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Full Length Research Paper

GENETIC VARIABILITY AND CHARACTER ASSOCIATION IN MUNGBEAN (*VIGNA RADIATA* (L.) WILCZEK)

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Abstract

The present experiment was conducted to evaluate the mungbean genotype to assess the magnitude of genetic variability and to understand the heritable component of variation for seed yield and its component traits traits. The estimates of genotypic coefficient of variability, heritability and genetic advance were high for seed yield per plant, 100-seed weight, number of seeds per pod, number of pods per plant and number of nodes on main stem. The estimates of correlation revealed that seed yield had positive and significant correlation with number of pods per plant, 100-seed weight, days to first picking maturity, primary branches per plant and number of pods per cluster. Path coefficient analysis indicated that number of pods per plant, number of seeds per pod, number of clusters per plant had maximum direct contribution on seed yield.

Keywords: Mungbean, genetic variability, heritability, path analysis

Introduction

Mungbean (*Vigna radiata* (L) Wilczek) is one of the important pulse crop because of its

short duration, adaptation to low water requirement and soil fertility. It is favored for consumption due to its easy digestibility and low production of flatulence (Shil and Bandopadhya, 2007) [11] Pulses are extensively grown in tropical regions of the world as a major protein rich crop bringing considerable improvement in human diet. Average protein content in the seed is around 24 percent. The protein is comparatively rich in the amino acid lysine but predominantly deficient in cereal grains (Baskaram *et al.*, 2009) [4]. Presently, the yield of mungbean is well below the optimum level to other pulses. The average yield of mungbean is very low not only in India (425kg/ka) but in entire tropical and sub-tropical Asia. India is the largest producer of mungbean in the world and accounts for 65 percent acreage and 54 percent production (Pratap *et al.*, 2012) [9]. Being the third largest pulse crop in India ,it occupies an area of about 3.55 million hectare area with total production 1,82 million tones and productivity of 512 kg/ha (All India Coordinated Research Project, 2012) [1].

Genetic variability studies provide basic information regarding the genetic properties of the population, based on which, breeding methods are formulated for further improvement of the crop. These studies are the helpful to know about the nature of extent variability attributable to different cases, sensitive nature of the crop to the environmental influences, heritability of the characters and genetic advance that can be realized in practical breeding .The extent of variability and heritability of the character among the genotypes is the basic source for the exploitation of superior potentiality of genotypes .Heritability gives the information of the magnitude of inheritance of quantitative traits ,while genetic advance will be helpful in formulating suitable selection procedures Seed yield per plant is a dependent trait ,which influenced by many independent traits, Studies on the correlation of the traits and their relative direct and indirect effects on seed yield are important ,as it is helpful in selection of desirable traits. Hense, an attempt was made to study thirteen quantitative traits, their correlations and effects on genotypes of mungbean.

Materials and Methods

The experimental material comprising of 40 genotypes of mungbean obtained from Narendera Dev University of Agriculture and Technology Kumarganj Faizabad and maintained at Research Farm of Department of Genetics and Plant Breeding, Post Graduate College Ghazipur-233001 India. The genotypes were grown in five rows of 3 meter length, adopting a spacing of 30x10 cm in a Randomized Block Design with three replications.

All the agronomic practices were followed to maintain the crop stand. Data were recorded on five randomly selected plants in each row for the characters *viz*. days to 50% flowering, days to first picking maturity, plant height (cm), primary branches per plant, number of nodes on main stem, number of clusters per plant, number of pods per cluster, pod length (cm), number of pods per plant, number of seeds per pod, 100-seed weight (g), protein content in seeds and seed yield per plant (g). The mean values of five plants were taken for the statistical analysis, statistical methods suggested by Burton (1952) for variability, Lush (1959) for heritability, Johnson *et al*., (1955) [15] for genetic advance as percentage of mean were adopted to find out the respective estimates. Further categorization of estimates was made based on the suggestions of Sivasubramanian and Madhavamenon (1973) for variability, Johnson *et al*. (1955) [15] for heritability and genetic advance as percentage of mean. genotypic and phenotypic correlations were partitioned into path coefficients analysis using the technique outlined by Dewey and Lu (1959) [5]. The biometrical observations on seed yield were recorded on single plant basis at the time of harvesting as per descriptions for *Vigna mungo* and *Vigna radiate* (revised) [IBPGR-biodiversity International, 1985] were used for estimation of genotypic and phenotypic coefficients of variation, heritability in broad sense and genetic advance as percentage of mean according to Johnson (1955) [15]. Correlation and path analysis according to Dewey and Lu (1959) [5].

