



## Phenotypic and Genetic Study on Native Pigeonpea Germplasm of Chhattisgarh for Yield Attributing Traits

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### Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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### ABSTRACT

**Aims:** To find out genetic variation of pigeon pea Germplasm population on Chhattisgarh, with *H. armigera*, *M. vitrata* Larvae Population.

**Study Design:** Augmented RBD Design in 4 block with 3 check varieties.

**Place and Duration of Study:** College of Agriculture Raipur, IGKV, Chhattisgarh. During *Kharif* 2019-2020.

**Methodology:** The experimental materials were used 100 local landraces of Pigeonpea and three popular standard checks. The Morphological observations on various agro-morphological characters including qualitative and quantitative characters and Incidence of major insects of Pigeonpea were recorded.

**Results:** outcome of the study revealed that Incidence of major insect of Pigeonpea 10 genotypes of pigeonpea are resistant and 10 are susceptible occurred. Analysis of variance indicated that the mean sum of squares due to genotypes were highly significant for all the characters with p-value of 0.001 and some traits check varieties 0.001. Results of genetic variability analysis state that's highest genetic advance as percent of the mean for traits are days to fifty percent flowering, plant height, seed protein content, and days to maturity.

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**Conclusion:** The Pigeonpea accession used in the study revealed significant variability for most of the morphological traits. Amongst the genotypes studied, high coefficients of variation were observed for most of the characters studied indicating the existence of sufficient variability.

**Keywords:** Coefficient of variation; augmented RBD; pigeonpea germplasms; *H. armigera*; *M. vitrata* larvae population.

## 1. INTRODUCTION

A leguminous wonder crop plant has coined the name “Pigeonpea” was in place in Barbados because of its use to feed pigeon by native farmers [1]. Pigeonpea [*Cajanus cajan* (L.) Millsp.], was extraordinary from the binging with rich nourishment protein in its seed (21%), provides protein supplies of vegetarian population. It has a great range for maturity days (95 days to 299 days) [2]. Only domesticated species in family *Cajaninae* is *Cajanus cajan*. Pigeonpea plays an essential role in providing food, shelter, medicine and other livelihood opportunities among the rural population. The grain is consumed as dal, the green seed serves as vegetable and the sticks are used as fuelwood. It is grown predominantly under rain-fed conditions of the semi- arid tropics. India is the largest producer of pulses, of which Pigeonpea is widely grown legume after chickpea, covering an area of 4.23 M ha with production 3.89 M tones and productivity of 917 kg/ha in india 2019-20, and it covers an area of 65.9 thousand ha with annual production of 39.9 thousand tons and productivity of 605 kg /ha in Chhattisgarh 2019-20 [3].

The knowledge of nature and extent of genetic variation is available in the Pigeonpea genotypes which is the prerequisite for any plant breeding experiment. Collection, conservation and characterization of genotype is the backbone of any crop improvement programme which in turn depends on the extent of genetic diversity present in gene pool. Diversity in plant genotypes provides the opportunity for plant breeders to develop new and improved cultivars with desirable characteristics. From the very beginning of agriculture, natural genetic variability has been exploited within crop species to meet subsistence food requirement, and now it is being focused on surplus food production to fulfill the requirements of increasing populations. Unfortunately, pigeon pea is considered an “orphan crop” in many countries. In India, the North-Eastern part of the Deccan Plateau along with the adjoining Chhotanagpur plateau, forming the parts of the present-day Odisha,

Chhattisgarh and Jharkhand germplasms. Therefore, there is a high probability of finding elite germplasms in the form of locally adapted landraces with desirable agro-morphological traits which may culminate into the breeding of Pigeonpea varieties with higher productivity. The role of genetic diversity in conducting successful plant breeding programmes involving productivity, quality parameters and stress tolerance is very important [4]. The market demand of Pigeonpea is bound to increase in demographically expanding India, where *per capita* pulse availability has declined from 69 grams in 1961 to 32 grams in 2005 [5]. The per capita availability of protein in the country is already one-third of its requirement and if production of this major pulse is not increased significantly, the problem of malnutrition among the poor will further aggravate. The characterization data provides valuable information about genetic diversity in the germplasms collections and this information is helpful in understanding the pattern of genetic variation in a crop species [6] and its further utilization.

