The Pharma Innovation

Vipin Kumar Pandey
Ph.D., Student, Department of
Genetics and Plant Breeding,
College of Agriculture, IGKV,
Raipur, Chhattisgarh, India

MK Singh
Principal Scientist, Department
of Genetics and Plant Breeding,
College of Agriculture, IGKV,
Raipur, Chhattisgarh, India

Prakriti Meshram
Ph.D., Student, Department of
Genetics and Plant Breeding,
College of Agriculture, IGKV,
Raipur, Chhattisgarh, India

Vishal Kumar Gupta
Ph.D., Student, Department of
Genetics and Plant Breeding,
College of Agriculture, IGKV,
Raipur, Chhattisgarh, India

Namita Singh
Ph.D., Student, Department of
Genetics and Plant Breeding,
College of Agriculture, IGKV,
Raipur, Chhattisgarh, India

Ashish Kumar Banjare
Ph.D., Student, Department of
Genetics and Plant Breeding,
College of Agriculture, IGKV,
Raipur, Chhattisgarh, India

Corresponding Author:
Vipin Kumar Pandey
Ph.D., Student, Department of
Genetics and Plant Breeding,
College of Agriculture, IGKV,
Raipur, Chhattisgarh, India

Genetic study of indigenous pigeon pea germplasm of Chhattisgarh based on morphological characters and key insect pest's larvae population

Vipin Kumar Pandey, MK Singh, Prakriti Meshram, Vishal Kumar Gupta, Namita Singh and Ashish Kumar Banjare

Abstract
The present investigation was carried out College of Agriculture Raipur, IGKVV, Chhattisgarh. The experimental materials were used 100 local landraces of pigeon pea and three popular standard checks during *Kharif* 2018 in an Augmented RBD Design for 15 qualitative and 20 qualitative characters observations recorded and analysis of variance for characters showed differences for different characters and the result of major pigeon pea 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: Coefficient of variation, augmented RBD, pigeon pea germplasms, *H. armigera*, *M. vitrata* larvae population

Introduction
Pigeon pea name was coined in Barbados (Gowda *et al*. 2011) [4]. Pigeon pea [*Cajanus cajan* (L.) Millsp.], gifted with rich nourishment protein in its seed (21%), provides protein requirements of the vegetarian population. It has a large variation for days to maturity (95 days to 299 days) (Remanandan 1988) [5]. *Cajanus cajan* only domesticated species in *Cajaninae*. Pigeon pea plays an important 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 a vegetable and the sticks are used as fuel wood. It is grown predominantly under rainfed conditions of the semi-arid tropics. India is the largest producer of pulses, of which pigeon pea 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 an annual production of 39.9 thousand tons and productivity of 605 kg/ha in Chhattisgarh 2019-20. (Anonymous, 2021) [6].

The knowledge of nature and extent of genetic variation is available in the Pigeon pea genotypes which is the prerequisite for any plant breeding experiment. Collection, conservation and characterization of genotype is the backbone of any crop improvement program which in turn 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 very beginning of agriculture, natural genetic variability has been exploited within crop species to meet subsistence food requirements, and now it is being focused on surplus food production to fulfil 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 germplasm. Therefore, there is a high probability of finding elite germplasm in the form of locally adapted landraces with desirable agro-morphological traits which may culminate into the breeding of pigeon pea 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) [3]. The market demand for pigeon pea 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) [1].

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 germplasm collections and this information helps understand the pattern of genetic variation in a crop species (Rao and Hodgkin 2002) [2] 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 responds poorly to the direct selection. Keeping these points in view, to find out suitable genotypes or donors to meet any current or future demand for improvement of the Pigeon pea crop, various indigenous Pigeon pea genotypes are taken to study.

Materials and Method

The experiment was carried out at Research cum Instructional Farm, Department of Genetics and Plant Breeding, College of Agriculture Raipur, Chhattisgarh, India. The experimental materials comprised of 100 local landraces of Pigeon pea and three popular standard checks. The experimental materials were received from different, part of Chhattisgarh. The experiment was conducted during *Kharif* 2018-19 in an Augmented Randomized Complete Block Design (RBD) to assess the agro-morphological characterization, genetic variability and genetic divergence among the 100 local landraces of Pigeon pea [*Cajanus cajan* (L.) Millsp.] and three popular standard checks namely Rajeevelochan, Asha and CGA-1 (Table 1.).

