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Assessment of genetic parameters for yield and yield components in f1 pigeon pea and their parents

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Abstract

The experiment was conducted at Research cum Instructional Farm, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh during *kharif* 2017-18 under the AICRP on Pigeonpea, Department of Genetics & Plant Breeding. Low estimates of PCV and GCV were identified for days to flower initiation days to 50% flowering, days to maturity, pod length, seeds/pod, 100 seed weigh, harvest index, protein%, and Dal recovery% that culminated into low genetic advance. The PCV and GCV were moderate for plant height, primary branches, Pod/plant. High heritability coupled with high genetic advance as percent of mean was more for plant height and no. of pod cluster/plant biological yield/plant, seed yield/plant. High heritability in these indicated the presence of additive gene effects. The secondary branches, pod cluster per plant and grain yield/plant were exhibited high genotypic and phenotypic coefficient of variation, heritability and genetic advance.

Keywords: Genetic variability, PCV, GCV, ECV, diallel, heritability and genetic advance, quantitative traits

Introduction

Pigeon pea or red gram [*Cajanus cajan* (L.) Millsp.], ($2n=2x=22$) is the globally covered fifth and second rank after chickpea in India. It is a rained crop and provides food, fuel, wood and fodder. It is major pulse crop of sustainable agriculture in the tropical and sub-tropical regions in the world. Pigeon pea has good soil rejuvenation qualities such as release of soil-bound phosphorous, recycling of soil nutrients, fixation of atmospheric nitrogen, and addition of organic matter and other nutrients etc. It is generally cultivated as a sole crop or as a mixed crop with short duration cereals or legumes as well as with other crops like cotton and groundnut. Pigeon pea is a hardy and drought tolerant crop assuring sustainable returns from marginal lands with minimum input, hence it is considered as very suitable crop for sustainable agriculture. Pigeon pea seeds contain 20%~24% protein and reasonable amounts of essential amino acid making it an important source of dietary protein, mainly in vegetarian-based diets. The seed and pod husks make quality feed, whereas dry branches and stems serve as domestic fuel. Fallen leaves from the plant provide vital nutrient to the plant also enriches soil through symbiotic nitrogen fixation^[1]. The trait of grain yield is controlled by complex gene action and hence traits contributing to yield must be considered and evaluated. It is therefore, necessary to estimate relative amounts of genetic and non-genetic variability exhibited by different characters using suitable parameters like genotypic coefficient of variability (GCV), Phenotypic coefficient of variability (PCV), heritability estimates (h^2) and genetic advance (GA) and genetic association between yield and yield contributing, the information on their aspects will help in the breeders to determine the selection criteria for isolating high yielded genotypes in Pigeon pea.

Materials and methods

The details of experimental site, period of experiment, materials used, and methods adopted for conduction of experiments and analysis of data during the course of investigation are described. The experiment was conducted at Research cum Instructional Farm, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh during *kharif* 2017-18 under the AICRP on Pigeon pea, Department of Genetics & Plant Breeding. In Hybridization programme 5 parents namely Rajeevlochan, BSMR-571, BSMR-2, RPS-2007-10 and ASHA were crossed to each other in full diallel fashion to generate set of hybrids. A total of 20 hybrids were synthesized by hand emasculation and pollination. Sufficient numbers of hand pollinated seeds were produced during 2016-17 rainy season.

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In emasculating the bud most likely to shed pollen the next day were selected. These buds were approximately 60 percent's the size of a mature bud and were tightly closed. It is best to select two buds per inflorescence for emasculating and two to ten buds can be emasculated on branch and other buds are removed [2]. A fairly leveled and uniform plot was selected for experimentation. Field was prepared by cross ploughing by tractor after the harvest of previous crop. The weeds and crop residues were removed to get neat and clear field.

