GENETIC VARIABILITY, CORRELATION AND PATHCOEFFICIENT ANALYSIS OF SOME YIELD COMPONENTS OF MUNGBEAN (*VIGNARADIATA* L.)

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Abstract: Genotypic and phenotypic coefficient of variation, heritability, genetic advance was evaluated for yield and its contributing characters in 30 moonbeam genotypes significant variations among the genotypes were observed for all the characters. Analysis of variance revealed that mean sum of squares due to genotypes were highly significant for all the characters except number of pod per clusters, 100 seed weight whereas, pod length shown significant differences thus revealing the existence of considerable variability in the material studied. Analysis of Variance was given in table no.4. High heritability coupled with high genetic advance was recorded for seed yield per plant, number of pod per cluster, plant height and days to 50% flowering. Indicating these characters would be best for phenotypic selection. The correlation coefficient analysis revealed high significant positive association of plant height, number of flower per raceme, number of seed per pod, petiole length, number of pod per clusters, pod length, days to 50% flowering and days to maturity and significant positive association of 100 seed weight with seed yield per plant. The path coefficient analysis showed that, days to 50% flowering had the highest direct effect on seed yield. The estimated Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) helped in getting a clear understanding of the variability present among the various genotypes. The GCV was maximum for seed yield per plant (32.70%). The phenotypic coefficient of variation was high for seed yield/plant (35.43%), number of pod per cluster (21.62%) and plant height (20.64%).

Keyword: Mungbean**,** correlation, variability, path analysis

INTRODUCTION

Mungbean (*Vignaradiata* L. Wilczek) is an important pulse crop which is annual legume. As compared to other legumes, these edsofmung bean are tasty, easily digestible and having more nutritional values. Its seed contains 24.7% protein, 0.6% fat, 0.9% fiber and 3.7% ash (Potter and Hotchkiss, 1997). Sprouts of mungbean are an important source of food and are very commonly used to protect from scurvy. The path analysis helps in partitioning the correlation coefficient of yield components with seed yield into its direct and indirect effects to ensure the actual contribution of an attribute as well as its influence through other traits. Correlation analysis provides the information of interrelationship of important plant characters and hence, leads to a directional model for direct or indirect improvement in seed yield per plant (Khan *et al*., 2004). Genetic variability with the help of suitable parameters such as genotypic coefficient of variation, phenotypic coefficient of variation, heritability and genetic advance are absolutely necessary to start an efficient breeding programme.

MATERIAL AND METHOD

Field experiments were conducted in 20012-2013 and was laid out in a Randomized Complete Block Design (RCBD) with three replication in spacing of 30 ×10 cm between rows and plants respectively Each genotype was represented by 4 rows of 4 m length with guard rows at either side. All the agronomical package of practices recommended for crop health stand was adopted. At instructional farm, Department of Genetics and Plant Breeding, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur (C.G.), to estimate genetic variability, heritability Genotypic and phenotypic coefficients of variance, heritabilityand genetic advance wereevaluatedforyieldanditscontributingcharactersin 30Mungbean genotypes. Details of the genotypes included in the experiment are given below in table no.1.Dataonfive randomly selected plant were recorded on ten characters *viz.*, daysto50%flowering(days), days tomaturity (days), plant height (cm), number of pods per cluster, pod length (cm), number of seeds per pod, 100 seed weight (g) and yield per plant (g). Genotypic and phenotypic coefficient of variations, heritability and genetic advance were estimated as per Singh and Chaudhury (1985) and Johns on *et al*. (1955). Details of the Genotypic (G), phenotypic (P) and environmental (E) correlation coefficients among different yield traits in mungbean given below in table no. 2.

RESULT AND DISCUSSION

Analysis of variance presented in Table 2 revealed that mean sum of squares due to genotypes were highly significant for all the characters except number of pod per clusters, 100 seed weight whereas, pod length shown significant differences. The estimate of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), heritability (h^2), genetic advance (GA), for ten different characters are presented in table no.5. The highest genotypic coefficient of variation was found for seed yield per plant followed by number of pod per cluster and the lowest for number of seeds per pod indicating higher degree of genetic variability for these characters. A higher heritability estimate associated with good estimates of genetic advance expected in the next generation for seed yield per plant, number of pod per cluster, plant height, number of seeds per pod and 100 seed weight suggesting these characters are governed by additive genetic effect to a great extent and improvement of these characters would be effective through phenotypic selection. Similar results were found by Vikas *et al*. (1998) for plant height, Sharma (1999) for 100-seed weight and seed yield per plant. High heritability estimates has been found to be helpful in making selection of superior genotypes on the basis of phenotypic performance. Johanson *et al*. *(*1955). Seed yield per plant exhibited highly significant positive correlation with number of pod per cluster at all phenotypic (0.814), genotypic (0.866) and environmental (0.491) level which were in accordance with the findings of Yaqoob *et al.* (1997), Sadiq and Abbas (2007) and Verma and Garg (2007). The character number of pod per cluster was identified as selection criteria for improving seed yield in mungbean as this character recorded strong positive correlation with seed yield. Days to 50% lowering had the highest direct effect (1.061) on seed yield per plant. It also had highly significant positive association with seed yield, complied with high heritability and high genetic advance. Hence, this character seems to be important contributor of seed yield and must be considered in selection for high seed yield details of the genotypic path coefficient of various characters influencing seed yield per plant in mungbeangiven below in table no. 3.

