



ISSN (E): 2277-7695

ISSN (P): 2349-8242

NAAS Rating: 5.23

TPI 2023; 12(12): 841-844

© 2023 TPI

www.thepharmajournal.com

Received: 02-09-2023

Accepted: 05-10-2023

SS Kamble

Senior Research Assistant, Plant Breeding, National Agricultural Research Project, Aurangabad, Maharashtra, India

Dr. DK Patil

Principal Scientist, Plant Breeding, National Agricultural Research Project, Aurangabad, Maharashtra, India

VB Rathod

M.Sc. Agri. (GPB), College of Agriculture, Badnapur, Maharashtra, India

Dr. VK Gite

Scientist, Plant Breeding, Agricultural Research Station Badnapur, Maharashtra, India

Correlation and path analysis for yield and yield contributing characters in greengram (*Vigna radiata* (L.) Wilczek)

SS Kamble, Dr. DK Patil, VB Rathod and Dr. VK Gite

Abstract

The correlation coefficient and path analysis studies undertaken for eleven yield and yield contributing characters in 40 germplasm lines along with one check BM 2003-2 in greengram during *Kharif* 2016-17 at Agricultural Research Station, Badnapur. Observations were recorded for 11 characters *viz.*, days to 50% flowering, days to maturity, plant height, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length, number of seeds per pod, 100 seed weight, protein content and seed yield per plant. The seed yield per plant was significantly and positively correlated with number of clusters per plant, number of pods per plant, 100 seed weight, pod length and number of seeds per pod. Path analysis revealed that pod length had the maximum positive direct effect on seed yield per plant followed by number of pods per plant, number of clusters per plant. These results suggested that selection could be practiced for the characters pod length, number of pods per plant, number of clusters per plant, 100 seed weight and seeds per pod for genetic improvement and high seed yield per plant in green gram.

Keywords: Greengram, genotype, correlation coefficient

Introduction

Greengram (*Vigna radiata* (L.) Wilczek) ($2n=2x=22$) is one of the most important edible food legumes of Asia and in India it contributes significant dietary protein supply in predominantly cereal rich diet. India is considered its native place. It is self-pollinated, semi-erect and short duration crop cultivated in *Kharif*, *Rabbi* and *summer* seasons. It's cultivation can improve all over properties of soil through nitrogen fixation from the atmosphere (Asthana, 1998) [2]. Greengram contains 22-28% protein, 60-65% carbohydrates, 3.5 -4.5 fiber, 1.0-1.5% fat and 4.5-5.5% ash. It is rich source of vitamins, essential amino acids and protein. Dal of greengram is widely used by most of the people as a rich source of digestible protein. In India during the year 2015-2016 greengram was grown on an area about 2.45 m ha with an annual production of 2.13 m tonnes and average yield of 632 kg/ha.

Character association provides information about the characters that are correlated in a desirable direction with each other and also with the seed yield in improving the yield. These correlations can be partitioned by path analysis into direct and indirect effects will be an added advantage and helps in selection to a greater extent for improvement of yield. Correlation analysis is a handy technique, which elaborate the degree and extent of relationship among important plant characters and it provides basic criteria for selection and leads to direction based on yield and yield components. On the other hand path analysis is an efficient statistical technique specially designed to quantify the interrelationship of different components and their direct and indirect effects on seed yield. Therefore the present study was undertaken to assess the correlation and path analysis in respect to various desirable characters in 41 genotypes of green gram.

Materials and Methods

The experiment was carried out to study the correlation and path analysis in Green gram (*Vigna radiata* (L.) Wilczek) with 40 germplasm lines of green gram alongwith one check BM 2003-2 during *Kharif* 2016-17 at Agriculture Research Station, Badnapur. The material used in the present study received from Agriculture Research Station, Badnapur. The material was sown in experimental field using a randomized block design with two replications and spacing was 45 cm X10 cm. Observations of five randomly selected plants from each replication were recorded for eleven characters *viz.*, days to 50% flowering, days to maturity,

Corresponding Author:

SS Kamble

Senior Research Assistant, Plant Breeding, National Agricultural Research Project, Aurangabad, Maharashtra, India

plant height, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length, number of seeds per pod, 100 seed weight, protein content and seed yield per plant. The genotypic co-variance was calculated as per Johnson *et al.* (1955) [5]. Appropriate variances and co-variances were used for calculating phenotypic and genotypic correlation coefficients (Johnson *et al.*, 1955) [5]. Path coefficient analysis was done according to the method suggested by Dewey and Lu (1959) [3].

