Plant height (cm)	43.20	33.96	31.28	12.94	13.49	92.09	11.06	25.59
Number of Primary Branches per Plant	2.26	0.05	0.02	6.00	10.21	34.53	0.16	7.26
Days to 50% Flowering	43.96	5.36	2.13	3.32	5.26	39.68	1.89	4.30
Number of Clusters Per Plant	8.96	2.17	1.72	14.64	16.44	79.31	2.41	26.86
Number of Pods Per Plant	20.41	9.12	7.09	13.04	14.79	77.73	4.84	23.69
Days to Maturity	68.83	8.39	3.25	2.62	4.21	38.75	2.31	3.36
Number of Seeds Per Pod	10.86	0.32	0.17	3.76	5.21	52.22	0.61	5.60
Pod Length (cm)	6.70	0.13	0.09	4.43	5.41	67.14	0.50	7.48
Seed Index (g)	3.20	0.04	0.03	4.95	5.94	69.34	0.27	8.48
Biological Yield Per Plant (g)	19.86	11.59	9.53	15.55	17.14	82.27	5.77	29.05
Harvest Index (%)	29.47	24.40	20.44	15.34	16.76	83.78	8.53	28.93
Protein Content (%)	22.49	0.33	0.17	1.82	2.56	50.86	0.60	2.68
Seed Yield Per Plant (g)	5.86	1.95	1.89	23.48	23.84	96.95	2.79	47.62

yield per plant). High heritability (>60%) was identified for pod length (67.14), seed index (69.34), number of pods per plant (77.73), number of clusters per plant (79.31), whereas very high heritability (>80%) were identified for biological yield per plant (82.27), harvest index (83.78), plant height (92.09) and seed yield per plant (96.95). High heritability of these traits indicates that there is a close correspondence between the genotype and phenotype and selection can be done for these characters. Similar results were also observed by Anand *et al* (2016) and Shiv *et al* (2017).

Genetic Advance:

A perusal of genetic advance (Table 3 & Figure 1) revealed that it was high for plant height (11.06) followed by harvest index (8.53) and biological yield per plant (5.77). Results also revealed high genetic advance as per mean (>20%) for seed yield per plant (47.62), biological yield per plant (29.05) and harvest index (28.93). The high values of genetic advance showed that these traits are governed by additive genes and selection will be rewarding. The characters viz., number of pods per plant, number of clusters per plant, biological yield per plant, harvest index, plant height, seed yield per plant showed high heritability accompanied with high genetic advance, which indicates that most likely the heritability is due to additive gene effects and selection may be effective.

CONCLUSION

The present study revealed significant differences for all the characters indicating sufficient variation among genotypes. The genotypes KM11 584, KM11 583, RMG 1030, MH 934, NAVYA and SHARIF were identified as desirable genotypes or utilization in the breeding programme with more number of primary branches per plant, clusters per plant, seeds per plant, harvest index and seed yield per plant. Harvest index, biological yield per plant, number of clusters per plant, number of seeds per pod exhibited high estimates of GCV, PCV, heritability and genetic advance as percent of mean. Thus it is concluded that priority should be given to these characters during selection for future greengram yield improvement programme.

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REFERENCES

Anand G, Anandhi K and Paulpandi VK. 2016. 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* **7**(2):434-434. url: https://dx.doi.org/10.5958/0975-928x.2016.00054.5. doi: 10.5958/0975-928x.2016.00054.5

Anonymous 2018. Annual Report 2017-18 Directorate of Pulse development DPD/Pub./TR/29/2017-18.

Biradar KS, Salimath PM and Ravikumar RL. 2007. Genetic studies in greengram and association analysis. *Karnataka Journal of Agricultural Sciences* **20**(4):843-844.

Burton GW. 1952. Quantitative inheritance in grasses proceedings. *International Grassland Congress* **1**:227-283.

Candolle AD 1959. Origin of cultivated plants (New York, N. Y.: Hafner Publication Company).

Fisher RA. 1936. The correlation between relative on the supposition of genotypes grown in Kumaun Himalaya. *Indian Journal of Genetics and Plant Breeding* **66**(1):37-38.

Gw B and Devane EH. 1953. Estimating heritability in tall Fesscue from replicated clonal marterial. *Agronomy Journal* **45**:474-481.

Johnson HW, Robinson HF and Comstock RE. 1955. Genotypic and Phenotypic Correlations in Soybeans and Their Implications in Selection 1. *Agronomy Journal* **47**(10):477-483. url: https://dx.doi.org/10.2134/agronj1955.00021962004700100008x. doi: 10.2134/agronj1955.00021962004700100008x

Karpechenko GD. 1925. Chromosomes of phaseonline. *Bulletin Application of Botany* **14**:143-148.

Khaimichho EB, Hijam L, Kk S and Mukherjee S. 2014. Genetic control and character association estimates of yield and yield attributing traits in some mungbean genotypes. *Journal of Crop and Weed* **10**(2):82-88.

Lush. 1949. Inter-se correlation and regression of characters. *Proceeding of American Society of Animal Production* **33**:293-301.

Narasimhulu R, Naidu NV, Priya SM, Reddy RV and Khp. 2013. Genetic variability and association studies for yield attributes in mungbean (Vigna radiata (L.) wilczek). *Indian Journal of Plant Sciences* **2**(3):82-86.

Pinchhyo B and N T. 2016. Studies on genetic variability, correlation and path analysis in greengram (Vigna radiata L. Wilczek) germplasm. *International Journal of Agriculture Sciences* **8**(51):2267-2272.

Shiv A, Ramtekey V, Vadodariya GD, Modha KG and Patel RK. 2017. Genetic Variability, Heritability and Genetic Advance in F3 Progenies of Mungbean [Vigna radiata (L.) Wilczek]. *International Journal of Current Microbiology and Applied Sciences* **6**(12):3086-3094. url: https://dx.doi.org/10.20546/ijcmas.2017.612.360. doi: 10.20546/ijcmas.2017.612.360

Singh AK and Bhatt BP. 2013. Effects of foliar application of zinc on growth and seed yield of late-sown lentil. *Indian J. Agril. Sci* **83**(6):622-626.

Singh AK, Kumar P and Chandra N. 2013. Studies on yield production of mung bean (Vigna radiate) sown at different dates. *J. Environ. Biol* **34**:1007-1011.

Singh AK, Singh SS, Prakash V, Kumar S and Dwivedi SK. 2015. Pulses production in India: Present status, bottleneck and way forward. *Journal* **2**(2):75-83.

Srivastava and Singh G. 2012. Genetic variability, correlation and path analysis in mungbean (Vigna radiata (L.) Wilczek). *Indian Journal of Life Science* **2**(1):61-65.

Vavilov NI. 1951. The Origin, Variation, Immunity and Breeding of Cultivated Plants. *Soil Science* **72**(6):482-482. url: https://dx.doi.org/10.1097/00010694-195112000-00018. doi: 10.1097/00010694-195112000-00018

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