CONCLUSION

Analysis of variance revealed that, mean sum of squares due to genotypes were highly significant for all the characters except pod length showing significant difference while, number of pod per cluster and 100 seed weight were non-significant. Thus revealing that the existence of considerable variability in the material studied**.** The Genotypic Coefficient of Variation (GCV) was noted high for seed yield per plant and number of pod per cluster while, the Phenotypic Coefficient of Variation (PCV) was high for number of seed yield per plant, number of pod per cluster and plant height. GCV for seed yield recorded high which shows considerable scope for yield improvement. However, plant height has considerable genetic variability which can also be exploited for yield improvement. High heritability was found in all the character while high genetic advance was found in all the character also. The path coefficient analysis showed that, days to 50% flowering had the highest direct effect on seed yield. The correlation coefficient analysis revealed high significant positive association of plant height, number of flower per raceme, number of seed per pod, petiole length, number of pod per clusters, pod length, days to 50% flowering and days to maturity and significant positive association of 100 seed weight with seed yield. Hence, improvement of seed yield per plant can be achieved by improving these characters.

Table 1: Designation of Mungbean germplasms

S. No.	Genotype	Source
1	Pusa Vishal	IARI, New Delhi
2	MalviyaJyoti	BHU Varanashi
3	Pragya	IGKV, Raipur
4	Pairymung	BARC/IGKV,Raipur
5	TM-99-2	BARC, Trombay
6	TM 2000-1	BARC, MUMBAI
7	K-851	IIPR, Kanpur
8	TARM-1	BARC/Akola
9	RM-03-71	IGKV, Raipur
10	RM-03-79	IGKV, Raipur
11	BM-4	ARS, Badanpur
12	AKM 8802	POKV, Akola
13	PKVAKM 4	POKV, Akola
14	KM 2293	CSA, Kanpur
15	GM-04-02	SDAV, S.K.Nagar
16	PM-09-11	GBPAUT,Pantnagar
17	RVSM 11-9	Sehore
18	MH 805	Hisar
19	NVL 638	Nirmal seeds
20	DGG - 1	Dharwad
21	UANNATI	MSSCL, Akoa
22	SKUA-M-300	SKUA&T, Srinagar

23	IPM 2K 15-4	IIPR, Kanpur
24	PUSA 1271	IARI, New delhi
25	TMB-36	BARC, Mumbai
26	ML-1907	PAU, Ludhiana
27	RMG-1004	ARS, Durgapura
28	AKM 10-13	POK, Akola
29	COGG 979	Coimbtore
30	VGG 04-011	NPRC, Vamban

Table 2: Genotypic (G), phenotypic (P) and environmental (E) correlation coefficients among different yield traits in mungbean**.**

Character		No. of flower per raceme	No. of seeds per pod	No. pod per cluster	Petiole length	Seed yield	100 seed weight (gm)	Pod length (cm)	Days to 50% flowering	Days to maturity
Plant height	P G E	0.646** 0.744** -0.069	0.595** 0.627** 0.292	0.681** 0.745** 0.213	0.616** 0.670** 0.123	0.568** 0.648** 0.032	-0.137 -0.181 0.122	0.361* 0.405* -0.077	0.648** 0.694** 0.024	0.632** 0.684** -0.163
No. of flower per raceme	P G E		0.687** 0.775** -0.090	0.756** 0.817** 0.340	0.771** 0.892** -0.216	0.805** 0.851** 0.526	0.193 0.246 -0.095	0.610** 0.679** 0.000	0.859** 0.945** -0.216	0.862** 0.939** -0.123
No. of seeds per pod	P G E			0.686** 0.743** 0.183	0.675** 0.745** -0.120	0.743** 0.812** 0.211	0.180 0.226 -0.148	0.792** 0.860** -0.069	0.719** 0.753** 0.047	0.679** 0.714** -0.059
No. pod per cluster	P G E				0.660** 0.755** -0.133	0.814** 0.866** 0.491**	0.048 0.112 -0.310	0.554** 0.631** -0.151	0.701** 0.768** -0.149	0.688** 0.753** -0.178
Petiole length	P G E					0.680** 0.788** -0.131	0.188 0.232 -0.099	0.610** 0.662** 0.016	0.870** 0.922** -0.007	0.841** 0.890** -0.033
Seed yield	P G E						0.326 0.400* -0.052	0.696** 0.768** 0.133	0.712** 0.788** -0.125	0.687** 0.758** -0.107
100 seed weight (gm)	P G E							0.510** 0.543** 0.321	0.242 0.272 -0.015	0.272 0.303 0.008
Pod length (cm)	P G E								0.625** 0.649** 0.162	0.568** 0.593** 0.056
Days to 50% flowering	P G E									0.978** 0.982** 0.772**