Results and Dissection

Analysis of variance expressed the significance differences for all the characters studied. The genotypic and phenotypic correlations for eleven characters studied are presented in Table 1. The correlation either in positive or negative directions are described in this result. In general, the genotypic correlations were higher than the corresponding phenotypic correlations indicating dominance of genetic variance on expression of characters. Seed yield per plant exhibited positive significant correlation with number of clusters per plant (0.7606, 0.5901), number of pods per plant (0.6791, 0.5110), 100 seed weight (0.2655, 0.1952), pod length (0.2475, 0.1909) and number of seeds per pod (0.2105, 0.2326). These results were in conformity with earlier findings of Maddewad (2005) [7] for 100 seed weight, pod length and number of seeds per pod and Sreelakshmi and Reddy (2011) [16] for number of clusters per plant, number of seeds per pod and number of pods per plant. Similar results were also observed by Titumeer *et al.* (2014) [19] for number of pods per plant, number of seeds per pod and pod length, Poonam Rathor *et al.* (2015) [8] for number of clusters per plant, number of pods per plant, 100 seed weight and by Thanga *et al.* (2015) [18] for number of clusters per plant, number of pods per plant, 100 seed weight and number of seeds per pod.

The characters plant height (0.1225, 0.1387), number of pods per cluster (0.0696, 0.0562) and days to 50% flowering (0.0571, 0.0754) showed positive but non-significant correlation with seed yield. These results are in agreement with the findings of Rahim *et al.* (2010) [10] for days to 50% flowering and Kumar *et al.* (2013) [6] and Rathor *et al.* (2015) [8] for plant height. The characters days to maturity (-0.0646, -0.0927) and protein content (-0.1193, -0.0814) display negative and non-significant correlation with seed yield. These results were in conformity with earlier finding of Kumar *et al.* (2013) [6] for protein content and Rathor *et al.* (2015) [8] for days to maturity. The number of clusters per plant showed positively significant correlation with number of pods per plant (0.9992, 0.6502) and protein content (0.5195, 0.3551) while it had the significant and negative correlation with pod length (-0.2867, -0.2989) and non-significant and negative correlation with number of seeds per pod (-0.2108, -0.0366), 100 seed weight (-0.1950, -0.1878) and number of pods per cluster (-0.0240, 0.1377). Similar results were reported by Srivastava and Singh *et al.* (2012) [17] for protein content and number of seeds per pod and Sreedevi and Reddy (2004) [15] and Priya and Reddy (2008) [9] number of pods per plant and Rathor *et al.* (2015) [8] for number of pods per plant and number of seeds per pod. The number of pods per plant showed significant positive correlation with protein content (0.3439, 0.2824), while significant and negative correlation with 100 seed weight (-0.5449, -0.4005) and pod length (-0.5494, -0.4809) and number of seeds per pod (-0.1080, -

0.2191) negatively significant. Similar results were reported by Srivastava and Singh (2012) [17] for 100 seed weight and pod length

The number of seeds per pod had positive but non-significant correlation with 100 seed weight (0.0554, 0.0416) while it was negatively significant with protein content (-0.4968, -0.4252). Similar results were reported by Raje and Rao (2000) [11] for protein content and Srivastava and Singh (2012) [17] for 100 seed weight. The pod length exhibited positive and significant correlation with number seeds per pod (0.6367, 0.4952) and 100 seed weight (0.8255, 0.7099) while it showed significant and negative correlation with protein content (-0.3853, -0.3637). Similar results were reported by Raje and Rao (2000) [11], Venkateswarlu (2001) [20] and Ramana (2003) [12] for number seeds per pod and 100 seed weight. Rathor *et al.* (2015) [8] for number of seeds per pod and 100 seed weight. The number of pods per cluster showed significant positive correlation with number of pods per plant (0.6273, 0.4839) while significant and negative correlation with 100 seed weight (-0.6694, -0.6124) and pod length (-0.5918, -0.5252) while non-significant and negative correlation with number of seeds per pod (-0.1051, -0.0557) and protein content (-0.0498, -0.0037).