Layout was done with the help of measuring tape, rope and sticks, etc. Sowing was done by hand dibbling in rows made with the help of *kudali*. 5 elite Pigeon pea genotypes and their Crossed in full diallel fashion were grown in Randomized Block Design (RBD) with two replications during *khari* 2017-18. All the agronomical Package of practices recommended was adopted and fertilizer dose of 20N: 50P: 20K kg ha⁻¹ was applied. Sowing of genotypes was on 03/07/2017 keeping inter and intra row spacing of 60 and 20 cm, respectively. Each genotype was represented by 2 rows of 4 m length with border rows at either side of replication.

Observations were recorded on single plant basis on five randomly selected competitive plants, separately from each replication. Whereas, observation on days to flower initiation, days to 50 per cent flowering and days to maturity were recorded on plot basis. Protein analysis work was done in the Quality Laboratory, Department of Genetics & Plant Breeding, College of Agriculture, IGKV, Raipur, Chhattisgarh, 492012.

Results and discussion

The analysis of variance indicating the mean sum of squares for all the sixteen characters studied, are summarized in (Table 1). The genotypic differences were highly significant for all the sixteen characters indicating considerable amount of genetic variability among the genotypes tested in the present study, suggesting ample scope for improvement of yield and various yield attributing characters. Success of any crop improvement program depends upon the variability in the material. A large amount of variation is necessary in a breeding population to enable the breeder to carry out effective selection.

Table 1: Analysis of variance (R.B.D) for 16 agro-economic traits in 25 elite genotype of Pigeon pea

Source of variation	Character	DF	DF (50%)	DM	PH	PB	SB	PC	P/P	PL	S/Pod	100 seed wt.	BY	HI	Protein (%)	Dal (%)	SY/P
DF	Replication	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	Treatment	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24
	Error	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24
MSS	Replication	12.5	10.58	18	2.04	2.88	30.4	369.9	42.32	0.156	0.0008	0.182	35.1	1.185	0.412	0.058	29.76
	Treatment	7.02	6.82	5.003	1036.6	6.428	60.20	1906.	205.8	0.2939	0.0458	0.9187	8670.7	4.7750	2.873	11.05	484.62
	Error	1.375	1.08	1.5	33.30	1.005	5.46	85.21	9.153	0.0193	0.084	0.0357	4.20	0.1245	0.140	0.736	5.34
F-Value	Replication	9.09**	9.79**	12**	0.065ns	2.86ns	5.56*	4.34*	4.62*	8.12**	0.009ns	5.10*	8.35**	9.52**	2.93ns	0.079ns	5.57*
	treatment	5.11**	6.31**	3.33**	31.12**	6.39**	11.02**	22.37**	22.48**	15.23**	0.54ns	25.69**	2062.7**	38.34**	20.49**	15.01**	90.72**

Significant at ** 1% & * 5%

**Bold figures indicates maximum and minimum values

The value of days to flower initiation ranged from 99.00 days to 107.00 days with mean value of 102.42 days. The variation in days to 50% flowering ranged from 110.00 days to 117.00 days having the general mean of 113.58 days was revealed that most are early genotypes. (Table 2). Day to maturity ranged from 184.50 days to 190.00 days comprising the general mean of 187.72 days confirming that most of the genotypes, belonging medium late maturity group. The range of plant height varying from 171.00 cm to 250.00 cm having the general mean of 218.00 cm. It revealed that the population very closed to medium tall stature. The number of primary branches/plant varied from 7.00 to 12.50 with general mean of 9.88 and the number of secondary branches/plant varied from 18.00 to 36.50 with general mean of 28.3. The pods/plant ranged from 96.00 to 230.00 pods their means 156.8 exhibiting that the majority of the genotypes

