Vislavath Ramvilas Pashwan
M.Sc. Scholar, Department of
Genetics and Plant Breeding,
NAI, SHUATS, Prayagraj,
Uttar Pradesh, India

Dr. Arun Kumar Chaurasia
Associate Professor, Department
of Genetics and Plant Breeding,
NAI, SHUATS, Prayagraj,
Uttar Pradesh, India

Deepak Rao
M.Sc Scholar, Department of
Seed Science and Technology,
CSAUT, Kanpur, Uttar Pradesh,
India

Rodda Spandana
M.Sc. Scholar, Department of
Genetics and Plant Breeding,
NAI, SHUATS, Prayagraj,
Uttar Pradesh, India

Mailaram Rajkumar
M.Sc. Scholar, Department of
Genetics and Plant Breeding,
NAI, SHUATS, Prayagraj,
Uttar Pradesh, India

Dr. Vislavath Surender
Ph.D Scholar, Department of
Physical Education and Sports.
Pondicherry University,
Pondicherry, India

Studies on genetic variability for quantitative characters, growth and yield parameters in pigeonpea (*Cajanus cajan* L.) genotypes

Vislavath Ramvilas Pashwan, Dr. Arun Kumar Chaurasia, Deepak Rao, Rodda Spandana, Mailaram Rajkumar and Dr. Vislavath Surender

Abstract
The Purpose of this study was to determine at the Field Experiment Research Center, "Department of Genetics and Plant Breeding, Sam Higginbottom University of Agricultural Technology and Sciences, Prayagaraj", during *Kharif* 2019 in a randomized, three-repetition block design to gain insight into the nature and range of genetic parameters and its use in developing for superior pigeonpea genotypes [*Cajanus cajan* (L.) Millsp.]. The genetic parameters examined are genotypic and phenotypic variation, genotypic and phenotypic coefficient of variation, heritability (h^2) and genetic advance. In addition, these parameters, correlation coefficients and path analysis for seed yield and the properties of its components were also examined in 12 different long-term experienced pigeonpea genotypes. Results showed that the genotypes of all traits studied showed significant variability, and the analysis of variance showed that there were highly significant differences among the 12 pigeon pea genotypes of the 14 quantitative traits studied. It can be concluded from the current investigation that among the 12 pigeon pea genotypes based on average yield, 912, 901, 902, and 907 were found to be superior and showed the maximum seed yield. Among these 12 genotypes, they were found to provide the best results for 912. The maximum genotype and phenotypic variation of biological/plant yield, plant height and harvest index were recorded. Record the maximum GCV and PCV of each plant, the number of pods per plant, and the weight of each pod. The high heritability of seed yield, plant height, harvest index, number of pods per plant and seed yield per plant were recorded for each plot. High heritability and high genetic progress are recorded as a percentage of the average seed yield for each plot.

Keywords: Genetic variation, variability parameters, correlation coefficient, path analysis, pigeon pea (*Cajanus cajan* L.)

Introduction
Leguminous are a better alternative source of protein, which is the basis of the daily diet of ordinary Indians and has a high biological value. Unfortunately, the beans grown by our farmers are not enough. One of the most difficult challenges facing our scientists is achieving self-sufficiency and increasing agricultural production to meet the needs of a rapidly growing population. Lack of protein in the diet is more harmful to human health than any other ingredient. Protein deficiency is most pronounced in Southeast Asia, including India. Beans are only a source of protein for vegetarians in India.

Cajanus cajan (L.) Millsp, it is an efficient and nutritionally important grain legume crop, which belongs to the sub-tribe of the family Cajaninae under the legume subfamily Papilionoideae. It is the only edible legume cultivated with 11 pairs of chromosomes ($2n = 2x = 22$) and a diploid genome with a size of 833.07 Mbp (Varshney *et al.,* 2012) [31]. Redgram is the sixth largest pulse producer in the world and are grown on 4.92 million ha (million ha) with an annual yield of 3.65 tonnes and a yield of 898 kg ha - 1. (FAOSTAT, 2013) [11]. In India alone, redgram is cultivated on an area of approximately 3.56 million hectares (76% of the world surface) with an average production of 2.31 million tons (70% of the world production) (FAOSTAT, 2013) [12]. The factors responsible for low productivity are lack of improved cultivars, number of pests and diseases affecting the crop, its sensitivity to abiotic stresses and underutilization of its genomic resources. The productivity of pigeonpea has been hampered by several abiotic factors such as waterlogging, salinity, heat and heavy metals. In India, the average yield loss of pigeon peas is estimated at 0.32 million tonnes at a cost of about US $ 22 million (ICRISAT, 2009).

