



ISSN (E): 2277-7695

ISSN (P): 2349-8242

NAAS Rating: 5.23

TPI 2023; 12(12): 849-853

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www.thepharmajournal.com

Received: 13-09-2023

Accepted: 16-10-2023

SS Kamble

Senior Research Assistant, Plant Breeding, National Agricultural Research Project, Aurangabad, Maharashtra, India

Dr. DK Patil

Principal Scientist, Plant Breeding, National Agricultural Research Project, Aurangabad, Maharashtra, India

VB Rathod

M.Sc. Agri. (GPB), College of Agriculture, Badnapur, Maharashtra, India

Dr. VK Gite

Scientist, Plant Breeding, Agricultural Research Station, Badnapur, Maharashtra, India

Genetic variability analysis for yield and yield components in mungbean (*Vigna radiata* (L.) Wilczek)

SS Kamble, Dr. DK Patil, VB Rathod and Dr. VK Gite

Abstract

The Genetic variability study was undertaken for 41 genotypes including one check viz. BM 2003-2 in mungbean at Agricultural Research Station, Badnapur during *kharif* 2016-17. Observations were recorded for eleven yield and yield component traits viz., days to 50% flowering, days to maturity, plant height, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length, number of seeds per pod, 100 seed weight, protein content and seed yield per plant. Significant differences were observed for all characters studied which revealed the presence of considerable amount of variability in the materials under study. The high PCV and GCV values were observed for seed yield per plant, number of pods per plant and pod length. The lowest GCV and PCV values were recorded for days of flowering, days to maturity and protein content indicating the narrow range of variation for these traits. All the characters recorded high magnitude of heritability indicating the high influence of genetic components. High heritability coupled with high genetic advance was observed for seed yield per plant, number of pods per plant, pod length, plant height, 100 seed weight, number of pods per cluster, number of clusters per plant and number of seeds per pod was suggesting the role of additive gene effects and possibilities of achieving progress through selection.

Keywords: Heritability, variability, genetic advance

Introduction

Mungbean (*Vigna radiata* (L.) Wilczek) ($2n=2x=22$) is widely grown pulse crop of Asia. It is self-pollinated crop and the third important pulse crop which is widely cultivated after Bengal gram and Red gram in India. It is a short duration crop cultivated throughout year in *Kharif*, *Rabbi* and *summer* seasons as a sole crop as an intercrop or mixed crop with cereals. Strong tap root system has an ability to fix atmospheric nitrogen and improves the nutrient status of soil (Asthana, 1998) [3]. Green gram is a vital source of digestible protein for human beings as they consumed green pods as vegetable and dried seeds as Daal. It is also useful as fodder for cattle. It is rich source of vitamin B and essential amino acids like leucine, lysine, tryptophan, and arginine. Compared to other legumes it has less antinutritional factors. In India green gram is grown in an area at 2.45 m ha with an annual production of 2.13 m tonnes and average yield of 632 kg/ha during the year 2015-2016. Whereas, Maharashtra accounts 5.11 lakh ha area and 2.89 lakh tonnes production with average productivity of 566 Kg/ha. Maharashtra is having 16.19 percent contribution in the area with 13.46 percent production share of the nation (average of last ten years) (Anonymous 2015-16) [1]. The major green gram producer states are Andhra Pradesh, Telangana, Maharashtra, Gujrat, Orrisa, and Tamilnadu.

Genetic variability is a metric character which is most important in crop improvement. Heritability is a parameter of particular significance to the breeder as it measures the degree of resemblance between the parents and the offsprings. The magnitude of variability identified the genotype by its phenotypic expression, while the genetic advance aids in exercising the necessary selection pressure. It is also important to study genetic parameters, like genotypic and phenotypic coefficient of variations for the most yield influencing traits for improving seed yield. Genetic variability can offer opportunity for the effective selection for a high yielding desirable plant.