Results and Discussion

The analysis of variance revealed highly significant differences among all the genotypes for all characters. Johnson (1955) [15] has suggested that GCV together with heritability would give best picture of amount of advance to be expected from selection. Seed yield per plant, 100 seed weight, number of seeds per pod, number of pods per plant, 100-seed weight, number of seeds per pod, number of pods per plant and number of nodes on main stem exhibited high estimates of GCV, PCV heritability, genetic advance and genetic advance as percentage of mean (Table-1). These traits can be used for selection as they respond well because of their high genetic variability. Parameswarappa (2005) [14] indicating that mungbean seed yield expressed high genetic advance coupled with high heritability and genotypic coefficient of variation. High heritability with low GCV, PCV and genetic advance were observed for days to 50% flowering and days to first picking maturity (Table-1). High heritability with moderate genetic advance, GCV, PCV for number of nodes on main stems, clusters per plant, plant height and number of pods per cluster indicate their limit

scope in the improvement through selection due to presence of moderate variability.

Table-2 represents the genotypic and phenotypic correlations between all pairs of characters. It was observed that genotypic correlations were greater than phenotypic correlations in all most the cases indicating that the environmental influences were not marked enough to alter the degree of association all the characters. Seed yield per plant possessed highly significant positive correlation with number of pods per plant, 100 seed weight, days to first picking maturity, primary branches per plant and number of pods per cluster. Days to 50% flowering showed positive significant correlation with days to first picking maturity. Similarly protein content had negative and significant correlation with number of clusters per plant; number of pods per plant with days to 50% flowering, days to first picking maturity and pod length; number of clusters per plant with days to 50% flowering. Similar result have been reported by Rahman *et al.* (2003) [12]. Ahmed *et al.* (1981)[2], Prakash (2006) [8], Verma and Garg (2007) [13].

Path coefficient analysis revealed that the trait, number of pods per plant had high positive direct effect on seed yield followed by number of seeds per pod and days to 50% flowering (Table-3). These traits also recorded strong positive correlation with seed yield per plant which are in accordance with the result of Rao (2006) [16]. The residual effect is low (0.214) indicating appropriateness of characters chosen. Number of clusters per plant, pod length, days to first picking maturity and protein content had negative direct effects.

Days to First picking maturity, plant height, primary branches per plant, number of pods per cluster, 100 seed weight, Protein content in seed recorded high positive indirect effect on seed yield *via* number of pods per plants. These findings are in agreement with Rao *et al.* (2006) [16], Verma and Garg (2007) [13], Prakash (2006) [8]. Hence number of pods per plant, days to first picking maturity, primary branches per plant, number of pods per cluster and 100-seed weight are the most important yield contributing components as they recorded high direct and indirect effects towards seed yield in mungbean.

Table 1: Estimation of grand mean, range, coefficient of variation. Heritability, Genetic advance and genetic advance as percentage of mean for different characters of Mungbean

Character	Grand Mean	Range	Coefficient of variation	Heritabilit	Genetic advance	Genetic advance at