Pigeonpea is the second largest legume in India after chickpea and is nutritionally well balanced. It is a versatile crop that provides food, feed, feed, fuel, functional utility, forestry

Corresponding Author:
Vislavath Ramvilas Pashwan
M.Sc. Scholar, Department of
Genetics and Plant Breeding,
NAI, SHUATS, Prayagraj,
Uttar Pradesh, India

use and fertilizer in the context of sustainable agriculture (Gowda *et al.,* 2015) [13]. It is an excellent source of dietary fibres (15.5g /100g), protein (21.7 g / 100 g), soluble vitamins, minerals and essential amino acids (Singh *et al.,* 1990) [28]. The pigeonpea is also used in traditional medicine. The flowers, leaves, roots, and seeds can be used to treat bronchitis, sores, and respiratory diseases. They can also be used as an an alexeritic, anthelmintic, expectorant, sedative, and vulnerary (Saxena and sultan, 2010) [27].

Yield is a complex trait determined by several constituent traits; therefore, performance selection must also consider related traits. Therefore, understanding the correlation between yield and its component characteristics is essential to increase seed yield through selection procedures. (Kumar *et al.*, 2015) [17]. Pea is a highly complex trait that is controlled by multiple genes and is interrelated with other performance components; therefore, it is often very difficult to directly improve performance. It can be achieved by improving closely related traits.

Yield is a complex trait determined by several component traits; hence selection for yield should take into account related traits as well. So, the knowledge of correlation between yield and its component traits is essential for seed yield improvement through selection programme (Kumar *et al.*, 2015) [17]. Pigeon pea is very complex trait which controlled by polygene and interlinked with other yield components; hence it is very difficult often to improve yield directly. It can be achieved by improving closely related traits.

The study of correlation coefficient gives a measure of the relationship between traits and provides the degree to which various traits are related to productivity. Black gram's systematic collection shows that the variability of biological and non-biological genes is insufficient. Because of its high degree of self-pollination and flowering, it is difficult to produce variability through crossbreeding. To improve performance and other polygenic features, mutation breeding can also be used effectively. Therefore, genetic variation is a basic requirement to promote crop improvement (Baudhbharti *et al.,* 2014) [4].

The genetic variation information of different traits has important economic significance and is also a prerequisite for the study of any plant species (Rathhaswammy, *et al.,* 1973) [23]. Pigeon pea (*Cajanus cajan* (L) Millsp.) is mainly self-pollinated, and occasionally cross-pollination (67%) can cause genetic variation. The degree of hybridization varies, and studies have shown that 877 representative collections of germplasm have variability (Reddy and Rao, 1975) [24]. In some varieties, different degrees of natural hybridization have occurred, up to 70%. Using natural variation, promising varieties were isolated and bred (Reddy & Singh, 1975) [25]. *Cajanus cajan* can survive well in various soils, from sandy to heavy clay, with a pH of 5.8 to 8.0. Deep loam with good drainage, without excess soluble salt and with a pH close to neutral is the most suitable for pigeon pea growth, while stagnant water is detrimental to its growth (Pathak, 1970) [21].

The progress of crops depends on the degree of genetic variation and the degree of inheritance of ideal traits. Studying genetic variation with appropriate genetic parameters (such as coefficient of variation, heritability estimates, and genetic progress) is essential for effective breeding programs. However, despite development of some high yielding, short duration, large seeded, disease resistant

varieties and improved production technology, a significant breakthrough in pigeonpea productivity has not been achieved so far. The average yield remains low at ~563 kg ha^{-1} (Singh *et al.,* 2012) [29].

Material and methods

This experiment includes 12 pigeon pea genotypes obtained from the IIPR, kanpur in 2019-20. The experiment was carried out in the field of "Department of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture, Technology and Sciences, Pryagraj (U.P.)" with three random block design (RBD) copies. Each genotype consists of three rows, the distance between plants is 25 cm, and the row spacing is 90 cm. Five competing plants randomly selected in each plot of three repetitions recorded the observation results, namely, field emergence, number of branches per plant, plant height, days to first flowering, days to flowering reached 50%, flowering The number of days. Maturity, number of pods per plant, number of seeds per pod, weight per plant, weight of 100 seeds, biological yield, harvest index, seed yield per plot and seed yield per plant. According to Burton, 1952 [5], various variability parameters are estimated. Panse and Sukhatme, analysis of variance estimated and recommended in 1967 [20]. Burton and Devane, 1953 [6] proposed estimating generalized heritability and genetic progress. The correlation coefficient between phenotype and genotype was calculated using the formula suggested by AlJibouri *et al.,* 1958 [2]. Path coefficient analysis was performed as described by Dewey and Lu, 1959 [10].

