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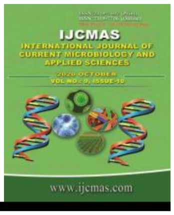

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Studies on Genetic Variability, Heritability and Genetic Advance in Pigeon Pea (*Cajanus cajan* (L.) Millsp.)

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ABSTRACT

Among various grain legumes grown, pigeon pea [*Cajanus cajan* (L.) millsp.] is the second most important crop of India. It is called by an array of names such as Arhar, Cango Pea, Angole, Rahar, Red Gram and Tur. The experiment under present investigation was during *Kharif* 2017 at Agriculture Farm, Nana Ji Deshmukh New Agriculture Campus, Mahatma Gandhi Chitrakoot Gramodaya Vishwavidyalaya, Chitrakoot, Satna (M.P.). The characters studied in the present study included plant stand, days to 50% flowering, primary branches per plant, number of pods per plant, plant height, 100-seed weight(g), seed yield per plant, seed yield (kg/ha), no. of seeds /pod and days to 80% maturity. Analysis of variance for the design of the experiment indicated highly significant differences for nine characters except for plant stand which was found to be non- significant. High PCV was obtained for pods per plant, primary branching, seeds per pod, seed yield per plant (g) and Yield kg/ ha. while high GCV was observed for the character pods per plant only. High heritability was observed for days to 50% flowering and pods per plant. High Genetic advance% of mean was observed only for pods per plant. High GCV, PCV, coupled with heritability and genetic advance% of mean was found only for character pod per plant.

Keywords

Genetic variability, Heritability and genetic advance, Pigeon pea

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Introduction

Pulse crop pays an important role in Indian economy. They are often referred to as "poor man's meat", since they are cheaper source of high quality protein. Grain legumes or pulses occupy an important place in man's food and nutritional requirements. They are important constituents in the diets of a very large number of people, especially in the developing countries and are good source of protein which helps to supplement cereal diets, improving their nutritive values. The presence of different types of proteins and their smaller molecules, including alkaloids, isoflavones, polyphenols and a variety of oligosaccharides, make legumes seeds unique in providing nutraceuticals. For centuries a combination of cereals and pulses has been good source of improved nutrition for people all over world. Besides, pulses are also important for increasing soil health through biological nitrogen fixation with sustainability of cropping system, crop diversification and natural resource management.

Among various grain legumes grown, pigeon pea [*Cajanus cajan* (L.) millsp.] is the second most important crop of India, belonging to tribe-Phaseoleae subtribe-cajaninae, family – leguminosae, genus – *Cajanus* and species – *cajan* with chromosome number 2n = 22. It is called by an array of names *viz*., Arhar, Cango Pea, Angole, Rahar, Red Gram and Tur. According to Vander Maesen (1986) pigeonpea originated in India and spread to other countries quite early endowed with several unique characteristics.

It is an important grain legume mostly being cultivated in Africa, Asia and Americas. It is mostly consumed as dry split dhal besides several other uses of various parts of pigeon pea plant. It is an excellent source of protein (20-22%), supplementing energy rich cereal diets in a mainly vegetarian population (Gawda *et al.*, 2015).

In India pigeonpea was cultivated on 4.65 mha with a total production of 3.02 MT and yield of 650.0 kg per ha during 2013. During 2013, ~83.09% of global pigeonpea production and ~85.50% of area was in Asia, 14.34% and 12.19% in Africa, 2.57% and 2.31% in America (FAOSTAT 2015).

It is grown as sole crop or intercrop with urdbean, mungbean, castor, sorghum, soybean, cotton, maize and groundnut in different states like Maharashtra, Karnataka, Andhra Pradesh, Madhya Pradesh, Uttar Pradesh, Gujarat, Rajasthan Odisha, Punjab and Haryana.

Pigeonpea has versatile use as food, feed, fuel and fodder. Pigeon pea is a multipurpose crop that fits very well in the context of sustainable agriculture. In addition to food, it can be used as fodder, feed, fuel, functional utility (for making baskets, huts, fences, etc.), fertilizer (fixes atmospheric nitrogen and releases phosphorus), forest use (re-forestation, lac production), and even for pharmaceutical purposes.

