RESEARCH ARTICLE

Morphological Characterization and Genetic Studies of Pigeonpea germplasm Accessions with Incidence of Insect Larvae Population Collected from Chhattisgarh, India

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ABSTRACT

The present study was conducted at the College of Agriculture Raipur, IGKVV, and Chhattisgarh**.** The experimental materials used 103 local landraces of pigeonpea, including three popular standard checks during Kharif 2019-20 in an augmented RBD Design for 15 qualitative and 20 qualitative characters observations recorded and analysis of variance for showed differences for different characters. High magnitude of the coefficient of variation GCV % and PC V% (more than 20 %) in some genotypes was observed for Duration of flowering (20.96, 21.41), Harvest Index (22.21, 22.82), *Maruca 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, rest all traits are in a medium value. Result of major pigeonpea insect's incidence 103 genotypes tested against different insect pests, 10 genotypes recorded most promising entries against key pest and 10 genotypes were recorded most susceptible entries against insect pest. A high coefficient of variation in the entire genotypes was observed for some traits.

Keywords: Augmented RBD, Coefficient of Variation, Incidence of insect Larvae Population, Pigeonpea Germplasms.

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INTRODUCTION

A leguminous wonder crop plant is coined the name "Pigeonpea" was in place in Barbados because of its uses to feed pigeon by native farmers (Gowda *et al*., 2011). Pigeonpea [*Cajanus cajan* (L.) Mill sp.], which was extraordinary from the binging with rich nourishment protein in its seed (21%), provides protein supplies for the vegetarian population. It has a great range for maturity days (95 days to 299 days) (Remanandan, 1988). Only domesticated species in family *Cajaninae* are *C. cajan*. Pigeonpea plays an essential role in providing food, shelter, medicine, and other livelihood opportunities among the rural population. The grain is consumed as dhal. The green seed serves as vegetable, and the sticks are used as fuel wood. 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 (Anonymous, 2021).

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 depends on the extent of genetic diversity present in the gene pool. Diversity in plant genotypes provides an opportunity for plant breeders to develop new and improved cultivars with desirable characteristics. From the 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 as an "orphan crop" in many countries. In India, the North-Eastern part of the Deccan Plateau and the adjoining Chhotanagpur plateau form 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 land races with desirable agro-morphological traits that may culminate into breeding pigeonpea varieties with higher productivity. The role of genetic diversity in conducting successful plant breeding programs involving productivity, quality parameters, and stress tolerance is very important (Walunjkar *et al*., 2015). The market demand for 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 (Swaminathan and Bhavani, 2013). 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

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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 clarifies the pattern of genetic variation in a crop species (Rao and Hodgkin 2002) and its further utilization.

Yield is a complex trait governed by many cumulative, duplicate and dominant genes and directly or indirectly influenced by the environment and responds 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.

MATERIALS AND METHOD

The research was conducted on Research Farm, Department of Genetics and Plant Breeding, College of Agriculture Raipur, Chhattisgarh, India. The trial resources comprised of hundred local landraces of Pigeonpea and three popular standard checks. The study materials were obtained from various part of Chhattisgarh. The study was started during *Kharif* 2019-20 in an Augmented Randomized Complete Block Design (augmented RCBD**)** in 4 blocks and three replications to assess the agro-morphological characterization, genetic variability and genetic divergence between the 100 local landraces of Pigeonpea [*C. cajan* (L.) Millsp.] and three standard checks, namely Rajeevelochan, Asha and CGA-1 (Table 1).

The Morphological observations on various agro-morphological characters, including qualitative and quantitative characters and Incidence of major insect and disease 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, *M. 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 mean (Table 1).

RESULT AND DISCUSSION

To determine variation and diversity between pigeonpea genotypes qualitative traits have been used. Qualitative traits are reflected as morphological markers for use as genotypes of pigeonpea because the environment less influences them. In the present study, the outcome of agro morphological traits states that categorization of germplasm genotypes determine variation among pigeonpea genotypes. It is vital for utilizing the appropriate attribute-based donors in breeding programs and important in the present era for conserving the unique pigeonpea. Outcomes from this study conform to the conclusions by (Majumdar *et al.,* 2008; Sharma *et al.,* 2009; Adegboyegun *et al.,* 2020; Devi *et al.,* 2020; Sharma *et al.,* 2020; Shruthi *et al.,* 2020; Tharageshwari *et al.,* 2020; Yohane *et al.,* 2020; Yuniastuti *et al.,* 2020; Kimaro *et al.,* 2021; Vanniaraja, 2021 and Yadav *et al.,* 2021).

The population occurrence on inflorescence of key insect pest of pigeonpea states that on the statement of *H. armigera* larvae population per inflorescence 10 lowermost genotypes with bottommost insect population are about as a resistance genotypes beside the *H. armigera* from the genotypes under

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
				CH3	CGA-1

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

study total of pigeonpea like T52, T5, T10, T45, T20, T21, T49, T23, T55 and T2. Whereas 10 topmost genotypes with uppermost insect population are considered capable susceptible genotypes beside the H. armigera from the under study total of pigeonpea genotypes like T80, T90, T89 T79, T78, T94, T88, T81, T83 and T99.