While comparing the present results in light of earlier findings, it was observed that showing significant association with yield contributing characters in desirable direction *viz.*, number of clusters per plant, number of pods per plant, 100 seed weight, pod length, number of seeds per pod could directly useful to construct the selection index which will help in identifying high yielding genotypes in green gram. Further path analysis provides basis for selection of superior genotypes from the diverse breeding population. Seed yield is the product of interaction of component traits. Apart from correlation studies, path coefficient analysis is important to obtain information about how the component characters influence the seed yield through each other. The genotypic correlation coefficients being more important are only partitioned to direct and indirect effects which are presented in Table 2. In the present investigation path coefficient analysis revealed that pod length (1.7416) recorded magnitudinally the highest positive direct effect on seed yield per plant followed by number of pods per cluster (0.5458), number of pods per plant (0.5213), number of clusters per plant (0.4996), days to maturity (0.0786). These direct effects are mainly responsible for significant positive association of these characters with seed yield per plant. These results are similar with findings of Shamuzzamam *et al.* (1981) [13], Srivastava and Singh (2012) [17] for number of pods per plant, Titumeer *et al.* (2014) [19] for pod length, Rathor *et al.* (2015) [8] and Thanga *et al.* (2015) [18] for number of pods per plant and number of clusters per plant. The character number of seeds per pod (-0.5560) recorded highest negative direct effect on seed yield per plant followed by 100 seed weight (-0.3489), plant height (-0.2065), days to 50% flowering (-0.0400) and protein content (-0.0290). These results are similar with findings of Rahim *et al.* (2010) [10] and Thanga *et al.* (2015) [18] for days to 50% flowering, Srivastava and Singh (2012) [17] for 100 seed weight and plant height, Titumeer *et al.* (2014) [19] for number of seeds per pod and Kumar *et al.* (2013) [6] for protein content. The character number of seeds per pod and 100 seed weight recorded negative direct effect on seed yield per plant. These character exhibited positive significant correlation with seed yield per plant. If the

correlation coefficient is positive, but the direct effect is negative, the indirect effects seem to be because of positive correlation. In such situations, the indirect causal factors are to be considered simultaneously for selection (Singh and Kaker, 1977) [14]. These results are similar to finding of Titumeer *et al.* (2014) [19] for number of seeds per pod and Srivastava and Singh (2012) [17] for 100 seed weight.

Days to 50 percent flowering showed negative indirect effect via days to maturity (-0.0270), number of clusters per plant (-0.0132), number of pods per cluster (-0.0001), number of pods per plant (-0.0117), protein content (-0.0132) and positive indirect effect via plant height (0.0080) and pod length (0.0105). The total correlation with seed yield per plant was positive and non-significant (0.0571). Number of

clusters per plant recorded positive indirect effect via days to 50% flowering (0.1649), days to maturity (0.1313), number of pods per plant (0.4992), protein content (0.2595) and negative indirect effect via plant height (-0.1813), number of pods per cluster (-0.0120), pod length (-0.1433), number of seeds per pod (-0.1053) and 100 seed weight (-0.0974). The total correlation with seed yield per plant was positive and significant (0.7606). Number of pods per cluster exhibited positive indirect effect of characters days to 50% flowering, plant height, number of pods per plant and negative indirect effect via days to maturity, number of clusters (0.0011) per plant (0.1302), pod length, number of seeds per pod, 100 seed weight and protein content. The total correlation with seed yield per plant was positive and non-significant.

