The Bioscan 8(4): 1551-1555, 2013 (Supplement on Genetics & Plant Breeding) www.thebioscan.in
AN INTERNATIONAL QUARTERLY JOURNAL OF LIFE SCIENCES

STUDY ON GENETIC VARIABILITY, CORRELATION AND PATH ANALYSIS WITH GRAIN YIELD AND YIELD ATTRIBUTING TRAITS IN GREEN GRAM [*VIGNA RADIATA* (L.) WILCZEK]

KAMLESHWAR KUMAR*, YOGENDRA PRASAD, S. B. MISHRA, S. S. PANDEY AND RAVI KUMAR
Department of Plant Breeding and Genetics,
Rajendra Agricultural University, Pusa - 848 125, Samastipur, Bihar, INDIA
e-mail: kamlesh.rani_bau@rediffmail.com

KEYWORDS
Variability
Correlation
Path analysis

Received on :
25.02.2013

Accepted on :
10.11.2014

***Corresponding author**

ABSTRACT
An experiment was conducted on green gram to study the genetic variability, correlation among the yield components their direct and indirect effects on grain yield. On the basis of genetic variability study only 100 seed weight exhibited high heritability estimates (narrow sense) coupled with high genetic advance, indicating the preponderance of additive gene action. Selection based on this trait will be rewarding. Phenotypic coefficient of variation was slightly higher in magnitude than the genotypic coefficient of variation. Number of secondary branches per plant, number of bunches per plant, number of pods per plant, number of grains per pod, pod length and 100 seed weight had shown positive and significant correlation along with their high positive direct effect with grain yield, suggesting that these parameters may be considered as prime traits during the course of selection to have the higher potential of yield in case of green gram.

INTRODUCTION

Legumes represent the second largest family of higher plants, second only to grasses in agricultural importance (Doyle and Luckow, 2003). Resource poor farmers across the developing world depend on grain legumes to sustain the health of their families and livestock and to enhance their economic well-being. Pulses are the principal source of dietary protein among vegetarians and are an integral part of daily diet because of their high protein content and good amino-acid balance in several forms world-wide. On account of balanced amino-acid composition of cereals and protein blend, which matches with the milk protein, pulses are often called as life line of human beings.

There is large disparity in yield of cereals and legumes. But as contrast to the impressive achievement in cereals, pulse production in our country remained almost stagnant with slight increase in productivity. There is also progressive decline in per capita availability of pulses from 70g per day in 1960-61 to less than 34g today as against 80g per day recommended by F.A.O/ W.H.O. (2010). It is estimated that the country's population will touch nearly 1.68 billion by 2030 AD. The country would then require a minimum of 32.00 million ton of pulses with an anticipated growth rate of 4.2 %. The global pulse production in 2009 was over 18 million ton over an area of 26 million hectares, and an average productivity of 701 kg/ha (FAO, 2009). In India, the total pulse production during 2007-08 was 15.12 million ton on 23.86 million hectares with an average productivity of 638 kg/ha (Agriculture Statistics at a glance, 2009). During 2009-10 the total area under green gram in Bihar was 1.8 lakh hectare with an average productivity of 550 kg/ha. Green gram is one of the important kharif and summer pulses of our country, which contains 25% protein and is an excellent and cheap source of high quality and easily digestible protein as compared to meat, fish, eggs etc. In addition to being a source of dietary proteins and income to the resource poor farmers, food legumes play an important role in sustainable crop production. They are an important component of cropping systems to maintain soil health because of their ability to fix atmospheric nitrogen, extract water and nutrients from the deeper layer of soil and add organic matter into the soil through leaf drop.

The entire success of plant breeding programme of any crop largely depends on the wide range of variability present in that crop. It is the range of genetic variability in respect of important economic characters present in the population upon which is based on the effectiveness of selection. Environment has a profound influence upon the economically important characters, which are quantitatively inherited. Hence, it is difficult to decide upon whether the observed variability is heritable or due to environment and it is therefore, necessary to partition the same into its heritable and non-heritable components with suitable parameters like genetic coefficient, heritability estimates and genetic advance.

Selection procedure is more difficult in a trait, where heritability is low or is not precisely measurable. Indirect selection in such a situation is more effective and study of correlation among different economic traits are therefore, essential for an effective selection programme because selection for one or more trait results in correlated response for several other traits (Searle,1965) and sequence of variation will also be influenced

(Waddington and Robertson,1966). Hence, the knowledge of genotypic and phenotypic correlation between yield and its contributing characters is very essential.

