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Component relationship and genetic variability of seed yield and its contributing traits in Greengram [Vigna radiata (L.) Wilezek]

Puri Satish Gajanan and Dr. GM Lal

Abstract

The present investigation consists of 21 genotypes of Green gram including one check, which were grown in the Field Experimentation Centre of the Department of Genetics and Plant breeding, SHUATS, Prayagraj during kharif 2021 following RBD with three replications. The data were recorded on 13 characters to study the amount of genetic variability, heritability, association of yield contributing components with yield and direct and indirect effects of yield contributing component with yield and direct and indirect effects of yield contributing components in the Green gram genotypes. Based on the mean performance genotype CO-7 followed by were identified as best genotypes for seed yield per plant. High significant variation was obtained for all characters studies. High heritability estimates were observed for days to 50% flowering followed by days to 50% pod setting, number of cluster per plant, seed index, number of primary branches, seed yield per plant, number of pod per plant, number of seed per plant, plant height, harvest index, days to maturity, biological yield per plant. High values for heritability indicates that it may be due to higher contribution of genotypic components. High genetic advance as percent of mean was recorded high for harvest index, days to 50% flowering, days to 50% pod setting, plant height, number of pod per plant, seed index, number of cluster per plant, days to maturity, biological yield per plant, seed yield per plant, while moderate genetic gain is observed number of seed per pod followed by number of primary branches and pod length. Traits exhibiting high heritability coupled with genetic advance as percent of mean suggest that the traits are governed by additive gene action, equal contribution of additive and non-additive gene action respectively. The present study revealed that grain yield per plant was positively and significantly correlated with Harvest index. Path analysis at phenotypic level identified Harvest index, seed index, number of seed per pod, and number of pods per plantimportant direct components for seed yield per plant.

Keywords: Greengram GCV, PCV, heritability, variability, genetic Advance, correlation analysis and path

Introduction

Pulses are a wonderful gift of nature, also known as grain legumes, are the major source of protein in Asia and constitute an important supplement to the predominantly cereal-based diet (Sahoo and Jaiwal, 2008). They are being sporadically grown under marginal lands of low fertility and moisture stress conditions; hence genotypes are more adaptable to poor management which registers limitation on yield, this does not reflect low genetic potential, but they may have higher genetic potential than cereals (Jain, 1978). Hence these are truly some of the best crops in the world and their production and availability assume special significance for the nutritional security of the people. India is a rare country which grows such a variety of pulse crops which none of the countries in the world grows.

Green gram [*Vigna radiata* (L.) R. Wilczek] has been cultivated in India since prehistoric times and is considered to be a native crop of India (Vavilov, 1926). The protein is comparatively rich in lysine, an amino acid which is predominantly deficit in cereal grains. Greengram seeds are rich in minerals like Calcium, iron, magnesium, phosphorus, potassium and vitamins like ascorbic acid, thiamine, riboflavin, niacin, pantothenic acid and vitamin A (Tang *et al.*, 2014).

Green gram is accentuated due to its nutritional value. Hundred gram of green gram seeds contains energy (234 cal), Protein (24.6%), fat (1.0%), fiber (2.2 g), carbohydrates (57.5%), calcium (0.08 g), phosphorus (0.045 g) and iron (5.7 mg), vitamin B (300 mg) and thiamin (0.525 mg) (Srivastava and Ali, 2004).

However, the productivity of greengram is low as in the case of other pulse crops.

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So, it is the need of the hour to develop varieties with high yield potential by using appropriate breeding programmes for selection of varieties having better yield potential.

As a result, it is necessary that we should have knowledge of magnitude of genetic variability and estimation of heritability for yield and its components in a crop population for determining the influence of environment for the expression of the characters, and the extent to which improvement is possible after selection to develop varieties with better yield potential.

Materials and Methods

The experiment was carried out at Field Experimentation Centre of the Department of Genetics and Plant Breeding, Naini Institute of Agriculture, Sam Higginbottom University of Agriculture, and Technology & Sciences. Prayagraj (U.P.), during Kharif-2021 season under Randomized Block Design.

