



Research Article

GENETIC ASSOCIATION AND PATH ANALYSIS FOR YIELD CONTRIBUTING TRAITS IN MUNGBEAN (*Vigna radiata* L. WILCZEK)

CHOUDHARY PRATIBHA^{1*}, PAYASI S.K.² AND URMALIYA KARISHMA³

^{1,2}Department of Genetics & Plant breeding, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur, Madhya Pradesh, 482004, India

³Department of Biotechnology, Mata Gujri Mahila Mahavidyalaya, Jabalpur, Madhya Pradesh, 482004, India

*Corresponding Author: Email- prratibha08@gmail.com

Received: July 10, 2016; Revised: August 18, 2016; Accepted: August 19, 2016; Published: October 30, 2016

Abstract- Genetic variability and character association in 18 advanced breeding lines (F_5) with two diverse parents of mungbean for different quantitative characters were studied in *kharif* 2012. The analysis of variance revealed highly significant difference for all characters, under study among the genotypes, indicating the presence of sufficient amount of variability in the genotypes. Thus, there is ample scope for selection of different quantitative characters for crop improvement. The highest GCV and PCV were observed for primary branches per plant and biological yield per plant respectively. High estimates of genetic advance as percent of mean were observed for plant height and biological yield per plant. High significant positive correlation was recorded for biological yield per plant and significant negative association for 100 grain weight at both genotypic and phenotypic levels with grain yield per plant and biological yield per plant, harvest index, pods per plant, plant height, days to maturity, pod length and 100 grain weight had direct positive effect on grain yield per plant.

Keywords- Variability, Heritability, Genetic advance, Correlation, Path analysis.

Citation: Choudhary Pratibha, et al., (2016) Genetic Association and Path Analysis for Yield Contributing Traits in Mungbean (*Vigna radiata* L. Wilczek). International Journal of Agriculture Sciences, ISSN: 0975-3710 & E-ISSN: 0975-9107, Volume 8, Issue 52, pp.-2465-2468.

Copyright: Copyright©2016 Choudhary Pratibha, et al., This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution and reproduction in any medium, provided the original author and source are credited.

Academic Editor / Reviewer: Dr Suresh Baban Dagade, A. K. Mall, Dr A. V. S. Durga Prasad, Bineeta Devi, Dr Narendra Kumar

Introduction

Mungbean (*Vigna radiata* L. Wilczek) is an important pulse crop which is annual legume. It is well suited to dry areas, mainly under irrigated conditions. It has the diploid chromosome number $2n = 2x = 22$ [1]. Mungbean is cultivated in tropical, subtropical and temperate zones of Asia including Bangladesh, India, Pakistan, Myanmar, Indonesia, Philippines, Sri Lanka, Nepal, China, Korea and Japan. The world average mungbean yield is about 400 kg/ha and India is the largest producer with more than 50% of world production. In India the area under mungbean production is 3.55 million hectare, the production of mungbean is 1.39mt, the productivity of the mungbean is 512 kg/ha [2]. It is a short duration crop and grown as sole as well as inter and multiple cropping system, hence it contributes to increase the income of marginal farmers. Mungbean occupies an important position due to its high seed protein content (22 to 24%) and ability to restore the soil fertility through symbiotic nitrogen fixation [3]. It is rich in essential amino acids specially lysine, which is deficient in most of the cereal grains. Therefore, it is very much essential to improve its yield. For yield improvement, it is essential to have knowledge on variability of different characters. The variability of a biological population is an outcome of genetic constitution of individuals making up that population in relation to prevailing environment. A survey of genetic variability with the help of suitable parameters such as genotypic coefficient of variation, heritability and genetic advance are absolutely necessary to start an efficient breeding program [4]. The coefficient of correlation between yield and its contributing traits show a complex relationship. Path coefficient analysis partitions the components of correlation coefficient into direct and indirect effects and visualizes the relationship in more meaningful way. Information regarding inheritance of grain yield and its closely related components is essential to efficiently exploit the available genetic diversity in mungbean for seed yield [5].