Correlation studies measure only mutual association between two traits and it does not imply the cause and effect of relationship. Path coefficient analysis has been found useful direct and indirect causes of association and allows a detailed examination of specific forces acting to produce a given correlation and measures the relative importance of each causal factor. The paper deals with the above aspects.

MATERIALS AND METHODS

The present investigation was carried out in the experimental area of Pulses Research Project of the Department of Plant Breeding and Genetics, Tirhut College of Agriculture, Dholi. Geographically, the research farm is situated at the site of Burhi Gandak river of North Bihar in the humid sub-tropical climatic zone at 25° 59 N latitude and 85° 75 E longitude with an altitude of about 51.2 meters above mean sea level with an average rainfall of about 1234 mm. The rainfall was 491.8 mm during the crop period i.e. April to June 2011. The soil type of the experimental block was alluvial with pH in the range of 7.7 to 8.5. The materials comprised of 50 F_1 crosses which were obtained by mating 10 lines with 5 testers in a line x tester mating design and their 15 parents. The experiment was laid out in Randomized Complete Block Design with three replications, during summer 2011. Row to row and plant to plant distance was 30 and 10 cm, respectively and per plot number of rows were three. Row length was four metres. The crop was raised in rainfed condition with all recommended agronomic package of practices to raise a good crop. Observations were recorded on five competitive and randomly selected plants in each replications for all the genotypes viz., plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of bunches per plant, number of pods per plant, number of grains per pod, pod length (cm), intensity of *Cercospora* infection, total protein, available protein, non available protein, 100- seed weight (g), harvest index (%) and grain yield (kg/ha).

RESULTS AND DISCUSSION

The variance of each character was analysed separately in randomised block design to test the significance of difference among the varietal means for fourteen quantitative as well as qualitative characters of green gram genotypes and results are presented in Table 1. From the table, it is clear that genotypes showed highly significant differences among themselves for all the characters except number of primary branches per plant. The materials taken under study was having the sufficient magnitude of variability, which is very much desirable to the breeder for identification of suitable high yielding genotypes to be used in crop improvement programme to enhance the grain yield of green gram.

Plant height varied from 34.70 to 51.50 cm with general mean 41.44 cm as in Table 2 showed that all the genotypes are having the semi-dwarf stature, number of primary branches per plant varied from 6.00 to 9.83 with general mean 8.15 suggesting that very few genotypes are closer to the higher range of traits, number of secondary branches per plant varied from 6.00 to 11.00 having general mean 8.33 indicating that most of the genotypes were having the moderate secondary branches per plant, number of bunches per plant ranged from 8.66 to 14.70 with general mean 12.04, number of pods per plant varied from 29.53 to 57.53 with general mean 43.06 which revealed that majority of genotypes were having the high number of pods per plant being a hybrid ,pod length ranged from 6.10 to 8.73 cm having general mean 7.34 cm, number of grains per pod varied from 7.27 to 12.87 pod and most of genotypes were having the eleven grains per pod as evident from general mean, intensity of *Cercospora* infection ranged from 6% to 32% with general mean 20%, 16 genotypes have shown significantly higher level of infection against *Cercospora* than the check Pant M-5, total protein varied from 19.56% to 24.56% with general mean 22.13%, available protein ranged from 15.40% to 18.83% having general mean 17.15 indicating that few genotypes were significantly higher in available protein to the check Pant M-5, non-available protein varied from 2.13% to 8.36% having general mean 4.98% indicating none of the genotypes were significantly superior over the check Pant M-5 for non-available protein, 100 seed weight ranged from 2.83 g to 5.40 g with general mean 4.31 g suggesting most of genotypes were significantly superior to the check Pant M-5, harvest index varied from 35.33% to 45.90% having general mean 41.57% exhibited most of the genotypes were significantly superior to check Pant M-5 and grain yield ranged from 8 q/ha to 15.60 q/ha with general mean 11.87 q/ha.

On perusal of Table 3, it was revealed that for all the characters phenotypic coefficient of variation (PCV) was slightly higher than the genotypic coefficient of variation (GCV), so it is evident that in expression of the characters mainly governed by the genotypes itself along with meagre effect of environment. This finding also get corroborated with Venkateswarlu (2001), Dikshit *et al*. (2002), Reddy *et al*. (2003) and Tejbir *et al*. (2009).