Sl. No.	Name of Genotype	Code	Source of Availability of Genotype
1.	901	V_1	'Indian institute of pulses research, (IIPR) Kanpur'
2.	902	V_2	IIPR, Kanpur'
3.	903	V_3	IIPR, Kanpur
4.	904	V_4	IIPR, Kanpur
5.	905	V_5	IIPR, Kanpur
6.	906	V_6	IIPR, Kanpur
7.	907	V_7	IIPR, Kanpur
8.	908	V_8	IIPR, Kanpur
9.	909	V_9	IIPR, Kanpur
10.	910	V_{10}	IIPR, Kanpur
11.	911	V_{11}	IIPR, Kanpur
12.	912	V_{12}	IIPR, Kanpur

Results and discussions

The analysis of variance (ANOVA) results for all traits showed differences between the genotypes studied (Table 1). Table 2 shows the average value, various parameters of variation, heritability in a broad sense, and genetic progress as a percentage of the average of all traits. A moderate estimate of the genotype coefficient of variation (GCV) was observed for biological performance. 2,37) Followed by plants height (21.91), the number of pods per plant (12.55), (Chandirakala *et al.,* 2010) [8]. The discovery of similar genotypic variation coefficients for plant height and maturity days (1, 47) showed low estimates of GCV. Highest magnitude of PCV is recorded as the height of the plant (22.02), followed by the number of pods per plant (13.63), the weight of pods per plant (13.32), the weight of 100 seeds (12.80), and each branch (11.24), harvest index (11.13), seed yield per plot (10.30), seed yield per plant (9.49), 50% flowering days (8.16), and it was found to be the lowest in mature days (1.84). The phenotypic coefficient of variation (PCV) value is higher than that of all

traits, but the PCV and GCV values of most traits are less different, indicating that the environmental impact on these traits is negligible. Therefore, it is possible to improve these traits through phenotypic selection of the most likely reason for the low estimates of PCV and GCV may be that the phenotypic plasticity that occurs in these traits is the main source of variation, rather than genetic variation. Rangere *et al*., (2013), Also obtained similar results. Chethana *et al.* (2015) [9] and Ajay *et al.* (2014) [1]. Idea of heritability is important for assessing the relative magnitude of the influence of genes and environment on total phenotypic variability. Reading Table 2 reveals the generalized heritability estimates (%) of the 14 characters studied. Seed yield per plot (99.42%), plant tallness (99.06%), gather record (87.48%), number of units per plant (84.81%) and showed high heritability. Banu *et al.,* (2007) [3] additionally detailed high heritability for cases per plant, gather list, and seed yield. Traits that exhibit high heritability do not necessarily produce high heritability progress. Johnson and Robinson (1955) [14] showed that high heritability should be accompanied by high heritability in order to draw more reliable conclusions. Breeders must be careful when selecting the best heritability, as it includes additive and non-additive genetic effects. The mean heritability is recorded as days of flowering (79.50%), pod weight per plant (70.53%) and days of maturity (64.44%), and in comparison with other genetic parameters, the number of seeds per pod (51.86%). (Table 2).

Genetic advance (GA) is the improvement of the underlying population that may be achieved through selection. High heritability does not always show high genetic advance. Therefore, compared with the heritability estimation alone, the heritability estimation combined with genetic advance is usually more useful in predicting the benefits of selection (Johnson *et al*., 1955) [14]. The readings of genetic advance (Table 2) show that seed yield/plot (2440.63), plant height (103.30), number of pods per plant (79.21), weight per plant (45,79), seeds are all high per plant Yield. (29.01). The high heritability associated with high genetic advance indicates the advantages of additive genetic effects and the effectiveness of selection for this trait. In this study, the high heritability recorded was accompanied by high genetic advance, as the percentage of plant height (44.93), number of pods/plant (23.82), seed yield/plot (21, 09), and average harvest index (20.05).), pod. Plant weight (19.35) and seed/plant yield (16.17) indicate that the inheritance of these traits is mainly controlled by additive genes, and selection based on