Results and Discussion

Table 1 shows Analysis of Variance for 13 different characters in Mungbean.

Characters		Mean Sum of Squares	
Characters	Replication (df =2)	Genotypes (df=20)	Error (df=40)
Days to 50% flowering	0.4910	35.507**	7.429
Days to 50% pod setting	2.7420	63.528**	14.858
Days to maturity	34.0090	62.666**	15.674
Plant height (cm)	3.1490	36.33**	6.631
Number of clusters per plant	0.7360	1.856**	0.766
Number of pods per plant	29.743*	34.629**	7.032
Pod length (cm)	0.3660	2.867**	0.324
Number of primary branches	0.0390	1.055**	0.036
Seed Index	0.0990	0.882**	0.038
Number of seeds per pod	0.2480	7.738**	0.599
Harvest index (%)	6.0450	32.876**	4.836
Biological yield per plant	12.083*	20.902**	3.202
Biological yield per plant	1.6680	3.22**	0.524
Seed yield/plant (gm)	0.4910	35.507**	7.429

Table 1: Analysis of Variance for 13 different characters in Mungbean

**,* significant 5% and 1% level of significance respectively

Data depicted in Table 2 shows Mean performance of 21 genotypes in Mungbean.

Table 2: Mean	performance	of 25	genotypes	in Mungbean
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Sl. No	Genotypes	DF50	DPS50	DM	PH	NCPP	NPPP	PL	NPB	SI	NSPP	HI	BYP	SYPP
01	PHULE G-94418	38.27	49.08	69.42	26.06	5.41	21.80	6.55	2.42	3.86	12.65	32.91	17.97	5.65
02	PS-16	34.72	43.80	67.57	26.97	5.24	16.58	8.37	2.02	4.87	10.58	38.23	16.27	5.83
03	CO-7	39.64	49.90	79.55	27.13	6.71	27.79	7.20	1.54	3.47	11.01	34.43	18.93	6.71
04	JALGAON 781	36.88	46.00	75.16	30.02	6.31	26.10	7.63	2.02	3.44	10.16	33.20	16.70	5.67
05	S.P.M. 2040	39.49	49.25	78.47	25.86	5.69	17.31	7.71	1.82	4.36	10.36	33.51	17.47	5.55
06	CO-8	41.56	51.68	71.03	31.25	6.06	21.47	9.14	1.15	4.18	13.61	27.64	18.19	5.09
07	T-44	31.60	39.66	65.00	20.97	3.98	14.37	6.17	0.52	3.73	8.11	35.05	11.24	3.92
08	SM-20-108	34.16	44.88	65.55	24.07	6.28	22.12	7.30	1.19	4.06	10.44	31.16	14.11	4.56
09	ML-337	42.96	56.81	75.07	26.00	6.00	21.97	8.31	1.45	2.85	11.52	33.39	16.79	5.40
10	PDM-139	34.59	43.66	67.70	26.19	5.61	22.97	6.90	1.18	3.26	9.14	33.35	14.56	4.90
11	GM-3	42.04	55.12	79.50	36.38	6.17	18.62	10.00	0.98	3.19	15.11	34.47	22.22	7.90
12	PHULE MOONG 9339	38.22	50.96	74.15	24.49	5.39	18.00	6.67	1.70	3.30	10.61	30.49	18.34	6.13
13	SHWETA	42.45	53.64	78.66	26.37	7.35	24.72	7.60	2.17	3.25	10.40	33.61	20.27	7.11
14	ML-131	41.68	52.34	76.46	29.91	5.44	23.48	6.29	0.79	3.27	9.43	33.23	19.18	6.49
15	TYPE-51	41.77	52.42	73.24	30.30	6.40	23.97	8.64	1.96	3.74	8.18	32.02	18.20	5.91
16	SML-1638	34.59	43.92	67.72	26.01	6.90	22.03	6.90	0.68	3.76	10.39	32.24	16.39	5.41
17	SM-20-103	32.61	41.39	71.99	25.71	6.65	22.28	7.00	2.43	3.35	10.16	33.96	20.24	7.28
18	SPM-20-47	40.17	51.85	74.73	28.95	5.45	20.23	6.51	0.87	3.32	11.30	27.30	20.28	5.40
19	VBN-2	40.37	51.46	76.42	23.54	4.97	18.70	7.13	0.69	3.97	10.44	26.02	17.01	4.37
20	BM 2002-1	36.96	49.66	70.27	33.03	4.72	16.51	7.88	0.97	4.53	11.16	24.59	16.35	4.19
21	SM-20-29 (CHECK)	38.70	50.33	74.91	26.19	5.64	19.39	7.06	1.35	2.77	10.07	29.15	22.41	6.37
	Mean	38.26	48.94	72.98	27.40	5.83	20.97	7.47	1.42	3.64	10.71	31.90	17.77	5.71
	C.V.	7.12	7.88	5.42	9.40	15.02	12.64	7.61	13.27	5.33	7.23	6.89	10.07	12.69
	S.E.(m)	1.57	2.23	2.29	1.49	0.51	1.53	0.33	0.11	0.11	0.45	1.27	1.03	0.42
	C.D. 5%	4.50	6.36	6.53	4.25	1.44	4.38	0.94	0.31	0.32	1.28	3.63	2.95	1.19
	C.D. 1%	6.02	8.51	8.74	5.69	1.93	5.86	1.26	0.42	0.43	1.71	4.86	3.95	1.60
	Range (Lowest)	31.60	39.66	65.00	20.97	3.98	14.37	6.17	0.52	2.77	8.11	24.58	11.24	3.92
	Range (Highest)	42.96	56.81	79.55	36.38	7.35	27.79	10.00	2.43	4.87	15.11	38.23	22.41	7.90