Yield is a complex trait being governed by a large number of cumulative, duplicate and dominant genes and directly or indirectly influenced by the environment as well as response poorly to the direct selection. Keeping these points in view, to find out suitable genotypes or donor to meet any current or future demand for improvement of the Pigeonpea crop, various indigenous Pigeonpea genotypes are taken to study.

## 2. MATERIALS AND METHODS

The research was conducted on Research Farm, Department of Genetics and Plant Breeding, College of Agriculture Raipur, Chhattisgarh, India. The trial resources comprised of 100 local landraces of Pigeonpea and three popular standard checks. The study materials were obtained from various, parts of Chhattisgarh. The study was started during *Kharif* 2019-20 in an Augmented Randomized Complete Block Design (RBD) to assess the agro-morphological

characterization, genetic variability and genetic divergence between the 100 local landraces of Pigeonpea [*Cajanus cajan* (L.) Millsp.] and three standard checks namely Rajeevelochan, Asha and CGA-1 (Table 1.)

Climatological data on temperature, rainfall, rainy days, relative humidity and sunshine hours recorded at the Meteorological Observatory Unit, Department of Agro- meteorology, IGKV Raipur, during the cropping period. The weather condition during investigation remained favorable for the growth and development of pulses. Weather during the crop period in all the seasons of two years was normal for Pigeonpea. The total

rains received during 2019-20 from 30<sup>th</sup> Standard Meteorological Week, were 1370.8 mm. Similarly, the maximum mean temperature ranged from 34.3°C to 23.6°C during 2019-20. It was higher at the time of sowing of the crop in July and a gradual decrease in temperature was noticed up to January and it again increased with the advancement of the crop period. The mean minimum temperature ranged between 7.3°C to 26.8°C during 2019-2020. The minimum temperature decreased gradually up to the third week of December and again increased. The Morphological observations on various agromorphological characters including qualitative

**Table 1. List of 100 local landraces of Pigeonpea and 3 popular standard checks used in the present study**

Entry No.	Genotype	Entry No.	Genotype	Entry No.	Genotype
T1	RP-1	T35	RP-36	T69	RP-85
T2	RP-2	T36	RP-37	T70	RP-89
T3	RP-3	T37	RP-38	T71	RP-91
T4	RP-4	T38	RP-41	T72	RP-92
T5	RP-5	T39	RP-42	T73	RP-93
T6	RP-6	T40	RP-43	T74	RP-94
T7	RP-7	T41	RP-44	T75	RP-95
T8	RP-8	T42	RP-45	T76	RP-96
T9	RP-9	T43	RP-46	T77	RP-97
T10	RP-10	T44	RP-48	T78	RP-98
T11	RP-12	T45	RP-53	T79	RP-99
T12	RP-13	T46	RP-54	T80	RP-100
T13	RP-14	T47	RP-55	T81	RP-101
T14	RP-15	T48	RP-56	T82	RP-102
T15	RP-16	T49	RP-57	T83	RP-103
T16	RP-17	T50	RP-60	T84	RP-104
T17	RP-18	T51	RP-61	T85	RP-105
T18	RP-19	T52	RP-62	T86	RP-106
T19	RP-20	T53	RP-63	T87	RP-107
T20	RP-21	T54	RP-64	T88	RP-108
T21	RP-22	T55	RP-66	T89	RP-109
T22	RP-23	T56	RP-67	T90	RP-110
T23	RP-24	T57	RP-69	T91	RP-112
T24	RP-25	T58	RP-70	T92	RP-113
T25	RP-26	T59	RP-72	T93	RP-115
T26	RP-27	T60	RP-73	T94	RP-116
T27	RP-28	T61	RP-74	T95	RP-118
T28	RP-29	T62	RP-75	T96	RP-119
T29	RP-30	T63	RP-76	T97	RP-120
T30	RP-31	T64	RP-77	T98	RP-121
T31	RP-32	T65	RP-78	T99	RP-122
T32	RP-33	T66	RP-79	T100	RP-123
T33	RP-34	T67	RP-80	CH1	Rajeevelochan
T34	RP-35	T68	RP-84	CH2	Asha

Note: CH=check variety, T=new treatment entry

and quantitative characters and Incidence of major insects of Pigeonpea were recorded viz. Biological Yield (gm/plant), Days to 50 % Flowering, Days to First Flowering, Days to Maturity, Duration of Flowering, Harvest Index, *Helicoverpa armigera* Larvae Population, *Maruca vitrata* Larvae Population, No. of Pods/plant, No. of Primary Branches, No. of Secondary Branches, No. of Seeds/Pod, Plant Height (cm), Pods Length (cm), Pod Width (cm), Protein %/100 gm Seeds, Shelling %, 100 Seed Weight (gm) and Seed Yield (gm/plant). The data recorded 100 local landraces of Pigeonpea and three popular standard checks for different quantitative and qualitative characters were subjected to the statistical analysis viz. analysis of variance, range, mean, standard deviation, standard error, heritability, genetic advance, Genetic advance as percentage of the mean (Table.1).