phenotypic performance may be useful. Banu *et al.* (2007) [3] also obtained similar harvest index results as Kumar *et al*. (2013) [18] for number of seeds per pod. Before proceeding with any crop improvement breeding program, it is necessary to obtain information on the relationship between different plant traits and yield, as this helps to quickly assess high-yielding genotypes in the selection program. Only by eliminating the genotype correlation of environmental impact can the real or true correlation be known. The results of this study indicate that in all the studied traits, the degree of genotype correlation coefficient is higher than that of the phenotypic counterpart (Table 3).

In the current study, seed yield per plant was found to be positively correlated with days to 50 percent flowering, number of pods per plant, plant height, days to maturity, number of seeds per pod, number of branches per plant, 100-seed weight, harvest index, and seed yield per plot at both genotypic and phenotypic level (Table 3). This shows that selection for these traits would be effective to improve total yield/plant in pigeonpea. This also suggested that above traits helped to improve total seed yield/plant. Very strong and positive correlations were also reported between seed yield and other characteristics obtained in this study by Sodavadiya *et al*. (2009) [30] and Chandana *et al*. (2012) [7] for plant height, days to 50 percent flowering, days to maturity, number of seeds per pod and 100-seed weight; Mittal *et al*. (2010) [19] for plant height and harvest index; Kumar *et al*. (2012) [16] for plant height, number of pods per plant, number of seeds per pod and harvest index. In the selection program, when less number of variable are considered, correlation study alone can serve the purpose.

However, when variables are increased, the situation becomes complex. For overcoming this complexity, path analysis (Dewey and Lu, 1959) [10] method was adopted to partition the correlation into direct and indirect effects, so that a relative merit of each trait is established and their number is reduced in selection programs. In the present study, the path coefficient analysis revealed that characters harvest index, biological yield, number of pods per plant, days to maturity, pods weight per plant, days to 50% flowering and field emergence have positive direct effect on seed yield per plant at genotypic and phenotypic levels (Table 4). These results were in conformity with of Sodavadiya *et al*. (2009) [30] and Chandana *et al.,* (2012) [7] for harvest index; Kumar *et al*. (2014) [15] and Rekha *et al.,* (2010) [26] for number of branches per plant

Table 1: Analysis of variance for 14 quantitative characters in pigeon pea.

Characters	Mean Sum of Squares		
	Replications	Treatments	Error
	(df= 2)	(df= 11)	(df=22)
Field emergence	0.194	38.528**	10.376
Number of branches / plant	1.19	2.38*	0.74
Plant height	56.69	7639.42**	24.15
Days to first flowering	10.53	32.47**	8.86
Days to 50% flowering	1.08	406.15**	32.14
Days to maturity	20.36	54.60**	8.48
Number of pods / plant	46.78	5542.08**	312.23
No. of seeds / pod	0.06	0.17*	0.04
Pods weight / plant	104.19	2394.35**	292.77
100 seed weight	3.23	3.60*	1.40
Biological yield / plant	309.82	1069.85**	415.86
Harvest index	0.673	28.375**	1.292
Seed yield / plot	4252.778	4243918.262**	8252.778
Seed yield / plant	89.58	769.70**	50.19

* And ** represents significant at 5% and 1% level of significance, respectively.

Table 2: Genetic parameters for 14 quantitative characters of pigeon pea.

Characters	Vg	Vp	GCV	PCV	HERTI	GA	GA as %
Field emergence	9.38	19.76	3.78	5.49	47.49	4.35	5.37
Number of branches / plant	0.55	1.28	7.32	11.24	42.42	0.99	9.82
Plant height	2538.42	2562.57	21.91	22.02	99.06	103.30	44.93
Days to first flowering	7.87	16.73	2.29	3.35	47.04	3.96	3.24
Days to 50% flowering	124.67	156.81	7.27	8.16	79.50	20.51	13.36
Days to maturity	15.37	23.85	1.47	1.84	64.44	6.48	2.44
Number of pods / plant	1743.28	2055.51	12.55	13.63	84.81	79.21	23.82
No. of seeds / pod	0.04	0.08	4.19	5.81	51.86	0.31	6.21
Pods weight / plant	700.53	993.30	11.18	13.32	70.53	45.79	19.35
100 seed weight	0.73	2.13	7.51	12.80	34.47	1.04	9.09
Biological yield / plant	218.00	633.86	2.37	4.05	34.39	17.84	2.87
Harvest index	9.03	10.32	10.41	11.13	87.48	5.79	20.05
Seed yield / plot	1411888.49	1420141.27	10.27	10.30	99.42	2440.63	21.09
Seed yield / plant	239.84	290.03	8.63	9.49	82.69	29.01	16.17

