

Original Research Article

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Trait Associations and Path Coefficient Analysis for Seed Yield and Morphological Characters in Greengram (*Vigna radiata* (L.) Wilczek.)

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ABSTRACT

Genetic variability, heritability along with genetic advance of traits, their association and direct and indirect effects on yield are essential for crop improvement. One hundred and three greengram genotypes were studied to assess variability and degree to which various plant traits associate with seed yield. Sufficient genetic variability was observed for plant height, pods per plant and seed yield. Number of primary branches per plant, number of clusters per plant and pod length showed lesser variability while 100 seed weight and harvest index exhibited intermediate range of variability. Moderate to high heritability estimates were found for all traits. Number of primary branches per plant, pod length and 100-seed weight exhibited negative and non significant genotypic and phenotypic correlations with seed yield. Plant height showed positive non-significant genotypic and significant phenotypic correlation. Number of clusters per plant, number of pods per plant and harvest index showed positive significant genotypic and phenotypic correlations with seed yield. Positive direct effects were exerted through number of pods per plant, pod length, 100 seed weight and harvest index while number of primary branches per plant, plant height and number of clusters per plant had negative direct effects. The present findings could be useful for establishing selection criteria for high seed yield in the greengram breeding.

Keywords

Correlation, Genetic variability, Greengram, Path analysis

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Introduction

Greengram (*Vigna radiata* L.) is an important pulse crop and occupies a good position due to its high seed protein content and ability to store the soil fertility through symbiotic nitrogen fixation. Thus, it contributed

significantly to enhancing the yield of subsequent crops. Additionally, it is well suited to both dry areas and irrigated conditions as well.

Primary objective of breeder is to increase the seed yield. Generally, yield represents the

final character resulting from many developmental and biochemical process which occur between germination and maturity. Before yield improvement can be realized, the breeder needs to identify the cause of variability in seed yield in any given environment, since fluctuations in environment generally effects yield through its components. Knowledge of heritability and genetic advance of the characters is a pre-requisite for the improvement through selection. Seed yield in greengram is a complex character like other crops, and is determined by various components. Knowledge of genetic variability existing among different parameters is important in crop improvement. Heritability, which measures phenotypic variance and is attributable to genetic causes, is another important consideration for a successful breeding program. Heritability with genetic advance helps in understanding the mode of inheritance of quantitative traits. Correlation coefficient analysis is a handy technique, which elaborates the degree and extent of relationship among important plant characters and it provides basic criteria for selection and leads to directional model based on yield and its components in the field experiments. Yet, the information it supplies about the nature of association is often incomplete. Path coefficient analysis, on the other hand, is an efficient statistical technique specially designed to quantify the interrelationship of different components and their direct and indirect effects on seed yield. Through this technique yield contributing characters can be ranked and specific traits producing a given correlation can be heeded Information regarding inheritance of grain yield and its closely related components is essential to efficiently exploit the available genetic diversity in greengram for seed yield.

Present research work was planned with the following objectives. First objective was to

assess the genetic variability existing among morphological as well as yield parameters along with their heritability and genetic advance for understanding the mode of inheritance of quantitative traits in greengram. Secondly, genetic correlations and direct and indirect effects of economically useful traits with seed yield were also investigated

Materials and Methods

The germplasm used in the present study consisted of about 103 greengram lines laid out in RBD design with two replications at College Farm, Rajendranagar during Kharif 2014. Each genotype was grown in a three rows of 4 m length, spaced 30 cm apart with a 10 cm distance between plants within the row. Appropriate agronomical operations and timely plant protection measures were followed to raise the healthy crop.

Data were recorded on five randomly selected plants in each entry of replication for plant height (cm), number of primary branches, number of cluster per plant, number of pods per plant, pod length (cm), 100 seed weight (g) and seed yield per plant (g) while, data relating to days to 50 per cent flowering, days to maturity, protein content (%) and harvest index (%) was recorded on whole plot basis. The data was statistically analyzed using average of five plants.

