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GENETIC VARIABILITY, CORRELATION, PATH ANALYSIS AND GENETIC DIVERSITY STUDIES IN PIGEON PEA (*CAJANUS CAJAN* L. MILLSP.)

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ABSTRACT

The fundamental goal of any crop improvement programme is to increase the yield potential of the crop. The character seed yield has a complex gene action. Many factors affecting the yield must be considered and evaluated for their contribution to yield. A successful breeding programme for yield improvement through phenotypic selection is mainly dependent on the nature and magnitude of variation in the available material. In this study we studied genetic variability along with correlation, path analysis and genetic diversity. A field experiment was carried out during *Kharif*-2024 at College farm, College of Agriculture, NAU, Bharuch. The experimental material comprised of 30 genotypes, was laid out in a randomized block design (RBD) with three replications. Each entry was presented by a single-row plot of 15 plants, spaced at 90 x 20 cm. The moderate to high genotypic and phenotypic coefficient of variances were observed for seed yield per plant followed by pods per plant, 100 seed weight, plant height, primary branches per plant and secondary branches per plant. Significant association of seed yield per plant in desirable direction at both genotypic and phenotypic levels was observed for various traits *viz.*, 100 seed weight, plant height, pods per plant and seeds per pod. Highest positive direct effect on seed yield per plant was recorded for 100 seed weight followed by protein content, seeds per pod, primary branches per plant and plant height. The maximum inter-cluster distance (D= 227.37) was found between Clusters III and V both carrying 2 genotypes followed by V and VI (D= 224.85) and III and VII (D= 194.64) indicating that genotypes included in these Clusters are genetically diverse and may give rise to high heterotic response.

Keywords **:** Variability, Correlation, Path Analysis, Genetic Diversity, Pigeon pea.

Introduction

Pigeon pea [*Cajanus cajan* (L.) Millsp.] is the fourth most important pulse crop in the world and the second most important pulse crop in India after chickpea. Pigeon pea is a drought-tolerant crop and one of the most important legumes grown in the tropics and subtropics. It belongs to the family *Fabaceae* and is also known as *Arhar* or *Tur*, generally used in preparing *dal* which is rich in protein, carbohydrates, vitamins, lipids and minerals and eaten by most of the Indian vegetarian population. It is a diploid (2n=2x=22) and often cross-pollinated (20-70%) crop (Saxena, 2006). It is perennial and has an indeterminate growth habit but is typically cultivated as an annual crop. It is an important *Kharif* crop mainly sown in June-July and harvested as per the maturity duration. India, considered as a native of pigeon pea (Van der Maesen, 1983) and the name ‘Pigeon pea’ probably originated in Africa. Pigeon pea is tall plant stature, long duration, non-synchronous maturity and continuous flowering further hampered the mechanization efforts and synchronized harvesting. The Harvest index of extra early genotypes was between 33.1 to 41.0% and in early genotypes it was 27.6 to 34.1. The medium duration genotypes recorded very low Harvest index of 20.4 to 24.1%. Pigeon pea is a widely adaptable, deep-rooted, drought-tolerant and leguminous food crop that can be cultivated in areas with annual rainfall of less than 650 mm. Being a legume, it has a symbiotic association with *rhizobium* which plays an important role in fixing atmospheric nitrogen. It provides 40-60 kg N/ha to the subsequent crop and improves soil fertility (Sarkar *et al.*, 2020). Almost all plant parts of this crop are used for one or another purpose the grains are used both as human food and animal feed, leaves can be used as animal fodder; green pods are used as vegetables in western India and after harvesting the grains the woody remains are used for fuel. It is a most versatile food legume with diversified uses as food, feed, fodder and fuel. It holds the prestigious position among all legumes because it plays an important role in food security and a balanced diet. In India, pigeon pea planted on about 4.13 million hectares of land and it occupies the first position in production with 3.42 million tonnes among all pigeon pea producing countries in the world. The productivity of India is 827 kg/ha among all pigeon pea producing countries in the world (Annon. 2024a). In Gujarat, pigeon pea occupies an area of 2.27 lakh hectares with a production of 2.90 lakh tonnes and a productivity of 1278 kg/ha (Annon. 2024b).

Material and Methods

A field experiment was will be carried out during *Kharif*-2024 at College farm, College of Agriculture, NAU, Bharuch. The experimental material for proposed study comprised of 30 genotypes, was laid out in a randomized block design (RBD) with three replications. Each entry was presented by a single-row plot of 15 plants, spaced at 90 x 20 cm. All recommended agronomic practices along with plant protection measures were followed uniformly and timely. In each replication and in each plot, five plants were randomly selected and tagged excluding border plants to minimize border effects. The observations were recorded for various characters *viz.,* Days to 50% flowering, Days to maturity, Plant height (cm), Primary branches per plant, Secondary branches per plant, Pods per plant, Pod length (cm), Seeds per pod, 100 seed weight (g), Seed yield per plant (g), Protein content (%).