Observation of *M. vitrata* insect population on plant 10 bottom most genotypes with bottommost insect population are regarded as a resistance genotypes against the *M. vitrata* from the understudy total of pigeonpea genotypes like T20, T52, T23, T42, T65, T11, T44, T5, T7 and T18. At the same time, 10 topmost genotypes with topmost insect populations are apropos as capable 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. The same conclusions are confirmed on verdicts by (Chakravarty *et al.,* 2016; Randhawa *et al.,* 2013 and Sharma *et al.,* 2009).

By using software R Studio, augmented design analysis was done by using observation data of *Kharif* 2019. 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 considerable variability in the material studied for the improvement of various traits (Table 2).

Outcomes from the ANOVA rejected the null hypothesis and determined that all 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 (Table 3 to 5).

Results of genetic variability analysis showed 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 (Jaggal *et al.,* 2012; Rekha *et al.,* 2013; Saroj *et al.,* 2013; Vange and Moses, 2009). Likewise, traits for pods per plant, seed yield per plant, number of primary and secondary branches per plant, biological yield per plant, and test weight are the high evaluation of genetic advance was detected by (Kesharam *et al.,* 2016; Pandey *et al.,* 2015 and Naik *et al.*, 2013).

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%.
**= significant at 1%.

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%.
**= significant at 1%.

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)

	Critical Difference Comparison			
Traits	*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	15.14	15.14	15.14	15.14
D 50 F	12.61	12.61	12.61	12.61
D F F	9.51	9.51	9.51	9.51
D M	19.82	19.82	19.82	19.82
D F	9.09	9.09	9.09	9.09
H I	3.06	3.06	3.06	3.06
H L P	0.46	0.46	0.46	0.46
M L P	0.65	0.65	0.65	0.65
N P P	9.09	9.09	9.09	9.09
N P B	1.82	1.82	1.82	1.82
N S B	1.91	1.91	1.91	1.91
N S P	0.34	0.34	0.34	0.34
P H	16.9	16.9	16.9	16.9
P L	0.59	0.59	0.59	0.59
P W	0.17	0.17	0.17	0.17
P S	1.35	1.35	1.35	1.35
S P	3.39	3.39	3.39	3.39
100 S W	1.01	1.01	1.01	1.01
S Y	5.46	5.46	5.46	5.46

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

	Standard errors comparison			
Traits	*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	1234567890ABCDEFGHIJKLMNOPQR STUVWX
RP-108	16.486	123	RP-16	23.286	1234567890ABCDEFGHIJKLMNOPQR STUV
RP-31	16.773	1234	RP-54	23.373	1234567890ABCDEFGHIJKLMNOPQ S U W Y
RP-29	16.773	1234	RP-121	24.886	1234567890ABCDEFGHIJKLMNOPQR STUVWXYZ
RP-45	16.773	1234	RP-42	25.173	1234567890ABCDEFGHIJKLMNOPQR STUVWXYZ
RP-97	17.086	1234	RP-27	28.173	1234567890ABCDEFGHIJKLMNOPQR STUVWXYZ
RP-98	17.686	1234	CH2	30.435	234567890ABCDEFGHIJKLMNOPQR STUVWXYZ
RP-78	17.856	123456	RP-6	30.486	1234567890ABCDEFGHIJKLMNOPQR STUVWXYZ
RP-122	18.286	1234	CH1	30.678	34567890ABCDEFGHIJKLMNOPQR STUVWXYZ
RP-35	19.173	123456789	CH3	31.545	4567890ABCDEFGHIJKLMNOPQR STUVWXYZ
RP-32	19.173	123456789	RP-20	34.686	234567890ABCDEFGHIJKLMNOPQR STUVWXYZ
RP-89	19.656	1234567 0	RP-123	36.886	567890ABCDEFGHIJKLMNOPQR STUVWXYZ
RP-77	19.656	1234567 0	RP-116	37.486	67 90 HIJKLMNOPQRSTUVWXYZ
RP-110	20.086	12345 8 ABCDEFG	RP-101	38.086	7 90 HIJKLMNOPQRSTUVWXYZ
RP-63	20.256	1234567 0 B EF HIJK	RP-106	38.086	7 90 HIJKLMNOPQRSTUVWXYZ
RP-67	20.256	1234567 0 B EF HIJK	RP-107	38.086	7 90 HIJKLMNOPQRSTUVWXYZ
RP-46	20.373	1234567890ABC H J LM	RP-96	38.086	7 90 HIJKLMNOPQRSTUVWXYZ
RP-70	20.856	1234567 0 B EF HIJK NO	RP-104	38.686	7 90 HIJKLMNOPQRSTUVWXYZ
RP-94	20.856	1234567 0 B EF HIJK NO	RP-105	38.686	7 90 HIJKLMNOPQRSTUVWXYZ
RP-14	20.886	1234567890A D F IJ L N P	RP-112	38.686	7 90 HIJKLMNOPQRSTUVWXYZ
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
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)
H. armigera Larvae Population	4.54	10.17	(Medium)	11.36	(Medium)	5.08	80.03	(High)	0.85	18.76	(Medium)
M. vitrata 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 genetic variability in any breeding material is a prerequisite as it provides a basis for selection and some valuable information regarding the selection of diverse parents for use in hybridization programs. Coefficient of variation truly provides a relative measure of variability among different traits. In the present investigation wide range of genetic variability was observed for most of the quantitative traits. High magnitude of coefficient of variation GCV % and PC V% (more than 20%) in some genotypes was observed for 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, rest all traits are in medium value. Heritability Broad sense is high for all traits and 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 that most of the traits are equally distributed in population but some are frequent and less diverse (Table 6).

CONCLUSION

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

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