comprising were having the greatest number of pods/plant being hybrids and pod cluster/plant ranged varying from 33.00 to 76.50 and general mean 52.72. The pod length ranged varying from 4.10 cm to 6.10 cm and general mean 5.26 cm besides the seeds/pod ranged from 3.70 to 4.00 seeds and their general mean of 3.77 seeds. The seed index (100 seed weight) ranged varying from 8.91 gm to 11.27 gm. and general mean 9.66 gm. Biological yield ranged varying from 194.00 gm. to 437.44 gm. and general mean is 319.15 gm. and their harvest index varies from 15.35% to 20.90% with mean of 18.88%. Besides grain yield/plant ranged from 29.80 gm. to 89.60 gm. and general mean 60.78 gm. suggesting hybrids have greater grain yield per plant followed by parents. Selection of elite transgressive sergeants may be obtained from F₂'s segregating population [3, 4, 5, 6, 7].

Table 2: Mean performance of F₁ and their Parents for different agro-economic traits

SL no.	Genotype	DF	DF (50%)	DM	PH	PB	SB	P/P	PC	PL	S/Pod	100 seed wt.	BY	HI	Protein (%)	Dal (%)	SY/P
1.	Rajeevlochan X BSMR-571	104.00	115.00	184.50	205.50	8.00	21.00	190.50	64.00	5.15	3.70	9.90	426.15	20.55	21.11	73.18	87.76
2.	Rajeevlochan X BSMR-2	103.50	114.00	187.50	203.95	7.00	18.00	169.50	57.00	4.10	4.00	9.47	436.40	19.15	23.26	70.61	83.70
3.	BSMR-571 X Rajeevlochan	103.00	114.00	187.50	207.10	7.50	18.50	137.00	45.50	5.15	3.70	9.34	410.45	20.15	22.21	72.83	82.90
4.	BSMR-2 X Rajeevlochan	101.00	112.00	187.50	211.50	9.00	24.50	161.50	55.50	5.15	3.80	9.80	389.95	18.00	23.08	75.95	70.20
5.	RPS-2007-10 X Rajeevlochan	101.50	112.50	186.00	227.70	9.50	27.00	189.00	64.00	5.20	3.70	9.25	437.40	20.45	22.22	79.05	89.60
6.	RPS-2007-10 X BSMR-571	102.50	114.00	185.00	171.00	7.50	22.00	196.50	65.50	5.20	3.60	9.18	286.00	18.30	23.97	77.00	52.50
7.	RPS-2007-10 X BSMR-2	103.50	116.50	187.00	197.00	8.50	24.00	155.00	52.00	5.10	3.90	10.27	314.90	20.00	20.35	75.85	63.00
8.	Rajeevlochan X ASHA	105.00	115.50	188.50	173.40	7.00	20.50	173.00	58.00	5.20	4.00	9.65	278.95	18.25	23.41	74.30	51.00
9.	ASHA X BSMR-571	107.00	117.00	190.00	190.80	7.00	23.00	163.50	54.50	5.40	3.70	9.46	339.30	19.00	21.87	72.57	64.50

