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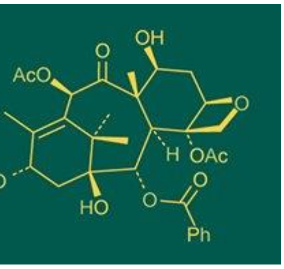

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Studies on variability for yield and yield attributing traits in pigeonpea [*Cajanus cajan* (L.) Millsp.]

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Abstract

Fifty pigeonpea genotypes were evaluated for the assessment of genetic variability, heritability and genetic advance expressed as *percent* of mean during *Kharif* 2021. The analysis of variance revealed the presence of sufficient variability among the fifty genotypes for different characters indicating the presence of sufficient genetic variability in the experimental material. The value of phenotypic coefficient of variations were slightly higher than genotypic coefficient of variations indicating the sufficient influence of environmental factor in most of the characters. High estimates of GCV and PCV were observed for the characters *viz*., biological yield per plant, number of branch per plant, harvest index, seed yield per plant and days to flowering. High heritability coupled with high genetic advance expressed as percent of mean were observed various characters like, days to flowering, days to maturity, number of seed per pod, pod length, number of pod per plant, number of branch per plant, seed yield per plant, harvest index and biological yield per plant, indicating the presence of additive gene action and less environmental influence on the characters and existence of sufficient heritable variation and wider scope for effective selection.

Keywords: Genetic variability, Pigeonpea, GCV, PCV, Heritability, Genetic advance

Introduction

Pigeonpea [*Cajanus cajan* (L.) Millsp.] is one of the most important pulse crops of India and rank second in area and production. It is commonly known as Arhar or Tur. Pigeonpea is a drought tolerant crop and one of the most important legumes grown in the tropics and sub tropics. It belongs to the family '*Fabaceae*'. Pigeonpea is often cross-pollinated crop having chromosome number 2n=22. Pigeonpea is the first "non-industrial crop" and the second food legume (after soybean) having a completed genome sequence. Pigeonpea is economically and nutritionally an important legume and is a major source of protein for the poor communities of many tropical and subtropical regions of the world. Protein content of commonly grown pigeonpea cultivars is 22 percent for whole grain samples. The high protein genotypes also contain higher (about 25%) Sulphur-containing amino acids namely, methionine and cysteine (Singh *et al.* 1990) [19]. Generally, it is used for preparing dal and it is also a good source of soluble vitamins, especially thiamine, riboflavin and niacin. Being a legume crop, the pigeonpea enriches soil through symbiotic nitrogen fixation. The major pigeonpea producing states in India are Andhra Pradesh, Karnataka, Gujarat, Madhya Pradesh, Maharashtra, Uttar Pradesh. Gujarat occupies 2.46 Lakh ha area with a production of 2.86 LMT and productivity of 1160 kg/ha (Anonymous, 2021-22) [2]. A systemic breeding program relies on knowledge of the type and degree of population variability resulting from genetic and non-genetic causes. The study of the level of genetic variability present in the existing genotype has become crucial, since genetic variability is necessary for the beginning of an efficient and effective breeding strategy. The study of genetic advance with heritability estimates could further clarify the nature of characters which can be improved through selection. Therefore, the present study was planned to estimate variability, heritability and genetic advance for yield and its attributing traits.

Materials and Methods

The present investigation was carried out during *kharif* 2021 at Agronomy instructional farm, C. P. C. A., Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar, Gujarat. The experimental materials used for study consisted of fifty genotypes of pigeonpea, which were procured from the Pulses Research Station, S. D. A. U., Sardarkrushinagar, Gujarat (Table 1). All the genotypes were raised in Randomized Block Design with four replications, each genotype sown in single row of 4.00 m length with spacing 60 cm between row and 20 cm between plants. The experimental material was evaluated for twelve characters *viz.*, days to flowering, days to maturity, plant height (cm), number of branch per plant, number of pod per plant, pod length (cm), number of seed per pod, seed yield per plant (g), biological yield per plant (g), test weight (g), harvest index (%) and protein content (%). Protein content was estimated with the help of Near Infrared Reflectance (NIR) spectroscopy technique. The data were subjected to statistical analysis. Analysis of variance calculated using formula suggested by Panse and Sukhatme (1978) [13]. Genetic variability parameters such as Phenotypic Coefficient of Variation (PCV), Genotypic Coefficient of Variation (GCV), Heritability and Genetic advance as *percent* of mean were worked out as per Burton (1952) [6], Allard (1960) [1] and Johnson *et al.* (1955) [10].