### 3. RESULTS AND DISCUSSION

Qualitative traits are reflected as morphological markers for use as genotypes of pigeonpea because they are less influenced by the environment. In the present study, the outcome of agro morphological traits states that categorization of germplasm genotypes determines variation among pigeonpea genotypes. It is not solitary vital for utilizing the appropriate attribute-based donors in breeding programs, but also important in the present era for conserving the unique pigeonpea. Outcomes from this study conformation on conclusions by [7-16] (Devi et al., 2020; Sharma et al., 2020).

Result of the population occurrence on the inflorescence of key insect pest of pigeonpea states that of *H. armigera* larvae population per inflorescence 10 lowermost genotypes that having bottommost insect population are about as a susceptible genotype beside the *H. armigera* from the understudy total of pigeonpea genotypes like T80, T90, T89, T79, T78, T94, T88, T81, T83 and T99. Whereas 10 top most genotypes that having uppermost insect population are regarding as a capable resistance genotypes beside the *H. armigera* from the genotypes under study total of pigeonpea like. T52, T5, T10, T45, T20, T21, T49, T23, T55 and T2.

Observation of *M. vitrata* insect population on plant 10 bottommost genotypes that having bottommost insect population are regarding as a susceptible germplasms beside the *M. vitrata*

from the understudy total of pigeonpea genotypes like T84, T76, T70, T85, T51, T53, T90, T62, T21 and T94. Whereas 10 topmost genotypes that having topmost insect population are apropos as a capable resistance genotypes against the *M. vitrata* from the under study total of pigeonpea genotypes like T20, T52, T23, T42, T65, T11, T44, T5, T7 and T18. These same conclusions are conformation on verdicts by [17,18,8].

By using software R Studio, augmented design analysis was done by using observation data of *Kharif* 2018 Analysis of variance indicated that the mean sum of squares due to genotypes were highly significant for all the characters. Significant mean squares due to seed yield and attributing characters revealed the existence of considerable variability in the material studied for the improvement of various traits (Table 2).

Outcomes from the ANOVA rejected the null hypothesis and determine that all of the population means are not equal. We use the post hoc test Tukey's multiple comparison test to define which population means among a set of means differ from the rest. In these outcomes, variances between means that share a letter are not statistically significant. Highest mean contenting germplasms T14 with group "a" letter and lowest mean containing germplasms T82 with group "1" letter, which indicates that germplasms T14 has a significantly higher mean than germplasms T82 and so on. Means of germplasms followed by the same letter in the table do not differ statistically. Similarly, check genotypes for Seed Yield (gm. /plant) all are not significantly different from each other. (Table 3 to 5).

Results of genetic variability analysis state that's (Table 6) highest genetic advance as percent of the mean for traits are days to fifty percent flowering, plant height, seed protein content and days to maturity is related to the conclusions by [19-22]. Likewise pods per plant, seed yield per plant, number of primary and secondary branches per plant, biological yield per plant and test weight detected by [23,24,25].

The genetic variability in any breeding material is a prerequisite as it does not only provide a basis for selection but also provide some valuable information regarding the selection of diverse parents for use in hybridization program. The coefficient of variation truly provides a relative measure of variability among different traits. In