			GCV	PCV	y		% of Mean
Days to 50% Flowering	37.19	34.33 - 42.67	4.36	4.76	0.839	3.06	8.22
Day to first picking maturity	69.61	62.89 - 73.11	2.83	3.16	0.803	3.64	5.22
Plant height	40.92	39.44 - 44.78	2.42	2.95	0.675	1.68	4.10
Primary branches/ plant	3.13	2.22 - 3.89	11.74	16.33	0.517	0.54	17.25
No. of Nodes on main stem	6.82	5.44 - 8.22	8.46	10.69	0.626	0.94	13.78
No. of Clusters/ plant	14.81	11.89 - 17.33	7.14	8.61	0.689	1.81	12.22
No. of Pods/ Cluster	4.11	2.89 - 5.34	12.36	16.70	0.548	0.77	18.73
Pod length	7.11	6.33 - 7.90	4.53	7.69	0.347	0.39	5.48
No. of Pods/ plant	57.25	42.00 - 63.88	9.45	9.62	0.966	10.96	19.14
No. of Seeds/ pod	6.52	5.21- 8.33	10.33	13.30	0.604	1.08	17.28
100 seed weight	3.18	2.00-4.13	11.31	14.18	0.637	0.59	18.55
Protein content in seed	21.21	20.16 - 22.67	2.75	3.64	0.571	0.91	4.29
Seed yield/ plant	12.97	06.93 - 16.40	18.10	18.78	0.929	4.66	35.92

Table 2: Genotypic (G) and Phenotypic (P) correlation among the 13 characters in Mungbean

Character		Days to first picking maturity	Plant height	Primary branches/ plant	No. of nodes on main stem	No. of Clusters/ plant	No. of Pods/ cluster	Pod length	No. of Pods/ plant	No. of Seeds/ pod	100 seed weight	Protein content in seed	Seed yield / Plant
Days to 50% Flowering	G	0.486**	-0.001	-0.217	0.174	-0.475**	-0.247*	0.341**	-0.372**	0.006	0.151	0.188	-0.252*
	P	0.395**	-0.006	-0.114	0.135	-0.364**	-0.191	0.236	-0.335**	0.001	0.124	0.119	-0.216
Days to first picking maturity	G		-0.187	-0.276*	0.291*	0.039	-0.205	0.377**	-0.564**	-0.025	0.428**	0.038	0.558**
	P		-0.133	-0.163	0.216	0.034	-0.191	0.156	-0.497**	0.002	0.318*	0.048	0.454**
Plant height	G			0.239	0.140	-0.196	0.300*	0.260*	.0263*	0.138	-0.083	0.203	0.286*
	P			0.129	0.135	-0.127	0.119	0.075	0.209	0.097	-0.035	0.126	0.243
Primary branches/ plant	G				0.097	0.074	0.386**	-0.036	0.302*	0.050	-0.199	0.106	0.402**
	P				0.080	0.091	0.200	0.091	0.215	0.020	-0.111	0.045	0.265*
Number of nodes on main stem	G					0.076	0.168	0.437**	-0.159	0.289*	0.198	-0.082	-0.064
	P					0.062	0.045	0.208	-0.123	0.133	0.096	-0.050	-0.027
No. of Cluster/pla	G						0.211	-0.244	0.065	-0.164	0.034	-0.371**	-0.024

nt	P						0.144	-0.116	0.060	-0.051	0.044	-0.262*	-0.038
No. of Pods/cluster	G							0.128	0.305*	0.065	-0.175	-0.059	0.361**
	P							0.090	0.225	0.029	-0.097	-0.065	0.265*
Pod length	G								-0.452**	-0.101	0.418**	-0.197	-0.369**
	P								-0.252*	-0.010	0.126	-0.124	-0.216
No. of Pods/plant	G									-0.016	-0.489**	0.203	0.905**
	P									-0.017	-0.379**	0.147	0.854**
No. of Seeds/pod	G										0.054	0.018	0.176
	P										0.086	0.011	0.151
100 seed weight	G											-0.156	0.470**
	P											-0.06	0.344**
Protein content in seed	G												0.217
	P												0.148
* Significant at 5% level of significance, ** Significant at 1% level of significance													

Table 3: Direct and indirect effects among their characters towards seed yield in Mungbean

Characters		**Days to 50% Flowering**	**Days to first picking maturity**	**Plant height**	**Primary branches/ plant**	**No. of nodes on main stem**	**No. of Clusters / plant**	**No. of Pods/ cluster**	**Pod length**	**No. of Pods/ plant**	**No. of Seeds/ pod**	**100 seed weight**	**Protein content in seed**	**G & P Correlation with yield/plant**
Days to	G	0.160	-0.062	0.000	-0.025	-0.005	-0.023	-0.011	0.035	-0.328	0.001	-0.00	0.008	-.252*