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 mungbean. Secondly, genetic correlations and direct and indirect effects of economically useful traits with seed yield were also investigated.

Materials and Methods

The experimental material comprised 18 advanced breeding lines (F_5) with two diverse parents of mungbean [Table-1] grown in Randomized Block Design with 4 replications at JNKVV, CoA, Rewa in *kharif* 2012. Standard agronomic package of practices was followed to raise a healthy crop. The data were recorded on eleven characters, viz., days to 50% flowering, days to maturity, plant height, number of primary branches, pods/plant, pod length, grains/pod, 100 grain weight, biological yield/plant, harvest index and grain yield/plant. The data for each trait was statistically analysed using analysis of variance recommended for randomized complete block design. F-test followed by least significant difference test was applied for means analysis. The mean values were used to obtain analysis of variance as per methodology advocated by [6]. PCV and GCV were calculated by the formula given by [7], heritability in broad sense (h^2) by [7,8] and genetic advance i.e. the expected genetic gain was calculated by using the procedure given by [9]. Correlation coefficient and path coefficient analysis was worked out as method suggested by [10,11] respectively. Genetic and phenotypic correlations among the traits were determined by [12] method.

Results and Discussion

Genetic variability analysis

The estimate of genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h^2) and genetic advance as 5% of mean (GAM) for 11 different characters were presented in [Table-2]. The coefficient of variation indicated that there were significant differences among the genotypes for measured characters. The phenotypic coefficient of variation (PCV) was slightly higher than the genotypic coefficient of variation (GCV) for all the characters suggesting the presence of environmental influence to some extent in the expression of these characters. The highest estimate of genetic variability was observed for biological yield followed by number of primary branches per plant, harvest index and plant height. Similarly, high magnitude of genotypic coefficient of variation was also reported by [13] for number of primary branches per plant and plant height in mungbean. Moreover, in the present study, high heritability was manifested by days to 50% flowering and plant height followed by days to maturity. Previously, high heritability for these traits has also been reported by [14,15] and for plant height observed by [16]. The estimate of genetic advance as percentage of mean high for biological yield per plant, number of primary branches per plant and harvest index in mungbean genotypes of present study. The high estimates of genetic advance as percentage of mean were also reported by [17] for biological yield per plant, [18] for harvest index.

5.	TJM 3 X Ganga 8	15.	PDM 139 X LGG 460
6.	HUM 1 X LGG 460	16.	HUM 1 X Ganga 8
7.	Ganga 8 X HUM 1	17.	Ganga 8 X K 851
8.	Ganga 8 X TJM 3	18.	HUM 1 X TJM 3
9.	HUM 1 X K 851	19.	Pusa Vishal (check)
10.	PDM 11 X TJM 3	20.	HUM 6 (check)

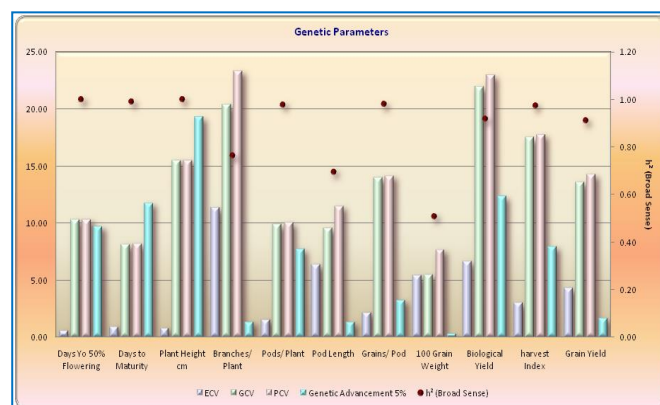


Fig-1 Genetic parameters of variation

Character association

Correlation coefficient analysis

Correlation coefficient analysis among grain yield and its contributing characters were shown in [Table-3].