**Table 2. Analysis of Variance (ANOVA) for Augmented Block Design on 2019 data of quantitative traits**

Source	Df	B Y	D 50 F	D F F	D M	D F	H I	H L P	M L P	N P P
Block unadj.	3	2092.7 **	1453.3 **	1258.2 **	2000.86 **	176.22 **	83.24 **	1.88 **	1.43 **	432.09 **
Trt. unadj.	102	1232.79 **	856.11 **	1668.18 **	586.48 **	279.13 **	121.19 **	1.11 **	2.26 **	341.43 **
Block adj.	3	302.25 **	209.81 **	132.8 **	329.39 *	21.27 ns	2.14 ns	0.27 **	0.17 ns	18.28 ns
Trt. adj.	102	1180.13 **	819.54 **	1635.08 **	537.31 **	274.57 **	118.8 **	1.06 **	2.23 **	329.26 **
Control	2	1304.86 **	906.3 **	847.72 **	972.33 **	3.79 ns	16.38 **	1.17 **	0.1 ns	3.79 ns
Augmented	99	1234.45 **	857.26 **	1700.91 **	583.66 **	285.03 **	121.86 **	1.11 **	2.31 **	344.77 **
Test vs augmented	1	924.59 **	642.28 **	68.85 *	93.19 ns	246.09 **	264.34 **	0.84 **	2 **	685.9 **
Test + Test.VS.aug.	100	1177.64 **	817.8 **	1650.83 **	528.61 **	279.99 **	120.85 **	1.06 **	2.27 **	335.77 **
Residuals	6	22.97	15.94	9.07	39.37	8.28	0.94	0.02	0.04	8.28

\*= significant at 5%. = P=0.05; \*\*= significant at 1%. = P=0.05

**Table 2. continued**

Source	Df	N P B	N S B	N S P	P H	P L	P W	P S	S P	100 S W	S Y
Block unadj.	3	7.05 **	50.32 **	0.55 **	1366.02 **	1.8 **	0.01 ns	8.74 **	54.64 **	4.92 **	63.44 **
Trt. unadj.	102	11.17 **	66.73 **	0.34 **	838.91 **	0.53 **	0.03 **	5.37 **	33.56 **	3.02 **	100.49 **
Block adj.	3	0.85 ns	5.31 **	0.08 *	195.11 *	0.3 *	0.01 ns	1.25 *	7.82 *	0.71 *	7.66 ns
Trt. adj.	102	10.98 **	65.4 **	0.32 **	804.47 **	0.48 **	0.03 **	5.15 **	32.18 **	2.9 **	98.85 **
Control	2	0.15 ns	33.91 **	0.4 **	1008.45 **	0.87 **	1 ns	6.46 **	40.35 **	3.62 **	1.36 ns
Augmented	99	11.4 **	68.04 **	0.33 **	836.7 **	0.53 **	0.03 **	5.35 **	33.47 **	3.01 **	102.61 **
Test vs augmented	1	9.85 **	2.76 *	0.29 **	718.53 **	0.08 ns	0.02 ns	4.6 **	28.75 **	2.59 **	88.63 **
Test + Test.VS.aug.	100	11.2 **	66.03 **	0.32 **	800.39 **	0.48 **	0.03 **	5.12 **	32.02 **	2.88 **	100.8 **
Residuals	6	0.33	0.36	0.01	28.62	0.04	0.003	0.18	1.15	0.1	2.99

\*= significant at 5%. = P=0.05; \*\*= significant at 1%. = P=0.05

Note: degree of freedom = Df, Biological Yield (gm/plant) = B Y, Days to 50 % Flowering = D 50 F, Days to First Flowering = D F F, Days to Maturity = D M, Duration of Flowering = D F, Harvest Index = H I, H. armigera Larvae Population = H L P, M. vitrata Larvae Population = M L P, No of Pods/plant = N P P, No of Primary Branches = N P B, No of Secondary Branches = N S B, No of Seeds/Pod = N S P, Plant Height (cm) = P H, Pods Length (cm) = P L, Pod Width (cm) = P W, Protein %/100 gm Seeds = P S, Shelling % = S P, 100 Seed Weight (gm) = 100 S W, Seed Yield (gm/plant) = S Y

**Table 3. Comparison of critical difference all traits of pigeonpea. (Alpha = 0.05)**

Traits	Critical Difference Comparison			
	A Test Treatment and a Control Treatment	A Test Treatment and a Control Treatment	A Test Treatment and a Control Treatment	A Test Treatment and a Control Treatment
BY	15.14	15.14	15.14	15.14
D 50 F	12.61	12.61	12.61	12.61
DFF	9.51	9.51	9.51	9.51
DM	19.82	19.82	19.82	19.82
DF	9.09	9.09	9.09	9.09
HI	3.06	3.06	3.06	3.06
HLP	0.46	0.46	0.46	0.46
MLP	0.65	0.65	0.65	0.65
NPP	9.09	9.09	9.09	9.09
NPB	1.82	1.82	1.82	1.82
NSB	1.91	1.91	1.91	1.91
NSP	0.34	0.34	0.34	0.34
PH	16.9	16.9	16.9	16.9
PL	0.59	0.59	0.59	0.59
PW	0.17	0.17	0.17	0.17
PS	1.35	1.35	1.35	1.35
SP	3.39	3.39	3.39	3.39
100 SW	1.01	1.01	1.01	1.01
SY	5.46	5.46	5.46	5.46