1. Weather conditions during the crop growing period

Meteorological data on temperature, rainfall, rainy days, relative humidity and sunshine hours recorded at the Meteorological Observatory Unit, Department of Agrometeorology, IGKV Raipur, during the cropping period are presented graphically in Fig. 1. The weather condition during the investigation remained favourable for the growth and development of pulses. Weather during the crop period in all the seasons of two years was normal for pigeon pea. The total rains received during 2018-19 from 30th Standard Meteorological Week, were 1402.8 mm. Similarly, the maximum mean temperature ranged from 32.3 ^{0}C to 25.6 ^{0}C during 2018-19. It was higher at the time of sowing of the crop in June 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 8.3 ºC to 25.8 ºC during 2018-2019. The minimum temperature decreased gradually up to the second week of December and again increase.

2. Agro-morphological characterization

The observations on various agro-morphological characters including qualitative and quantitative characters and the Incidence of major insect and disease of pigeon pea were recorded *viz.* Biological Yield (gm/plant), Days to 50% Flowering, Days to First Flowering, Days to Maturity, Duration of Flowering, Harvest Index, *H. 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 pigeon pea 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).
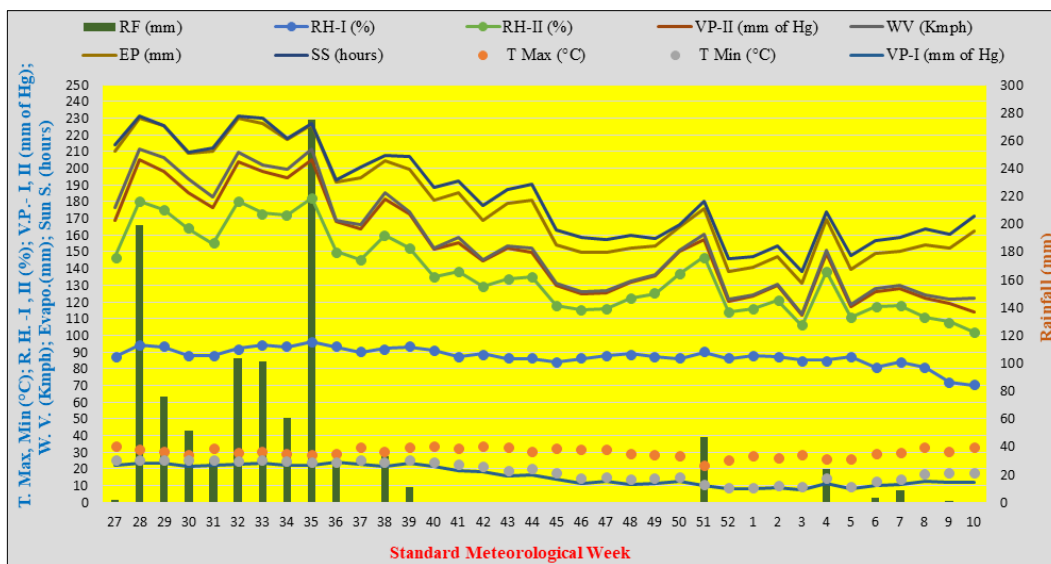
Fig 1: Weekly meteorological data during crop growth period (July 2018 to March 2019)

Table 1: List of 100 local landraces of pigeon pea 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.		CH3		CGA-1	

Result and Discussion

To establish distinctiveness among pigeon pea genotypes qualitative characters have been used. Qualitative traits are considered as morphological markers in the identification of genotypes of pigeon pea because they are less influenced by the environment. In the present investigation, the Result of agro morphological characterization reviled that characterization of germplasm genotypes establishes distinctiveness among pigeon pea genotypes. It is not only important for utilizing the appropriate attribute-based donors in breeding programs, but also essential in the present era for protecting the unique pigeon pea. These outcomes are confirmation on findings 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) [8, 9, 11-17].

Result of the population occurrence on the inflorescence of key insect pest of pigeon pea states that on the statement 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 pigeon pea genotypes like T80, T90, T89, T79, T78, T94, T88, T81, T83 and T99. Whereas 10 topmost genotypes that having uppermost insect population are regarding as capable resistance genotypes beside the *H. armigera* from the genotypes under study total of pigeon pea 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 pigeon pea genotypes like T84, T76, T70, T85, T51, T53, T90, T62, T21 and T94. Whereas 10 top most genotypes that having topmost

insect population are apropos as a capable resistance genotype against the *M. vitrata* from the understudy total of pigeon pea genotypes like T20, T52, T23, T42, T65, T11, T44, T5, T7 and T18. These same conclusions are confirmed on verdicts by (Chakravarty *et al*. 2016; Randhawa *et al*. 2013 and Sharma *et al*. 2009) [8, 18, 19].