10.	ASHA X BSMR-2	101.50	112.50	188.00	198.50	9.50	28.00	177.00	59.50	5.25	3.90	8.91	304.40	20.20	22.42	77.27	61.60
11.	ASHA X RPS-2007-10	103.00	114.50	187.50	249.00	10.50	29.50	189.00	63.00	5.60	3.80	9.01	265.85	19.07	20.42	76.43	50.70
12.	Rajeevlochan X RPS-2007-10	102.50	113.00	187.50	250.00	11.50	33.00	156.00	52.50	4.65	3.80	10.19	268.30	18.35	23.43	73.55	49.25
13.	BSMR-571 X RPS-2007-10	99.50	110.00	187.00	237.90	12.00	34.50	160.50	53.50	5.35	3.70	8.91	284.20	20.25	21.68	79.18	57.65
14.	BSMR-2 X RPS-2007-10	99.00	110.00	186.50	236.40	11.00	32.50	110.00	38.00	5.50	3.80	9.02	194.00	15.35	24.07	72.20	29.80
15.	Rajeevlochan X ASHA	100.00	113.00	184.50	211.10	10.50	33.00	134.00	45.50	5.45	3.80	8.47	240.30	16.10	23.39	74.99	38.70
16.	BSMR-571 X ASHA	101.50	112.50	187.00	233.40	9.50	28.50	135.50	48.00	5.65	3.70	9.26	251.15	17.25	22.50	71.99	43.35
17.	BSMR-2 X ASHA	101.00	113.50	188.00	245.90	12.50	36.00	151.00	52.00	5.35	3.70	10.12	286.05	20.90	23.49	75.50	59.85
18.	RPS-2007-10 X ASHA	104.00	115.00	189.50	237.00	12.50	36.50	173.50	58.50	5.40	3.90	11.01	298.95	19.45	23.79	75.39	58.20
19.	BSMR-571 X BSMR-2	106.00	117.50	190.00	243.10	9.50	28.00	114.50	38.50	5.05	3.80	11.27	248.05	16.48	22.51	76.68	40.90
20.	BSMR-2 X BSMR-571	102.00	112.50	189.00	245.70	10.50	31.50	162.00	52.00	5.45	3.80	8.85	269.30	16.40	23.53	72.66	44.20
21.	Rajeevlochan	101.50	112.00	188.00	207.00	11.00	31.50	96.00	33.00	5.30	3.50	10.06	377.00	19.10	21.56	73.99	72.26
22.	BSMR-571	102.50	112.50	189.50	209.00	11.00	31.50	130.00	42.00	4.90	3.50	10.36	328.90	20.15	21.34	73.41	65.50
23.	BSMR-2	102.00	113.50	189.00	205.10	11.00	29.00	149.50	50.50	5.10	4.00	10.11	350.40	19.70	21.74	79.25	65.58
24.	RPS-2007-10	102.50	113.50	189.50	223.50	11.50	33.00	230.00	76.50	6.15	3.50	9.88	339.85	20.30	21.02	76.47	68.50
25.	ASHA	101.00	113.50	189.00	229.50	12.00	33.00	116.00	39.00	5.80	4.00	9.86	352.65	19.25	19.98	75.89	68.55
	GM	102.42	113.58	187.72	218.0	9.88	28.3	156.8	52.72	5.26	3.77	9.66	319.15	18.88	22.33	75.04	60.78
	CV	1.14	0.91	0.65	2.64	10.14	8.25	5.88	5.73	2.63	7.68	1.95	0.64	1.86	1.67	1.14	3.80
	CD	2.42	2.14	2.52	11.91	2.06	4.82	19.05	6.24	0.28	0.59	0.39	4.23	0.72	0.77	1.77	4.77

Substantial difference were observed in the populations viz., parents and F1's hybrids with respect of various genetic parameters for quantitative traits viz., coefficient of variation, genotypic, phenotypic and environmental, GCV, PCV and ECV, heritability (Broad sense) and genetic advance (Table 3). The phenotypic variance was partitioned into genotypic (heritable) and environmental (non heritable) components of

variance. Obviously, the phenotypic variance was higher than the genotypic and environmental variance in all the studied traits. High estimates of GCV and PCV, heritability and genetic advance were observed for number of pods per plant, grain yield/plant and secondary branches/plant of the population. The same results were conformity with earlier workers [4, 7, 8, 9, 10].

Table 3: Genetic parameters of variability for grain yield and ancillary agro-economic traits in 25 Pigeon pea genotype