Materials and Methods

The experiment was conducted to study the genetic diversity in Mungbean (*Vigna radiata* (L.) Wilczek) with 40 germplasm lines of mungbean along with one check viz. BM 2003-2 during *Kharif* 2016-17 at Agricultural Research Station, Badnapur. The forty genotypes of mungbean along with one check BM 2003-2 were grown in a randomized block design with two

Corresponding Author:

SS Kamble

Senior Research Assistant, Plant Breeding, National Agricultural Research Project, Aurangabad, Maharashtra, India

replications during *Kharif 2016-17*. Each genotype was sown in a double row of 4 m length with spacing of 45 cm between rows and 10 cm between plants. Data on five randomly selected plants from each replication were recorded for eleven yield and its component traits *viz.*, days to 50% flowering, days to maturity, plant height, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length, number of seeds per pod, 100 seed weight, protein content and seed yield per plant. Data was subjected to analysis of variance for testing the significance of variance. The phenotypic and genotypic variances were calculated using the respective mean squares from variance table (Johnson *et al.* 1955) [8]. The genotypic and phenotypic coefficients of variation were calculated according to formula suggested by Burton, (1952) [4]. Heritability in broad sense was estimated for various characters as suggested by Hanson *et al.* (1956) [7]. Genetic advance (at 5% selection intensity) was calculated using the formula given by Allard (1960) [2] and Johnson *et al.* (1955) [8].

Results and Discussion

The analysis of variance revealed highly significant differences for all eleven characters among the genotype indicating the presence of high magnitude of variability present among the genotypes. (Table 1)

The mean values of the genotypes for different characters studied are presented in Table 2. Days to 50 percent flowering ranged between 35.00 (BM 2003-2) to 45.00 (BMG 54-2) days while mean value for this character was 39.63 days. The variation for days to maturity ranged between 53.00 (BMG 54-2) to 73.50 (BWM 40-1-10) days with mean value of 63.59 days. The plant height was maximum in case of BMG 42-1 (70.80 cm) while it was minimum in case of BWMUC 5-1-8 (35.00 cm). Mean value for this character was 54.98 cm. Number of clusters per plant ranged from 5.90 (BMG 64-2) to 10.51 (BWM 40-1-6) with mean value of 7.47. Number of pods per cluster ranged from BMG 66 (3.00) to BMG 61-2 (5.70) with mean value of 3.92. Number of pods per plant ranged from 14.10 BM (2003-2) to 39.00 (BWMCD 1-6) with mean value of 24.44. Average pod length ranged from 5.37 cm (BWMUC 22-1-2-1) to 11.60 cm (BMG 1-3) with mean of 8.92cm. The variation for number of seeds per pod ranged from 5.90 (BWMUC 5-1-8) to 14.70 (BM 2003-2) and the general mean value for this character was 12.18. The variation for 100 seed weight ranged between 2.67g (BWMCD 61) to 5.53g (BMG 1-3) and mean value for this character was 4.35g. The variation for seed yield per plant was ranged between 4.61 g (BWMCD 61) and 18.49g (BMG 1-3) with mean value of 10.72g. The variation for protein content (%) ranged from 20.04 (BMG 63)% to 25.32 (BWMUC 6-1)% with mean value of 22.03%.

The estimates of genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (b.s.), genetic advance as percent of mean for the different characters studied are presented in Table 3. Graphical comparisons of GCV and PCV for these characters are shown in Fig. 1. The phenotypic coefficients of variation was higher than genotypic coefficients of variation for all the characters under study. The highest estimates of GCV (25.91%) and

PCV (28.44%) were observed for seed yield per plant followed by number of pods per plant GCV (24.21%) and PCV (27.06%) and pod length GCV (22.08%) and PCV (23.01%) indicating good amount of variation for these characters and there is scope for improvement through selection. Hence, direct selection for these traits would be effective for the improvement of this crop. This result confirmed the earlier findings of Das *et al.* (1998) [5], Momin and Mishra (2004) [10], Eswari and Rao (2006) [6] and Thanga *et al.* (2015) [17]. The moderate magnitude of genotypic as well as phenotypic coefficients of variations were observed for plant height GCV (17.17%) and PCV (18.67%), number of pods per cluster GCV (15.69%) and PCV(17.51%), number of clusters per plant GCV (14.04%) and PCV (17.74%) and number of seeds per pod GCV (12.45%) and PCV (14.59%). Similar results were reported by Rahim *et al.* (2010) [13], Suresh *et al.* (2013) [16] and Thanga *et al.* (2015) [17]. The low magnitude of genotypic as well as phenotypic coefficients of variations were observed for days to 50% flowering GCV(5.49%) and PCV (5.77%), days to maturity GCV (5.49%) and PCV(5.82%) and protein content GCV (6.53%) and PCV(7.51%). Similar result were reported by Rohman *et al.* (2003) [15], Titumeer *et al.* (2014) [18] and Kumar *et al.* (2013) [9].

