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RESEARCH ARTICLE

GENETIC VARIABILITY, HERITABILITY, EXPECTED GENETIC ADVANCE AND CHARACTER ASSOCIATION IN MUNGBEAN (*Vigna radiata* L.Wilczek)

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Abstract

Fourty five advance lines including four varieties of mungbean were studied for genetic variability, heritability, genetic advance and character association for seed yield per plant and its component traits. The maximum variability was observed for seed yield per plant followed by pods per plant, 100-seed weight, number of seeds per pod and branches per plant. Heritability estimates were observed to be high for all the traits. High expected genetic advance coupled with high heritability estimates were for seed yield per plant, pods per plant and plant height indicating least influenced by the environmental variation. Seed yield per plant had significant and positive association with pods per plant, plant height, harvest index and seeds per pod.

INTRODUCTION

Mungbean (*Vigna radiata* L. Wilczek), also known as green gram is one of the most important pulse crops of Asia. In countries like India, food legumes, commonly known as pulses, are major source of dietary (24-27%) protein, which is 2 to 2.5 times higher than that of cereals. Its productivity is low which may be improved through employing the genetic variability appropriately. The estimates of heritable variances give a clue for possible improvement of the character under study. Association studies are helpful while making selection in the field for upgrading the seed yield. The present investigation was, therefore, under taken to predict an appropriate plant type for selection so as to improve the seed yield keeping in view the inter relation between traits and heritability.

MATERIAL AND METHODS

Fourty five advance genotypes alongwith four check varieties viz. PDM 139, KM 2241, IPM 02-3 and K 851were evaluated in three replications during *kharif* season at C.S.Azad University of Agriculture and Technology, Kanpur. Each genotype having six rows plot of 4 meter length with spacing 25 cm between and 10 cm within row. The observations were recorded for ten quantitative traits viz. days to 50 per cent flowering, days to maturity, plant height (cm), number of branches per plant, number of pods per plant, pod length (cm), number of grains per pod, harvest index, 100-seed weight and seed yield per plant (Table 1). Genotypic and phenotypic coefficient of variation was also estimated as Burton (1952). Heritability and Genetic Advance according to Hanson *et al*. (1956) and correlation coefficients were calculated as per formula suggested by Robinson *et al*. (1951).

RESULTS AND DISCUSSION

There were significant differences among genotypes for all the traits under study. Genetic parameters of variation, heritability and expected genetic advance as percentage over mean for seed yield and related traits are given in Table 1 & Fig.1. The genotypic and phenotypic coefficient variation ranged from 1.90 to 14.44 and 2.88 to 18.06, respectively. The maximum phenotypic and genotypic coefficient of variability were observed for branches per plant (15.70%) followed by cluster per plant (12%), seeds per pod (11.50%), pods per plant (9%) and seed yield per plant (10.69%). The least variability to the tune of 2-3% was recorded for days to flower and maturity. Similar findings have also been reported by Singh (1985); Saini *et al.*(1994); Rao (1994); Tyagi *et al*. (1997), Kumar *et al*.(1998), Khedar *et al*. (2006), Kumar *et al*. (2010), Babu *et al.* (2012), Farhan (2013), Nand *et al.* (2013) and Prasanna *et al.* (2013).

Table-1: Range, grand mean, genotypic (GCV) and phenotypic (PCV), Coefficient of variability, heritability (%), genetic advance per cent of mean for ten characters