Results and Discussion

The analysis of variance showed significant differences among the genotypes for all the characters under studied (Table 3). These gives the evidence of sufficient amount of variability among the genotypes. The values of various parameters like, GCV, PCV, heritability and GAM was displayed in Table 4. Based on estimates of the genotypic and phenotypic coefficient of variation, the value of phenotypic coefficient of variations were slightly higher than genotypic coefficient of variations, revealing the sufficient influence of environmental factor in most of the characters. The estimates of GCV and PCV were high in number of branch per plant, seed yield per plant, harvest index, biological yield per plant and days to flowering, offering better scope for selection as there was less influence of environment. Similar results for high GCV and PCV were obtained by Thanga *et al.* (2019) [20] and Bathini *et al.* (2021) [4] for number of branch per plant, Rao and Rao (2020) [16], Pashwan *et al.* (2021) [14] and Bathini *et al.* (2021) [4] for seed yield per plant, Rangare *et al.* (2013) [15] and Pashwan *et al.* (2021) [14] for harvest index, Pandey *et al.* (2015) [12] and Pashwan *et al.* (2021) [14] for biological yield per plant and Yerimani *et al.* (2013) [21] and Sharma *et al.* (2012) [18] for days to flowering. Moderate estimates of genotypic and phenotypic coefficient of variation were observed for number of seed per pod, number of pod per plant, pod length, plant height and days to maturity, indicates moderate amount of variability present in the population. Similar results for moderate GCV and PCV were recorded by Kumar *et al.* (2014) [11] for number of seed per pod, Yerimani *et al.* (2013) [21] for pod length and plant height. While lowest estimates of genotypic and phenotypic coefficient variation were observed for protein content and test weight, indicated that there was low diversity present in population and it limits the future improvement programs. Similar results for low GCV and PCV obtained by Yerimani *et al.* (2013) [21] for test weight and Baskaran and Muthaiah (2006) [3] and Rekha *et al.* (2013) [17] for protein content. The close association between GCV and PCV were observed for all the traits indicated that the variability was primarily due to genotypic differences. In the present study, phenotypic coefficient of variation were more than genotypic coefficients of variation in all the traits. This might be due to environmental effect. Similar finding was reported by Sharma *et al.* (2012) [18].

Heritability is one of the important means of ensuring success in selection programmes for the genetic improvement. It is a good index of the transmission of characters from parents to their offspring (Falconer, 1989) [7]. Genetic advance is the measure of genetic gain under selection. High estimates of heritability obtained for most of the character, indicating that these characters were least influenced by environment. While, moderate estimates of heritability were observed in plant height and test weight. Genetic advance expressed as percent of mean was also high for mostly characters, indicating the presence of additive gene action and there was better scope for further improvement. Moderate GAM were observed for plant height and test weight. High heritability coupled with high genetic advance expressed as percent of mean were observed for days to flowering, days to maturity, number of seed per pod, pod length, number of pod per plant, number of branch per plant, seed yield per plant, harvest index and biological yield per plant, indicating the presence of additive gene action and less environmental influence on the characters and existence of sufficient heritable variation and wider scope for effective selection. Similar results for high heritability and high GAM were recorded by Rangare *et al.* (2013) [15] and Sharma *et al.* (2012) [18] for days to flowering, Rao and Rao (2020) [16] for days to maturity, number of branch per plant and number of pod per plant, Pandey *et al.* (2015) [12] for number of seed per pod and seed yield per plant, Gupta *et al.* (1975) [9] for pod length, Rangare *et al.* (2013) [15] and Pashwan *et al.* (2021) [14] for harvest index. Moderate heritability coupled with moderate genetic advance as percent of mean was observed for trait *viz.*, plant height and test weight, indicating additive gene action in their inheritance. Similar result was observed by Biniwal *et al.* (1981) [5] for plant height. High heritability coupled with low genetic advance as percent of mean was observed for protein content. In spite of all, limited scope of improvement in this character can be made by direct selection. The similar finding was earlier reported by Rekha *et al.* (2013) [17] for protein content.