Materials and Methods

The experiment under present investigation was conducted in a well prepared field during *Kharif* 2017 at Agriculture Farm, Nana Ji Deshmukh New Agriculture Campus, Mahatma Gandhi Chitrakoot Gramodaya Vishwavidyalaya, Chitrakoot, Satna (M.P.). The place of experiment in Chitrakoot is situated at $25^0$10' North latitude and $80^0$85' East longitude. The altitude is about 200m above mean sea level.

The experiment was laid out fallowing Randomized Block Design (RBD) with three replications during *Kharif* 2017. The experimental material was sown on 18th July, 2017and harvested on 19th, February, 2018 . Each treatment was grown in 4× 5.40 m sized plots with 6 rows per plot spaced 90 cm apart. The plant to plant distance was maintained 25cm by thinning. Five competitive plants from each plot were randomly selected for recording of observations on seven characters (Table 1). Average of the data from the sampled plants of each plot in respect of different characters was used for various statistical analyses. The data were recorded for the following characters.

Estimation of genetic parameters

The mean data of all traits was exposed to ANOVA analysis to obtain the estimates of mean sum of squares and mean sum of products and these were utilised for the calculation of following parameters.

Coefficient of variation

The coefficient of variation (CV) being a unit less measurement, is a good basis for comparing the extent of variation between different characters with different scales.

$$\mathbf{CV} = \frac{\mathbf{SD}}{\bar{\mathbf{X}}} \times \mathbf{100}$$

The genotypic and phenotypic variance was calculated as per the formulae proposed by Burton (1952).

Genotypic variance σg^2 =

$$\frac{\textit{Number of raplications}}{\textit{MSS due to genotypes} - \textit{MSS due to error}}$$

Phenotypic variance $\sigma p^2 = \sigma g^2 + \sigma e^2$

σg^2 = Genotypic variance

σp^2 = Phenotypic variance

σe^2 = Error variance

Phenotypic and genotypic components of variance were estimated by using the formula suggested by Burton and De Vane (1953).

$$\textbf{Genotypic coefficient of variability (GCV)} = \frac{\sigma g}{\bar{X}} \times 100$$

$$\textbf{Phenotypic coefficient of variability (PCV)} = \frac{\sigma P}{\bar{X}} \times 100$$

Where,
σg = Genotypic standard deviation
σp = Phenotypic standard deviation
$\bar{X}$ = General mean of character

Sivasubramanian and Menon (1973) categorised PCV and GCV estimates as follows,

20.1 percent and above = High
10.1-20 percent = Moderate
1-10 percent = Low

Heritability (h^2)

Broad sense heritability was computed as “the ratio of genetic variance to the total phenotypic variance as suggested by Hanson *et al.*, (1956) and expressed as percentage”.

$$\textbf{Heritability } (\mathbf{h}^2) = \frac{\sigma_g^2}{\sigma_p^2} \times \mathbf{100}$$

Where,
$\sigma^2 p$ = Phenotypic variance
$\sigma^2 g$ = Genotypic variance

The heritability percentage was categorized as high, moderate and low as given by Robinson *et al.*, (1949).
60.1 percent and above = High
30.1- 60 percent = Moderate
0-30 percent = Low

Genetic Advance (GA)

The expected genetic gain for each character was analysed by using the following method suggested by Johnson *et al.*, (1955).

$$\textbf{Genetic advance(GA)} = \mathbf{K} \times \mathbf{h}^2 \times \sigma_p$$

Where,
K = A constant, the value equal to 2.06 at 5 % selection intensity
h^2 = broad sense heritability
σ_p = phenotypic standard deviation
Genetic advance as percentage of mean (GAM)

$$\mathbf{GAM} = \frac{\mathbf{GA}}{\bar{\mathbf{X}}} \times \mathbf{100}$$

The range of genetic advance as percent of mean is classified as suggested by Johnson *et al.*, (1955),

GA < 10 per cent = Low
GA > 10 – 20 per cent = Moderate
GA > 20 per cent = High

Results and Discussion

Analysis of variance for the design of experiment parameters

Analysis of variance for the design of the experiment indicated highly significant differences for all the characters except for plant stand which was found to be non-significant. The characters studied in the present study viz- plant stand, days to 50% flowering, primary branches per plant, number of pods per plant, plant height(cm), 100-seed weight(g), seed yield per plant(g), seed yield (kg/ha), no. of seeds /pod and days to 80% maturity (Table 2).