A perusal of the table, revealed that high heritability estimates coupled with high genetic advance was observed for 100 seed weight, indicating the preponderance of additive and fixable genetic variance; suggesting that this trait may be subjected to any selection scheme to develop the stable genotypes and selection pressure may be exercised in early generation. High heritability coupled with moderate genetic advance for number of pods per plant as well as high heritability coupled with low genetic advance indicating the presence of additive as well as non-additive gene action. For these traits improvement can be made opting the two to three cycles of recurrent selection followed by pedigree or single seed descent methods of breeding. These findings were corroborated with Dadepeer *et al*. (2009), Dhananjay *et al*. (2009) and Rahim *et al*. (2010).

In the present investigation Table 4, showed that plant height exhibited significant and positive correlation with number of bunches per plant, number of primary branches per plant and number of pods per plant, suggesting that plant height may be directly/indirectly responsible to enhance the magnitude of these aforesaid traits. This finding is corroborated

Table 1: Analysis of variance in RBD for 14 characters in green gram

S. No.	Characters	Mean sum of squares Replications (df = 2)	Treatments (df = 64)	Error (df = 128)
1	Plant height (cm)	8.34	44.14**	5.50
2	Number of primary branches/plant	0.38	1.74	2.03
3	Number of secondary branches/plant	1.89	3.79**	1.43
4	Number of bunches/plant	0.15	5.52**	0.71
5	Number of pods/plant	0.28	75.75**	6.82
6	Pod Length (cm)	0.15	0.88**	0.04
7	Number of grains/pod	1.09	3.77**	0.60
8	Intensity of *Cercospora* infection (%)	21.44	146.43**	16.15
9	Total protein (%)	0.16	4.76**	0.14
10	Available protein (%)	0.23	2.19**	0.09
11	Non available protein (%)	0.32	4.21**	0.25
12	100 seed weight (g)	0.02	0.99**	0.02
13	Harvest index (%)	1.98	14.42**	5.97
14	Yield (kg/ha)	0.01	0.01**	0.01

df - Degree of freedom, ** - Significant at p = 0.01

Table 2: Range and mean of 14 characters in green gram

S. No.	Characters	Range	Mean	CV (%)
1	Plant height (cm)	34.70 - 51.50	41.44	5.79
2	Number of primary branches/plant	6.00 - 9.83	8.15	17.36
3	Number of secondary branches/plant	6.00 - 11.00	8.33	14.33
4	Number of bunches/plant	8.66 - 14.70	12.04	7.41
5	Number of pods/plant	29.53 - 57.53	43.06	6.06
6	Pod Length (cm)	6.10 - 8.73	7.34	2.82
7	Number of grains/pod	7.27 - 12.87	11.34	6.85
8	Intensity of *Cercospora* infection (%)	6.00 - 32.33	20.13	20.12
9	Total protein (%)	19.56 - 24.56	22.13	1.67
10	Available protein (%)	15.40 - 18.83	17.15	1.78
11	Non available protein (%)	2.13 - 8.36	4.98	9.92
12	100 seed weight (g)	2.83 - 5.40	4.31	3.51
13	Harvest index (%)	35.33 - 45.90	41.57	8.85
14	Yield (q/ha)	8.00- 15.60	11. 87	13.11

Table: 3. Genetic parameters for 14 characters in greengram

Characters	σ^2p	σ^2g	PCV	GCV	Heritability (narrow sense)	Genetic advance	Genetic advance in % of mean	SEm ±
Plant height (cm)	18.33	12.56	10.33	8.55	68.50	6.05	14.59	1.96
Primary branches/plant	1.93	0.53	17.03	8.93	27.46	0.79	15.33	1.15
Secondary branches/plant	2.19	0.77	17.79	10.55	35.00	1.07	12.89	0.97
Bunches/plant	2.30	1.57	12.59	10.39	68.00	2.13	17.68	0.69
Pods/plant	29.43	22.62	12.59	11.04	76.90	8.59	19.95	2.13
Pod length (cm)	0.32	0.27	7.66	7.13	86.50	1.00	13.66	0.17
Grains/pod	1.66	1.05	11.35	9.05	63.60	1.69	14.87	0.63
Intensity of *Cercospora* infection (%)	60.21	44.27	38.55	33.05	73.50	11.75	58.39	3.26
Total protein (%)	1.67	1.54	5.85	5.60	91.9	2.45	11.07	0.30
Available protein (%)	0.79	0.69	5.18	4.87	88.00	1.61	9.41	0.25
Non available protein(%)	1.59	1.35	25.35	23.33	84.70	2.20	44.22	0.40
100 seed weight (g)	0.36	0.34	13.90	13.45	93.60	1.16	26.81	0.12
Harvest index (%)	8.91	3.00	7.18	4.17	33.70	2.07	4.98	1.99
Yield (q/ha)	0.01	0.01	15.55	8.35	28.80	0.05	9.23	0.05