Table 3: (a) Estimation of Phenotypic Correlation coefficient and its components in 12 pigeon pea genotypes

Characters	Field emergence	Number of branches / plant	Plant height	Days to first flowering	Days to 50% flowering	Days to maturity	Number of pods / plant	No. of seeds / pod	Pods weight / plant	100 seed weight	Biological yield / plant	Harvest index	Seed yield / plot	Seed yield / plant
Field emergence	1.000	0.125	-0.294	-0.326	-0.214	-0.299	0.065	-0.502**	0.228	0.179	0.261	-0.042	0.155	0.089
Number of branches/ plant		1.000	0.011	0.049	-0.217	-0.304	0.418*	-0.493**	0.524**	0.417*	0.211	0.430**	0.444**	0.624**
Plant height			1.000	-0.025	-0.193	0.267	0.043	0.125	-0.021	-0.138	-0.134	0.087	-0.113	0.012
Days to first flowering				1.000	0.474**	0.279	-0.341*	-0.184	-0.348*	0.325	0.104	-0.167	-0.215	-0.136
Days to 50% flowering					1.000	0.441**	-0.517**	0.032	-0.493**	0.123	0.366*	-0.514**	-0.406*	-0.420*
Days to maturity						1.000	-0.702**	0.240	-0.721**	-0.018	0.238	-0.634**	-0.615**	-0.620**
Number of pods / plant							1.000	0.035	0.924**	-0.274	-0.429**	0.880**	0.769**	0.815**
No. of seeds / pod								1.000	-0.101	-0.621**	-0.430**	0.109	-0.010	-0.078
Pods weight / plant									1.000	-0.220	-0.289	0.781**	0.715**	0.778**
100 seed weight										1.000	0.284	-0.093	-0.146	0.037
Biological yield / plant											1.000	-0.472**	-0.051	-0.071
Harvest index												1.000	0.777**	0.884**
Seed yield / plot													1.000	0.866**
Seed yield / plant														1.000

Table 3: (b) Estimation of Genotypic Correlation coefficient and its components in 12 pigeon pea genotypes

Characters	Field emergence	Number of branches/plant	Plant height	Days to first flowering	Days to 50% flowering	Days to maturity	Number of pods / plant	No. of seeds / pod	Pods weight / plant	100 seed weight	Biological yield / plant	Harvest index	Seed yield / plot	Seed yield / plant
Field emergence	1.000	-0.425**	-0.490**	-0.604**	-0.322	-0.568**	0.074	-0.460**	0.057	-0.027	0.267	-0.004	0.424**	0.029
Number of branches/plant		1.000	-0.173	0.434**	-0.182	-0.702**	0.738**	-0.406*	0.599**	0.243	-0.766**	0.814**	0.812**	0.714**
Plant height			1.000	-0.056	-0.204	0.402*	0.012	0.371*	-0.095	-0.438**	-0.426**	0.056	-0.223	-0.019
Days to first flowering				1.000	0.477**	0.424**	-0.496**	-0.468**	-0.501**	0.930**	0.546**	-0.261	-0.279	-0.142
Days to 50% flowering					1.000	0.581**	-0.569**	-0.058	-0.552**	0.222	0.901**	-0.646**	-0.574**	-0.504**

	Days to maturity	Number of pods / plant	No. of seeds / pod	Pods weight / plant	100 seed weight	Biological yield / plant	Harvest index	Seed yield / plot	Seed yield / plant
Days to maturity	1.000	-0.886**	0.371*	-0.990**	-0.209	0.251	-0.878**	-1.004**	-0.947**
Number of pods / plant		1.000	0.113	1.015**	-0.202	-0.611**	0.995**	1.002**	1.002**
No. of seeds / pod			1.000	0.122	-0.660**	-0.666**	-0.000	-0.510**	-0.164
Pods weight / plant				1.000	-0.203	-0.636**	1.036**	1.010**	1.003**
100 seed weight					1.000	-0.081	-0.053	0.240	-0.118
Biological yield / plant						1.000	-0.757**	-0.528**	-0.639**
Harvest index							1.000	1.001**	1.000**
Seed yield / plot								1.000	1.001**
Seed yield / plant									1.000