The heritability estimates are better indicator of heritable portion of the variation. The broad sense heritability includes the contribution of additive gene effects and allelic interaction due to dominance and epistatis. Burton (1952) [4] suggested that the genetic coefficient of variation heritability estimates together give better idea about the amount of genetic advance expected through selection. The estimates of heritability (B.S.), genetic advance as percent of mean for the different characters studied are presented in Table 3. Graphical comparisons of heritability and genetic advance as percent of mean for these eleven yield and yield contributing characters are shown in Fig. 2. In the present investigation the range of broad sense heritability was from 62.67% for number of pods per cluster to 92.07% for pod length. The highest broad sense heritability recorded for pod length (92.07%) followed by days to 50% flowering (90.54%), days to maturity (88.83%), plant height (84.52%), seed yield per plant (82.98%), number of pods per cluster (80.22%), number of pods per plant (80.06%), 100 seed weight (80.03%), protein content (75.59%), number of seeds per pod (72.77%) and number of clusters per plant (62.67%). The broad sense heritability refers to the genetic portion of the phenotypic variability. It indicates major role of genotype and less environmental influence. The character having maximum broad sense heritability, there is a scope for selection for that character. High broad sense heritability estimates indicated both additive and non-additive variances and selection based on heritability estimates alone may not be useful. Since heritability alone does not give a correct measurement of the genotypic variation, it should be observed along with genetic advance as percent of mean. Similar results were reported for the characters 50% flowering, days to maturity, plant height, seed yield per plant and number of pods per plant by Rahim *et al.* (2010) [13], Titumeer *et al.* (2014) [18] and for pod length and protein content by Kumar *et al.* (2013) [9].

Table 1: Analysis of variance yield and it's component traits in Mungbean

Source of variation	d. f.	Mean sum of square										
		Days to 50 percent flowering	Days to maturity	Plant height (cm)	No. of clusters per plant	No. of pods per cluster	No. of pods per plant	Pod length (cm)	No. of seeds per pod	100 seed weight (gm)	Seed yield per plant (gm)	Protein content (%)
Replications	1	0.20	0.30	0.92	0.01	0.01	2.14	0.68	0.10	0.01	3.32	1.58
Genotypes	40	9.98**	25.87**	194.60**	2.85**	0.85**	78.83**	8.09**	5.46**	1.46**	17.02**	4.80**
Error	40	0.50	1.53	16.33	0.65	0.09	8.72	0.33	0.86	0.16	1.58	0.67

* significant at 5 percent level of probability **significant at 1 percent level of probability

Table 2: Mean performance for eleven yield and yield contributing characters in forty one genotypes of Mungbean