Results and Discussion

The analysis of variance (Table 1) revealed highly significant ($p < 0.01$) to significant ($p < 0.05$) differences for all characters. This suggested adequate amount of genetic variability among genotypes that may be helpful for yield improvement by selection. A thorough probe into mean data revealed that primary branches ranged from 1.20 to 3.40 (Table 2). Maximum primary branches were produced by KM 11 564 (3.13) whereas the

minimum number was recorded for LGG 574 (1.20). Plant height ranged from 25.03 to 49.37 cm with maximum contribution from RM 12 -12 while minimum contribution by ML 267. Clusters per plant ranged from 5.40 to 10.83. Co 3 ranked first in cluster per plant and SML 134-9 had lowest production. Pods per plant ranged from 11.76 to 29.63. K 851 produced maximum number of pods per plant and minimum number was produced by HUM 12. Maximum and minimum pod length was recorded in IPM 02-13 and MGG 398 respectively. Maximum and minimum 100-seed weight was recorded in SML 668 and CZMS 1 respectively. Contemplation of mean values for seed yield per plant that cultivar KM 11-564 proved its superiority by contributing maximum towards this trait while IPM 2-03 was found poor with lowest contribution. Harvest index ranged from 27.07 to 38.90. Maximum harvest index was produced by LGG 562 and minimum was produced by Madhira Mung.

Genetic components

The magnitude of phenotypic coefficients of variation was higher than genotypic coefficients for all the traits under study (Table 2) showing greater influence of environment on these traits. These results are in accordance with the finding of Yadav *et al.*, (2017) who also reported similar effects of environment. In the present study, number of pods per plant were shown to have maximum genotypic coefficient of variation GCV (32.84 %) followed by seed yield (29.52%) suggesting substantial amount of genetic variability and are in accordance with Degefa *et al.*, (2014). Sufficient genetic variability was observed for plant height, number of primary branches, pods per plant and seed yield which showed that these traits can be recommended for direct selection. Variability in green gram for different traits have been studied earlier by many workers Aparna *et*

al.,(2014), Ahmed *et al.*,(2014), Roy and Yadav *et al.*, (2017). The extent of variability among the genotypes with respect to different quantitative characters was estimated in terms of PCV and GCV. The PCV and GCV ranged from 7.73 (harvest index) to 33.01 (number of pods per plant) and respectively 5.15 (pod length) to 32.84 (number of pods per plant). Moreover, in the present study, high heritability was manifested by plant height, number of pods per plant, number of clusters per plant, 100 seed weight seed yield and harvest index. Previously, high heritability for these traits has also been reported by Itafa *et al.*, (2014), Das and Barua (2015). These traits were expected to remain stable under varied environmental conditions, as environment is less influential on highly heritable traits and could easily be improved by applying selection pressure. Narasimhulu *et al.*, (2014) also observed high genetic advance for pods per plant as suggested by our findings. In present study, lowest genetic advance was observed (0.93) for days to maturity followed by pod length (0.94) and is comparable to the findings of Lalinia and Khameneh (2014) who also reported lowest genetic advance for these traits. High heritability coupled with high genetic advance was seen in number of primary branches per plant and number of pods per plant and seed yield per plant indicating that these traits were controlled by additive genes and can easily be transferred to succeeding generations. Under present investigation heritability was calculated in broad sense that includes both additive as well as non-additive gene effects of heritable nature of these two characters. Whereas, despite of higher GCV and PCV, number of seeds per pod and pod length were recorded with relatively lesser heritability portion of variation indicating that heritability is a property not only of a character but also of the population and the environment to which genotypes were subjected to. Therefore, its ultimate value depends on the magnitude of all

the component variance in totality and not to be viewed independent of each other to determine heritable portion of variation. Significantly higher estimates of genetic components (GCV, PCV, h^2 and GA) for seed yield per plant, number of pods per plant and number of primary branches per plant have also been reported by Pavan *et al.*, (2019) in different sets of greengram germplasm.

Genotypic and phenotypic correlations

The phenotypic correlation (r_p) estimates among the 12 characters are presented in Table 3. The r_p estimates ranged from 0.647 between number of clusters per plant and seed yield per plant to -0.152 between 100-seed weight and seed yield per plant. Of these 66 r_p estimates, 15 were significant. The genotypic correlation (r_g) estimates (Table 3) ranged from 0.697 between number of clusters per plant and seed yield per plant to -0.303 between days to maturity and pod length. Eighteen of 66 r_g estimates were found to be significant. In general the r_p and r_g estimates followed almost similar trend for all the characters under study. The magnitude of r_g was greater than r_p in almost all cases indicating higher genotypic correlation in case of positive association and lower in case of negative association would reinforce selections based on phenotype. Of the association of character components plant height, number of clusters per plant, and number of pods per plant, pod length and number of seeds per pod showed highly significant positive correlation with seed yield per plant both at phenotypic and genotypic level. Similar high positive correlation was reported by many workers Itefa *et al.*, (2014) for number of pods per plant, number of seeds per pod, plant height and 100 seed weight. Keerthiga *et al.*, (2017) for number of pods per plant, number of clusters per plant and