By using software R Studio, augmented design analysis were 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 (Jaggal *et al*. 2012; Rekha *et al*. 2013; Saroj *et al*. 2013; Vange and Moses, 2009) [20-23]. 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) [24-26].

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 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 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 a medium value. 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).

Table 2: Analysis of variance (ANOVA) for augmented block design on 2018 data of quantitative traits

Source	Df	BY	D50F	DFF	DM	DF	HI	HLP	MLP	NPP
Block unadj.	3	135.3 ns	675.17 **	175.4 **	701.58 **	13.08 ns	22.3 *	0.25 ns	2.76 **	340.77 **
Trt. unadj.	102	603.2 **	1111.77 **	375.21 **	1500.86 **	41.84 **	14.62 *	1.31 **	2.72 **	335.94 **
Block adj.	3	189.49 ns	131.53 ns	60.82 ns	243.29 ns	17.05 ns	8.78 ns	0.39 ns	0.33 **	40.41 **
Trt. adj.	102	604.79 **	1095.78 **	371.84 **	1487.38 **	41.95 **	14.22 *	1.32 **	2.65 **	327.11 **
Control	2	128.11 ns	17.79 ns	8.22 ns	32.9 ns	2.31 ns	11.76 ns	0.04 ns	0.04 ns	5.24 ns
Augmented	99	502.62 **	1145.05 **	386.42 **	1545.67 **	42.89 **	11.77 ns	1.34 **	2.79 **	344.77 **
Test vs. augmented	1	11510.68 **	4.03 ns	0.1 ns	0.39 ns	16.33 ns	301.72 **	0.77 ns	1 **	123.94 **
Test + Test. vs. aug.	100	614.33 **	1117.34 **	379.12 **	1516.47 **	42.75 **	14.27 *	1.34 **	2.7 **	333.55 **
Residuals	6	61.34	32.9	15.21	60.86	4.26	3.18	0.15	0.03	3.41

* = Significant at 5%.

** = Significant at 1%.

Table 2: Continued……..

Source	Df	NPB	NSB	NSP	PH	PL	PW	PS	SP	100 SW	SY
Block unadj.	3	5.59 **	5.98 **	2.76 **	1388.44 **	0.0013 ns	0.4 **	10.58 **	63.14 **	26.8 *	19.99 **
Trt. unadj.	102	3.44 **	9.98 **	2.72 **	846.79 **	0.0042 **	0.86 **	6.5 **	135.08 **	42.18 **	12.19 **
Block adj.	3	0.8 *	1.97 ns	0.33 **	208.46 *	0.0017 ns	0.14 ns	1.51 *	21.9 ns	15.28 ns	3 *
Trt. adj.	102	3.3 **	9.86 **	2.65 **	812.09 **	0.0042 **	0.86 **	6.23 **	133.86 **	41.84 **	11.69 **
Control	2	4.14 **	0.27 ns	0.04 ns	1045.54 **	0.00023 ns	0.02 ns	7.82 **	2.96 ns	2.31 ns	15.06 **
Augmented	99	3.43 **	9.89 **	2.79 **	843.66 **	0.0043 **	0.89 **	6.48 **	139.11 **	43.29 **	12.15 **
Test vs. augmented	1	2.94 **	38.2 **	1 **	758.86 **	0.0016 ns	0.00023 ns	5.56 **	0.04 ns	11.47 ns	10.93 **
Test + Test. vs. aug.	100	3.28 **	10.05 **	2.7 **	807.42 **	0.0043 **	0.87 **	6.2 **	136.48 **	42.63 **	11.63 **
Residuals	6	0.12	0.49	0.03	34	0.00043	0.04	0.22	5.48	4.26	0.49

* = Significant at 5%.

** = Significant at 1%.

Note: Degree of freedom = Df, Biological yield (gm/plant) = BY, Days to 50% flowering = D50F, Days to first flowering = DFF, Days to maturity = DM, Duration of flowering = DF, Harvest index = HI, *H. armigera* larvae population = HLP, *M. vitrata* larvae population = MLP, No. of pods/plant = NPP, No. of primary branches = NPB, No. of secondary branches = NSB, No. of seeds/pod = NSP, Plant height (cm) = PH, Pods length (cm) = PL, Pod width (cm) = PW, Protein %/100 gm seeds = PS, Shelling % = SP, 100 seed weight (gm) = 100 SW, Seed yield (gm/plant) = SY

Table 3: Comparison of critical difference all traits of pigeon pea. (Alpha = 0.05)