Sr. No.	Name of genotypes	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of clusters per plant	No. of pods per cluster	No. of pods per plant	Pod length (cm)	No. of seeds per pod	100 seed weight (g)	Seed yield per plant (g)	Protein Content (%)
1.	BMG 1-3	37.00	63.00	60.00	9.61	3.75	32.00	11.60	13.00	5.53	18.49	20.74
2.	BMG 4-9-2	38.50	60.00	62.30	6.71	3.25	16.90	10.92	12.60	5.51	13.71	21.03
3.	BMG 11-1	39.00	65.00	67.40	7.11	4.55	24.20	7.68	12.20	4.14	10.48	20.98
4.	BMG 14-1	39.50	63.00	62.20	6.41	3.75	18.48	10.60	12.00	4.83	9.51	22.75
5.	BMG 31-1	38.00	62.00	62.80	6.20	3.45	16.80	10.90	12.80	5.34	8.88	21.35
6.	BMG 37	40.00	66.50	62.00	7.31	4.95	29.26	6.75	11.70	3.11	8.26	21.44
7.	BMG 42-1	39.00	65.00	70.80	5.91	5.45	25.00	7.45	12.00	3.57	12.71	20.83
8.	BMG 43-1	41.00	64.00	63.20	7.81	3.95	26.18	11.00	12.50	5.11	14.23	20.92
9.	BMG 43-2	38.50	63.50	61.90	6.61	3.95	18.76	10.85	12.30	5.25	10.69	22.23
10.	BMG 44	39.50	60.00	66.50	7.01	3.35	20.86	11.20	12.70	5.02	10.38	23.54
11.	BMG 45	39.50	62.50	60.00	7.21	3.95	20.86	10.45	12.50	5.19	11.72	20.47
12.	BMG 45-2	38.50	58.50	56.50	7.81	4.00	29.32	8.45	13.80	3.55	11.28	21.97
13.	BMG 54-2	36.00	53.00	49.20	7.51	4.95	27.58	6.40	12.70	3.42	10.17	22.23
14.	BMG 59-1	40.50	62.00	60.00	7.76	3.45	26.66	11.05	12.80	5.05	12.92	21.14
15.	BMG 60-1	38.50	62.00	63.10	8.21	4.05	22.54	9.80	13.00	5.09	11.73	23.10
16.	BMG 61-2	40.50	65.00	63.20	6.71	5.70	28.84	6.65	10.90	3.18	7.59	20.48
17.	BMG 62	41.50	64.00	66.20	7.20	4.30	27.16	6.05	12.00	3.26	7.82	20.48
18.	BMG 63	38.50	62.00	62.50	5.92	3.75	20.30	11.33	12.20	5.13	10.38	20.04
19.	BMG 64	38.50	60.50	55.60	6.06	3.35	18.06	11.55	13.10	5.19	9.26	20.39
20.	BMG 64-2	36.50	62.00	54.90	5.90	3.35	14.84	10.25	12.70	5.02	7.25	20.48
21.	BMG 64-3	37.50	61.50	62.00	6.01	3.35	16.80	11.00	12.50	5.13	7.51	20.30
22.	BMG 65	37.00	61.00	64.60	6.51	3.45	18.48	11.12	12.45	4.21	9.28	20.22
23.	BMG 66	38.00	63.00	62.40	6.81	3.00	20.16	11.00	12.60	5.16	10.72	20.78
24.	BMG 69-1	38.00	61.00	45.80	8.41	3.55	25.16	6.89	11.10	2.95	8.49	21.09
25.	BWMT 1-6	39.50	61.50	50.20	10.11	4.95	39.00	6.94	11.90	3.07	15.81	23.88
26.	BWMT 6-39	43.00	63.00	41.80	6.61	4.05	20.16	7.85	13.10	3.27	9.90	21.90
27.	BWMT 51	42.50	63.00	68.90	8.31	4.65	33.64	7.80	13.50	3.54	12.73	21.10
28.	BWMT 61	40.50	63.50	36.70	6.71	3.95	19.46	5.72	12.00	2.67	4.61	21.01
29.	BWMT 2-1	44.00	67.00	43.50	8.51	3.65	28.14	8.67	12.20	3.48	10.21	21.03
30.	BWMT 40-1-6	40.50	63.00	37.70	10.51	4.15	37.98	7.80	13.10	3.56	16.51	22.10
31.	BWMT 40-1-10	42.00	73.50	48.45	8.39	3.78	27.03	8.25	13.20	4.35	12.35	23.40
32.	BWMT 42-1-2	40.50	64.50	46.10	7.24	3.45	16.66	9.50	14.20	4.14	7.05	23.34
33.	BWMT 1-3	43.00	64.50	52.00	9.81	3.10	29.26	11.16	14.50	5.26	16.48	23.15
34.	BWMT 2-1	45.00	70.50	50.90	6.91	3.15	18.76	9.65	11.90	5.11	10.17	24.01
35.	BWMT 3-1	40.00	63.00	46.50	7.41	3.95	29.30	7.20	11.80	4.23	12.33	23.07
36.	BWMT 16	39.00	65.00	51.90	7.71	4.05	28.84	7.20	12.00	3.86	11.90	23.97
37.	BWMT 5-1-8	41.00	71.00	35.00	7.31	3.55	23.94	5.70	5.90	4.85	6.71	24.98
38.	BWMT 6-1	44.00	70.50	51.30	8.21	4.15	28.14	7.50	10.70	3.78	8.77	25.32
39.	BWMT 8-1	37.50	63.00	48.10	8.01	4.95	35.46	7.30	10.10	4.29	11.93	25.20
40.	BWMT 22-1-2-1	39.00	68.50	36.35	9.49	3.13	26.85	5.37	6.50	4.99	11.18	25.07
41.	BM 2003-2	35.00	62.00	43.85	6.11	3.50	14.10	11.10	14.70	4.83	7.63	21.58
	Mean	39.63	63.59	54.98	7.47	3.92	24.44	8.92	12.18	4.35	10.72	22.03
	C. V. %	1.78	1.95	7.35	10.84	7.79	12.08	6.48	7.61	9.27	11.73	3.71
	S. E. ±	0.50	0.87	2.86	0.57	0.22	2.09	0.41	0.66	0.28	0.89	0.58
	C. D. 5%	1.42	2.50	8.17	1.64	0.62	5.97	1.17	1.87	0.81	2.54	1.65