Table 1: List of pigeonpea genotypes included in study

Sr No.	Genotype	Sr No.	Genotype
1	IC 274037	26	Maruti
2	IC 274076	27	BDN 2004-1
3	IC 274082	28	BDN 2013-41
4	IC 274086	29	PA 16
5	IC 274087	30	PA 992
6	IC 274103	31	PAU 881
7	IC 311718	32	JKM 189
8	IC 312380	33	TJT 501
9	IC 323233	34	AL 201
10	IC 323239	35	Rajiv Lochan
11	IC 323250	36	Rajeshwari
12	IC 323258	37	BRG 4
13	IC 323264	38	BRG 5
14	IC 323274	39	Asha
15	IC 323282	40	JA 4
16	IC 323284	41	RVSA 16-1
17	IC 525346	42	SGA 1
18	IC 525456	43	GT 104
19	IC 525487	44	GT 105
20	IC 525639	45	GJP 1
21	IC 525666	46	BDN 711
22	IC 525737	47	GT 101
23	ICPL 11318	48	GT 103
24	ICPL 20202	49	SKNP 1608
25	ICPL 99074	50	SKNP 1614

Source: Pulses Research Station, S. D. A. U., Sardarkrushinagar

Table 2: Categorization of genetic estimates

Estimates	GCV&PCV (%)	Heritability (h^2_b) (%)	GAM (%)
Low	0 to 10	0 to 30	0 to 10
Moderate	10 to 20	30 to 60	10 to 20
High	More than 20	More than 60	More than 20

Table 3: Analysis of variance (ANOVA) for different characters of pigeonpea genotypes

Sr. No.	Character	Mean sum of square		
		Replications	Genotypes	Error
	Degree of freedom	3	49	147
1	Days to flowering	18.23	3437.80**	16.08
2	Days to maturity	0.12	3440.88**	6.39
3	Plant height (cm)	641.83	1481.76**	240.78
4	Number of branch per plant	1.84	20.35**	0.49
5	Number of pod per plant	13.85	408.19**	28.33
6	Pod length (cm)	0.08	2.22**	0.03
7	Number of seed per pod	0.05	1.14**	0.07
8	Test weight (g)	0.15	3.63**	0.70
9	Seed yield per plant (g)	4.69	64.19**	2.84
10	Biological yield per plant (g)	41.46	3302.62**	74.51
11	Harvest index (%)	4.98	126.25**	6.54
12	Protein content (%)	0.01	3.24**	0.18

*, ** Significant at 0.05 and 0.01 percent of significance level, respectively.

Table 4: Genetic parameters of variation for seed yield and its contributing characters in pigeonpea

Sr. No.	Characters	Range	Mean	GCV (%)	PCV (%)	$h^2_{(b)}$ (%)	GAM (%)
1	Days to flowering	60.00-176.00	123.50	23.68	23.91	98.16	48.34
2	Days to maturity	99.77-210.75	161.30	18.10	18.16	99.26	37.14
3	Plant height (cm)	101.33-183.00	144.75	12.17	16.22	56.30	18.81
4	Number of branch per plant	2.90-11.85	7.72	28.85	30.24	91.05	56.72
5	Number of pod per plant	41.54-99.27	63.88	15.26	17.38	77.02	27.58
6	Pod length (cm)	3.10-6.89	4.57	16.18	16.63	94.66	32.43
7	Number of seed per pod	2.70-6.47	3.57	14.52	16.22	80.21	26.80
8	Test weight (g)	8.88-12.50	10.24	8.35	11.69	51.11	12.30
9	Seed yield per plant (g)	9.03-25.55	15.88	24.66	26.85	84.38	46.67
10	Biological yield per plant (g)	29.40-135.13	82.52	34.43	35.98	91.55	67.85
11	Harvest index (%)	11.26-34.40	20.92	26.15	28.87	82.06	48.80
12	Protein content (%)	16.64-21.15	18.57	4.71	5.23	81.15	8.74