Table 3: Genotypic path coefficient of various characters influencing seed yield per plant in mungbean

Character	Plant height	No. of flower per raceme	No. of seeds per pod	No. of pod per cluster	Petiole length	100 seed weight (gm)	Pod length (cm)	Days to 50% flowering	Days to maturity	Genotypic correlation coefficient
Plant height	**0.140**	0.556	0.400	0.383	0.073	-0.120	-0.296	0.737	-1.224	0.648**
No. of flower per raceme	0.104	**0.747**	0.494	0.420	0.097	0.164	-0.497	1.002	-1.682	0.851**
No. of seeds per pod	0.088	0.579	**0.638**	0.382	0.081	0.151	-0.629	0.799	-10278	0.812**
No. pod per cluster	0.105	0.610	0.474	**0.514**	0.082	0.075	-0.462	0.815	-1.348	0.866**

Petiole length	0.094	0.666	0.475	0.388	**0.109**	0.154	-0.484	0.979	-1.594	0.788**
100 seed weight (gm)	-0.025	0.184	0.144	0.058	0.025	**0.666**	-0.397	0.288	-0.542	0.400*
Pod length (cm)	0.057	0.507	0.548	0.325	0.072	0.362	**-0.731**	0.689	-1.061	0.768**
Days to 50% flowering	0.097	0.706	0.481	0.395	0.101	0.181	-0.475	**1.061**	-1.759	0.788**
Days to maturity	0.096	0.702	0.455	0.387	0.097	0.202	-0.433	1.042	**-1.790**	0.758**

Table 4: Analysis of Variance

Source of variation	D.F.	Plant height	No. of flower per raceme	No. of seeds per pod	No. pod per cluster	Petiole length	Seed yield	100 seed weight (gm)	Pod length (cm)	Days to 50% flowering	Days to maturity
Replication	2	27.421*	1.106*	0.021	0.102	0.114	0.348	0.796**	0.511	2.359	1.250
Treatment	29	179.21**	5.491**	2.991**	1.127	3.043**	4.217**	0.499	1.83*	275.07**	281.12**
Error	58	7.143	0.260	0.076	0.052	0.095	0.231	0.034	0.046	2.114	1.715

*Significant at 5% probability level

** Significant at 1% probability level

Table 5: Genetic parameter of variation

Character	GCV (%)	PCV (%)	h^2 (%)	GA	GA as % of mean
Plant height	19.47	20.64	88.9	14.71	37.81
No. of flower per raceme	14.55	15.60	87.0	2.54	28.00
No. of seeds per pod	10.11	10.50	92.7	1.96	20.10
No. pod per cluster	20.20	21.62	87.3	1.15	38.85
Petiole length	13.02	13.63	91.2	1.95	25.62
Seed yield	32.70	35.43	85.2	2.19	62.21
100 seed weight (gm)	11.36	12.55	81.9	0.73	21.09
Pod length (cm)	12.51	12.99	92.8	1.53	24.79
Days to 50% flowering	17.12	17.32	97.7	19.43	34.87
Days to maturity	11.16	11.26	98.2	19.70	22.77

GCV= Genotypic Coefficient of Variation, PCV= Phenotypic Coefficient of Variation
h^2= heritability, GA= Genetic Advance

REFERENCES

Johanson, H. W., Robinson, H. F., Comstock, R. E., (1955). Estimates of genetic and environmental variability insoybean.*AgronJ* **47**:314-318.

Khan, M. D., I. H. Khalil, M. A. Khan and Ikramullah, (2004). Genetic divergence and association for yield and related traits in mung bean.*Sarhad J. Agric*., 20: 555–61.

Potter,N. N.,Hotchkiss, J. H., (1997). FoodScience.*CBSPublishers*,NewDelhi, India.403.

Sadiq, M. S. and Abbas, G. (2007). Selection indices for seed yield in mungbean. *International J. of Biology and Biotechnology*. **4**(4): 421-423.

Sharma, R. N. (1999) Heritability and character association in non segregating populations of Mungbean (*Vignaradiata*L.Wilczek). *Journalof Interacademicia***3**:5-10.

Singh,R. K.,Chaudhury,B. D., (1985) Biometrical Method in Quantitative Genetic Analysis. *Kalyani Publishers*.NewDelhi,India.

Verma, P. and Garg, D. K. (2007). Correlation and path coefficient studies in mungbean. *J. of Arid Legumes*.**4**(2): 88-91.

Vikas ,V. R. S. P.,Singh,S. P. (1998). Geneticvariability in mungbean(*Vignaradiata*L. Wilczek) over environments in *kharif* season. *Annals of Agri Bio Research* **3**:211-215.

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 Agriculture*.**13**(2): 129-133.