Table 3: Estimates of variability parameters for eleven yield and yield contributing characters in Mungbean

	Name of the characters	Range		Mean	σ^2g	σ^2p	σ^2e	GCV (%)	PCV (%)	h^2 (b.s.) (%)	G.A.	G.A. as% of mean
		Minimum	Maximum									
1.	Days to 50% flowering	35.00	45.00	39.63	4.74	5.24	0.50	5.49	5.77	90.54	4.27	10.77
2.	Days to maturity	53.00	73.50	63.59	12.17	13.70	1.53	5.49	5.82	88.83	6.77	10.65
3.	Plant height (cm)	35.00	70.80	54.98	89.13	105.46	16.33	17.17	18.67	84.52	17.88	35.51
4.	Number of clusters per plant	5.90	10.51	7.47	1.10	1.75	0.65	14.04	17.74	62.67	1.71	22.91
5.	Number of pods per cluster	3.00	5.70	3.92	0.38	0.47	0.09	15.69	17.51	80.22	1.13	28.94
6.	Number of pods per plant	14.10	39.00	24.44	35.01	43.73	8.72	24.21	27.06	80.06	10.91	44.63
7.	Pod length (cm)	5.37	11.60	8.92	3.88	4.21	0.33	22.08	23.01	92.07	3.89	43.65
8.	Number of seeds per pod	5.90	14.70	12.18	2.30	3.16	0.86	12.45	14.59	72.77	2.66	21.87
9.	100 seed weight (g)	2.67	5.53	4.35	0.65	0.81	0.16	18.55	20.74	80.03	1.49	34.19
10.	Seed yield per plant (g)	4.61	18.49	10.72	7.72	9.30	0.58	25.91	28.44	82.98	5.21	48.62
11.	Protein content (%)	20.04	25.32	22.03	2.07	2.73	0.67	6.53	7.51	75.59	2.58	11.69

The estimates of genetic advance as percent of mean ranged from 10.65 to 48.62 with the highest estimate in case of seed yield per plant (48.62%) followed by number of pods per plant (44.63%), pod length (43.65%), plant height (35.51%), 100 seed weight (34.19%), number of pods per cluster (28.94%), number of clusters per plant (22.91%), and number of seeds per pod (21.87%) indicating that these traits are under control of additive gene action and potential possibilities exist for the improvement of these characters through simple selection. Similar findings supported for seed yield per plant, number of pods per plant, plant height, 100 seed weight, number of seeds per pod by Suresh *et al.* (2013) [16], for number of pods per cluster, number of clusters per plant by Thanga *et al.* (2015) [17]. Moderate genetic advance as percent of mean were observed for character days to 50% flowering, days to maturity and protein content. Similar findings reported by Rohman M. *et al.* (2003) [15]. In the present investigation, high heritability for seed yield per plant, number of pods per plant, pod length, plant height, 100 seed weight, number of pods per cluster, number of clusters