number of seeds per pod. Hundred seed weight, exhibited moderate positive correlation with yield at both phenotypic and genotypic level. Forty two out of 55 phenotypic correlation among the yield components were positive out of which five were significant where as only one phenotypic correlation was negatively significant. In general the phenotypic and genotypic correlation estimates followed almost similar trend. The characters number of seeds per pod, number of pods per plant and number of clusters per plant showed high positive correlation among themselves both at genotypic and phenotypic level which is in close agreement with the report of Kanimoli *et al.*, (2018) and Pavan *et al.*, (2019). Number of primary branches per plant showed moderate but significant positive association with plant height, and plant height with number of pods per plant and harvest index. Number of seeds per pod also had moderate positive association with 100 seed weight whereas days to maturity also have moderate non-significant positive correlation with number of clusters per plant. Days to maturity had a moderate but negative correlation with pod length. Number of clusters per plant showed highly significant positive correlation with number of pods per plant but low non-significant positive correlation with survival harvest index. Correlation of number of seeds per pod was non significantly negative correlated with protein content. Correlation study in greengram for different biometrical traits have been reported by earlier scientist Lalinia and Khameneh (2014), Aparna *et al.*, (2015) and Pavan *et al.*, (2019). Thus the significant association of number of clusters per plant, number of pods per plant and number of seeds per pod with seed yield per plant and among them indicated that selection of genotype based on these characters will be effective for yield improvement (Table 4).

Table.1 Analysis of variance (mean squares) for yield and yield component characters in Greengram

Source of variation	df	Days to 50 % flowering	Days to maturity	No.of primary branches	Plant height (cm)	No.of clusters/plant	No.of pods/plant	Pod length (cm)	No.of seeds/pod	100 seed wt. (g)	Seed yield /plant (g)	Protein content (%)	Harvest index (%)
Replications	2	6.96	24.77	4.49	40.28	10.24	24.94	31.12	1.19	0.06	18.91	0.59	1.14
Treatments	102	11.94**	38.53**	5.67**	72.03**	14.04**	214.63**	2.52**	1.48**	0.26**	49.37**	6.74**	24.76**
Error	204	5.66	7.14	0.85	3.76	2.95	9.19	1.49	0.64	0.01	2.38	0.39	1.21

Significant at 5% (*) and 1% (**) levels, respectively

Table.2 Estimation of genetic parameters and percentage contribution of different characters towards genetic divergence

Characters	Mean	Range		Coefficient of variation		Heritability (Broad sense)	Genetic advance as % over mean	% Contribution of different characters towards divergence
		Min	Max	Genotypic (GCV)	Phenotypic (PCV)			
Days to 50% flowering	33.63	33.28	42.43	12.95	18.87	68.63	6.39	0.29
Days to maturity	71.28	64.54	77.31	5.57	7.84	71.08	9.32	2.17
No. of primary branches per plant	2.16	1.20	3.40	21.76	32.24	67.49	71.04	5.34
Plant height (cm)	36.40	25.03	49.37	15.91	17.41	91.39	32.63	8.2
No. of clusters/plant	7.79	5.40	10.80	15.31	15.71	91.84	44.46	2.86
No. of Pods per plant	20.84	11.76	29.63	32.84	33.01	93.37	74.65	22.51
Pod length (cm)	7.15	4.92	11.83	5.15	8.33	57.02	9.38	0.13
No. of seeds per pod	10.52	8.40	12.40	15.42	20.2	34.07	24.2	0.25
100 Seed weight (g)	3.25	2.20	4.80	11.61	14.79	78.50	20.26	2.03
Protein content (%)	21.77	19.76	24.35	2.61	3.03	75.06	16.3	4.41
Harvest index (%)	33.70	27.07	38.90	5.34	7.73	68.21	15.99	16.86
Seed yield per plant (g)	7.56	4.13	11.02	29.52	31.12	94.86	89.14	34.95