Table 4: (a) Estimation of direct and indirect effects of yield and its component characters in 12 pigeon pea genotypes (phenotypic path)

Characters	Field emergence	Number of branches/plant	Plant height	Days to first flowering	Days to 50% flowering	Days to maturity	Number of pods / plant	No. of seeds / pod	Pods weight / plant	100 seed weight	Biological yield / plant	Harvest index	Seed yield / plot	Seed yield / plant
Field emergence	0.052	0.011	-0.006	-0.035	0.013	0.012	0.020	-0.105	0.007	0.026	0.106	-0.026	0.015	0.052
Number of branches / plant	0.006	0.090	0.000	0.005	0.013	0.012	0.129	-0.103	0.016	0.060	0.086	0.266	0.044	0.090
Plant height	-0.015	0.001	0.021	-0.003	0.011	-0.010	0.013	0.026	-0.001	-0.020	-0.054	0.054	-0.011	0.021
Days to first flowering	-0.017	0.004	-0.001	0.107	-0.028	-0.011	-0.105	-0.039	-0.011	0.047	0.042	-0.103	-0.021	0.107
Days to 50% flowering	-0.011	-0.020	-0.004	0.051	-0.059	-0.017	-0.160	0.007	-0.015	0.018	0.149	-0.318	-0.040	-0.059
Days to maturity	-0.016	-0.027	0.006	0.030	-0.026	-0.038	-0.217	0.050	-0.022	-0.003	0.097	-0.392	-0.061	-0.038
Number of pods / plant	0.003	0.038	0.001	-0.036	0.031	0.027	0.309	0.007	0.029	-0.039	-0.174	0.544	0.076	0.309
No. of seeds / pod	-0.026	-0.044	0.003	-0.020	-0.002	-0.009	0.011	0.210	-0.003	-0.089	-0.175	0.067	-0.001	0.210
Pods weight / plant	0.012	0.047	0.000	-0.037	0.029	0.028	0.285	-0.021	0.031	-0.032	-0.118	0.483	0.071	0.031
100 seed weight	0.009	0.037	-0.003	0.035	-0.007	0.001	-0.085	-0.130	-0.007	0.143	0.116	-0.058	-0.014	0.143
Biological yield / plant	0.014	0.019	-0.003	0.011	-0.022	-0.009	-0.132	-0.090	-0.009	0.041	0.407	-0.292	-0.005	0.407
Harvest index	-0.002	0.039	0.002	-0.018	0.030	0.024	0.272	0.023	0.024	-0.013	-0.192	0.619	0.077	0.619
Seed yield / plot	0.008	0.040	-0.002	-0.023	0.024	0.024	0.237	-0.002	0.022	-0.021	-0.021	0.481	0.099	0.099

Residual are 0.03597

Table 4: (b) Estimation of direct and indirect effects of yield and its component characters in 12 pigeon pea genotypes (genotypic path)