**Table 4. Comparison of standard errors all traits of pigeonpea**

Traits	Standard Errors Comparison			
	A Test Treatment and a Control Treatment	A Test Treatment and a Control Treatment	A Test Treatment and a Control Treatment	A Test Treatment and a Control Treatment
B Y	6.19	6.19	6.19	6.19
D 50 F	5.15	5.15	5.15	5.15
D F F	3.89	3.89	3.89	3.89
D M	8.1	8.1	8.1	8.1
D F	3.71	3.71	3.71	3.71
H I	1.25	1.25	1.25	1.25
H L P	0.19	0.19	0.19	0.19
M L P	0.27	0.27	0.27	0.27
N P P	3.71	3.71	3.71	3.71
N P B	0.74	0.74	0.74	0.74
N S B	0.78	0.78	0.78	0.78
N S P	0.14	0.14	0.14	0.14
P H	6.91	6.91	6.91	6.91
P L	0.24	0.24	0.24	0.24
P W	0.07	0.07	0.07	0.07
P S	0.55	0.55	0.55	0.55
S P	1.38	1.38	1.38	1.38
100 S W	0.41	0.41	0.41	0.41
S Y	2.23	2.23	2.23	2.23

Note: Biological Yield (gm/plant) = B Y, Days to 50 % Flowering = D 50 F, Days to First Flowering = D F F, Days to Maturity = D M, Duration of Flowering = D F, Harvest Index = H I, *H. armigera* Larvae Population = H L P, *M. vitrata* Larvae Population = M L P, No of Pods/plant = N P P, No of Primary Branches = N P B, No of Secondary Branches = N S B, No of Seeds/Pod = N S P, Plant Height (cm) = P H, Pods Length (cm) = P L, Pod Width (cm) = P W, Protein %/100 gm Seeds = P S, Shelling % = S P, 100 Seed Weight (gm) = 100 S W, Seed Yield (gm/plant) = S Y

**Table 5. HSD method applies for population mean comparisons for Seed Yield (gm/plant)**

Treatment	Adjusted Means	Group	Treatment	Adjusted Means	Group
RP-102	14.086	1	RP-19	22.086	1234567890A D F IJ L N PQRST
RP-99	14.086	1	RP-18	22.086	1234567890A D F IJ L N PQRST
RP-100	15.886	12	RP-13	22.086	1234567890A D F IJ L N PQRST
RP-119	15.886	12	RP-109	23.086	1234567890ABCDEFGHIJKLMN OPQRSTUVWXYZ
RP-108	16.486	123	RP-16	23.286	1234567890ABCDEFGHIJKLMN OPQRSTUVWXYZ
RP-31	16.773	1234	RP-54	23.373	1234567890ABCDEFGHIJKLMN OPQ S U W Y
RP-29	16.773	1234	RP-121	24.886	1234567890ABCDEFGHIJKLMN OPQRSTUVWXYZ
RP-45	16.773	1234	RP-42	25.173	1234567890ABCDEFGHIJKLMN OPQRSTUVWXYZ
RP-97	17.086	1234	RP-27	28.173	1234567890ABCDEFGHIJKLMN OPQRSTUVWXYZ
RP-98	17.686	1234	CH2	30.435	234567890ABCDEFGHIJKLMN OPQRSTUVWXYZ
RP-78	17.856	123456	RP-6	30.486	1234567890ABCDEFGHIJKLMN OPQRSTUVWXYZ
RP-122	18.286	1234	CH1	30.678	34567890ABCDEFGHIJKLMN OPQRSTUVWXYZ
RP-35	19.173	123456789	CH3	31.545	4567890ABCDEFGHIJKLMN OPQRSTUVWXYZ
RP-32	19.173	123456789	RP-20	34.686	234567890ABCDEFGHIJKLMN OPQRSTUVWXYZ
RP-89	19.656	1234567 0	RP-123	36.886	567890ABCDEFGHIJKLMN OPQRSTUVWXYZ
RP-77	19.656	1234567 0	RP-116	37.486	67 90 HIJKLMN OPQRSTUVWXYZ
RP-110	20.086	12345 8 ABCDEFG	RP-101	38.086	7 90 HIJKLMN OPQRSTUVWXYZ
RP-63	20.256	1234567 0 B EF HIJK	RP-106	38.086	7 90 HIJKLMN OPQRSTUVWXYZ
RP-67	20.256	1234567 0 B EF HIJK	RP-107	38.086	7 90 HIJKLMN OPQRSTUVWXYZ
RP-46	20.373	1234567890ABC H J LM	RP-96	38.086	7 90 HIJKLMN OPQRSTUVWXYZ
RP-70	20.856	1234567 0 B EF HIJK NO	RP-104	38.686	7 90 HIJKLMN OPQRSTUVWXYZ
RP-94	20.856	1234567 0 B EF HIJK NO	RP-105	38.686	7 90 HIJKLMN OPQRSTUVWXYZ
RP-14	20.886	1234567890A D F IJ L N P	RP-112	38.686	7 90 HIJKLMN OPQRSTUVWXYZ
RP-7	21.486	1234567890A D F IJ L N PQR	RP-61	38.856	89 A CD G LM PQRSTUVWXYZ