Traits	Critical difference comparison			
	A test treatment and a control treatment	Control treatment means	Two test treatments (Different blocks)	Two test treatments (Same block)
BY	24.74	13.55	31.29	27.1
D50F	18.12	9.92	22.92	19.85
DFF	12.32	6.75	15.59	13.5
DM	24.64	13.5	31.17	27
DF	6.52	3.57	8.25	7.15
HI	5.63	3.09	7.13	6.17
HLP	1.22	0.67	1.54	1.33
MLP	0.53	0.29	0.67	0.58
NPP	5.84	3.2	7.38	6.39
NPB	1.08	0.59	1.37	1.19
NSB	2.22	1.21	2.81	2.43
NSP	0.53	0.29	0.67	0.58
PH	18.42	10.09	23.3	20.18
PL	0.07	0.04	0.08	0.07
PW	0.59	0.32	0.75	0.65

PS	1.49	0.82	1.88	1.63
SP	7.39	4.05	9.35	8.1
100 SW	6.52	3.57	8.25	7.15
SY	2.21	1.21	2.8	2.42

Table 4: Comparison of standard errors all traits of pigeon pea

Traits	Standard errors comparison			
	A test treatment and a control treatment	Control treatment means	Two test treatments (Different blocks)	Two test treatments (Same block)
BY	10.11	5.54	12.79	11.08
D50F	7.41	4.06	9.37	8.11
DFF	5.04	2.76	6.37	5.52
DM	10.07	5.52	12.74	11.03
DF	2.67	1.46	3.37	2.92
HI	2.3	1.26	2.91	2.52
HLP	0.5	0.27	0.63	0.55
MLP	0.21	0.12	0.27	0.24
NPP	2.39	1.31	3.02	2.61
NPB	0.44	0.24	0.56	0.48
NSB	0.91	0.5	1.15	0.99
NSP	0.21	0.12	0.27	0.24
PH	7.53	4.12	9.52	8.25
PL	0.03	0.01	0.03	0.03
PW	0.24	0.13	0.31	0.26
PS	0.61	0.33	0.77	0.67
SP	3.02	1.65	3.82	3.31
100 SW	2.67	1.46	3.37	2.92
SY	0.9	0.49	1.14	0.99

Note: Biological yield (gm/plant) = BY, Days to 50% flowering = D50F, Days to first flowering = DFF, Days to maturity = DM, Duration of flowering = DF, Harvest index = HI, *H. armigera* larvae population = HLP, *M. vitrata* larvae population = MLP, No. of pods/plant = NPP, No. of primary branches = NPB, No. of secondary branches = NSB, No. of seeds/pod = NSP, Plant height (cm) = PH, Pods length (cm) = PL, Pod width (cm) = PW, Protein %/100 gm seeds = PS, Shelling % = SP, 100 seed weight (gm) = 100 SW, Seed yield (gm/plant) = SY

Table 5: HSD method applies for population mean comparisons for seed yield (gm/plant)

Treatment	Adjusted means	Group	Treatment	Adjusted means	Group
T84	12.73313225	1	T53	18.68621242	1234567890ABCDEFGHI
T91	13.5221255	12	T48	18.85867547	1234567890ABCDEFGHIJKLMN
T95	13.57751372	12	T8	18.87831971	1234567890ABCDEFGHIJKLMN
T89	14.47775388	1234	T51	19.49455408	1234567890ABCDEFGHIJK
T36	14.48303069	123 5	T1	19.60759228	1234567890ABCDEFGHIJKLMN
T86	14.6595212	1234	T23	19.60887971	1234567890ABCDEFGHIJKLMN
T24	15.28018494	123456	T45	19.83607971	1234567890ABCDEFGHIJKLMN
T26	15.56078036	123456	T65	19.8508865	1234567890ABCDEFGHIJKLM
T94	15.621916	123456	T67	20.07822919	1234567890ABCDEFGHIJKLMN
T43	15.74788778	123456	T9	20.09123812	1234567890ABCDEFGHIJKLMN
T72	15.8064865	123456	T22	20.35948449	1234567890ABCDEFGHIJKLMN
T85	15.99399788	123456	T25	20.51970278	1234567890ABCDEFGHIJKLMNO
T92	16.02478968	123456	T99	20.67680754	34567890ABCDEFGHIJKLMNO
T90	16.52681502	1234567890	T12	20.78140651	234567890ABCDEFGHIJKLMNOPQRS
T74	16.70035809	12345678 AB	T47	21.04196205	234567890ABCDEFGHIJKLMN P
T13	16.94807971	1234567890ABCD	T17	21.12123729	234567890ABCDEFGHIJKLMNOPQRS
T32	17.26515658	1234567 9 A C EF	T77	21.14142412	34567890ABCDEFGHIJKLMNOPQRSTUVW
T49	17.29807196	1234567 9 A C EF	T82	21.37317454	34567890ABCDEFGHIJKLMNOPQRSTUVWXYZabcde
T21	17.32367971	1234567890ABCDE G	T3	21.39257971	234567890ABCDEFGHIJKLMNOPQRS XYZa
T70	17.72442074	1234567890ABCDEFGHI	T6	21.63780773	34567890ABCDEFGHIJKLMNOPQRS XYZa fghijklmno
T62	17.99076214	1234567890ABCDEFGHI	T73	21.67599589	34567890ABCDEFGHIJKLMNO R UV XY bc fg i pqr
T10	18.17573041	1234567890ABCDEFGHIJK	T41	21.74276341	4 67890ABCDEFGHIJKLMNOPQ T V X Z b d ij mn q stu
T76	18.5730852	1234567890ABCDEFGH J L	T98	21.7873968	567890ABCDEFGHIJKLMNOPQRSTUVWXYZabcdef h k n p t vw
T7	18.66807971	1234567890ABCDEFGHIJKLM	T5	22.16207971	34567890ABCDEFGHIJKLMNOPQRS XYZa fghijklmno xy