50%												4		
Flowering	P	0.078	-0.018	0.000	-0.009	0.008	0.027	-0.013	-0.013	-0.273	0.001	-0.003	-0.001	-0.216
Days to first picking	G	0.078	-0.127	0.012	-0.032	-0.008	0.002	-0.009	0.039	0.497	-0.005	-0.012	0.002	0.558**
maturity	P	0.031	-0.045	-0.003	-0.013	0.013	-0.003	-0.013	-0.008	0.405	0.000	-0.008	0.000	0.454**
Plant height	G	0.000	0.024	-0.066	0.028	-0.004	-0.009	0.014	0.027	0.232	0.029	0.002	0.009	0.286*
	P	0.000	0.006	0.021	0.010	0.008	0.009	0.008	-0.004	0.170	0.015	0.001	-0.001	0.243
Primary branches/ plant	G	-0.035	0.035	-0.016	0.115	-0.003	0.004	0.018	-0.004	0.226	0.011	0.005	0.005	0.402**
	P	-0.009	0.007	0.003	0.077	0.005	-0.007	0.014	-0.005	0.175	0.003	0.003	0.000	0.265*
Number of nodes on main stem	G	0.028	-0.037	-0.009	0.011	-0.026	-0.004	0.008	0.045	-0.140	0.061	-0.005	-0.004	0.064
	P	0.011	-0.010	0.003	0.006	0.058	-0.005	0.003	-0.011	-0.100	0.020	-0.002	0.000	-0.027
No. of Cluster/plant	G	-0.076	-0.005	0.013	0.009	-0.002	0.048	0.010	-0.025	0.057	-0.035	-0.001	-0.016	-0.024
	P	-0.029	-0.002	-0.003	0.007	0.004	-0.074	0.010	0.006	0.049	-0.008	-0.001	0.002	-0.038
No. of	G	0.040	0.026	-0.02	0.045	-0.004	0.010	0.046	0.013	0.268	0.014	0.005	-0.003	0.361**

Pods/cluster				0										
	P	-0.015	0.009	0.003	0.015	0.003	-0.010	0.070	-0.005	0.180	0.004	0.002	0.000	0.256*
Pod length	G	-0.055	-0.048	-0.017	-0.004	-0.011	-0.012	0.006	0.103	-0.399	-0.022	-0.012	-0.009	-0.369**
	P	-0.019	-0.007	0.002	0.007	0.012	0.009	0.006	-0.054	-0.205	-0.002	-0.003	0.001	-0.216
No. of Pods/plant	G	-0.060	0.072	-0.017	0.035	0.004	0.003	0.014	-0.046	0.881	-0.003	0.014	0.009	0.905**
	P	-0.026	0.022	0.004	0.016	-0.007	-0.004	0.016	0.014	0.841	-0.003	0.009	-0.001	0.854**
No. of Seeds/pod	G	0.001	0.003	-0.009	0.006	-0.008	-0.008	0.003	-0.010	-0.014	0.213	-0.001	0.001	0.176
	P	0.000	0.000	0.002	0.002	0.008	0.004	0.002	0.001	-0.014	0.149	-0.002	0.000	0.151
100 seed weight	G	0.024	-0.054	0.005	-0.023	-0.005	0.002	-0.008	-0.043	0.431	0.011	-0.028	-0.007	0.470**
	P	0.010	-0.014	-0.001	-0.008	0.006	-0.003	-0.007	-0.007	0.308	-0.013	0.024	0.000	0.344**
Protein content in seed	G	0.030	-0.005	-0.013	0.012	0.002	-0.018	-0.003	-0.020	0.179	0.004	0.004	0.044	0.217
	P	0.009	-0.002	0.003	0.003	-0.003	0.019	-0.005	0.007	0.119	0.002	0.001	-0.006	0.148
Residual (G) = 0.1057		Residual (P) = 0.2147												

* significant at 5% level of significance, ** significant at 1% level of significance

Bold diagonal figures are the direct effects;

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