Table-1 List of mungbean genotypes used in the study

S. No.	Name of genotypes	S. No.	Name of genotypes
1.	TJM 3 X Pusa Vishal	11.	TJM 3 X HUM 1
2.	PDM 11 X K 851	12.	Ganga 8 X Pusa Vishal
3.	HUM 1 X PDM 11	13.	HUM 1 X Pusa Vishal
4.	PDM 11 X HUM 1	14.	PDM 139 X TJM 3

Table-2 Estimation of mean, range, co-efficient of variation (PCV and GCV) heritability, genetic advance and genetic gain in mungbean genotypes

Parameters	Days to 50% Flowering	Days to Maturity	Plant Height cm	Primary Branches/Plant	Pods/Plant	Pod Length	Grains/ Pod	100 Grain Weight	Biological Yield	harvest Index	Grain Yield /plant
Mean	45.91	70.49	60.51	3.73	38.35	8.03	11.45	3.98	28.47	22.32	6.17
Range											
Lowest	39.32	61.77	46.13	2.19	31.44	6.50	8.88	3.55	19.66	17.34	4.80
Highest	54.16	80.47	75.19	5.38	44.13	10.21	13.72	4.37	43.06	28.52	7.92
GCV	10.02	7.80	15.03	20.35	9.40	9.56	13.30	5.46	21.96	16.52	13.60
PCV	10.32	8.21	15.49	23.30	10.00	11.47	14.14	7.66	22.94	17.75	14.26
h^2 (Broad Sense)	0.97	0.95	0.97	0.76	0.94	0.69	0.94	0.51	0.92	0.93	0.91
GAM 5%	21.19	16.69	31.84	36.60	20.11	16.42	28.44	8.00	43.30	35.51	26.71

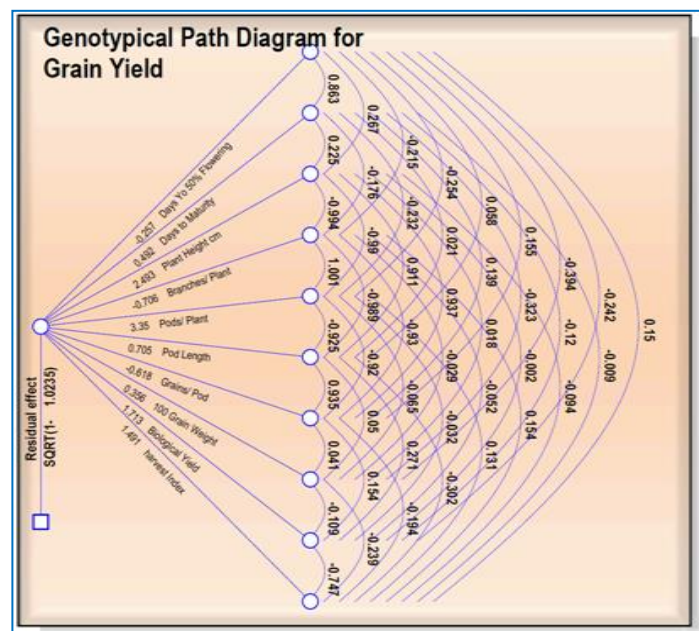
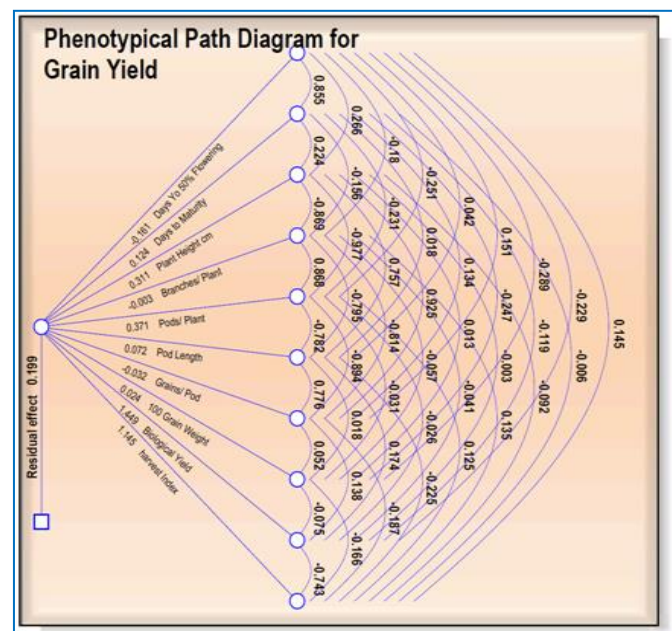