with Raje and Rao (2000). Number of primary branches per plant was found to be positively and highly significantly correlated with number of bunches per plant, number of pods per plant and number of secondary branches per plant. This finding was in agreement with the observations of Yaqoob *et al*. (1997). Number of secondary branches per plant exhibited positive and significant correlation with number of bunches per plant, number of pods per plant and grain yield. Similar results were also observed by Mishra *et al*. (1995) and Dhuppe *et al*. (2005). Number of bunches per plant showed positive and highly significant correlation with number of pods per plant and grain yield; indicating that this character may be responsible to enhance the yield. This result corroborated with the findings of Singh and Pathak (1993) and Singh *et al*. (1995). Positive and significant correlation for number of pods per plant was observed with grain yield. This finding is in conformity with Rajan *et al* (2000), Venkateshwarlu (2001), Haritha and Shekhar (2002), Dhuppe *et al*. (2005), Anil and Lokendra (2006), Saxena *et al*. (2007) and Dhananjay *et al*. (2009). Number of grains per pod showed positive and

Table 4: Path Coefficient analysis showing direct (diagonal) and indirect effects on yield of other component traits at phenotypic level

Character	Plant height (cm)	Primary branches/ plant	Secondary branches/ plant	Bunches/ plant	Pods/ plant	Grains/ pod	Pod length (cm)	100 seed weight (g)	Intensity of *Cercospora* infection(%)	Harvest index (%)	Total protein (%)	Available protein (%)	Yield (q/ha)
Plant height (cm)	0.019	0.006	0.004	0.007	0.005	-0.001	-0.001	-0.003	-0.002	-0.001	-0.003	-0.001	0.115
Primary branches/plant	-0.021	-0.069	-0.017	-0.023	-0.014	-0.004	-0.008	-0.003	0.007	-0.014	0.008	0.007	0.100
Secondary branches/plant	0.016	0.017	0.070	0.032	0.026	0.004	0.004	-0.005	-0.006	0.008	0.004	0.003	0.236*
Bunches/plant	0.030	0.026	0.036	0.080	0.036	-0.004	0.001	-0.012	-0.008	0.007	-0.002	0.002	0.244*
Pods/plant	0.105	0.082	0.155	0.189	0.420	-0.022	-0.025	-0.099	-0.103	0.092	-0.015	0.066	0.382**
Grains/pod	-0.006	0.008	0.008	-0.001	-0.008	0.146	0.051	0.065	0.032	0.004	-0.035	-0.037	0.317**
Pod length (cm)	-0.005	0.017	0.008	0.003	-0.009	0.054	0.156	0.068	0.012	0.002	-0.024	-0.028	0.320**
100 seed weight (g)	-0.041	0.013	-0.021	-0.043	-0.070	0.135	0.133	0.302	0.042	-0.001	-0.054	-0.133	0.332**
Intensity of *Cercospora* infection(%)	0.006	0.007	0.006	0.007	0.019	-0.016	-0.006	-0.011	-0.076	0.010	-0.009	0.008	-0.092
Harvest index(%)	0.004	-0.019	-0.010	-0.008	-0.009	-0.004	-0.010	0.001	0.012	-0.091	-0.007	0.007	0.015
Total protein (%)	0.009	0.007	-0.004	0.001	0.002	0.014	0.009	0.010	-0.006	-0.005	-0.057	-0.022	-0.208
Available protein (%)	0.01	0.004	-0.002	-0.001	-0.006	0.010	0.007	0.017	0.004	0.003	-0.014	-0.038	-0.165

Residual effect = 0.467, * - Significant at p = 0.05, ** - Significant at p = 0.01