S. N.	characters	Range of mean		Grand mean	Coefficient of variability		Heritability (%)	Genetic advance	Genetic advance in percent of mean	C.V.
		Min.	Max.		GCV	PCV				
1.	**Days to 50 per cent flowering**	30.33	39.00	33.89	6.41	7.32	76.60	5.02	14.18	3.53
2.	**Days to maturity**	65.66	72.00	68.58	1.90	2.88	43.20	2.26	3.29	2.17
3.	**Plant height**	30.06	43.40	37.77	7.98	8.85	81.30	7.17	18.99	3.83
4.	**No .of primary branches per plant**	2.33	4.00	3.11	8.92	18.06	24.40	0.36	11.64	15.70
5.	**No. of clusters per plant**	4.33	8.66	7.05	12.26	17.12	51.30	1.64	23.19	11.94
6.	**No. of pods per plant**	16.00	29.00	20.84	14.44	16.97	72.40	6.76	32.45	8.90
7.	**Pod length**	6.46	8.16	7.14	5.72	7.51	58.00	0.82	11.50	4.87
8.	**No. of seeds per pod**	6.33	9.33	7.85	6.11	12.63	23.00	0.61	7.74	11.16
9.	**100- seed weight**	2.91	4.15	3.55	10.05	10.19	97.10	0.93	26.14	1.72
10	**Seed yield per plant**	3.71	6.81	4.94	13.88	14.87	87.20	1.69	34.21	5.32

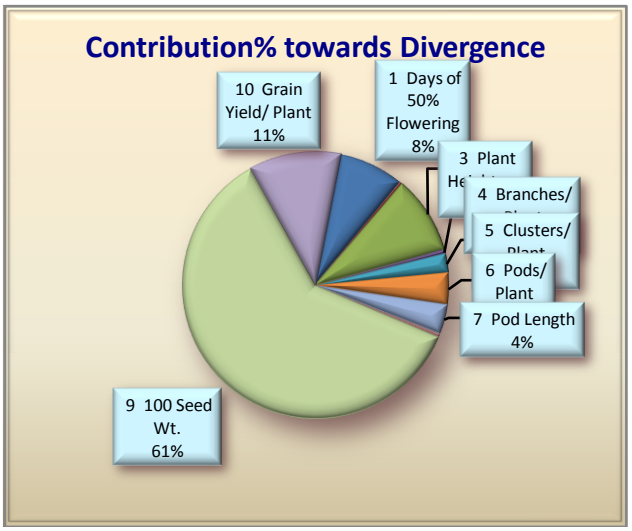

Fig.1: Estimates of Variability

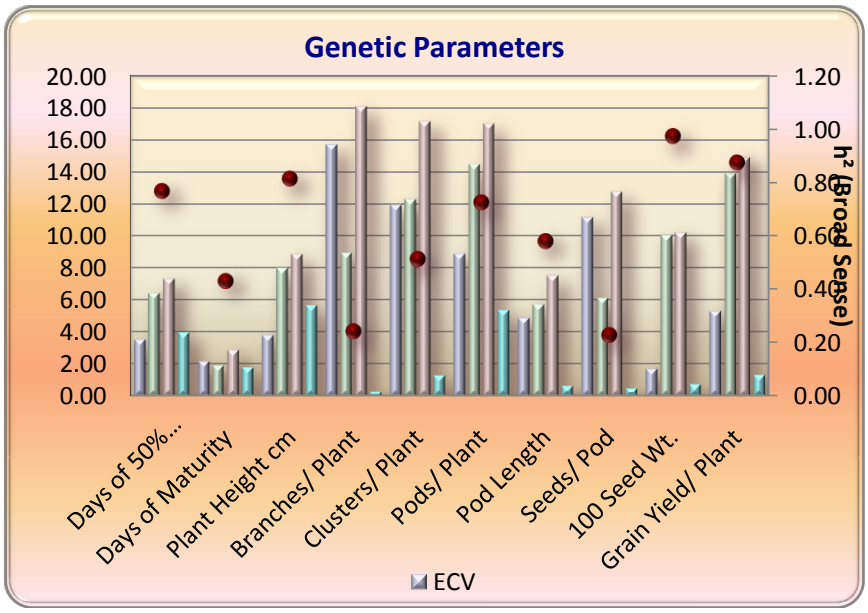

Fig.1: Estimates of coefficient of variation, heritability and genetic advance.