Result and Discussion

A great quantity of variation is necessary in a breeding population to enable the breeder to carry out effective selection. All the genotypes displayed wide range of variation in their mean performance with respect to all the characters studied. This had been exampled by the analysis of variances which showed highly significant mean differences for these characters indicating that the genotypes under study were genetically diverse (Table 1).

Table 1: Analysis of variance (mean sum of square) for various characters in pigeon pea

Source of variation	Degree of freedom	Mean of sum square				
		Days to 50% flowering	Days to maturity	Plant height	Primary branches per plant	Secondary branches per plant
Replication	2	56.14	166.14*	34.68	0.03	2.54
Genotypes	29	100.97**	105.38**	1298.68**	8.04**	33.06**
Error	58	25.85	44.54	116.48	0.45	4.26
S. Em. (±)		2.93	3.85	6.23	0.39	1.19
CD at 5%		8.31	10.90	17.63	1.10	3.37
CV (%)		4.39	4.17	7.08	5.34	7.87

Source of variation	Degree of freedom	Mean of sum square					
		Pods per plant	Pod length	Seeds per pod	100 seed weight	Seed yield per plant	Protein content
Replication	2	588.31	0.04	0.01	0.83*	57.41	3.62**
Genotypes	29	4800.21**	0.92**	0.38**	5.85**	614.60**	5.43**
Error	58	241.59	0.13	0.06	0.26	42.91	0.48
S.Em. (±)		8.97	0.21	0.15	0.29	3.78	0.40
CD at 5%		25.40	0.59	0.42	0.84	10.70	1.14
CV (%)		6.45	5.87	6.40	5.62	10.04	3.12

** Significant at 1% level * Significant at 5% level

Among the evaluated 30 genotypes, BP-16-184, PE-23-74, GT-105 and PE-23-71 were observed most potential high yielder genotypes and PE-23-77, PE-23-73, PE-23-81 and PME-23-116 were found to be most promising early genotypes in respect of days to 50% flowering while, PE-23-77, PME-23-116, PE-23-64, PE-23-76 and PME-23-129 were found early genotypes in respect of days to maturity. Moderate to high estimates of genotypic and phenotypic variances were observed for days to 50% flowering, days to maturity, plant height (cm), pods per plant and seed yield per plant (g) (Table 2). Similar result was observed by Baria *et al.* (2023) for days to maturity, plant height, secondary branches per plant, pods per plant and seed yield per plant, Burhade *et al.* (2023) for plant height, Kaur *et al.* (2023) for pods per plant in pigeon pea. The genotypic variance followed the trend of phenotypic variance and was greater than environmental variance for most of the characters. This implied that phenotypic variability may be considered as a reliable measure of genotypic variability. In the present study, phenotypic and genotypic variances were greater than environmental variance for most of the characters under study except days to 50% flowering and days to maturity, which indicated that influence of environment on expression of traits was lower or negligible, hence selection would be effective for plant height, secondary branches per plant, pods per plant and seed yield per plant due to their high to moderate estimates of genotypic and phenotypic variances. The moderate to high genotypic and phenotypic coefficient of variances were observed for seed yield per plant followed by pods per plant, 100 seed weight, plant height, primary branches per plant and secondary branches per plant (Table 3). Similar results were also obtained by Ranjani *et al.* (2018) for plant height and pods per plant, Anuradha and patro (2019) for pods per plant, Rao and Rao (2020) for seed yield per plant and pods per plant, Bhagat *et al.* (2022) for seed yield per plant, Sarkar *et al.* (2020) for pods per plant, Kaur *et al.* (2023) for pods per plant, Kumar *et al.* (2023) for days to maturity and days to 50% flowering.