Characters	Field emergence	Number of branches / plant	Plant height	Days to first flowering	Days to 50% flowering	Days to maturity	Number of pods/ plant	No. of seeds / pod	Pods weight / plant	100 seed weight	Biological yield / plant	Harvest index	Seed yield /plot	Seed yield/ plant
Field emergence	-0.217	0.004	-0.034	-0.031	0.079	0.108	0.025	-0.021	0.008	-0.002	0.108	-0.002	0.003	-0.217
Number of branches / plant	0.092	-0.010	-0.012	0.022	0.045	0.134	0.248	-0.019	0.089	0.015	-0.310	0.413	0.006	-0.010
Plant height	0.106	0.002	0.068	-0.003	0.050	-0.077	0.004	0.017	-0.014	-0.027	-0.173	0.029	-0.002	0.068
Days to first flowering	0.131	-0.004	-0.004	0.052	-0.118	-0.081	-0.167	-0.021	-0.074	0.057	0.221	-0.133	-0.002	0.052
Days to 50% flowering	0.070	0.002	-0.014	0.025	-0.246	-0.111	-0.192	-0.003	-0.082	0.014	0.365	-0.328	-0.004	-0.246
Days to maturity	0.123	0.007	0.028	0.022	-0.143	-0.191	-0.298	0.017	-0.147	-0.013	0.102	-0.445	-0.008	-0.191
Number of pods / plant	-0.016	-0.007	0.001	-0.026	0.140	0.169	0.336	0.005	0.151	-0.012	-0.247	0.505	0.007	0.336
No. of seeds / pod	0.100	0.004	0.025	-0.024	0.014	-0.071	0.038	0.046	0.018	-0.041	-0.270	0.000	-0.004	0.046
Pods weight / plant	-0.012	-0.006	-0.006	-0.026	0.136	0.189	0.341	0.006	0.149	-0.013	-0.258	0.526	0.008	0.149
100 seed weight	0.006	-0.002	-0.030	0.048	-0.055	0.040	-0.068	-0.030	-0.030	0.062	-0.033	-0.027	0.002	0.062
Biological yield / plant	-0.058	0.008	-0.029	0.028	-0.222	-0.048	-0.205	-0.030	-0.095	-0.005	0.405	-0.384	-0.004	0.405
Harvest index	0.001	-0.008	0.004	-0.014	0.159	0.168	0.335	0.000	0.154	-0.003	-0.307	0.507	0.007	0.507
Seed yield / plot	-0.092	-0.008	-0.015	-0.014	0.141	0.228	0.344	-0.023	0.168	0.015	-0.214	0.515	0.007	0.007

Residual are -0.0170

Conclusion

From the present investigation it is concluded that among 12 genotypes of pigeon pea on the basis of mean performance 912, 901, 902 and 907 were found to be superior and showed possessed maximum seed yield. Among 12 genotypes found to be gave best result by 912.

Plant height, number of pods per plant and pods weight per plant exhibited high GCV, PCV and genetic parameters revealed that heritability (broad sense) and genetic advance as % of mean values were high for seed yield per plot, plant height, harvest index, number of pods per plant, seed yield per plant indicating that selection would be fruitful for improvement of these traits.

Correlation coefficient analysis revealed that seed yield per plant exhibited positive and significant correlation associated with pods weight per plant, number of pods per plant, seed yield per plot, harvest index and number of branches per plant at genotypic and phenotypic levels. Path coefficient analysis revealed that characters harvest index, biological yield, number of pods per plant, days to maturity, pods weight per plant, days to 50% flowering and field emergence have positive direct effect on seed yield per plant at genotypic and phenotypic levels.

Acknowledgement

Future scope

The further investigation needs to conduct for the field trial in the research farm using effected soils in the different region of the country as the Pigeon pea used in this study genotype which is widely recommended in the different states in this India.