Table 5. Continued

Treatment	Adjusted Means	Group	Treatment	Adjusted Means	Group
RP-73	38.856	89 A CD G LM PQRSTUVWXYZ	RP-74	40.656	QRSTUVWXYZ
RP-80	38.856	89 A CD G LM PQRSTUVWXYZ	RP-53	40.773	R T V X Z
RP-75	38.856	89 A CD G LM PQRSTUVWXYZ	RP-66	41.256	STUVWXYZ
RP-103	39.286	0 HIJKLMNOPQRSTUVWXYZ	RP-91	41.256	STUVWXYZ
RP-115	39.286	0 HIJKLMNOPQRSTUVWXYZ	RP-64	41.256	STUVWXYZ
RP-118	39.286	0 HIJKLMNOPQRSTUVWXYZ	RP-85	41.256	STUVWXYZ
RP-79	39.456	A CD G LM PQRSTUVWXYZ	RP-8	41.286	WXYZ
RP-2	39.486	BC E GH K M O UVWXYZ	RP-26	41.286	WXYZ
RP-34	39.573	DEFG I K NOPQRSTUVWXYZ	RP-5	41.286	WXYZ
RP-28	39.573	DEFG I K NOPQRSTUVWXYZ	RP-24	41.286	WXYZ
RP-60	39.573	DEFG I K NOPQRSTUVWXYZ	RP-17	41.286	WXYZ
RP-113	39.886	HIJKLMNOPQRSTUVWXYZ	RP-4	41.286	WXYZ
RP-120	39.886	HIJKLMNOPQRSTUVWXYZ	RP-56	41.373	T V X Z
RP-76	40.056	LM PQRSTUVWXYZ	RP-57	41.373	T V X Z
RP-62	40.056	LM PQRSTUVWXYZ	RP-30	41.373	T V X Z
RP-72	40.056	LM PQRSTUVWXYZ	RP-41	41.373	T V X Z
RP-69	40.056	LM PQRSTUVWXYZ	RP-84	41.856	UVWXYZ
RP-95	40.056	LM PQRSTUVWXYZ	RP-93	41.856	UVWXYZ
RP-36	40.173	NOPQRSTUVWXYZ	RP-25	41.886	WXYZ
RP-43	40.173	NOPQRSTUVWXYZ	RP-44	41.973	V X Z
RP-55	40.173	NOPQRSTUVWXYZ	RP-33	41.973	V X Z
RP-37	40.173	NOPQRSTUVWXYZ	RP-38	41.973	V X Z
RP-48	40.173	NOPQRSTUVWXYZ	RP-9	42.486	WXYZ
RP-92	40.656	QRSTUVWXYZ	RP-22	43.086	YZ

Table 5. Continued

Treatment	Adjusted Means	Group
RP-12	43.086	YZ
RP-1	43.086	YZ
RP-3	43.686	Z
RP-21	43.686	Z