Character	DF	DF (50%)	DM	PH	PB	SB	PC	P/P	PL	S/Pod	100 seed wt.	BY	HI	Protein (%)	Dal (%)	SY/P
PCV (%)	2.001	1.749	0.9606	10.60	19.51	20.24	20.12	19.66	7.5184	6.759	7.1500	20.63	8.28750	5.4967	3.23558	25.747
GCV (%)	1.641	1.491	0.705	10.274	16.667	18.487	19.245	18.8102	7.0399	0.221	6.876	20.625	8.074	5.234	3.0267	25.465
Hb ^{2%}	67.27	72.65	53.8698	93.774	72.95	83.36	91.44	91.484	87.6782	29.435	92.5075	99.90	94.91656	90.6939	87.5067	97.819
GA	2.8407	2.9747	2.0010	44.680	2.897	9.840	59.44	19.53	0.71482	0.1546	1.31649	135.53	3.06036	2.29333	4.37711	31.539
GA (% of mean)	2.77	2.61	1.06	20.49	29.32	34.77	37.91	37.06	13.57	4.09	13.62	42.46	16.20	10.26	5.83	51.88
CV (%)	1.14	0.91	0.65	2.64	10.14	8.25	5.88	5.73	2.63	7.68	1.95	0.64	1.86	1.67	1.14	3.80
CD	2.42	2.14	2.52	11.91	2.06	4.82	19.05	6.24	0.28	0.59	0.39	4.23	0.72	0.77	1.77	4.77

Low estimates of PCV and GCV were identified for days to flower initiation days to 50% flowering, days to maturity, pod length, seeds/pod, 100 seed weigh, harvest index, protein%, and Dal recovery% that culminated into low genetic advance. High heritability in these traits indicated the presence of additive gene effects. The PCV and GCV were moderate for plant height, primary branches, Pod/plant results is accordance with [11]. The ECV was generally low for all traits assessed the observed variation will enhance the genetic improvement of the crop for any of these traits evaluated. This indicate that environmental influences were low compared to genetic factors in the variability observed suggesting that the traits have broad genetic base and hence improvement can be achieved through selection. The secondary branches, pod cluster per plant and grain yield/plant were exhibited high genotypic and phenotypic coefficient of variation, heritability and genetic advance [7, 12, 13]. Whereas high heritability indicates the effectiveness of selection on the basis of phenotypic performance, it does not show any indication of the amount of genetic progress for selecting the best individuals.

The high genetic advance was recorded in characters viz., Plant height, biological yield/plant, number of pods cluster/plant (24.76%) and grain yield plant. However, low genetic advance was recorded in characters viz. days to flowering initiation, days to 50% flowering (11.52%), days to maturity, number of secondary branches/plant, 100-seed weight (9.76%), number of primary branches plant-1(6.62%),

dal recovery% (5.23%), seed protein content (3.23%) and number of seeds pod-1 (1.33%). According to Johnson [14], heritability estimates along with the genetic gain are usually more useful. High heritability coupled with high genetic advance as percent of mean was more for seed yield (kg/ha), yield/plant, biological yield/plant, plant height and no. of pod cluster/plant. Indicating the role of additive gene in expressing these traits, suggesting better scope for improvement of these traits through direct selection. Jagan Mohan Rao and Thirumala Rao [15] also reported similar results in Pigeon pea. The coefficient of variation reveals the presence of extent variability for different yield traits and it does not provide the information of the heritable portion. But, it is essential to know that the heritability estimates of the different characters. The heritability estimate leads to separation of variance due to environmental effects from the total variability and indicates the accuracy with which a genotype can be identified by its phenotypic performance, thus making the selection more effective for the isolation of superior genotype.

Conclusion

The trait of grain yield is controlled by complex gene action and hence traits contributing to yield must be considered and evaluated. High heritability and genetic advance might be due to additive gene action, while non-additive and additive gene interactions could be associated with traits possessing high heritability estimates coupled with moderate genetic advance.

In the present investigation, high heritability coupled with high per cent mean genetic advance was obtained in favor of the characters, viz., plant height, number of primary and secondary branches/plant, pod length, pods/plant, 100 seed weight and grain yield/plant. These traits were confirming that the presence of adequate variability in concern genotypes. The greatest variation was observed in number of pods/plant. Which indicated that the character controlled by additive gene effects. These characters would be more effective for selection of elite genotypes.

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