High estimates of heritability was recorded by 100 seed weight (87.58%), pods per plant (86.28%), primary branches per plant (84.65%), seed yield per plant (81.62%), plant height (77.19%), protein content (77.13%), secondary branches per plant (69.22%), pod length (66.32%) and seeds per pod (60.92%). whereas, moderate amount of heritability was recorded by days to 50% flowering (49.20%) and days to maturity (31.28%). The high genetic advance was obtained for pods per plant (74.59%) and plant height (35.92%). Seed yield per plant (25.69%) reported moderate genetic advance expressed as per cent of mean and low genetic advance was found in days to 50% flowering (7.23%), secondary branches per plant (5.30%), days to maturity (5.18%), primary branches per plant (3.01%), 100 seed weight (2.63%), protein content (2.32%), pod length (0.86%) and seeds per pod (0.52%). High heritability coupled with high genetic advance as per cent of mean were observed for pods per plant, 100 seed weight and seed yield per plant, which indicated better scope of their improvement through selection, as these characters were predominantly governed by additive genetic variance. Similar findings were earlier reported by Hemavathy *et al.* (2019) for plant height, pods per plant, pod length, primary branches per plant and 100 seed weight, Sahu and Ekka (2020) for pods per plant, secondary branches per plant and seed yield per plant, Gaur *et al.* (2020) for secondary branches per plant and pods per plant. Burhade *et al.* (2023) for seed yield per plant.

When selection is applied for improvement of any single trait, changes are likely to occur, not only for the trait under selection but on the other trait also. This is because of inter-relationship between two or more traits due to genetic or environmental factors. Though true association can only be depicted by genotypic correlation coefficient. Hence, understanding the extent of genetic association between yield and its contributing characters are useful in isolating the most desirable genotypes. The genotypic (rg) and phenotypic (rp) correlation coefficients of elevan characters are presented in Table 4. In present investigation, the data showed that correlation at genotypic and phenotypic levels had the same trend. Values of genotypic correlation coefficients were higher than those of their respective phenotypic correlation coefficients in most of the cases, suggesting that there was a strong and inherent association between two characters. Significant association of seed yield per plant in desirable direction at both genotypic and phenotypic levels was observed for various traits *viz.*,100 seed weight, plant height, pods per plant and seeds per pod, while, days to maturity show significant and positive association at genotypic level only, indicating that these attributes were mainly influencing the seed yield in pigeon pea. These traits would be useful in selecting the high yielding genotypes in pigeon pea from the available genotypes. Similar results were also reported by Kesha *et al.* (2016) for grain yield per plant, primary branch per plant, pods per plant, days to maturity, 100 seed weight and plant height, Meena *et al.* (2017) for number of pods per plant and 100-seed weight, Pashwan *et al.* (2021) for pod weight per plant, number of pods per plant, seed yield per plot, harvest index and number of branches per plant and Akshaya *et al.* (2024) for days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of pods per plant and 100 seed weight.

Association studies provides only the relation between two variables, whereas, path coefficient analysis allows separation of the direct and their indirect effects through other traits by partitioning the correlation. Thus, correlation combined with path analysis gives better understanding of the relationship between different traits. The direct and indirect effects of various quantitative traits on yield were presented in Table 5. In the present investigation, highest positive direct effect on seed yield per plant was recorded for 100 seed weight followed by protein content, seeds per pod, primary branches per plant and plant height. This result is in accordance with Alaka *et al.* (2020) for pods per plant, plant height, number of secondary branches, harvest index and days to maturity, Rathore *et al.* (2020) for biological yield, harvest index, plant height, number of seeds per pod, days to 50% flowering and number of primary branches, Chaudhary *et al.* (2022) for number of pods per plant, number of branches, days to maturity and 100-seed weight, Parmar *et al.* (2023) for number of pods per plant and 100 seed weight, Akshaya *et al.* (2024) for days to 50% flowering, days to maturity, number of primary branches per plant, number of pods per plant, pod width, number of seeds per pod and 100 seed weight and Bhatt *et al.* (2024) for 100 seed weight. Negative direct effects on seed yield per plant were unveiled by days to 50% flowering, days to maturity, pods per plant and pod length. Comparable outcomes were revealed by Verma *et al.* (2018) for days to 50% flowering, Devi *et al.* (2020) for days to 50% flowering and primary branches per plant, Sharma *et al.* (2021) for primary branches per plant, Tharageshwari and Hemavathy (2020) for days to maturity, raceme number, pod bearing length and number of seeds per pod and Vanniarajan *et al.* (2023) for plant height, days to maturity. An imperative concern for formulating the path diagram is that all the key causal factors affecting the seed yield per plant are included. Since, yield is very multifaceted trait being exaggerated by so many causes, it might not be feasible to include all the characters. Under these circumstances, provision is made for a residual path which would take care of all such factors excluded. In present study the residual effect at genotypic level was 0.1827 which suggested that there might be few component traits responsible to influence the seed yield per plant than those studied.