Table 5: Continued………

Treatment	Adjusted means	Group
T57	22.20920312	34567890ABCDEFGHIJKLMNOPQRSTUVWXYZabcdefghij l pqrs v x z1
T56	22.2668865	34567890ABCDEFGHIJKLMNOPQRSTUVWXYZabcdefghij l pqrs v x z1
T39	24.01750216	7890ABCDEFGHIJKLMNOPQRSTUVWXYZabcdefghijklmnopqrstuvwxyz1z2z3z4z5
T68	24.0854465	90 CDEFGHIJKLMNOPQRSTUVWXYZabcdefghijklmnopqrstuvwxyz1z2z3z4z5z6z7z8z9
T88	24.17130679	ABCDEFGHIJKLMNOPQRSTUVWXYZabcdefghijklmnopqrstuvwxyz1z2z3 z6z7
T42	24.30807971	8 0 B D GHIJKLMNOPQRSTUVWXYZabcdefghijklmnopqrstuvwxyz1z2z3z4z5
T75	24.623704	CDEFGHIJKLMNOPQRSTUVWXYZabcdefghijklmnopqrstuvwxyz1z2z3z4z5z6z7z8z9z0
T18	24.68886361	F HIJKLMNOPQRSTUVWXYZabcdefghijklmnopqrstuvwxyz1z2 z4 z6 z8 zA
T44	25.06807971	GHIJKLMNOPQRSTUVWXYZabcdefghijklmnopqrstuvwxyz1z2z3z4z5z6z7z8z9z0
T81	25.13301278	EFGHIJKLMNOPQRSTUVWXYZabcdefghijklmnopqrstuvwxyz1z2z3z4z5z6z7z8z9z0zAzBzC
T87	25.44393128	HIJKLMNOPQRSTUVWXYZabcdefghijklmnopqrstuvwxyz1z2z3z4z5z6z7z8z9z0zAzBzCzDzE
T78	25.62817659	I K MNOPQRSTUVWXYZabcdefghijklmnopqrstuvwxyz1z2z3z4z5z6z7z8z9z0zAzBzCzDzE
T54	25.85163748	JKLMNOPQRSTUVWXYZabcdefghijklmnopqrstuvwxyz1z2z3z4z5z6z7z8z9z0zAzBzC
T69	26.51685332	LMNOPQRSTUVWXYZabcdefghijklmnopqrstuvwxyz1z2z3z4z5z6z7z8z9z0zAzBzCzDzE
T61	26.83270205	NOPQRSTUVWXYZabcdefghijklmnopqrstuvwxyz1z2z3z4z5z6z7z8z9z0zAzBzCzDzEzF
C1R1	27.26151192	XYZabcdefghijklmnopqrstuvwxyz1z2z3z4z5z6z7z8z9z0zAzB zD
T30	28.34793949	O QRSTUVWXYZabcdefghijklmnopqrstuvwxyz1z2z3z4z5z6z7z8z9z0zAzBzCzDzEzFzGzH
T46	28.36843759	O QRSTUVWXYZabcdefghijklmnopqrstuvwxyz1z2z3z4z5z6z7z8z9z0zAzBzCzDzEzFzGzHzIzJ
T58	28.71193674	PQ ST W Za de h jklmno stuvwxyz1z2z3z4z5z6z7z8z9z0zAzBzCzDzEzFzG zI zKzLzMzNzOzPzQ
T38	28.7239525	RS U W Y a c efgh kl op r vwxyz1z2z3z4z5z6z7z8z9z0zAzBzCzDzEzFzGzHzIzJ zL zOzP zRzSzT
T16	29.07748657	TUVW bcde pqrstuvw z1z2z3z4z5z6z7z8z9z0zAzBzCzDzEzFzGzHzIzJzK zM zP zS zUzV
T28	29.3865526	fgh kl op r vwxyz1z2z3z4z5z6z7z8z9z0zAzBzCzDzEzFzGzHzIzJzKzLzMzNzOzPzQzRzSzTzUzVzWzX
T34	29.48407971	fgh kl op r vwxyz1z2z3z4z5z6z7z8z9z0zAzBzCzDzEzFzGzHzIzJzKzLzMzNzOzPzQzRzSzTzUzVzWzX
T100	29.5045151	g ij lm o qrs u xyz1z2z3z4z5z6z7z8z9z0zAzBzCzDzEzFzGzHzIzJzKzL zN zR zU zW