(Abbreviations: DF50: Days to 50% flowering, DPS50: Days to 50% pod setting, DM: Days to maturity, PH: Plant height, NPB: Number of primary branches per plant, NCPP: Number of clusters per plant, NPPP: Number of pods per plant, NSPP: Number of seeds per pod, PL: Pod

length, SI: Seed index, BY: Biological Yield per plant HI: Harvest index, SYPP: Seed yield per plant) Table 3 represents Mean performance of 21 genotypes in Mungbean.

Table 3: Mean Performance of superior genotypes for seed yield per plant along with attributing characters in Mungbean

Genotypes	DF50	DPS50	DM	PH	NCPP	NPPP	PL	NPB	SI	NSPP	HI	BYP	SYPP
CO-7	39.64	49.90	79.55	27.13	6.71	27.79	7.20	1.54	3.47	11.01	34.43	18.93	6.71
GM-3	42.04	55.12	79.50	36.38	6.17	18.62	10.00	0.98	3.19	15.11	34.47	22.22	7.90
ML-131	41.68	52.34	76.46	29.91	5.44	23.48	6.29	0.79	3.27	9.43	33.23	19.18	6.49
SM-20-103	32.61	41.39	71.99	25.71	6.65	22.28	7.00	2.43	3.35	10.16	33.96	20.24	7.28
SM-20-29 (CHECK)	38.70	50.33	74.91	26.19	5.64	19.39	7.06	1.35	2.77	10.07	29.15	22.41	6.37

(Abbreviations:- DF50: Days to 50% flowering, DPS50: Days to 50% pod setting, DM: Days to maturity, PH: Plant height, NPB: Number of primary branches per plant, NCPP: Number of clusters per plant, NPPP: Number of pods per plant, NSPP: Number of seeds per pod, PL: Pod length, SI: Seed index, BY: Biological Yield per plant HI: Harvest index, SYPP: Seed yield per plant)

Presented Table 4 shows Genetic parameters for 14 characters in Mungbean.