Fig-2 Genotypic and Phenotypic path diagram

Path analysis

Path coefficient analysis [Table-4] revealed that positive direct effect of plant height, pods per plant, biological yield and harvest index is confirmed by [16,18,19,23,25-27]. These traits also recorded strong positive correlation with grain yield per plant (except plant height, which had non-significant negative association with grain yield) which was in accordance with the result of [17]. Similarly primary branches per plant had recorded high positive indirect effect on grain yield via number of pods per plants and highly negative indirect effect through harvest index and biological yield per plant. This indicates that the high yielding mungbean genotypes could be obtained by selecting plants having more pods per plant, and a direct selection through these characters should be effective. These findings are in agreement with [17,28,29].

Conclusion

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 mungbean could be brought through selection of component characters directly concerned with final yield in pulse crops like days to 50% flowering, days to maturity, plant height along with pods per plant and biological yield per plant for the improvement of grain yield in mungbean.

Conflict of Interest: None declared

References

- [1] Karpechenko G.D. (1925) Chromosomes of Phaseolinae. *Bull. Appl Bot Leningrad*, 14,143-148.
- [2] Anonymous. (2014-15) Second Advance Estimates of Production of Food grains. Department of Agriculture and Cooperation - www.agricoop.nic.in
- [3] Malik B.A. (1994) Grain legumes. In: *Crop Production*. (Ed.): M.S. Nazir. p. 301. National Book Foundation, Islamabad.
- [4] Mishra S.P., Asthana A.N. and Yadav L. (1988) *Plant Breeding*, 100(3), 228-229.
- [5] Khattak G.S., Ashraf M. and Khan M.S. (2004) *Pak. J. Bot.*, 36(3), 583-588.
- [6] Panse V.G. and Sukhatme P.V. (1967) *Statistical Methods of Agricultural Workers*, 2nd Edition, p. 381, I.C.A.R Publishing, New Delhi.
- [7] Burton G.W. (1952) *Agronomy J.*, 51, 515-518.
- [8] Burton G.W. and De Vane E.H. (1953) *Agron. J.*, 45, 478-481.
- [9] Johnson H.W., Robinson H.F. and Comstock R.E. (1955) *Agronomy J.*, 47, 477-483.
- [10] Al-Jibouri H.A., Miller R.A. and Robinson H.F. (1958) *Agron.J.*, 50,633-637.
- [11] Dewey D.R. and Lu K.H. (1959) *Agron. J.*, 51, 1207-1211.
- [12] Singh R.K. and Chaudhary B.D. (2005) *Biometrical Methods in Quantitative Genetic Analysis*. Kalyani Publishers, New Delhi.
- [13] Dikshit H.K., Singh B.B. and Dua R.P. (2002) *Indian J. Pulse. Res.*, 15(2), 125-127.
- [14] Rohman M.M., Iqbal Hossain A.S.M., Arifin M.S., Akhter Z. and Hasanuzzaman M. (2003) *Asian Journal of Plant Sciences*, 2, 1209-1211.
- [15] Siddique M., Malik F.M.A. and Awani S.I. (2006) *Int. J. Agri. Biol.*, 8(6), 793-795.
- [16] Baisakh B., Swain S.C., Panigrahi K.K., Das T.R. and Mohanty A. (2016) *Legume Genomics and Genetics*, 7(2), 1-9.
- [17] Rao C., Rao Y.K. and Reddy M. (2006) *Legume Res.*, 29 (3), 216-218.
- [18] Kumar N.V., Lavanya G.R., Singh S.K. and Pandey P. (2010) *AAB Bioflux*, 2(3), 251-257.
- [19] Mittal V.P., Singh P. and Brar K.S. (2007) *Internat. J. Agric. Sci.*, 3(1), 80-81.
- [20] Gul R., Khan H., Mairaj G., Ali S., Farhatullah and Ikramullah (2008) *Sarhad J. Agric.*, 24(1), 37-42.
- [21] Khajudparn P. and Tantasawat P. (2011) *African Journal of Biotechnology*, 10(49), 9992-10000.
- [22] Hozayn M., El-Habbasha S.F., El-Lateef L.M. and Abd El-Monem A.A. (2013) *Journal of Applied Sciences Research*, 9(1), 643-651.
- [23] Singh C.M., Mishra S. B. and Pandey A. (2016) *Legume Research*, 39(1), 20-25.
- [24] Hakim L. (2008) *Indonesian Journal of Agricultural Science*, 9, 24-28.
- [25] Kumar R., Ravi K. and Ojha C.B. (2004) *Legume Research*, 27(1), 32-36.
- [26] Idress A., Sadiq M.S., Hanif M., Abbas G. and Haider S. (2006) *J. Agric. Res.*, 44(3), 181-189.
- [27] Srivastava R.L. and Singh G. (2012) *Indian J. L.Sci.*, 2(1), 61-65.
- [28] Verma P. and Garg D.K. (2007) *Journal of Arid Legume*, 4(2), 88-91.
- [29] Prakash V. (2006) *Crop Improv.*, 33(2), 175-180.