Table 5: Continued………

Treatment	Adjusted means	Group
T66	29.51265857	k mno tu w y z2z3z4z5z6z7z8z9z0zAzBzCzDzEzFzGzHzIzJzKzLzMzNzOzPzQzRzSzTzUzVzWzX
C2R1	29.82420819	z2z3z4z5z6z7z8z9z0zAzBzCzDzEzFzGzHzIzJ
T50	29.87624457	xyz1z2z3z4z5z6z7z8z9z0zAzBzCzDzEzFzGzHzIzJzKzLzMzNzOzPzQzRzSzTzUzVzWzX
T80	30.48450823	z2z3z4z5z6z7z8z9z0zAzBzCzDzEzFzGzHzIzJzKzLzMzNzOzPzQzRzSzTzUzVzWzXzY
T71	30.59170883	z2z3z4z5z6z7z8z9z0zAzBzCzDzEzFzGzHzIzJzKzLzMzNzOzPzQzRzSzTzUzVzWzX
T52	30.6668865	z2z3z4z5z6z7z8z9z0zAzBzCzDzEzFzGzHzIzJzKzLzMzNzOzPzQzRzSzTzUzVzWzX zZ
T40	30.91077253	z2z3z4z5z6z7z8z9z0zAzBzCzDzEzFzGzHzIzJzKzLzMzNzOzPzQzRzSzTzUzVzWzXzY
C3R1	31.06600363	zC zEzFzGzHzIzJzKzLzMzNzOzPzQzRzSzTzUzVzWzX
T83	31.16666507	z4z5 z8z9z0zAzBzCzDzEzFzGzHzIzJzKzLzMzNzOzPzQzRzSzTzUzVzWzXzYzZza
T35	31.35852947	z6z7z8z9z0zAzBzCzDzEzFzGzHzIzJzKzLzMzNzOzPzQzRzSzTzUzVzWzXzY
T11	31.65073385	z3 z5 z7 z9z0 zBzCzDzEzFzGzHzIzJzKzLzMzNzOzPzQzRzSzTzUzVzWzXzYzZza
T2	32.31776406	z0 zBzCzDzEzFzGzHzIzJzKzLzMzNzOzPzQzRzSzTzUzVzWzXzYzZzazb
T27	32.66017239	zAzBzCzDzEzFzGzHzIzJzKzLzMzNzOzPzQzRzSzTzUzVzWzXzYzZzazb
T64	33.21935221	zDzEzFzGzHzIzJzKzLzMzNzOzPzQzRzSzTzUzVzWzXzYzZzazbzc
T96	34.50731123	zFzGzHzIzJzKzLzMzNzOzPzQzRzSzTzUzVzWzXzYzZzazbzczd
T59	34.69548288	zGzHzIzJzKzLzMzNzOzPzQzRzSzTzUzVzWzXzYzZzazbzczd
T33	35.27750862	zIzJzKzLzMzNzOzPzQzRzSzTzUzVzWzXzYzZzazbzczdze
T14	35.44897072	zGzHzIzJzKzLzMzNzOzPzQzRzSzTzUzVzWzXzYzZzazbzczd
T60	35.631421	zH zJ zRzSzTzUzVzWzXzYzZzazbzczdze
T29	36.09387671	zK zMzN zQ zUzVzWzXzYzZzazbzczdze
T19	36.53996778	zL zNzO zQzR zT zWzXzYzZzazbzczdze
T93	36.63633158	zM zOzPzQ zSzT zV zXzYzZzazbzczdze
T63	38.08875909	zY zazbzczdzezf
T55	38.17483416	zY zazbzczdzezf