The cluster analysis revealed that, thirty genotypes were grouped into seven clusters. The Cluster I was largest having 18 genotypes. Cluster I had a minimum mean value for seeds per pod (3.98) and seed yield per plant (8.36). Cluster II was the second largest which contained four genotypes. The Cluster II revealed maximum mean values for pods per plant (309.33) and primary branches per plant (15.33). Cluster III, IV and V had 2 genotype whereas, Cluster VI and VII had 1 genotype. Cluster III had a minimum mean value for days to 50% flowering (112.66), days to maturity (156.83), plant height (123.16) and 100 seed weight (54.50). The Cluster IV revealed maximum values for seeds per pod (4.50). The Cluster V had high mean values for 100 seed weight (86.50). The Cluster VI had high mean values for days to 50% maturity (136.66), days to maturity (178.66), plant height (187.66), secondary branches per plant (32.00) and pod length (7.53), seed yield per plant (12.53) and protein content (24.66). Cluster VII had a minimum mean value for primary branches per plant (11.00), secondary branches per plant (21.66), pods per plant (178.33), pod length (5.33) and protein content (21.36).

Inter and intra cluster distance values are given in Table 8. The maximum inter-cluster distance (D= 227.37) was found between Clusters III and V both carrying 2 genotypes followed by V and VI (D= 224.85) and III and VII (D= 194.64) indicating that genotypes included in these Clusters are genetically diverse and may give rise to high heterotic response. The minimum inter-cluster distance was (D= 76.90) found between Clusters II and VII indicating a close relationship among the genotypes included in these Clusters. The lowest intra-cluster distance were in Clusters VI and VII (D= 0.00) indicating that genotypes within these Clusters were similar. Whereas, the highest intra-cluster distance was in Cluster V (D= 66.18).

Conclusion

Ample amount of genetic variability is observed in the experimental materials, suggesting good scope for development of early maturing and high yielding genotypes. Based on per se performance BP-16-184, PE-23-74, GT-105 and PE-23-71 were observed as most potential high yielder genotypes High heritability coupled with high genetic advance as per cent of mean were observed for seed yield per plant, pods per plant and 100 seed weight which indicated better scope of their improvement through selection. Significant association of seed yield per plant in desirable direction at both genotypic and phenotypic levels was observed for 100 seed weight, plant height, pods per plant and seeds per pod. The overall picture of path analysis revealed that for improving yield in pigeon pea, selection advantage should be given to 100 seed weight followed by protein content, seeds per pod, primary branches per plant and plant height as they recorded high positive direct effect on seed yield per plant. Further, it is interesting to note that significant correlation of 100 seed weight, seeds per pod and plant height came from their own high positive direct effect. Hence, direct selection for these traits may be useful for further improvement of seed yield in pigeon pea. Based on the maximum genetic distance, it is advisable to attempt a crossing of the genotypes from Clusters III (PE-23-64, PE-23-83) with Cluster V (PE-23-65, PE-23-76), Cluster V (PE-23-65, PE-23-76) and Cluster IV (PE-23-79, PE-23-81) for developing a broad spectrum of favorable genetic variability for yield improvement in pigeon pea.

Table 2: Descriptive statistics of 11 traits in pigeon pea

Sr. No.	**Characters**	**Range**		**Mean**	**Variance**		
		Minimum	**Maximum**		**Genotypic**	**Phenotypic**	**Environmental**
1.	Days to 50% flowering	108.67	136.67	115.65	25.03	50.89	25.85
2.	Days to maturity	152.33	178.67	159.72	20.27	64.82	44.54
3.	Plant height (cm)	117.07	194.93	152.39	394.06	510.54	116.48
4.	Primary branches per plant	10.47	16.00	12.66	2.52	2.98	0.45
5.	Secondary branches per plant	21.53	33.93	26.22	9.59	13.86	4.26
6.	Pods per plant	175.87	310.13	240.87	1519.53	1761.13	241.59
7.	Pod length (cm)	5.32	7.50	6.24	0.26	0.39	0.13
8.	Seeds per pod	3.53	5.13	3.86	0.03	0.09	0.06
9.	100 seed weight (g)	6.93	12.53	9.13	1.86	2.12	0.26
10.	Seed yield per plant (g)	39.73	103.67	65.22	190.56	233.47	42.91
11.	Protein content (%)	20.43	25.10	22.35	1.64	2.13	0.48

Table 3: Genotypic and phenotypic coefficient of variation, heritability, genetic advance and genetic advance as per cent of mean for 11 traits of pigeon pea