per plant, and number of seeds per pod was associated with high genetic advance as percent of mean, indicating that these characters are controlled by additive gene action and direct selection for such traits is rewarding in crop improvement. Similar results were finding by Verraswamy *et al.* (1973) [19], Das *et al.* (1998) [5], Paramsivan and Rajasekaran (1980) [12] for the character plant height and number of pods per plant. Ramana and Singh (1987) [14] and Suresh *et al.* (2013) [16] find similar results for seed yield per plant, number of pods per plant, number of clusters per plant, plant height and for seed yield per plant, number of pods per plant, plant height, 100 seed weight, number of seeds per pod. The character days to 50% flowering, days to maturity and protein content with high heritability was associated with moderate genetic advance Rohman M. *et al.* (2003) [15], reported that these characters are controlled by non-additive gene action i.e. dominance deviation or epistasis, hence there is limited scope for further improvement through selection for these characters. Hybridization is the best way to improve this character.

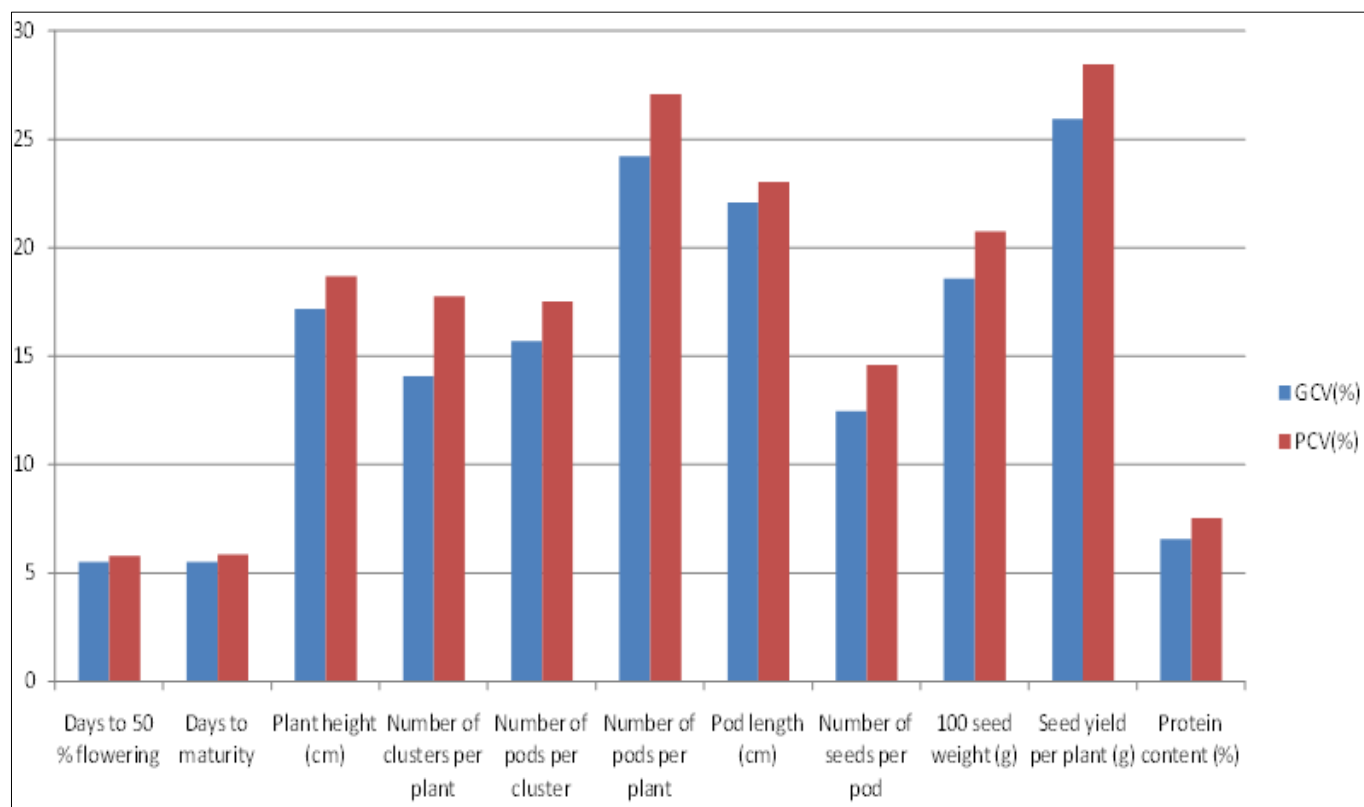


Fig 1: Graphical comparison of GCV and PCV of eleven characters in mungbean

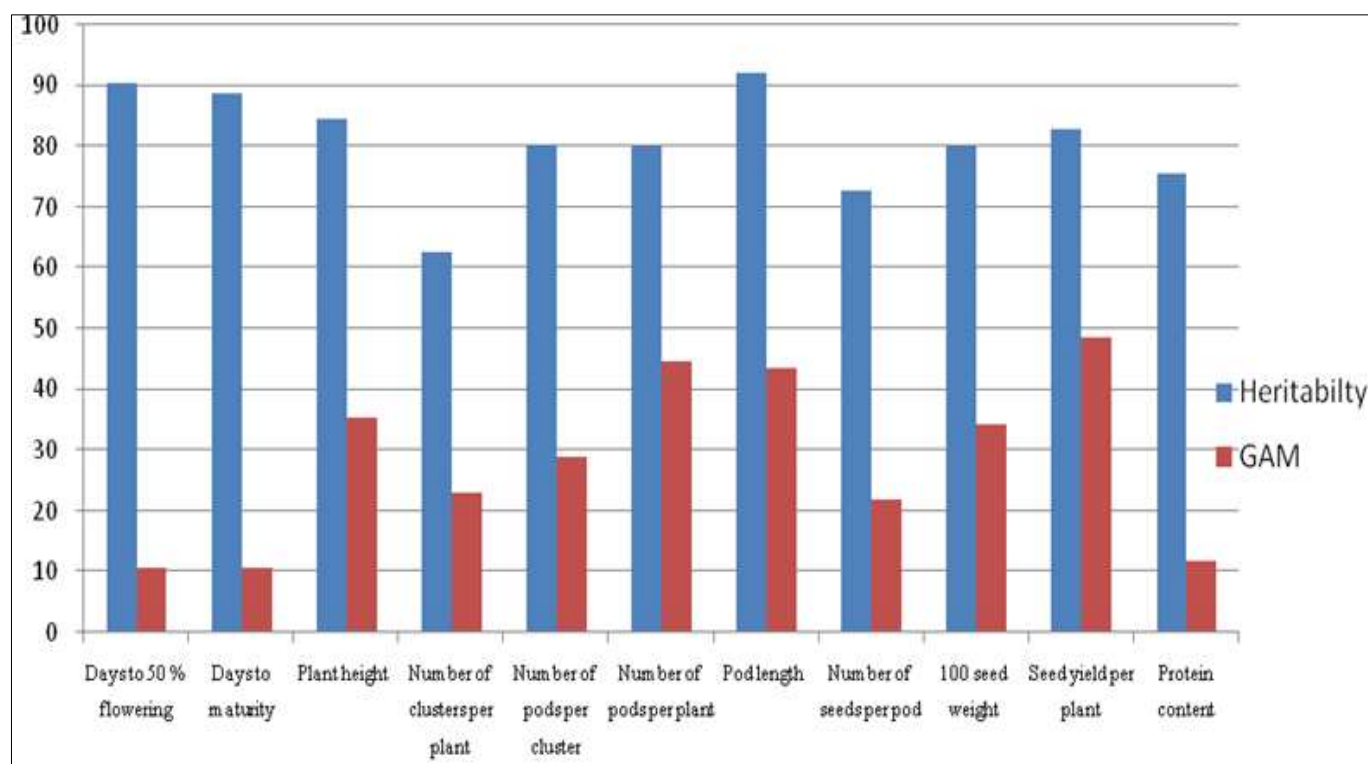


Fig 2: Graphical comparison of heritability and genetic advance as percent of mean for eleven characters in mungbean

Conclusion

By considering the estimates of genetic parameters like genotypic coefficient of variation, heritability and genetic advance as percent of means, it can be pointed out that, the characters like seed yield per plant, 100 seed weight, number of pods per plant, number of clusters per plant, number of pods per cluster and number of seeds per pod, pod length are the most important characters for crop improvement in mungbean.

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