Table 5: Phenotypic and genotypic correlation for 14 characters in greengram

Character		Primary branches/ plant	Secondary branches/ plant	Bunches/ plant	Pods/ plant	Grains/ pod	Pod length (cm)	100 seed weight (g)	Intensity of *Cercospora* infection (%)	Harvest index (%)	Total protein (%)	Available protein (%)	Yield (q/ha)
Plant height (cm)	P	0.312*	0.231	0.375**	0.249*	-0.044	-0.033	-0.135	-0.084	-0.039	-0.149	-0.004	0.115
	G	-1.127	0.301	0.422	0.268	-0.201	-0.029	-0.169	-0.130	-0.378	-0.193	0.001	0.071
Primary branches/plant	P		0.241*	0.327**	0.196**	0.053	0.111	0.044	-0.096	0.207	-0.115	-0.102	0.100
	G		0.331	-0.733	-0.976	0.225	-0.250	-0.089	0.537	0.247	0.463	0.619	-0.463
Secondary branches/plant	P			0.455**	0.369**	0.053	0.054	-0.069	-0.083	0.112	0.062	0.045	0.236*
	G			0.692	0.480	-0.139	-0.074	-0.091	-0.125	0.005	0.119	0.075	0.228
Bunches/plant	P				0.450**	-0.008	0.016	-0.143*	-0.094	0.086	-0.019	0.024	0.244*
	G				0.559	-0.083	-0.049	-0.199	-0.158	-0.037	-0.026	0.011	0.367
Pods/plant	P					-0.051	-0.059	-0.233	-0.245*	0.219	-0.036	0.157	0.382**
	G					-0.207	-0.123	-0.277	-0.306	0.345	-0.057	0.192	0.312
Grains/pod	P						0.349**	0.446**	0.218	0.027	-0.242*	-0.255*	0.317**
	G						0.451	0.603	0.315	-0.151	-0.356	-0.355	0.328
Pod length (cm)	P							0.439**	0.077	0.009	-0.153	-0.182	0.320**
	G							0.481	0.143	-0.023	-0.165	-0.203	0.529
100 seed weight (g)	P								0.139	-0.001	-0.180	-0.440**	0.332**
	G								0.157	0.022	-0.191	-0.489	0.619
Intensity of *Cercospora* infection (%)	P									-0.136	0.112	-0.110	-0.092
	G									-0.171	0.144	-0.134	-0.176
Harvest index(%)	P										0.079	-0.072	0.015
	G										0.171	-0.103	0.140
Total protein (%)	P											0.381**	-0.208
	G											0.431	-0.492
Available protein (%)	P												-0.165
	G												-0.342

* - Significant at p = 0.05, ** - Significant at p = 0.01

significant correlation with pod length, 100 seed weight and grain yield. Similar results were also observed by Raje and Rao (2000), Rajan *et al*. (2000), Sreedevi and Sekhar (2004), Anbumalarmathi *et al*. (2005) and Singh *et al*. (2009). Pod length exhibited positive and significant correlation with grain yield. This result is corroborated with Mishra *et al*. (1995), Wani *et al*. (2007) and Dadepeer *et al*. (2009). 100 seed weight showed positive and highly significant correlation with grain yield. Similar results were reported by Venkateswarlu (2001), Dhuppe *et al*. (2005), Reddy et al. (2005) and Eswari and Rao (2006).

As evident from Table 5, number of secondary branches per plant, number of bunches per plant, number of pods per plant, number of grains per pod, pod length and 100 seed weight exhibited positive and significant correlation along with their positive and high direct effect on grain yield indicating that these characters may be considered as prime traits during the course of selection for enhancing the grain yield of green gram. The residual effect was obtained less than 0.5, suggesting that some of the characters have not been included in the present investigation, which may be responsible to enhance the yield of green gram. These findings are corroborated with Venkateswarlu (2001), Haritha and Sekhar (2002), Sreedevi and Sekhar (2004), Duppe *et al*. (2005), Reddy *et al*. (2005), Mittal *et al*. (2007), Dhananjay *et al*. (2009) and Singh *et al*. (2009).

REFERENCES

Anbumalarmathi, J., Rangasamy, P. and Sheeba, A. 2005. Association analysis for yield and quality traits in greengram [*Vigna radiata* (L.) Wilczek]. *Crop Research Hisar*. **30(1):** 54-58.

Anil, Sirohi and Lokendra Kumar 2006. Studies on correlation and path analysis in mungbean [*Vigna radiata* (L.) Wilczek]. *International J. Of Plant Sciences*. **1(1):** 61-63.

Agriculture Statistics at a Glance (2009).

Dadepeer, Peerajade, Ravi Kumar, R. L. and Salimath, P.M. 2009. Genetic variability and character association in local green gram genotypes. *Environment and Ecology*. **27(1):** 165-169.

Dhananjay, Ramakant, Singh, B. N. and Singh, G. 2009. Studies on genetic variability, correlations and path coefficients analysis in mung bean. *Crop Res. Hisar*. **38(1/3):** 176-178.