Table 5: Mean performance of genotypes for yield and yield contributing characters of fifty genotypes of pigeonpea

Sr. No.	Genotypes	Days to flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of pods per plant	Pod length (cm)	Number of seed per pod	Test weight (g)	Seed yield per plant(g)	Biological yield per plant(g)	Harvest index (%)	Protein content (%)
1.	IC 274037	153.50	198.25	161.31	10.80	61.62	3.32	2.70	9.38	12.29	48.27	25.48	19.56
2.	IC 274076	118.00	162.76	134.46	9.10	66.66	3.80	3.56	9.25	18.01	80.37	22.39	18.45
3.	IC 274082	119.00	163.75	122.28	9.55	63.33	4.95	3.67	10.88	16.78	76.53	22.01	18.95
4.	IC 274086	148.25	190.26	142.01	8.85	59.31	4.56	3.66	10.38	21.34	135.13	15.74	18.68
5.	IC 274087	122.25	164.50	145.91	9.85	68.06	4.09	3.66	11.50	24.01	109.24	21.98	18.53
6.	IC 274103	112.50	157.75	139.87	9.90	69.53	5.13	3.67	10.25	25.55	100.84	25.28	18.34
7.	IC 311718	150.00	190.25	162.51	5.75	52.61	4.82	3.59	10.00	15.43	107.17	14.48	19.13
8.	IC 312380	154.25	191.02	167.18	6.15	55.67	5.25	3.64	9.13	13.84	119.97	11.52	18.50
9.	IC 323233	120.50	165.25	150.90	9.40	99.27	5.25	4.34	9.38	24.70	114.10	21.65	18.98
10.	IC 323239	135.25	174.26	183.00	9.35	65.30	4.37	3.52	9.88	18.46	84.34	22.09	19.01
11.	IC 323250	135.25	176.02	154.57	11.85	62.12	4.01	3.55	9.75	14.09	125.51	11.26	19.32
12.	IC 323258	176.00	210.25	174.25	10.75	65.08	4.64	3.54	9.13	14.78	122.49	12.25	18.72
13.	IC 323264	175.50	210.75	170.85	10.55	66.92	4.80	3.60	9.75	11.45	62.53	18.35	18.44
14.	IC 323274	175.50	205.25	138.90	8.60	64.86	5.50	3.55	10.50	11.21	60.95	18.46	18.96
15.	IC 323282	165.25	198.01	167.56	10.95	64.82	5.54	3.54	8.75	12.59	50.34	25.25	18.10
16.	IC 323284	162.50	207.25	143.31	8.75	63.83	5.17	3.56	10.25	13.60	81.99	16.65	18.64
17.	IC525346	120.00	165.76	161.38	8.65	51.04	3.35	2.92	8.88	11.85	34.44	34.40	19.49
18.	IC525456	116.00	153.26	138.24	7.80	60.44	5.32	3.34	9.38	12.55	55.92	22.53	19.43
19.	IC 525487	135.25	174.75	168.98	7.60	43.36	5.44	3.59	12.50	10.30	36.73	28.20	21.15
20.	IC 525639	104.25	134.50	118.82	8.10	48.97	3.82	2.96	9.50	11.66	44.42	26.29	19.95
21.	IC 525666	139.50	172.50	132.80	8.95	60.73	5.09	3.65	9.13	17.50	80.71	21.96	17.52
22.	IC525737	123.50	171.26	159.16	4.95	70.02	3.81	3.68	12.25	15.90	116.74	14.11	19.56
23.	ICPL 11318	60.00	99.77	127.54	2.90	60.33	3.94	3.50	9.38	16.74	108.08	15.60	19.58
24.	ICPL 20202	139.50	175.76	165.30	5.10	63.77	4.81	3.78	10.25	9.03	29.40	30.75	17.95
25.	ICPL 99074	104.50	145.01	161.31	10.80	41.54	4.19	3.62	9.75	16.32	105.54	15.53	16.64