Table-3 Phenotypic and genotypic correlations between seed yield and its component characters

Character		Days to 50% Flowering	Days to Maturity	Plant Height cm	Primary Branches Per Plant	Pods Per Plant	Pod Length	Grains per Pod	100 Grain Weight	Biological Yield per Plant	harvest Index	Grain Yield per Plant
Days to 50% Flowering	P	--	0.8552**	0.2664*	-0.1801	-0.2508*	0.0416	0.1511	-0.289**	-0.2286*	0.1455	-0.2372*
	G	--	0.8627	0.2670	-0.2154	-0.2539	0.0576	0.1550	-0.3942	-0.2420	0.1500	-0.2514
Days to Maturity	P		--	0.2236*	-0.1560	-0.2310*	0.0184	0.1341	-0.2468*	-0.1185	-0.0059	-0.2158
	G		--	0.2252	-0.1759	-0.2317	0.0208	0.1389	-0.3232	-0.1200	-0.0094	-0.2259
Plant Height cm	P			--	-0.8688**	-0.9773**	0.7565**	0.9251**	0.0131	-0.0033	-0.0923	-0.1482
	G			--	-0.9940	-0.9902	0.9106	0.9366	0.0181	-0.0020	-0.0937	-0.1534
Branches / Plant	P				--	0.8676**	-0.7954**	-0.8142**	-0.0566	-0.0405	0.1347	0.1202
	G				--	1.0008	-0.9894	-0.9304	-0.0291	-0.0519	0.1536	0.1441
Pods / Plant	P					--	-0.7816**	-0.8941**	-0.0312	-0.0262	0.1251	0.1519
	G					--	-0.9250	-0.9197	-0.0651	-0.0325	0.1308	0.1580
Pod Length	P						--	0.7761**	0.0178	0.1745	-0.2247*	-0.0128
	G						--	0.9354	0.0498	0.2714	-0.3023	-0.0246
Grains / Pod	P							--	0.0523	0.1379	-0.1869	-0.0373
	G							--	0.0411	0.1540	-0.1939	-0.0296
100 Grain Weight	P								--	-0.0747	-0.1659	-0.2662*
	G								--	-0.1090	-0.2393	-0.3877
Biological Yield	P									--	-0.7433**	0.6157**
	G									--	-0.7468	0.5827
Harvest Index	P										--	0.0465
	G										--	0.0866
Grain Yield	P											--
	G											--