Table 4: Genetic parameters for 14 characters in Mungbean

Sl. No	Characters	GCV (%)	PCV (%)	h2 (Heritability Broad Sense)	GA (5% LOS)	GA as % of mean
01	Days to 50% flowering	7.997	10.71	55.749	4.706	12.3
02	Days to 50% pod setting	8.23	11.391	52.196	5.995	12.248
03	Days to maturity	5.423	7.671	49.984	5.764	7.898
04	Plant height(cm)	11.483	14.839	59.887	5.016	18.306
05	Number of clusters per plant	10.343	18.24	32.153	0.704	12.082
06	Number of pods per plant	14.462	19.211	56.675	4.704	22.429
07	Pod length(cm)	12.321	14.482	72.381	1.614	21.593
08	Number of primary branches	40.949	43.045	90.5	1.142	80.248
- 09	Seed Index	14.555	15.5	88.169	1.026	28.153
10	Number of seeds per pod	14.408	16.12	79.886	2.84	26.528
11	Harvest index (%)	9.583	11.805	65.902	5.113	16.026
12	Biological yield per plant	13.671	16.98	64.822	4.029	22.674
13	Seed yield/plant(gm)	16.613	20.902	63.17	1.552	27.2

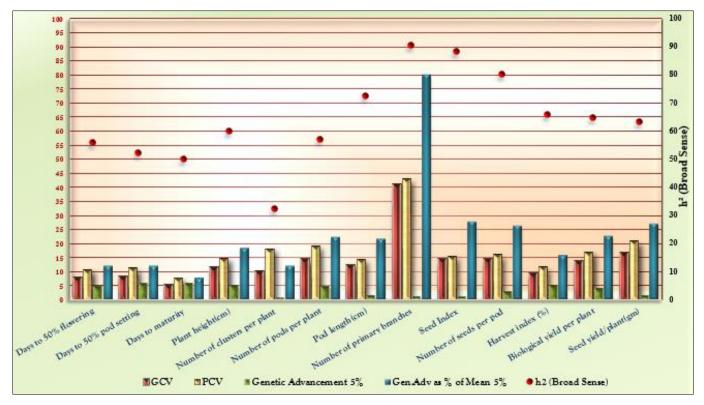


Fig 1: Bar chart representing the relationship among the GCV, PCV, Heritability, Genetic Advance and Genetic Advance as percent of mean in Mungbean

Table 5 shows Estimates of phenotypic correlation coefficients among different quantitative characters in mungbean genotypes

Characters	DF50	DPS50	DM	PH	NCPP	NPPP	PL	NPB	SI	NSPP	HI	BYP	SYPP
DF50	1.00	0.90**	0.45**	0.32*	0.13	0.16	0.28*	0.02	-0.21	0.28*	-0.18	0.37*	0.24
DPS50		1.00	0.45**	0.35*	0.06	0.05	0.23	-0.02	-0.23	0.41**	-0.23	0.38*	0.21
DM			1.00	0.31*	0.24	0.24	0.18	0.15	-0.37*	0.26*	0.03	0.53**	0.45**
PH				1.00	0.02	0.06	0.50**	-0.04	0.02	0.44**	-0.14	0.31*	0.21
NCPP					1.00	0.70**	0.13	0.32*	-0.22	0.14	0.18	0.49**	0.55**
NPPP						1.00	-0.01	0.30*	-0.31*	-0.03	0.19	0.34*	0.44**
PL							1.00	0.08	0.17	0.44**	0.02	0.20	0.21
NPB								1.00	0.01	0.00	0.38*	0.26*	0.41**
SI									1.00	0.02	-0.08	-0.38*	-0.39*
NSPP										1.00	-0.05	0.38*	0.28*
HI											1.00	-0.07	0.42**
BYP												1.00	0.77**
SYPP													1.00

**,* significant 1% and 5% level of significance respectively

Data depicted in Table 6 Estimates of genotypic correlation coefficients among different quantitative characters in mungbean genotypes