Table 1: Estimation of correlation coefficient of eleven characters in mungbean

Character Number	Days to 50% flowering	Days to maturity	Plant height	Number of clusters per plant	Number of pods per cluster	Number of pods per plant	Pod length	Number of seeds per pod	100 seed weight	Protein content	Seed yield per plant	
	1	2	3	4	5	6	7	8	9	10	11	
1. GP	1.0000	1.0000	0.6752** 0.5886**	-0.1998 - 0.1649	0.3301** 0.2549*	0.0021 0.0097	0.2928** 0.2304*	-0.2618* - 0.2318*	-0.1178 - 0.0602	-0.2412* - 0.2335*	0.3305** 0.2592*	0.0571 0.0754
2. GP		1.0000	-0.3190** -0.2220*	0.2629** 0.1139	-0.0586 - 0.0764	0.0528 0.1504	-0.3044* - 0.2573*	-0.4219** - 0.4478**	-0.0016 0.0092	0.4827** 0.3929**	-0.0646 - 0.0927	
3. GP			1.0000 1.0000	-0.3629** - 0.3759**	0.2385* 0.1757	-0.1950 - 0.1120	0.4700** 0.4330**	0.4359** 0.2669*	0.2658* 0.2374*	-0.5354** -0.4664**	0.1225 0.1387	
4. GP				1.0000 1.0000	-0.0240 0.1377	0.9992** 0.6502**	-0.2867** -0.2989**	-0.2108 - 0.0366	-0.1950 - 0.1878	0.5195** 0.3551**	0.7606** 0.5901**	
5. GP					1.0000 1.0000	0.6273** 0.4839**	-0.5918** -0.5252**	-0.1051 - 0.0557	-0.6694** -0.6124**	-0.0498 - 0.0037	0.0696 0.0562	
6. GP						1.0000 1.0000	-0.5494** -0.4809**	-0.1080 - 0.2191*	-0.5449** -0.4005**	0.3439** 0.2824*	0.6791** 0.5110**	
7. GP							1.0000 1.0000	0.6367** 0.4952**	0.8255** 0.7099**	-0.3853** -0.3637**	0.2475* 0.1909	
8. GP								1.0000 1.0000	0.0554 0.0416	-0.4968** -0.4252**	0.2105* 0.2326*	
9. GP									1.0000 1.0000	0.0109 - 0.0070	0.2655* 0.1952	
10. GP										1.0000 1.0000	-0.1193 - 0.0814	
11. GP											1.0000 1.0000	

*, ** indicates significant at 5 and 1% level of probability respectively, G= genotypic correlation P= phenotypic correlation

Table 2: Estimate of direct and indirect effect of ten causal variables on seed yield in mungbean

Sr. No.	Characters	Days to 50% flowering	Days to maturity	Plant height	Number of clusters per plant	Number of pods per cluster	Number of pods per plant	Pod length	Number of seeds per pod	100 seed weight	Protein content	Total genotypic correlation with seed yield / plant
1.	Days to 50% flowering	-0.0400	-0.0270	0.0080	-0.0132	-0.0001	-0.0117	0.0105	0.0047	0.0097	-0.0132	0.0571
2.	Days to maturity	0.0531	0.0786	-0.0251	0.0207	-0.0046	0.0041	-0.0239	-0.0332	-0.0001	0.0379	-0.0646
3.	Plant height	0.0413	0.0659	-0.2065	0.0750	-0.0492	0.0403	0.0971	-0.0900	-0.0549	0.1106	0.1225
4.	No. of clusters per plant	0.1649	0.1313	-0.1813	0.4996	-0.0120	0.4992	0.1433	-0.1053	-0.0974	0.2595	0.7606**
5.	No. of pods per cluster	0.0011	-0.0320	0.1302	-0.0131	0.5458	0.3434	0.3230	-0.0574	-0.3654	-0.0272	0.0696
6.	Number of pods per plant	0.1526	0.0275	-0.1017	0.5209	0.3270	0.5213	0.2864	-0.0563	-0.2841	0.1793	0.6791**
7.	Pod length	-0.4560	-0.5303	0.8166	-0.4994	-1.0307	-0.9568	1.7416	1.1089	1.4378	-0.6711	0.2475*
8.	Number of seeds per pod	0.0655	0.2346	-0.2424	0.1172	0.0584	0.0601	0.3540	-0.5560	-0.0308	0.2762	0.2105*
9.	100 seed weight	0.0841	0.0006	-0.0927	0.0680	0.2335	0.1901	0.2880	-0.0193	-0.3489	-0.0038	0.2655*
10.	Protein content	-0.0096	-0.0140	0.0155	-0.0150	0.0014	-0.0100	0.0112	0.0144	-0.0003	-0.0290	-0.1193

Residual effect = 0.207, Bold and Underlined figures = Direct effect.