Treatment	Adjusted Means	Group
RP-23	43.686	Z
RP-10	43.686	Z
RP-15	63.486	a

**Table 6. genetic variability analysis for different characters of Pigeonpea**

Trait	Mean	GCV	GCV category	PCV	PCV category	ECV	hBS	Hbs category	GA	GAM	GAM category
Biological Yield (gm/plant)	156.82	13.8	(Medium)	13.94	(Medium)	2	97.94	(High)	44.18	28.17	(High)
Days to 50 % Flowering	134.94	10.53	(Medium)	11.02	(Medium)	3.26	91.25	(High)	28	20.75	(High)
Days to First Flowering	94.68	14.47	(Medium)	14.72	(Medium)	2.65	96.75	(High)	27.81	29.37	(High)
Days to Maturity	188.58	11.66	(Medium)	12.18	(Medium)	3.52	91.66	(High)	43.45	23.04	(High)
Duration of Flowering	53.86	20.96	(High)	21.41	(High)	4.39	95.8	(High)	22.79	42.32	(High)
Harvest Index	21.05	22.21	(High)	22.82	(High)	5.23	94.75	(High)	9.39	44.6	(High)
<i>H. armigera</i> Larvae Population	4.54	10.17	(Medium)	11.36	(Medium)	5.08	80.03	(High)	0.85	18.76	(Medium)
<i>M. vitrata</i> Larvae Population	4.76	22.58	High	22.77	(High)	2.96	98.31	(High)	2.2	46.19	(High)
No of Pods/plant	49.64	25.9	High	26.16	(High)	3.67	98.03	(High)	26.26	52.9	(High)
No of Primary Branches	10.88	12.09	(Medium)	12.69	(Medium)	3.85	90.79	(High)	2.59	23.77	(High)
No of Secondary Branches	17.06	23.17	High	23.33	(High)	2.77	98.59	(High)	8.1	47.46	(High)
No of Seeds/Pod	4.66	19.55	(Medium)	19.65	(Medium)	1.95	99.01	(High)	1.87	40.13	(High)
Plant Height (cm)	239.72	11.86	(Medium)	12.08	(Medium)	2.3	96.38	(High)	57.59	24.02	(High)
Pod Width (cm)	0.57	19.04	(Medium)	19.99	(Medium)	6.07	90.79	(High)	0.21	37.44	(High)
Pods Length (cm)	5.09	11.12	(Medium)	11.64	(Medium)	3.47	91.14	(High)	1.11	21.89	(High)
Protein %/100 gm Seeds	20.39	11.71	(Medium)	11.92	(Medium)	2.21	96.57	(High)	4.84	23.74	(High)
Shelling %	52.85	8.64	(Low)	9.11	(Low)	2.87	90.07	(High)	8.94	16.92	(Medium)
100 Seed Weight (gm)	15.51	17.03	(Medium)	18.5	(Medium)	7.23	84.72	(High)	5.02	32.34	(High)
Seed Yield (gm/plant)	31.04	13.42	(Medium)	13.9	(Medium)	3.63	93.18	(High)	8.29	26.72	(High)

the present investigation wide range of genetic variability was observed for most of the quantitative traits. High magnitude of the coefficient of variation GCV% and PC V% (more than 20%) in some genotypes was observed for the duration of flowering (20.96, 21.41), Harvest Index (22.21, 22.82), *M. vitrata* larvae population (22.58, 22.77), No of Secondary branches (23.17, 23.33) while shelling percentages are low 8.64 and 9.11 respectively, while rest of the traits recorded low to medium values. Heritability Broad sense is high for all traits and also genetic advance is high for all traits but genetic advance as percent of mean are all for high except for *H. armigera* larvae population and Shelling percent in medium category value estimated. In frequencies distribution of qualitative traits, we found most of the traits are equally distributed in population but some are frequent in population and less diverse (Table 6).

#### 4. CONCLUSION

The above mention characters showing a high estimate of genetic advance as the percent of the mean are governed by additive genes and selection for them will be rewarded. The pigeonpea accession used in the study revealed significant variability for most of the morphological traits. Amongst the genotypes studied, high coefficients of variation were observed for most of the characters studied indicating the existence of sufficient variability. Out of 100 genotypes tested against different insect pests, 10 were categorized at most promising entries against key insect pests the desirable traits from these promising sources can be incorporated into elite entries with higher yield potential or utilized for advanced genetic analysis studies.

#### COMPETING INTERESTS

Authors have declared that no competing interests exist.

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