Characters	DF50	DPS50	DM	PH	NCPP	NPPP	PL	NPB	SI	NSPP	HI	BYP	SYPP
DF50	1.00	0.89**	0.91**	0.60**	0.41**	0.39**	0.55**	0.03	-0.35*	0.50**	-0.28*	0.77**	0.46**
DPS50		1.00	0.98**	0.59**	0.36*	0.30*	0.60**	-0.02	-0.40*	0.52**	-0.39*	0.77**	0.43**
DM			1.00	0.40*	0.48**	0.38*	0.32*	0.16	-0.45**	0.30*	-0.11	0.88**	0.77**
PH				1.00	0.41**	0.21	0.80**	-0.04	0.01	0.64**	-0.19	0.64**	0.51**
NCPP					1.00	0.84**	0.47**	0.54**	-0.39*	0.19	0.31*	0.39*	0.69**
NPPP						1.00	-0.02	0.36*	-0.47**	-0.06	0.14	0.18	0.34*
PL							1.00	0.15	0.20	0.66**	0.08	0.31*	0.32*
NPB								1.00	0.04	0.01	0.42**	0.28*	0.50**
SI									1.00	0.03	-0.07	-0.49**	-0.53**
NSPP										1.00	-0.21	0.50**	0.34*
HI											1.00	-0.17	0.44**
BYP												1.00	0.83**
SYPP													1.00

**,* significant 1% and 5% level of significance respectively

Presented Table 7 shows Estimates of phenotypic path for seed yield per plant in mungbean genotypes.

Table 7: Estimates of phenotypic path for seed yield per plant in mungbean genotypes

Characters	DF50	DPS50	DM	PH	NCPP	NPPP	PL	NPB	SI	NSPP	HI	BYP	SYPP
DF50	0.0267	0.0240	0.0120	0.0086	0.0035	0.0043	0.0076	0.0005	-0.0057	0.0076	-0.0048	0.0099	0.2407
DPS50	-0.0144	-0.0160	-0.0072	-0.0056	-0.0009	-0.0007	-0.0037	0.0004	0.0037	-0.0065	0.0036	-0.0061	0.2106
DM	-0.0074	-0.0074	-0.0166	-0.0052	-0.0040	-0.0040	-0.0030	-0.0024	0.0062	-0.0043	-0.0004	-0.0088	0.449**
PH	0.0112	0.0123	0.0110	0.0349	0.0006	0.0023	0.0174	-0.0014	0.0007	0.0155	-0.0050	0.0108	0.2070
NCPP	0.0104	0.0046	0.0196	0.0014	0.0806	0.0561	0.0105	0.0261	-0.0176	0.0111	0.0143	0.0394	0.553**
NPPP	0.0046	0.0013	0.0070	0.0019	0.0201	0.0289	-0.0002	0.0085	-0.0089	-0.0008	0.0055	0.0097	0.438**
PL	0.0113	0.0092	0.0073	0.0199	0.0052	-0.0003	0.0400	0.0033	0.0068	0.0175	0.0010	0.0081	0.2085
NPB	0.0003	-0.0003	0.0022	-0.0006	0.0048	0.0044	0.0012	0.0148	0.0001	0.0000	0.0056	0.0039	0.405**
SI	0.0142	0.0151	0.0245	-0.0012	0.0144	0.0203	-0.0112	-0.0004	-0.0661	-0.0013	0.0051	0.0253	-0.391*
NSPP	-0.0042	-0.0061	-0.0038	-0.0066	-0.0021	0.0004	-0.0065	0.0000	-0.0003	-0.0150	0.0008	-0.0057	0.275*
HI	-0.0794	-0.1006	0.0111	-0.0630	0.0788	0.0846	0.0109	0.1682	-0.0342	-0.0244	0.4444	-0.0330	0.417**
BYP	0.2673	0.2746	0.3818	0.2226	0.3516	0.2418	0.1456	0.1875	-0.2751	0.2752	-0.0534	0.7188	0.772**
SYPP	0.2407	0.2106	0.449**	0.2070	0.553**	0.438**	0.2085	0.405**	-0.391*	0.275*	0.417**	0.772**	1.0000
Partial R ²	0.0064	-0.0034	-0.0074	0.0072	0.0446	0.0127	0.0083	0.0060	0.0258	-0.0041	0.1852	0.5551	

Table 8 shows Estimates of genotypic path for seed yield per plant in mungbean genotypes.