26.	MARUTI	104.25	144.76	115.24	5.65	55.51	4.13	3.12	10.88	12.94	50.01	25.91	20.29
27.	BDN 2004-1	122.75	171.02	123.39	9.55	53.73	4.95	3.73	10.13	14.73	117.04	12.64	17.52
28.	BDN 2004-41	139.25	175.76	125.17	5.30	68.15	4.98	3.64	11.75	17.96	74.17	24.33	17.51
29.	PA 16	62.50	101.76	101.33	4.00	70.39	4.89	3.82	9.38	12.62	50.82	24.81	19.17
30.	PA 992	62.75	102.25	164.45	6.55	52.86	4.09	3.83	10.25	11.33	43.10	26.32	19.33
31.	PAU 881	63.25	102.75	160.91	5.00	72.04	4.26	3.72	9.25	15.56	95.00	16.42	17.71
32.	JKM 189	134.50	177.50	177.15	9.15	75.45	4.07	2.87	11.13	16.36	101.09	16.35	17.66
33.	TJT 501	105.25	146.26	130.92	5.55	75.79	3.67	2.98	10.63	25.49	108.15	23.66	19.59
34.	AL 201	69.75	110.76	129.74	5.30	63.22	3.81	3.49	9.00	13.43	86.53	15.48	19.38
35.	RAJIV LOCHAN	124.00	159.26	141.03	6.50	69.55	4.27	3.43	11.00	23.90	110.58	21.53	18.75
36.	RAJESHWARI	118.50	152.76	107.18	3.05	67.04	3.93	3.70	10.13	14.60	111.80	13.59	18.97
37.	BRG 4	122.00	156.25	140.08	5.30	55.31	3.37	3.42	11.75	16.71	108.52	15.53	17.63
38.	BRG 5	139.25	187.76	160.55	5.75	59.83	3.10	2.96	9.25	14.01	75.85	18.55	18.11
39.	ASHA	121.50	155.50	139.82	9.10	61.55	5.25	3.62	10.50	19.88	71.91	27.68	18.31
40.	JA 4	70.00	105.75	128.86	7.90	70.16	3.88	3.20	11.13	17.73	95.71	18.57	17.82
41.	RVSA 16-1	105.75	140.01	132.29	8.15	72.23	4.07	2.89	9.00	18.20	109.12	16.70	17.06
42.	SGA 1	118.00	151.02	137.94	7.20	65.85	4.16	2.98	10.88	16.70	65.31	25.59	18.83
43.	GT 104	139.50	181.76	147.47	5.55	51.19	6.89	6.47	11.00	13.84	62.35	22.41	17.79
44.	GT 105	106.00	135.25	138.83	7.00	75.89	5.10	3.88	10.88	17.11	83.88	20.49	17.78
45.	GJP 1	144.00	178.26	154.31	9.80	70.91	5.05	3.57	12.25	16.81	109.14	15.47	17.07
46.	BDN 711	122.25	154.25	149.64	7.60	54.71	4.98	3.65	10.25	11.32	35.82	31.72	17.37
47.	GT 101	104.50	138.26	157.25	7.60	83.42	5.26	4.25	11.13	18.08	76.91	23.55	18.17
48.	GT 103	122.25	153.76	166.97	11.50	72.37	5.40	3.58	10.50	16.92	78.60	21.66	17.77
49.	SKNP 1608	121.75	155.50	137.66	8.00	74.47	4.88	3.87	10.88	17.10	77.90	22.13	18.79
50.	SKNP 1614	165.25	200.01	118.85	10.85	52.92	5.37	3.54	9.88	10.72	35.07	30.57	18.48
General Mean		123.50	161.30	144.75	7.72	63.88	4.57	3.57	10.24	15.88	82.52	20.92	18.57
Range	Minimum	60.00	99.77	101.33	2.90	41.54	3.10	2.70	8.88	9.03	29.40	11.26	16.64
	Maximum	176.00	210.75	183.00	11.85	99.27	6.89	6.47	12.50	25.55	135.13	34.40	21.15
S.Em±		1.48	1.24	7.76	0.35	2.66	0.09	0.13	0.42	0.84	4.32	1.28	0.21
C.D at 5%		5.60	3.53	21.68	0.98	7.44	0.25	0.36	1.17	2.35	12.04	3.57	0.59
C.V %		3.25	1.56	10.72	9.05	8.33	3.84	7.21	8.17	10.61	10.46	12.23	2.27