Dhuppe, M. V., Madrap, I. A., Chandankar, G. D. and More, S. S. 2005. Correlation and path analysis in mungbean. *J. of Soil and Crops*. **15(1):** 84-89.

Dikshit, H. K., Singh, B. B. and Dua, R. R. 2002. Genetic variation in mungbean. *Indian J. Pulses Res.* **15(2):** 125-127.

Doyle, J. J. and Luckow, M. A. 2003. The rest of iceburg. Legume diversity and evolution in a phylogenetic context. *Plant Physiology,* **131:** 900-910.

Eswari, K. B. and Rao, M. V. B. 2006. Analysis of genetic parameters for yield and certain yield components in green gram. *International J. of Agric. Sciences.* **2(1):** 143-145.

F. A. O. 2009. News letter.

Haritha, S. and Sekhar, M. R. 2002. Correlation and path analysis in mungbean. *Legume Res.* **25(3):** 180-183.

Mishra, A. K., Yadav, L. N. and Raghu, J. S. 1995. Variability of metric traits and character association in *Vigna radiata Agri. Sci. Digest.* **15(2):** 51-54.

Mittal, V. P., Paramjit, Singh, and Brar, K. S. 2007. Component characters influencing seed yield in moongbean. *International J. of Agric. Sciences*. **3(1):** 80-81.

Rahim, M. A., Mia, A. A., Mahmud, F., Zeba, N. and Afrin, K. S. 2010. Genetic variability, character association and genetic divergence in mungbean (*Vigna radiata* (L.) Wilczek). *Plant Omics*. **3(1):** 1-6.

Rajan, R. E. B., Wilson, D., and Vidyaraghava, Kumar 2000. Correlation and path analysis in greengram. *Madras Agric. J.* **87(10/12):** 590-593.

Raje, R. S. and Rao, S. K. 2000. Association analysis for yield and its components in mungbean. *Legume Res.* **23(1):** 42-48.

Reddy, N. B. R., Lad, D. B. and Mukhekar, G. D. 2005. Correlation and path analysis studies in green gram. *J. of Maharastra Agric. Univ*. **30(2):** 156-159.

Reddy, V. L. N., Reddi Sekhar, M., Reddy, K. R. and Reddy, K. H. 2003. Genetic variability for yield and its components in mungbean (*Vigna radiata* (L.) Wilczek). *Legume Res.* **26(4):** 300-302.

Saxena, R. R. Singh, P. K. and Saxena, R. R. 2007. Correlation and path analysis in mungbean cultivars (*Vigna radiata* (L.) Wilczek). *J. of Inter Academicia.* **11(2):** 143-148.

Searle, S. R. 1965. The value of indirect selection I. *Mass Selection Biometrics*. **21:** 682-708.

Singh, I. S., Hue, N. T. N. and Gupta, A. K. 1995. Associations and cause effect analysis in some F_2 populations of greengram. *Legume Res.* **18(3/4):** 137-142.

Singh, R. P. and Pathak, M. M. 1993. Correlation studies in mungbean. *Indian J. Pulses Res.* **6:** 35-37.

Singh, S. K., Singh, I. P., Singh, B. B. and Omkar, Singh 2009. Correlation and path coefficient studies for yield and its components in mungbean. *Legume Res.* **32(3):** 180-185.

Sreedevi., G. and Sekhar, M. R. 2004. Character association and path analysis of morphological attributes in green gram. *Annals of Agric Res.* **25(1):** 149-152.

Tejbir, Singh., Amitesh, Sharma. and Alie, F. A. 2009. Impact of environment on heritability and genetic gain for yield and its component traits in mung bean. *Legume Res*. **32(1):** 55-58.

Venkateswarlu, O. 2001. Correlation and path analysis in greengram. *Legume Res*. **24(2):** 115-117.

Venkateswarlu, O. 2001. Genetic variability in green gram (*Vigna radiata* (L.) Wilczek]. *Legume Res.* **24(1):** 69-70.

Waddington, C. H. and Robertson, E. 1996. Selection for developmental canalization. *Genetics Res*. **7:** 03-312.

Wani, B. A. Marker, S. and Lavanya, G. R. 2007. Genetic variability, correlation and path analysis in greengram. *J. of Maharastra Agric. Univ.* **32(2):** 216-219.

W. H. O. 2010. News letter.

Yaqoob, M., Malik, A. J., Malik, B. A., Khan, H. U. and Nawab, K. 1997. Path co-efficient analysis in some mungbean mutants under rainfed conditions. *Sarhad J. of Agric.* **13(2):** 129-133.