		1 abi	e 8: Estim	ates of ge	notypic pa	ath for see	ea yiela p	er plant in	mungbear	i genotyp	es		
Characters	DF50	DPS50	DM	PH	NCPP	NPPP	PL	NPB	SI	NSPP	HI	BYP	SYPP
DF50	0.3038	0.3134	0.3214	0.1826	0.1253	0.1173	0.1680	0.0085	-0.1047	0.1520	-0.0841	0.2336	0.457**
DPS50	-0.6758	-0.6551	-0.6448	-0.3881	-0.2362	-0.1978	-0.3920	0.0112	0.2616	-0.3415	0.2550	-0.5054	0.434**
DM	0.0166	0.0154	0.0156	0.0063	0.0075	0.0059	0.0049	0.0025	-0.0070	0.0048	-0.0017	0.0138	0.771**
PH	-0.1420	-0.1399	-0.0949	-0.2362	-0.0956	-0.0502	-0.1882	0.0092	-0.0030	-0.1517	0.0451	-0.1506	0.510**
NCPP	0.3694	0.3228	0.4303	0.3624	0.8952	0.7547	0.4221	0.4822	-0.3510	0.1734	0.2806	0.3518	0.690**
NPPP	-0.1302	-0.1018	-0.1266	-0.0717	-0.2844	-0.3373	0.0076	-0.1237	0.1595	0.0215	-0.0476	-0.0601	0.341*
PL	-0.0623	-0.0674	-0.0355	-0.0898	-0.0531	0.0026	-0.1127	-0.0164	-0.0220	-0.0738	-0.0094	-0.0351	0.322*
NPB	-0.0105	0.0064	-0.0608	0.0147	-0.2022	-0.1377	-0.0546	-0.3754	-0.0139	-0.0033	-0.1591	-0.1039	0.504**
SI	-0.0627	-0.0726	-0.0812	0.0023	-0.0713	-0.0859	0.0356	0.0067	0.1817	0.0055	-0.0119	-0.0895	-0.525**
NSPP	0.0143	0.0149	0.0087	0.0183	0.0055	-0.0018	0.0187	0.0003	0.0009	0.0286	-0.0061	0.0141	0.341*
HI	-0.1046	-0.1470	-0.0399	-0.0721	0.1183	0.0532	0.0316	0.1600	-0.0248	-0.0802	0.3776	-0.0624	0.436**
BYP	0.9413	0.9444	1.0788	0.7807	0.4810	0.2181	0.3814	0.3388	-0.6026	0.6061	-0.2024	1.2241	0.830**
SYPP	0.457**	0.434**	0.771**	0.510**	0.690**	0.341*	0.322*	0.504**	-0.525**	0.341*	0.436**	0.830**	1.0000
Partial R ²	0.1389	-0.2840	0.0121	-0.1204	0.6179	-0.1150	-0.0363	-0.1891	-0.0955	0.0097	0.1646	1.0164	

Table 8: Estimates of genotypic path for seed yield per plant in mungbean genotypes

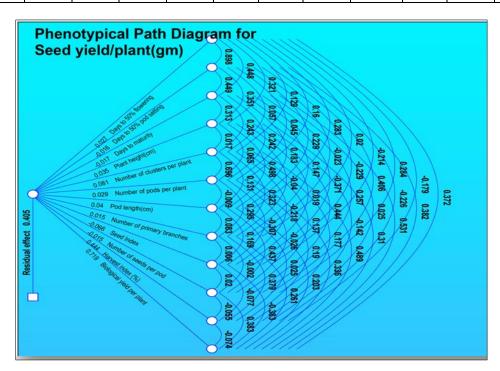


Fig 2: Phenotypic path diagram for seed yield per plant

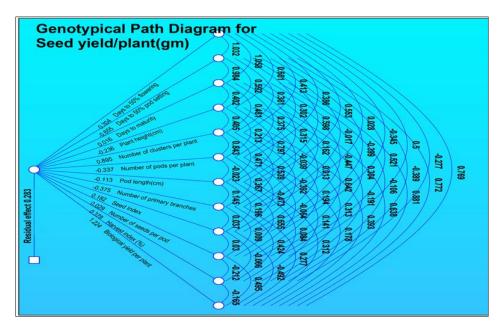


Fig 3: Genotypic path diagram for seed yield per plant

Summary

The present study entitled "Component relationship and genetic variability of seed yield and its contributing traits in Greengram [*Vigna radiata* (L.) Wilezek]" was conducted at central research farm, Department of Genetics and Plant breeding, SHUATS. The experiment was done in randomized block design with three replications using 21 genotypes during Kharif 2021.