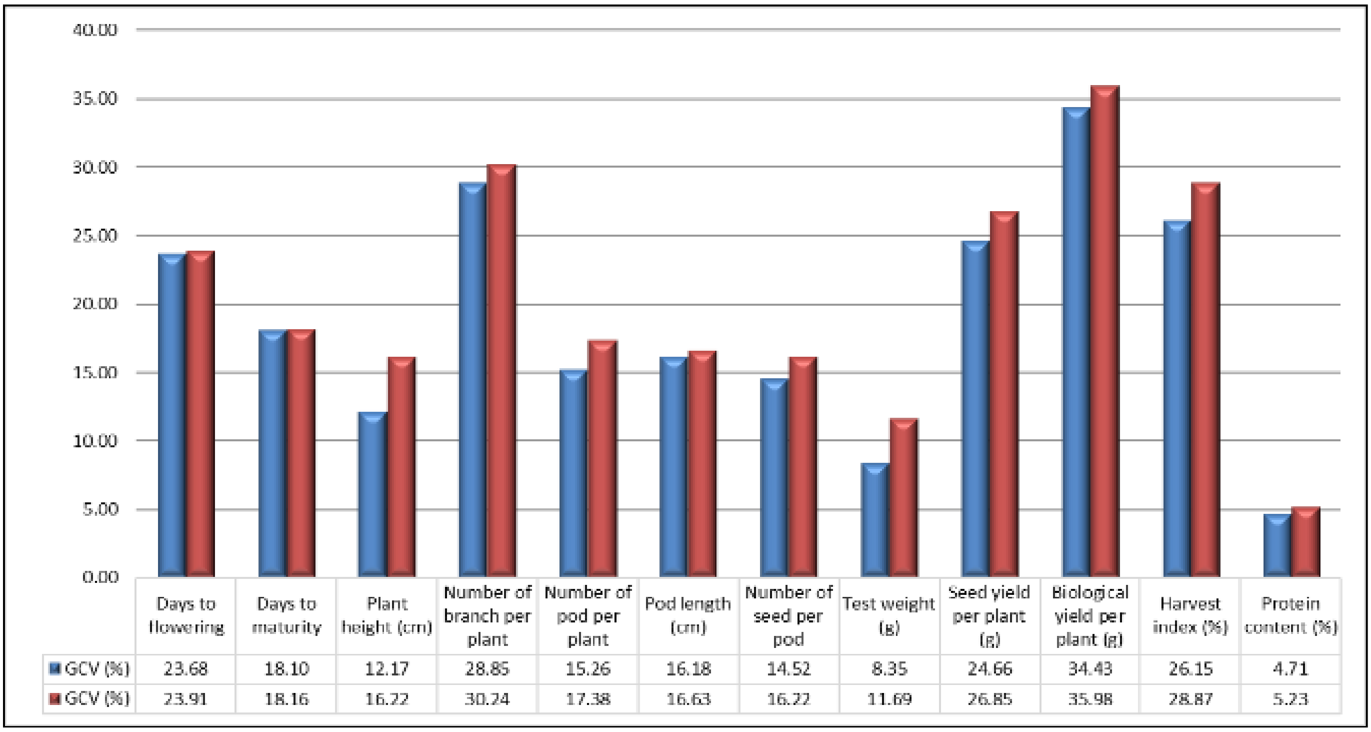

Fig 1: Graphical comparison of GCV, PCV as percent of mean for 12 characters in pigeonpea