*, ** indicates significant at 5 and 1% level of probability respectively Normal figures = Indirect effect

Conclusion

The residual effect determines how best the causal factors account for the variability of the dependent factor, the seed yield, in this case. In present study, residual effect was low (0.207) indicating appropriateness of characters chosen. It is suggested that on the basis of genetic parameter correlation and path analysis, number of clusters per plant, number of pods per plant, pod length, seeds per pod and 100 seed weight should be given topmost priority while formulating a selection strategy for improvement of yield in green gram

References

1. Anonymous. Indian Institute of Pulses Research, Kanpur; c2015-16. p. 103-110.
2. Asthana AN. Pulse crops research in India. Indian J Agric Sci. 1998;68:448-452.
3. Dewey DR, Lu HK. A correlation and path coefficient analysis of components of crested wheat grass and seed production. Agron J. 1959;51(6):515-518.
4. Gupta SN, Lal S, Rai L. Correlation and path analysis in green gram [*Vigna radiata* (L.) Wilczek]. Haryana Agric Univ J Res. 1982;12(2):287-291.
5. Johnson HW, Robinson HF, Comstock RE. Estimation of genetic and environmental variability in soybean. Agron J. 1955;47:314-318.
6. Kumar K, Prasad Y, Mishra SB, Pandey SS, Kumar R. Study on genetic variability, correlation and path analysis with grain and yield attributing traits in green gram [*Vigna radiata* (L.) Wilczek]. The Bioscan. 2013;8(4):1551-1555.
7. Maddewad MW. Variability studies in M3 lines of green gram [*Vigna radiata* (L.) Wilczek]. M.Sc. (Agri.) Thesis submitted to M.P.K.V., Rahuri; c2005.
8. Rathor P, Singh A, Imran M, Ali K, Fatma R. Character association and path analysis for yield and yield component traits in green gram [*Vigna radiata* (L.) Wilczek]. Indian Res J Genet Biotech. 2015;7(1):93-97.
9. Priya MS, Reddy KHP. Character association and path analysis in twenty-one F3 progenies of mungbean (*Vigna radiata* (L.) Wilczek). J Res ANGRAU. 2008;36(1):16-20.
10. Rahim MA, Mia AA, Mahmud F, Zeba N, Afrin KS. Genetic variability, character association and genetic divergence in Green gram [*Vigna radiata* (L.) Wilczek]. Plant Omics J. 2010;3(1):1-6.
11. Raje RS, Rao SK. Association analysis for yield and its components in green gram (*Vigna radiata* (L.) Wilczek). Legume Res. 2000;23(1):42-48.
12. Ramana MV. Genetic studies on soyabean (*Glycine max* (L.) Merrill) in nontraditional areas and seasons. Ph.D. Thesis ANGRAU, Hyderabad; c2003.
13. Rathore Shamsuzzamam KM, Khan MRH, Shaikh MAQ. Genetic variability and character association in green gram [*Vigna radiata* (L.) Wilczek]. Bangladesh J Agric Res. 1981;8(1):1-5.
14. Singh RK, Kaker SN. Control of individual trait means during index selection. Proc. Third. Cong. SABRAO (Canberra). 1977;3:22-25.
15. Sreedevi G, Reddy SM, Sekar MR. Character association and path analysis of morphological attributes in greengram. Ann Agric Res. 2004;25(1):149-152.
16. Sreelakshmi C, Reddy SM. Comparison between correlation and path analysis studies in the full sib progenies and F3 bulk population among yield and its attributes in two crosses of greengram (*Vigna radiata* (L.) Wilczek). Electron J Plant Breed. 2011;2(2):258-262.
17. Srivastava RL, Singh G. Genetic variability correlation and path analysis in green gram [*Vigna radiata* (L.) Wilczek]. Indian J L Sci. 2012;2(1):61-65.
18. Thanga A, Shunmugavalli N, Anand G. Genetic variability correlation and path co-efficient studies on yield and its components in green gram. Legume Res. 2015;38(4):442-446.
19. Titumeer SM, Rahim MA, Zeba N. Genetic variability, character association and genetic divergence in green gram (*Vigna radiata* L. Wilczek). Agronomski glasnik. 2014;6:305-324.
20. Venkateshwarlu O. Correlation and path analysis in greengram. Legume Res. 2001;24(2):115-117.