Genetic variability

The results pertaining to genetic parameters *viz.*, range, mean, phenotypic coefficient of variation, genotypic coefficient of variation, heritability and genetic advance as per cent of mean were calculated to estimate the amount of genetic variability for different characters. The results related to genetic parameters are presented in the Table 3.

The data of mean and range reveals the extent of phenotypic and genotypic variability of characters under study. Results obtained from these components of genetic parameter indicate presence of abundant amount of genetic variability in the material under present investigation. Variability in quantitative characters of pigeonpea was also reported by. vavilon *et al.,* (1926), Pandey and Singh (2002), Linge, Singh, Mahiboobsa *et al.*, Patel *et al.*, (1998), Jahagirdar *et al.*, (1994) for seed yield.

Data obtained from the experiment displayed the high GCV for the characters pods per plant (45.02), Moderate GCV for primary branching (12.55), Seeds per Pod (12.55), Plant Height (cm.) (11.38), Seed Yield per Plant (g) (11.24) and Yield kg/ ha. (11.70) whereas Low GCV was shown by plant Stand (3.49), Days to 50% Flowering (9.47), Days to 80% Maturity (2.31) and 100 Seed Wt.(g) (6.00). High PCV was obtained for pods per Plant (48.45), primary Branching (22.49), seeds per Pod (24.22), seed Yield per Plant (g) (20.90) and Yield kg/ ha. (21.51), moderate PCV was obtained for days to 50% Flowering (10.85), plant Height (cm.) (17.85), 100 Seed Wt.(g) (10.89) whereas Low PCV was shown by days to 80% maturity (4.98). High GCV coupled with high PCV was observed for the character pods per plant. Vange and Egbe Moses (2009) and Varshney (2010).

Table.1 Name of genotypes/varieties used during experimentation

BDN 2	**RKPV 310-09**	**NPMK 15-05**	**IBTDRG-1**
ICPL 87119	RKPV 455-02	VRG 08-004	RVSA 15-8
JKM 189	BDN 2014-2	TRG 87	IPA 17B-11
CRG 2015-007	IBTDRG-2	WRG 311	RVSA 15-9
PT0723-1-2-3	BAUPP 15-22	GJP 1606	SKNP 1416
LRG 208	GJP 1601	RPS 2008-5	IPA 17B-10
IBTDRG 3	WRG 303	BAUPP 15-21	

Table.2 Analysis of variance for ten quantitative characters in pigeon pea

S. No.	Characters	Mean Sum of Square		
		Replication	Treatments	Error
	d.f.	2	21	42
1	Plant Stand	39.81	52.39**	21.46
2	Days to 50% Flowering	10.72	251.13***	23.73
3	Primary Branching	15.77	28.52**	12.10
4	Pods Per Plant	4104.48	96724.24***	4835.23
5	Seeds Per Pod	0.46	1.23*	0.59
6	Plant Height (cm.)	1052.02	2184.97***	715.90
7	Days to 80% Maturity	1.57	102.61*	56.16
8	100 Seed Wt.(g)	0.38	2.39**	1.04
9	Seed Yield Per Plant (g)	93.38	95.39**	42.96
10	Yield kg/ ha.	18926.82	17754.88**	7846.57

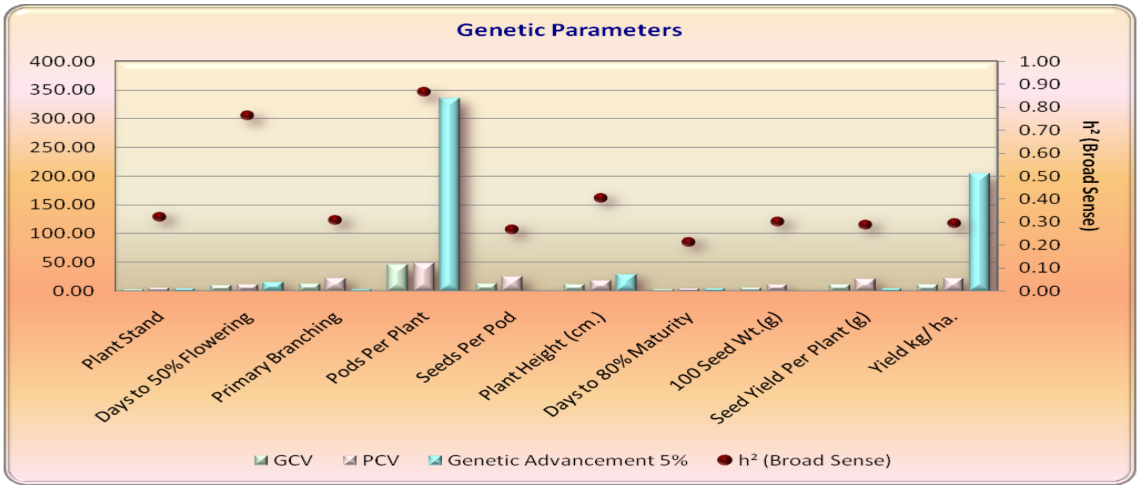
Table.3 Heritability (%) in broad sense, genetic advance in percent of Mean, range, genotypic, phenotypic and error variance and coefficient of variation for 10 quantitative characters in Pigeon pea