Table.3 Correlation coefficient between seed yield and yield contributing characters in greengram

		days to 50 % flowering	days to maturity	primary branches	plant height	No.of clusters/plant	no.of pods/plant	pod length	no.of seeds/pod	100 seed wt	protein content (%)	harvest index (%)	seed yield /plant (g)
Days to 50% flowering	P	1.00	0.206	0.251	-0.003	0.136	0.067	-0.202	-0.044	-0.046	0.029	-0.173	0.225
	G	1.00	0.239	0.261	-0.001	0.141	0.077	-0.204	-0.055	-0.051	0.052	-0.186	0.275*
Days to maturity	P		1.00	0.378**	0.146	0.242	0.163	-0.026	-0.016	-0.074	-0.069	0.168	0.269*
	G		1.00	0.386**	0.169	0.257	0.174	-0.303*	-0.012	-0.090	-0.071	0.177	0.298*
Primary braches	P			1.00	0.285*	0.269	0.069	0.162	0.048	0.126	0.115	0.106	0.237*
	G			1.00	0.298*	0.277	0.102	0.187	0.055	0.130	0.120	0.123	0.251*
Plant height	P				1.00	0.518**	0.373*	0.059	0.032	0.025	0.019	0.247*	0.323*
	G				1.00	0.575**	0.435**	0.137	0.023	0.076	0.114	0.273*	0.392*
No. of clusters/plant	P					1.00	0.640**	0.056	0.123	0.184	0.077	-0.409	0.647**
	G					1.00	0.672**	0.072	0.138	0.192	0.160	-0.463	0.697**
No. of pods/plant	P						1.00	0.308**	0.198	0.149	0.136	-0.142	0.521**
	G						1.00	0.350**	0.220	0.178	0.231	-0.133	0.546**
Pod length	P							1.00	0.070	0.422**	-0.005	0.113	0.246
	G							1.00	0.081	0.595**	-0.045	0.114	0.292*
No. of seeds/pod	P								1.00	0.311*	-0.196	0.088	0.560**
	G								1.00	0.316*	-0.286	0.091	0.594**
100 Seed wt	P									1.00	0.017	0.076	-0.152
	G									1.00	0.032	0.085	-0.165
Protein content	P										1.00	0.086	0.144
	G										1.00	0.097	0.138
Harvest index (%)	P											1.00	0.021
	G											1.00	0.032

Significant at 5% (*) and 1% (**) levels respectively

Table.4 Direct and indirect (genotypic) effects of different contributing traits towards seed yield in greengram

		Days to 50 % flowering	Days to maturity	Primary Branches	Plant height	No.of clusters /plant	No.of pods/plant	Pod length	No.of seeds /pod	100 seed wt	Protein content (%)	Harvest index (%)	Seed yield /plant (g)
Days to 50% flowering	P	0.023	0.028	0.001	0.001	0.001	0.004	-0.003	-0.003	-0.014	0.001	0.093	0.225
	G	0.092	0.114	0.112	0.008	0.057	0.037	-0.018	-0.026	0.025	-0.014	0.104	0.275*
Days to maturity	P	0.002	0.051	0.022	0.002	0.004	-0.023	0.001	-0.006	-0.009	-0.005	0.076	0.269*
	G	0.006	0.175	0.111	0.014	0.068	-0.084	0.022	0.336	0.077	-0.009	0.124	0.298*
Primary braches	P	0.045	0.024	0.049	0.001	0.001	0.015	0.000	0.025	-0.009	0.001	0.061	0.237*
	G	0.062	0.118	0.266	0.005	0.059	0.119	-0.141	0.256	0.031	0.005	0.13	0.251*
Plant height	P	0.025	0.029	-0.004	0.076	0.021	0.003	-0.010	0.107	-0.016	-0.002	0.012	0.323*
	G	0.008	0.115	-0.199	0.299	0.152	-0.022	-0.121	0.222	0.030	-0.008	0.044	0.392*
No. of clusters/ plant	P	0.119	0.043	-0.043	0.012	0.319	0.010	0.013	0.064	0.123	0.001	0.051	0.647**
	G	0.013	0.146	-0.201	0.501	0.363	0.185	0.215	0.156	0.056	0.004	0.073	0.697**
No. of pods/plant	P	0.007	0.000	-0.041	0.009	0.009	0.511	0.015	0.003	-0.006	-0.003	0.019	0.521**
	G	0.095	0.031	0.354	0.103	0.103	0.579	0.128	0.102	0.261	0.041	0.058	0.546**
Pod length	P	-0.022	0.003	0.231	0.003	0.019	0.049	0.255	0.001	-0.006	0.004	0.001	0.246
	G	-0.097	-0.053	0.387	0.108	0.103	0.172	0.274	0.037	0.103	0.126	0.011	0.292*
No. of seeds/pod	P	-0.005	-0.002	0.002	0.001	0.018	0.032	0.001	0.005	0.174	0.001	0.009	0.560**
	G	-0.173	-0.014	0.121	0.157	0.037	0.106	0.006	0.462	0.498	0.009	0.021	0.594**
100 Seed wt	P	0.007	0.001	0.006	0.009	0.002	0.019	0.001	0.001	-0.016	0.002	0.003	-0.152
	G	0.015	-0.065	0.017	0.002	0.157	0.115	0.019	0.017	-0.222	0.006	0.075	-0.165
Protein content	P	0.002	0.000	0.002	0.017	-0.122	0.004	0.002	0.003	0.032	-0.013	0.004	0.144
	G	0.073	-0.087	0.050	0.050	-0.207	0.127	0.135	0.009	0.092	-0.064	0.02	0.138
Harvest index (%)	P	0.022	0.002	0.018	0.061	0.005	0.000	0.017	0.002	0.052	0.003	0.111	0.121
	G	0.074	-0.010	0.151	0.151	0.074	0.201	0.092	0.031	0.174	0.011	0.133	0.132