Table 5: Continued………

Treatment	Adjusted means	Group
T37	38.64243359	zZzazbzczdzezf
T31	38.65207971	zazbzczdzezf
T97	40.03366738	zbzczdzezf
T4	41.08358058	zczdzezf
T79	41.29623711	zdzezf
T20	43.17438657	zezf
T15	45.69230221	zf

Table 6: Genetic variability analysis for different characters of pigeon pea

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)

Table 7: Frequencies distribution of agro-morphological characters on three checks with 100 local landraces of pigeon pea

S. No.	Traits	Categories	Freq. No.	Freq. percentages
1	Anthocyanin colour on hypocotyl	Present	0	0.00
		Absent	103	100.00
2	Flower pattern of streaks on petal	Absent	16	15.53
		Dense	6	5.83
		Medium	25	24.27
		Sparse	51	49.51
		Mosaic	5	4.85
3	Pod constriction	Prominent	30	29.13
		Slight	73	70.87
4	Pod pubiscience	Present	103	100.00
		Absent	0	0.00
5	Plant branching pattern	Erect	37	35.92
		Semi spreading	64	62.14
		Spreading	2	1.94
6	Stem colour	Green	100	97.09
		Purple	3	2.91
7	Pod colour	Dark purple	6	5.83
		Green	1	0.97
		Green with brown streak	8	7.77
		Green with purple streak	85	82.52
		Purple	3	2.91
8	Leaf shape	Narrowly oblong	5	4.85
		Oblong	96	93.20
		Obovat	2	0.97
9	Leaf pubescence on lower surface of the leaf	Present	0	0.00
		Absent	103	100.00
10	Pod surface stickiness	Present	103	100.00
		Absent	0	0.00
11	Colour of flower base of petal	Light yellow	21	20.39
		Orange yellow	31	30.10
		Purple	14	13.59
		Red	1	0.97
		Yellow	36	34.95
12	Plant growth habit	Determinate	52	50.49
		Indeterminate	51	49.51
13	Seed colour	Brown	42	40.777
		Cream	10	9.709
		Dark brown	37	35.922
		Grey	10	9.709
		Purple	4	3.883
14	Seed colour pattern	Mottled	18	17.476
		Uniform	85	82.524

15	Seed shape	Elongate	5	4.854
		Globular	43	41.748
		Oval	55	53.398

Conclusion

The above mention characters showing high estimate of genetic advance as the percent of the mean are governed by additive genes and selection for them will be rewarded. The pigeon pea 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.