S. No.	Characters	Range		Coefficient of Variation		Heritability (Broad Sense)	Genetic Advance %of Mean
		Min.	Max.	GCV	PCV		
1	Plant Stand	80.00	96.00	3.49	6.13	32.46	4.1
2	Days to 50% Flowering	78.67	113.00	9.47	10.85	76.16	17.02
3	Primary Branching	11.47	22.67	12.55	22.49	31.14	14.43
4	Pods per Plant	99.33	861.33	45.02	48.45	86.37	86.2
5	Seeds per Pod	3.00	5.67	12.55	24.22	26.84	13.39
6	Plant Height (cm.)	138.33	236.00	11.38	17.85	40.62	14.94
7	Days to 80% Maturity	159.33	179.00	2.31	4.98	21.61	2.22
8	100 Seed Wt.(g)	9.67	12.67	6.00	10.89	30.34	6.81
9	Seed Yield per Plant (g)	19.67	50.00	11.24	20.90	28.92	12.45
10	Yield kg/ ha.	816.33	2137.33	11.70	21.51	29.62	13.12

Appendix.I Mean performance of genotypes for 10 quantitative characters in pigeon pea

Appendix I: Mean Performance of genotypes for 10 quantitative characters in Pigeon pea											
No	**Varieties/ Genotypes**	**Plant Stand**	**Days to 50% Floweri**	**Primary Branching**	**Pods Per Plant**	**Seeds Per Pod**	**Plant Height (cm.)**	**Days to 80% Maturi**	**100 Seed Wt.(g)**	**Seed Yield Per Plant (g)**	**Seed Yield (kg/ ha.)**
1	BDN 2	95.67	88.00	17.33	575.67	3.33	166.60	166.00	12.33	38.33	1692.33
2	ICPL 87119	95.00	95.67	22.67	861.33	3.00	204.87	166.00	9.67	38.67	1706.00
3	JKM 189	94.00	95.00	20.27	737.00	3.33	234.67	168.67	12.67	50.00	2137.33
4	CRG 2015-007	95.33	86.00	22.40	578.00	4.00	232.40	168.67	11.00	35.00	1394.33
5	PT0723-1-2-3	93.33	85.67	18.93	416.00	4.00	194.47	172.67	11.00	39.67	1592.33
6	LRG 208	93.00	98.00	19.20	495.67	4.33	191.20	176.00	11.33	32.00	1445.33
7	IBTDRG 3	93.00	82.00	17.13	142.00	3.00	157.80	179.00	10.67	19.67	816.33
8	RKPV 310-09	95.00	88.67	11.47	372.33	3.33	145.13	173.33	11.00	40.33	1662.00
9	RKPV 455-02	93.67	90.00	11.80	244.67	4.00	175.67	174.33	10.00	41.33	1736.00
10	BDN 2014-2	83.67	83.33	21.60	441.67	3.67	138.33	164.67	10.33	43.00	1730.67
11	IBTDRG-2	92.00	94.33	17.47	387.33	4.00	170.87	162.00	10.00	33.00	1441.00
12	BAUPP 15-22	94.33	103.33	22.33	99.33	3.33	155.80	162.00	12.33	36.67	1629.33
13	GJP 1601	94.33	104.33	19.00	247.00	3.00	194.93	172.00	10.67	38.67	1681.00
14	WRG 303	96.00	82.67	17.87	458.00	4.00	206.27	173.33	12.33	33.33	1280.67
15	NPMK 15-05	94.33	83.67	20.60	596.00	5.67	222.00	179.00	12.00	34.00	1314.33
16	VRG 08-004	94.33	96.00	22.33	456.33	4.67	177.67	170.33	10.33	33.33	1434.67
17	TRG 87	87.67	94.33	20.27	297.33	3.33	181.60	171.33	10.33	32.00	1376.33
18	WRG 311	92.67	90.67	17.60	212.00	4.67	191.33	176.00	11.67	38.00	1598.67