**Significant at 1% level of significance

*Significant at 5% level of significance

Table- 4 Phenotypic and genotypic path coefficients of ten yield components to yield in F_5 population

Character		Days to 50% Flowering	Days To Maturity	Plant Height cm	Primary Branches/ Plant	Pods/ Plant	Pod Length	Grains/ Pod	100 Grain Weight	Biological Yield per plant	harvest Index	Grain Yield (r)
Days to 50% Flowering	P	-0.1608	0.1064	0.0829	0.0006	-0.0930	0.0030	-0.0048	-0.0069	-0.3313	0.1665	-0.2373*
	G	-0.2565	0.4242	0.6658	0.1521	-0.8506	0.0406	-0.0958	-0.1404	-0.4146	0.2237	-0.2515
Days to Maturity	P	-0.1375	0.1244	0.0696	0.0005	-0.0856	0.0013	-0.0043	-0.0059	-0.1718	-0.0067	-0.2159*
	G	-0.2213	0.4917	0.5616	0.1242	-0.7764	0.0147	-0.0858	-0.1151	-0.2056	-0.0140	-0.2260
Plant Height cm	P	-0.0428	0.0278	0.3114	0.0028	-0.3623	0.0543	-0.0293	0.0003	-0.0048	-0.1057	-0.1482
	G	-0.0685	0.1107	2.4934	0.7019	-3.3174	0.6420	-0.5788	0.0065	-0.0034	-0.1398	-0.1534
No. of Primary Branches/ Plant	P	0.0290	-0.0194	-0.2705	-0.0033	0.3216	-0.0570	0.0258	-0.0013	-0.0588	0.1542	0.1203
	G	0.0553	-0.0865	-2.4784	-0.7062	3.3527	-0.6975	0.5750	-0.0104	-0.0890	0.2291	0.1442
Pods/ Plant	P	0.0403	-0.0287	-0.3043	-0.0028	0.3707	-0.0561	0.0284	-0.0007	-0.0380	0.1432	0.1519
	G	0.0651	-0.1139	-2.4690	-0.7067	3.3501	-0.6521	0.5684	-0.0232	-0.0556	0.1951	0.1581
Pod Length	P	-0.0067	0.0023	0.2356	0.0026	-0.2897	0.0717	-0.0246	0.0004	0.2528	-0.2572	-0.0128
	G	-0.0148	0.0102	2.2705	0.6987	-3.0989	0.7050	-0.5781	0.0177	0.4650	-0.4508	-0.0246
Grains/ Pod	P	-0.0243	0.0167	0.2880	0.0027	-0.3314	0.0557	-0.0317	0.0012	0.1998	-0.2140	-0.0373
	G	-0.0398	0.0683	2.3353	0.6570	-3.0811	0.6595	-0.6180	0.0146	0.2637	-0.2892	-0.0296
100 Grain Weight	P	0.0465	-0.0307	0.0041	0.0002	-0.0116	0.0013	-0.0017	0.0238	-0.1083	-0.1899	-0.2663*
	G	0.1011	-0.1589	0.0452	0.0205	-0.2181	0.0351	-0.0254	0.3562	-0.1867	-0.3568	-0.3878
Biological Yield per Plant	P	0.0368	-0.0147	-0.0010	0.0001	-0.0097	0.0125	-0.0044	-0.0018	1.4489	-0.8509	0.6158**
	G	0.0621	-0.0590	-0.0050	0.0367	-0.1087	0.1914	-0.0952	-0.0388	1.7130	-1.1137	0.5828
harvest Index	P	-0.0234	-0.0007	-0.0287	-0.0004	0.0464	-0.0161	0.0059	-0.0039	-1.0771	1.1447	0.0466
	G	-0.0385	-0.0046	-0.2337	-0.1085	0.4382	-0.2131	0.1199	-0.0852	-1.2792	1.4914	0.0866

r = Correlation coefficient between traits