The analysis of variance for all characters of mungbean genotypes revealed good extant of significant differences among the genotypes for all traits. Henceforth, the data for all 13 characters that showed sufficient amount of significant differences were subjected to further statistical analysis.

Out of 21 genotypes, evaluated for 13 different characters, 4 genotypes were found to be superior for seed yield per plant over Check variety SM-20-29. These genotypes comprised of released varieties CO-7, GM-3, ML-131, SM-20-103. Therefore, these genotypes may be used in future breeding programme to develop superior varieties with desirable economic traits beneficial for mankind by creating variability by hybridization followed by selection.

Both high GCV and PCV was recorded for Number of primary branches per plant. While both moderate GCV and PCV were recorded for plant height, number of clusters per plant, number of pods per plant, Pod length, Seed Index, number of seeds per pod and biological yield per plant which suggests that improvement in these characters might be gained to a reasonable extent. Both low GCV and PCV were recorded for days to maturity.

High estimates of heritability coupled with high genetic advance as % of mean was recorded for pod length, Number of primary branches per plant, seed index, number of seeds per pod, biological yield per plant (g) and seed yield per plant (g). High estimates of heritability coupled with moderate genetic advance as % of mean was recorded for harvest index, while moderate estimates of heritability coupled with moderate genetic advance as % of mean was observed for Days to 50% flowering, days to 50% pod setting, plant height and number of clusters per plant. These traits are governed by additive gene action and thus can be improved through direct selection.

Moderate GCV along with high heritability was observed for pod length, seed index, number of seeds per pod biological yield (g) and Seed yield per plant (g). This indicated that these traits are comparatively under less influence of environment henceforth, desirable for selection in breeding programme.

Positive and significant correlation was observed for days to maturity, number of clusters per plant, number of pods per plant, number of primary branches per plant, number of seeds per pod, harvest index and biological yield per plant at both phenotypic and genotypic level. Therefore, these characters emerged as most important attributing associates of seed yield per plant in mungbean. Thus, selection practiced for the improvement in one character will automatically result in the improvement has not been made for the yield character.

Path Coefficient analysis revealed that days to 50% flowering, days to maturity, number of clusters per plant, Seed index, number of seeds per pod, biological yield per plant and harvest index had direct positive effect on seed yield at genotypic level. While plant height, number of clusters per plant, number of pods per plant, pod length, number of primary branches per plant, biological yield and harvest index had direct positive effect on seed yield per plant at phenotypic level. Selection in these traits will lead to higher efficiency in breeding programme for improving yield. Thus these traits may be ranked as most important attributing traits for seed yield per plant in mungbean.

Conclusion

From the present investigation it is concluded that among 21 genotypes of mungbean on the basis of mean performance 4 genotypes viz CO-7, GM-3, ML-131, and SM-20-103 possessed maximum seed yield per plant over the check variety SM-20-29. It is also concluded that analysis of variance showed significant variation among different genotypes for all characters studied. Number of primary branches per plant exhibited high estimates of GCV and PCV. While characters like plant height, number of clusters per plant, number of pods per plant, Pod length, Seed Index, number of seeds per pod and biological yield per plant exhibited moderate estimates of GCV and PCV both. Genetic parameters also revealed that high heritability (broad sense) was observed for all characters except for days to 50% flowering, days to 50% pod setting, days to maturity, plant height, number of clusters per plant and number of pods per plant. Correlation coefficient analysis revealed that seed yield per plant exhibited significant and positive association with days to maturity, number of clusters per plant, number of pods per plant, number of primary branches per plant, number of seeds per pod, harvest index and biological yield per plant at both genotypic and phenotypic level. Path coefficient analysis revealed that characters like number of clusters per plant, biological yield and harvest index exhibited direct positive effect at both phenotypic and genotypic level. Therefore, these characters should be given priority during selection for improvement in mungbean.

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