19	GJP 1606	80.00	101.00	19.73	227.00	4.00	222.40	161.33	11.33	42.00	1866.33
20	RPS 2008-5	93.33	81.33	20.07	531.33	3.33	204.93	167.33	12.67	46.67	1755.00
21	BAUPP 15-21	93.67	82.33	14.27	208.00	3.00	222.73	175.33	10.33	37.33	1421.67
22	IBTDRG-1	93.00	108.33	17.13	376.33	3.33	193.20	175.33	11.00	34.67	1540.00
23	RVSA 15-8	92.67	78.67	20.33	371.33	4.00	236.00	160.00	12.33	36.67	1336.00
24	IPA 17B-11	81.67	113.00	21.27	234.33	3.00	206.47	168.33	10.67	39.33	1747.67
25	RVSA 15-9	88.00	80.67	20.33	342.33	3.67	217.13	159.33	12.00	40.00	1496.00
26	SKNP 1416	91.67	99.00	15.67	236.67	3.00	197.27	175.67	11.67	31.67	1406.67
27	IPA 17B-10	90.67	96.33	14.20	350.00	3.67	209.13	174.67	10.67	39.00	1684.67
	Mean	**91.93**	**91.94**	**18.64**	**388.70**	**3.69**	**194.48**	**170.10**	**11.20**	**37.20**	**1552.69**
	C.V.(%)	5.04	5.30	18.66	17.89	20.72	13.76	4.41	9.09	17.62	18.04
	F ratio	2.44	10.58	2.36	20.00	2.10	3.05	1.83	2.31	2.22	2.26
	S.E.±m	2.67	2.81	2.01	40.15	0.44	15.45	4.33	0.59	3.78	161.73
	C.D. 5%	7.59	7.98	5.70	113.93	1.25	43.84	12.28	1.67	10.74	458.95
	Range Lowest	80.00	78.67	11.47	99.33	3.00	138.33	159.33	9.67	19.67	816.33
	Range Highest	96.00	113.00	22.67	861.33	5.67	236.00	179.00	12.67	50.00	2137.33



Heritability and genetic advance

High heritability was observed for days to 50% flowering (76.65), pods per plant (86.37), moderate heritability was observed for plant stand (32.46), primary branching (31.14), plant height (40.62), 100 Seed Wt. (30.34) while low heritability was observed for seeds per pod (26.84), days to 80% maturity (21.61), seed yield per plant (28.92) and Yield kg/ ha. (29.62). Hanson *et al.*, (1956), Ghodke *et al.*, (1994).

High Genetic advance% of mean was observed only for pods per plant (86.82), moderate genetic advance% of mean was observed for days to 50% Flowering (17.02), primary branching (14.43), seeds per pod (13.39), plant height (14.94), seed yield per plant (12.45) and yield kg/ha. (13.12) while low genetic advance% of mean was shown by traits plant stand (4.1), days to 80% maturity (2.22) and 100 Seed Wt (6.81).High GCV, PCV, coupled with heritability and genetic advance% of mean was found for character pod per plant. Findings of the present experiment were in confirmation with the findings of Manju. and Sreelatha Kumar (2002) and Ghodke *et al.*, (1994).
Conclusions are as follows:

Analysis of variance for the design of experiments revealed highly significances among treatments for all the characters except for plant sta, indications wide variation among genotypes.

Phenotypic coefficients of variability (PCV) were higher than genotypic coefficients of variability (GCV) for all the characters.

The heritability values ranged from 21.61 per cent for days to 80% maturity to 86.37 per cent for pods / plant. High heritability was found for pods / plant and days to 50% flowering

The expected genetic advance in per cent of mean ranged from 4.1 per cent for plant stand to 86.2 per cent for pods / plant. High heritability was found for pods / plant followed by days to 50% flowering

The heritability coupled with genetic advance was found high with pods per plant, yield kg/ha, plant height and days to 50% flowering

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