References

1. Swaminathan MS, Bhavani RV. Food production & availability - Essential prerequisites for sustainable food security. Indian J Med Res 2013;138:383-391.
2. Rao VR, Hodgkin T. Genetic diversity and conservation and utilization of plant genetic resources Plant Cell, Tissue and Organ Culture 2002;68:1-19.
3. Walunjkar CB, Parihar A, Singh NK, Parmar LD. Genetic diversity of wild and cultivated genotypes of pigeon pea through RAPD and SSR markers J Environ. Biol 2015;36:461-466.
4. Gowda CLL, Saxena KB, Srivastava RK, Upadhyaya HD, Silim SN. Pigeon pea: From an orphan to leader in food legumes. In Biodiversity in Agriculture: Domestication, Evolution and Sustainability (Gepts P, Bettinger RL, Brush SB, Famula TR, McGuire PE, Qualset CO and Damania AB eds.). Cambridge University Press. University of California, Davis, USA 2011, 361-373.
5. Remanandan Sastry P, DVSSR, Mengesha MH. ICRISAT pigeon pea germplasm catalog: passport information. Patancheru, A.P. 502 324, India: International Crops Research Institute for the Semi-Arid Tropics 1988.
6. Anonymous. All India Coordinate Research Project on Pigeon pea Annual Kharif Pulses Group Meet 2021.
7. Majumder ND, Singh F, Tiwari SK, Mishra DK. Identification of characteristics for DUS testing in pigeon pea (*Cajanus cajan* (L.) Millsp.). Food Legumes for Nutritional Security and Sustainable Agriculture 2008;2:86-93.
8. Sharma HC, Sujana G, Rao DM. Morphological and chemical components of resistance to pod borer, *Helicoverpa armigera* in wild relatives of pigeon pea. Arthpo. Pla. Interac 2009;3(2009):151-161.
9. Adegboyegun K, Okpanachi FE, Akpanikot KE. Morphological Characterization of 22 Accessions of Pigeon Pea [*Cajanus cajan* (L) Millsp.]. Asi. J of Biochem. Gene and Mol. Bio 2020;4(3):2582-3698.
10. Sharma OP, Gopali JB, Yelshetty S, Bambawale OM, Garg DK, Bhosle BB. Pests of pigeon pea [*Cajanus cajan* (L.) Millsp.]. and their management. NCIPM, IARI. New Delhi. India 2010.
11. Shruthi HB, Hingane AJ, Reddi MS, Kumar SCV, Prashanthi L, Reddy BBV *et al*. Genetic Divergence for Yield, Physiological and Quality Traits in Super-Early Pigeon pea (*Cajanus cajan.* (L.) Millsp.). Int. J Curr. Microbiol. App. Sci 2020;9(1):2422-2433.
12. Tharageshwari LM, Hemavathy AT. Correlation and Path Analysis in Pigeon pea [*Cajanus cajan* (L.) Millsp.]. Int. J Curr. Microbiol. App. Sci 2020;9(01):80-86. doi: https://doi.org/10.20546/ijcmas.2020.901.009
13. Yohane EN, Shimelis H, Laing M, Mathew I, Shayanowako A. Phenotypic Divergence Analysis in Pigeon pea [*Cajanus cajan* (L.) Millspaugh] Germplasm Accessions. Agronomy 2020;10(11):1682.
14. Yuniastuti Sukaya E, Dewi LC, Delfianti MNI. The Characterization of Black Pigeon Pea (*Cajanus cajan)* in Gunungkidul, Yogyakarta. Caraka Tani: J of Sust. Agri 2020;35(1):78-88.
    doi: http://dx.doi.org/10.20961/carakatani.v35i1.28400.
15. Kimaro D, Melisa R, Sibiya J, Shimelis H. Agro-morphological characterization of pigeon pea (*Cajanus cajan* (L.) Millsp.): Basis to breeding. Agr. Nat. Resour 2021;55:23-32.
16. Vanniarajan C, Magudeeswari P, Gowthami R, Indhu SM, Ramya KR, Monisha K *et al*. Assessment of Genetic Variability and Traits Association in Pigeon pea [*Cajanus cajan* (L.) Millsp.] Germplasm. Legu. Res.-An Int. J 2021;44(2). DOI: 10.18805/LR-4442.
17. Yadav SK, Kumar N, Prasad K, Mahto CS, Lal HC, Choudhary AK *et al*. Morphological characterization of pigeon pea [*Cajanus cajan* (L.) Millsp] germplasm for selection of elite genotypes. J of Pharmacognosy and Phytochemistry 2021;10(1):1170-1173.
18. Chakravarty S, Bera T, Agnihotri M, Jagdish J. Screening of Short Duration Pigeon pea [*Cajanus cajan* (L.) Millsp.] Genotypes against Major Insect Pests. J of Pure and App. Microb 2016;10(4):2-9.
19. Randhawa HS, Kumar A. Evaluation of Pigeon pea Genotypes for Their Resistance against Pod borer, *Maruca vitrata* Geyer under Natural Conditions. Tren. in Biosci 2013;6(5):562-563.
20. Jaggal LG, Talikoti MM, Jakkeral SA. Correlation and path analysis studies in pigeon pea [*Cajanus cajan* (L.) Millsp]. Legume Res 2012;9(2):64-67.
21. Rekha R, Prasanthi L, Sekhar MR, Priya MS. Variability, character association and path analysis for yield and yield attributes in pigeon pea [*Cajanus cajan* (L.) Millsp.]. Electronic J Plant Breeding 2013;4(4):1331-1335.
22. Saroj SK, Singh MN, Kumar R, Singh T, Singh MK. Genetic Variability, Correlation and Path Analysis for Yield attributes in Pigeon pea. An international Quarterly Journal of life science 2013;8(3):941-944.
23. Vange T, Moses OE. Studies on genetic characteristics of pigeon peagermplasm at otobi, Benue State of Nigeria. World J of Agri. Sci 2009;5(6):714-719.
24. Kesharam Saxena K, Tushar MS, Bisnoi G. A Study on Genetic Variability, Correlation and Path Analysis in Pigeon pea [*Cajanus cajan* L. Millspaugh]. Int. J of Agri. Sci 2016;8(51):2287-2289. ISSN: 0975-3710 & E-ISSN: 0975-9107.
25. Pandey P, Pandey VR, Tiwari DK, Yadav SK. Studies on direct selection parameters for seed yield and its component traits pigeon pea [*Cajanus cajan* (L.) Millsp.].

African J Agric. Res 2015;10(6):485-490.
26. Naik SJ, Satheesh Gowda B, Dinesh M, Miyan HB, Asif, Pushpa HD. Genetic analysis in advanced breeding lines (F5) of pigeon pea [*Cajanus cajan* (L.) Millisp.]. A Quarterly J Life Sci 2013;10(1):196-200.