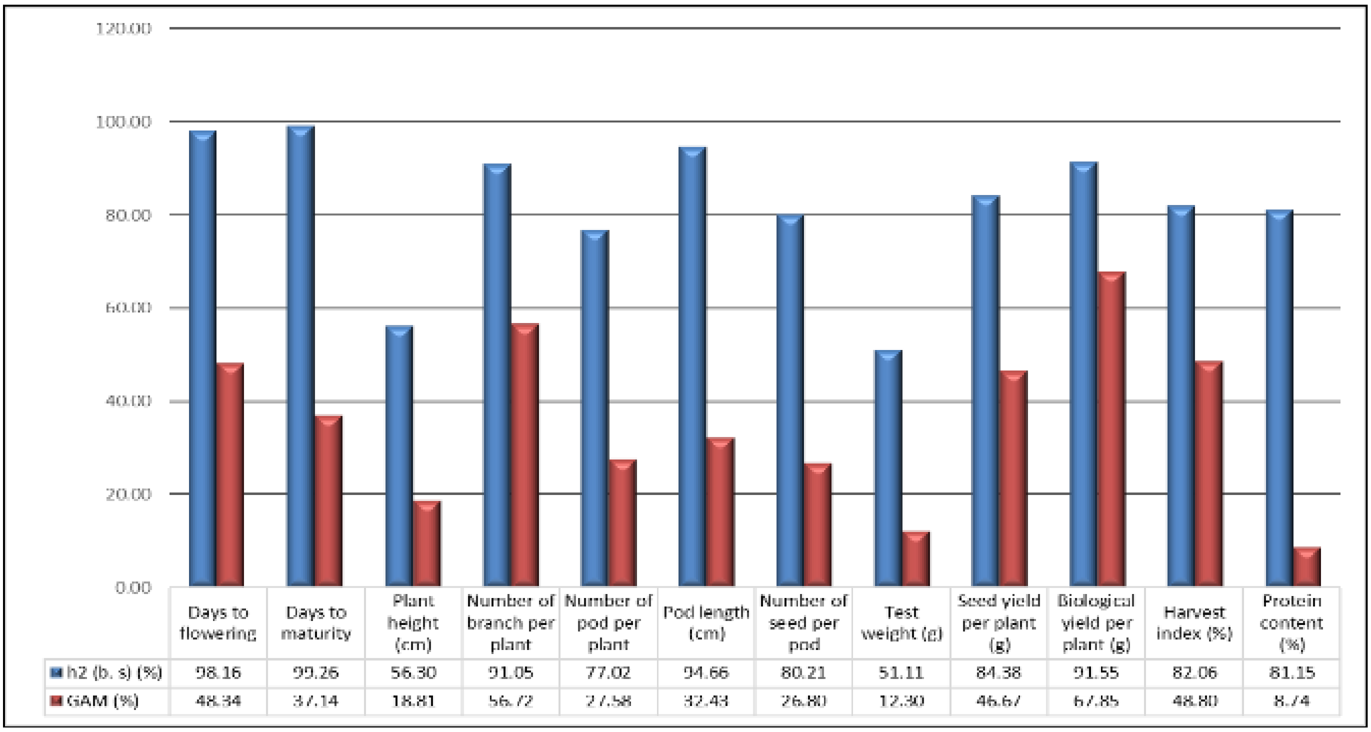

Fig 2: Graphical comparison of heritability h^2 (b) and expected genetic advance as percent of mean for 12 characters in pigeonpea

Conclusion

The analysis of variance showed sufficient variability among all the genotypes of pigeonpea. Based on the mean performance, five genotypes *viz*., IC 274103, TJT 501, IC 323233, IC 274087, RAJIV LOCHAN were found elite genotypes. These, genotypes could be further exploited by employing mass selection and pedigree selection. High heritability coupled with high genetic advance expressed as percent of mean were observed for days to flowering, days to maturity, number of seed per pod, pod length, number of pod per plant, number of branch per plant, seed yield per plant, harvest index and biological yield per plant indicating the presence of additive genes, less environmental influence on the characters, existence of sufficient heritable variation and wider scope for effective selection.

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