References

1. Ajay BC, Byregowda M, Babu HP, Kumar GNV, Reena M. Variability and transgressive segregation for yield and yield contributing traits in pigeonpea crosses. *Electronic Journal of Plant Breeding.* 2014;5(4):786-791.
2. Al-Jibouri HA, Muller PA, Robinson HF. Genetic and environmental variances and co-variances in an upland cotton cross of inter specific origin. *Journal of Agronomy,* 1958;50:633-636.
3. Banu MR, Muthaiah AR, Ashok S. Heterosis studies in pigeonpea. *Advances in Plant Sciences.* 2007;20(1):37-38.
4. Baudhbharti Rajesh K, Bind HN, Arun K, Vijay S. Correlation and path analysis for yield and yield components in black gram [*Vigna mungo* (L.) Hepper]. *Progressive Research.* 2014;8(Special):473-476.
5. Burton GW. Quantitative Inheritance of Grasses. Proc. *6th Int. Grassland congress.* 1952;1:277-283.
6. Burton GW, De Vane EM. Estimating heritability in tall fesses from replicated cloned material. *Journal of Agronomy,* 1953;45(3):474-481.
7. Chandana KC, Prasanthi L, Reddi Sekhar M, Reddy BV. Studied on correlation and path analysis for yield and its attributes in rabi redgram. Indian J Agric. Res. 2012;48(1):47-51.
8. Chandirakala R, Subbaraman N, Hameed A. Heterosis for yield in pigeonpea [*Cajanus cajan* (L.) Millsp.]. *Electronic Journal of Plant Breeding.* 2010;1(2):205-208.
9. Chethana CK, Muniswamy PS, Gangadhara K, Nagaraju CH. Genetic variability in stable male sterile, maintainer and restorer lines of pigeonpea [*Cajanus cajan* (L.) Millsp.]. Trends in Biosciences. 2015;8(1):203-400.
10. Dewey DR, Lu KH. A correlation and path analysis of components of crested wheat grass seed production. *Agronomy Journal.* 1959;51:513-518.
11. FAOSTAT. Online agricultural statistics, 2013. http//www.faostat.org.
12. FAOSTAT Online agricultural statistics, 2013. http//www.faostat.org.
13. Gowda CLL, Chaturvedi SK, Gaur PM, Kumar CVS, Jukanti AK. 2015. www.commodityindia.com/mailer/Pulses_handbook_2015_EBook.pdf.http://nsdl.niscair.res.in/jspui *bitstream/123456789/528/1/Pulses%20-%20Formatted.pdf*
14. Johnson HW, Robinson HF, Comstock RE. Estimates of Genetic and Environmental Variability in Soybeans. *Agronomy Journal.* 1955;47:314-318.
15. Kumar S, Kumar S, Singh S, Shivani. Genetic variability and inter-relationship among yield contributing characters in pigeonpea grown under rainfed lowland of eastern region of India. Journal of Food Legumes. 2014;27(2):104-107.
16. Kumar S, Kumar S, Singh S, Shivani. Genetic variability and inter-relationship among yield contributing characters in pigeonpea grown under rainfed lowland of eastern region of India. Journal of Food Legumes. 2012;27(2):104-107.
17. Kumar GV, Vanaja M, Sathish P, Vagheera P, Lakhsmi. Correlation analysis for quantitative traits in blackgram (*Vigna mungo* (L.) Hepper) in different seasons. *International Journal of Scientific and Research Publications.* 2015;5(4):1-4.
18. Kumara NB, Santoshagowda GB, Nishanth GK, Dharmaraj PS. Genetic diversity, variability and correlation studies in advanced genotypes of pigeonpea [*Cajanus cajan* (L.) Millsp.]. Acta Biologica Indica. 2013;2(2):406-411.
19. Mittal VP, Singh P, Brar KS. Character association and path coefficient analysis for yield components in pigeonpea. [*Cajanus cajan* (L.) Millsp.] Madras Agric. J. 2010;97(10-12):319-320.
20. Panse VG, Sukhatme PV. Statistical methods for agricultural workers. *2nd edition* ICAR, New Delhi, 1967, 361.
21. Pathak GN. Red gram in pulse crops of India. New Delhi Indian: ICAR, 1970, 17-20.
22. Rangare NR, Reddy GE, Kumar SR. Heritability, genetic advance and variability for yield contributing characters in pigeonpea (*Cajanus cajan* L. Millsp). Trends in Biosciences. 2010;6(5):660-662.
23. Rathaswammy R, Veeraswamy R, Raghupathy GA. Studies on genetic variability of certain quantitative characters in red gram (*Cajanus cajan*) (L.) Millsp. Madras Agricuultural Journal. 1973;60:204-206.
24. Reddy RP, Rao NGP. Somatic variation in *Cajanus cajan*. Current Science Journal. 1975;44:816-817.
25. Reddy RP, Singh D. Character association in pigeon pea.

Indian Journal of Genetics. 1975;35:119-122.

26. Rekha R, Prasanthi L, Reddy M, Latha P, Sudhakar S. Variability, character association and path analysis for yield and yield attributes in pigeonpea. Electronic Journal of Plant Breeding. 2010;4(4):1331-1335.

27. Saxena K, Sultana R. *Health*. 2010;2:1335-1344. doi: 10.4236/health.211199.

28. Singh *et al.* Nutrition quality evaluation of newly developed highprotein genotypes of pigeonpea (*Cajanus cajan*). *Journal of the Science of Food and Agriculture.* 1990;50:201-209.

29. Singh NK, Gupta DK, Jayaswal PK, Mahato AK, Dutta S, Singh S, *et al*. The first draft of the pigeonpea genome sequence. J. Plant Biochem. Biotechnol. 2012;21(1): 98-112.

30. Sodavadiya PR, Pithia MS, Savaliya JJ, Pansuriya AG, Korat VP. Studies on characters association and path analysis for seed yield and its components in pigeonpea (*Cajanus cajan* (L.) Millsp.). Indian journals.com. 2009;32(3):203-205.

31. Varshney R, *et al*. Agricultural biotechnology for crop improvement in a variable climate: hope or hype? Trends Plant Sci. 2012;16:363-371.