A perusal of results revealed greater genotypic correlations than their corresponding phenotypic correlations indicating the preponderance of genetic variance in expression of characters. The characters, number of pods per plant, number of clusters per plant and plant height showed strong and positive correlation with seed yield and also among themselves. Therefore, these are considered to be the most important characters on which selection pressure can be exercised to improve the yield potential of greengram. Though correlation coefficients are important in determining the yield components, the extent of contribution of a particular trait to a dependable variable like yield may hardly be judged from them. In such cases, path coefficient analysis helps in partitioning the association into direct and indirect effects. Positive correlations occur due to the changes of genes supplying precursors. On the other hand negative correlations arise due to competition among traits for common precursors which is restricted supply (Manoj and Kumar, 2015).

Path analysis

The correlation values decide only the nature and degree of association existing between pairs of characters. A character like seed yield is dependent on several mutually associated component characters and change in any one of the components is likely to affect the whole network of cause and effect relationship. This in turn might affect the true association of component characters, both in magnitude and direction and tend to vitiate association of yield and yield components. Hence it is necessary to partition the phenotypic correlations of component characters into direct and indirect effects (Itefa *et al.*, 2014)

Critical analysis of the results of path analysis for seed yield revealed that direct effect of number of pods per plant, number of primary

branches and number of clusters per plant were high and positive followed by direct effects of plant height, pod length and harvest index, indicating that they are the major contributing characters to seed yield in greengram. These three characters also showed significant and positive correlation among themselves and with plant height, number of clusters per plant and number of pods per plant indicating that indirect selection based on these characters may be given importance while formulating the selection criteria. Direct effect of days to 50 per cent flowering, number of pods per plant and 100 seed weight was low and negative.

Similar trends were evident from the studies of Bisht *et al.*, (2014), Itefa *et al.*, (2014) and Narasimhulu *et al.*, (2013). Plant height followed by number of pods per plant had negative direct influence on seed yield but they had significant and positive association with seed yield. This may be due to their high positive indirect contribution via harvest index. Hence, the indirect effects of most of the characters were found positive and high via harvest index. Thus, harvest index emerged as most important direct yield contributing traits in present study. The direct effects of remaining characters on seed yield at phenotypic level were not consistent in nature to corresponding direct effect at genotypic level. Phenotypic path analysis, number of primary branches per plant, clusters per plant, and seeds per pod showed negligible positive direct effect on seed yield per plant while its direct effects at genotypic level was considerably negative. At genotypic level, number of pods per plant had high positive direct effects. Thus, number of pods per plant also appeared as important direct yield components at genotypic level. Number of pods per plant was identified as important yield component by Lalinia and Khameneh (2014), Kanimoli *et al.*, (2017) and Pavan *et al.*, (2019).

Days to flowering, days to maturity, plant height, pod length, 100 seed weight and protein content exhibited substantial positive indirect effects via other traits. Occurrence of negative as well as positive indirect effects of yield attributing traits on seed yield via one or other traits simultaneously presents a complex situation wherein a compromise has to be made for different yield attributes in determining the ideotype for high seed yield in greengram. It was concluded that characters with positive effects should be significantly considered in selection criteria for yield improvement in mungbean breeding programs.