High heritability estimates to the level of (>70%) were found for all the characters, except number of branches per plant where it was only 24% (Table 1 & Fig.1). The high heritability for economic traits including seed yield per plant gave pleasant indication for success in selection because of their heritable in nature and can gave anticipated gain in selection. The genetic advance in per cent of mean was the highest for seed yield per plant (34.21%), followed by pods per plant (32.45%) and 100-seed weight (26.14%) whereas it was lowest for days to maturity (3.29%). Similar findings were reported by Singh *et al*. (1978); Rao (1994), Singh(1999), Khedar *et al*. (2006), Kumar *et al*. (2010), Babu *et al*. (2012), Farhan (2013), Nand *et al*. (2013) and Prasanna *et al*. (2013). High heritability coupled with high expected genetic advance was observed for seed yield per plant, pods per plant and 100-seed weight indicated that these traits were least influenced by environmental interaction. Thus selection for these traits would be quite effective in enhancing grain yield per plant and also simultaneously its related attributes.

Correlation coefficients of seed yield per plant with other traits are given in Table 2. Seed yield per plant exhibited significant and positive correlation with branches per plant, 100-seed weight, number of seeds per pod, number of pods per plant and 100-seed weight with number of seeds per pod and pod length; number of seeds per pod with pod length, number of clusters per plant and number of pods per plant; number of pods per plant with number of clusters per plant and number of branch per plant; plant height with days to maturity had positive and significant association.

Table 2: Genotypic correlation coefficient for different characters in mungbean

Characters	Days to 50 per cent flowering	Days to maturity	Plant height	No.of primary branches per plant	No. of clusters per plant	No. of pods per plant	Pod length	No. of seeds per pod	100 -seed weight	Grain yield per plant
Days to 50 per cent flowering	-	0.869	-0.267	0.190	0.076	0.146	-0.172	0.020	0.105	0.165
Days to maturity		-	0.433	0.169	-207	0.258	-0.054	-0.443	0.168	0.070
Plant height			-	-0.140	0.212	-0.222	-0.200	-0.027	-0.182	-0.192
No.of primary branches per plant				-	0.112	0.045	0.092	-0.159	0.167	0.332
No. of clusters per plant					-	0.332	-0.167	-0.292	-0.256	0.242
No. of pods per plant						-	-0.052	-0.553	-0.555	-0.037
Pod length							-	-0.02	0.214	0.189
No. of seeds per pod								-	0.318	0.259
100- seed weight									-	0.332

grain yield per plant										-

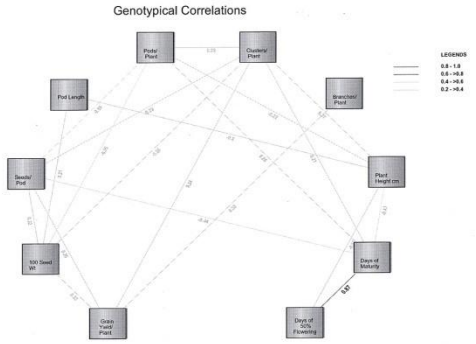

Fig.3: Correlation coefficients

The studies revealed that seed yield per plant is the product of seeds per plant and 100-seed weight, where as seeds per plant, depends on pods per plant, seeds per pod, plant height, branching and pod length. Therefore, due emphasis need to be given on above mentioned traits for improving the productivity during selection. Moreover these traits are also highly heritable and inter related. Harvest index is the proportion of seed yield of total biomass. Therefore, it refers to the physiological efficiency of the genotype which is also criteria for selection.

Thus, present investigation revealed that the advance lines viz. IP1118, IP 1127, KM 2324, KM 2325, KM 2326, SML 1127 and KM 2353 were found superior and can be utilized for further breeding programmes aimed to developing high yielding and stable varieties. Above advanced lines have been incorporated in our breeding programme for developing new high yielding genotypes.

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