In aforesaid discussion it can be concluded that the magnitude of all the phenotypic variances was higher than genotypic variances showing the pronounced effects of environment. Higher heritability showed additive effects and more gain of selection in next generations when coupled with high genetic advance. The seed yield is an important parameter among all the morphological as well as yield traits. Improvement in seed yield in greengram could be brought through selection of component characters directly concerned with final yield in pulse crops like number of primary branches per plot, number of pods per plant, pod length, plant height and harvest index which showed positive direct effects.

References

- Ahmad HB, Rauf S, Rafiq CM, Mohsin AU, Shahbaz U and Sajjad, M. Genetic variability for yield contributing traits in mungbean (*Vigna radiata* L.). *Journal of Global Innovation in Agricultural and Social Sciences*. 2014; 2(2): 52-54.
- Aparna Raturi, Singh SK, Vinay Sharma and Rakesh Pathak. Genetic variability, heritability, genetic advance and path analysis in mungbean [*Vigna radiata* (L.) Wilczek]. *Legume Research*. 2015; 38 (2): 157-163.
- Bisht IS, Niharika Singh DP and Khulbe RK. Genetic variability and correlation studies in advance inter-specific and inter-varietal lines and cultivars of Mungbean (*Vigna radiata*). *Journal of Food Legumes*. 2014; 27(2): 155-157.
- Das RT and Barua PK. Association Studies for Yield and its components in Green Gram. *International Journal of Agriculture, Environment and Biotechnology*. 2015; 8(3): 561.
- Degefa I, Petros Y and Andargie M. Genetic variability, heritability and genetic advance in Mungbean (*Vigna radiata* (L.) Wilczek) accessions. *Plant Science Today*. 2014; 1(2): 94-98.
- Dhoot R, Modha KGD, Kumar and Dhoot M. Correlations and Path Analysis Studies on Yield and its Components in Mungbean (*Vigna radiata* (L.) Wilczek). *International Journal of Current Microbiology and Applied Sciences*. 2017; 6(5): 370-378.
- Itefa D, Yohannes P and Mebeaselassie A. Correlation and path coefficient analysis among seed yield traits of Mungbean (*Vigna radiata* (L.) Wilczek) accessions in Ethiopia. *Annual Research & Review in Biology*. 2014; 4(1): 269-284.
- Kanimoli Mathivathana M, Samyuktha SM, Deepa Priya R, Mariyammal I, Bharathi P, Jagadeeshselvam N, Karthikeyan A, Sudha M, Pandiyan M, Karthikeyan G, Vanniarajan C, Raveendran M, Senthil N. Association and Path Analysis of Yield and Yield Components in the RIL Population of *Vigna radiata* × *Vigna umbellata*. *International Journal of Current Microbiology and Applied Sciences*. 2018; 7(4): 1231-1235
- Keerthiga, S., S. Sen., H.R. Pandya and K.G.

- Modha. Correlation and Path Analysis in F4 Progenies of Green Gram [*Vigna radiata* (L.) R. Wilczek] for Seed Yield and its Attributes. *International Journal of Current Microbiology and Applied Sciences*. 2018; 7(1): 710-719.
- Lalinia AA and Khameneh MM. Multivariate statistical method for determining interrelationships among seed yield and related characters in Mungbean. *International Journal of Farm and Allied Sciences*. 2014; 3(3): 274-281.
- Manoj Katiyar, Amit Kumar. Genetics Analysis of Yield and Its Component Traits in Mungbean (*Vigna radiata* L. Wilczek). *International Journal of Innovative Research and Development*. 2015; 4 (2):119-121.
- Narasimhulu R, Naidu NV, Shanthi P, Rajarajeswari V and Reddy K.H.P. Genetic variability and association studies for yield attributes in mungbean (*Vigna radiata* L. Wilczek). *Indian Journal of Plant Sciences*. 2013; 2 (3): 82-86.
- Pavan K, Reddy P and Chandra Mohan Mehta. Estimation of variability through genetic parameters and identification of superior pure lines for yield attributing traits in green gram [*Vigna radiata* (L.)]. *Journal of Pharmacognosy and Phytochemistry*. 2019; SP3: 55-61
- Yadav SM, Ved Prakash and Khedar, OP. Gene action of yield and its contributing characters in Mungbean [*Vigna radiata* (L.) Wilczek] under different Environments. *Journal of Pharmacognosy and Phytochemistry*. 2017; 6(5): 999-1003.
- Narasimhulu R, Naidu NV, Shanthi P, Rajarajeswari V and Reddy K.H.P.

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