Sr. No.	**Characters**	**GCV%**	**PCV%**	**Heritability Broad Sense (%)**	**Genetic Advance**	**Genetic Advance (% of mean)**
1.	Days to 50% flowering	4.32	6.16	49.20	7.23	6.25
2.	Days to maturity	2.81	5.04	31.28	5.18	3.24
3.	Plant height	13.02	14.82	77.19	35.92	23.57
4.	Primary branches per plant	12.55	13.64	84.65	3.01	23.79
5.	Secondary branches per plant	11.81	14.20	69.22	5.30	20.24
6.	Pods per plant	16.18	17.42	86.28	74.59	30.96
7.	Pod length	8.24	10.11	66.32	0.86	13.82
8.	Seeds per pod	7.99	10.24	60.92	0.52	12.85
9.	100 seed weight	14.94	15.97	87.58	2.63	28.81
10.	Seed yield per plant	21.16	23.42	81.62	25.69	39.38
11.	Protein content	5.74	6.53	77.13	2.32	10.39

Table 4: Genotypic and phenotypic correlations of seed yield per plant with other characters in 30 genotypes of pigeon pea

Characters		**Days to 50% flowering**	**Days to maturity**	**Plant height**	**Primary branches per plant**	**Secondary branches per plant**	**Pods per plant**	**Pod length**	**Seeds per pod**	**100 seed weight**	**Protein content**
Seed yield per plant	r_g	0.26	0.37*	0.42*	0.24	0.06	0.42*	-0.09	0.37*	0.46**	0.25
	r_p	0.12	0.18	0.35**	0.21*	0.07	0.38**	-0.05	0.31**	0.44**	0.23*
Days to 50% flowering	r_g	1	0.99**	0.31	0.33	0.47**	0.18	0.49**	0.34	0.80**	0.46**
	r_p	1	0.61**	0.16	0.25*	0.24*	0.04	0.32**	0.15	0.55**	0.22*
Days to maturity	r_g		1	0.04	0.42*	0.40*	0.14	0.48**	0.25	0.79**	0.68**
	r_p		1	0.03	0.25*	0.12	0.08	0.27**	0.23*	0.42**	0.27**
Plant height	r_g			1	0.15	0.46**	0.36*	-0.04	0.08	0.21	-0.04
	r_p			1	0.14	0.35**	0.32**	0.04	0.06	0.15	0.0006
Primary branches per plant	r_g				1	0.52**	0.42*	0.05	0.05	0.23	0.08
	r_p				1	0.38**	0.33**	0.04	0.04	0.19	0.04
Secondary branches per plant	r_g					1	0.52**	0.06	0.01	0.39*	-0.13
	r_p					1	0.39**	0.09	0.02	0.31**	-0.06
Pods per plant	r_g						1	-0.12	0.21	0.14	0.23

	r_p						1	-0.09	0.18	0.12	0.21*
Pod length	r_g							1	0.45*	0.31	0.13
	r_p							1	0.37**	0.23*	0.13
Seeds per pod	r_g								1	0.12	0.01
	r_p								1	0.03	0.05
100 seed weight	r_g									1	0.17
	r_p									1	0.17
Protein content	r_g										1
	r_p										1

** Significant at 1% level * Significant at 5% level

Table 5: Direct and Indirect effects of ten causal variables on seed yield per plant in 30 genotypes of pigeon pea

Characters	Days to 50% flowering	Days to maturity	Plant height	Primary branches per plant	Secondary branches per plant	Pods per plant	Pod length	Seeds per pod	100 seed weight	Protein content	Seed yield per plant
Days to 50% flowering	**-0.709**	-0.985	0.106	0.140	0.099	-0.072	-0.174	0.289	1.076	0.499	0.269
Days to maturity	-0.828	**-0.844**	0.014	0.175	0.084	-0.058	-0.170	0.215	1.058	0.732	0.379*
Plant height	-0.223	-0.035	**0.339**	0.064	0.097	-0.145	0.015	0.069	0.286	-0.044	0.425*
Primary branches per plant	-0.239	-0.355	0.052	**0.417**	0.109	-0.165	-0.019	0.049	0.315	0.086	0.249
Secondary branches per plant	-0.335	-0.341	0.157	0.218	**0.209**	-0.208	-0.023	0.013	0.520	-0.147	0.063
Pods per plant	-0.130	-0.126	0.125	0.175	0.111	**-0.394**	0.044	0.176	0.193	0.251	0.427*
Pod length	-0.353	-0.409	-0.015	0.023	0.014	0.050	**-0.350**	0.379	0.419	0.142	-0.099
Seeds per pod	-0.245	-0.217	0.028	0.024	0.003	-0.083	-0.158	**0.838**	0.170	0.011	0.371*
100 seed weight	-0.574	-0.672	0.073	0.098	0.080	-0.057	-0.110	0.107	**1.329**	0.189	0.465**
Protein content	-0.331	-0.579	-0.014	0.034	-0.029	-0.092	-0.046	0.008	0.236	**1.067**	0.252

Residual effect= 0. 1827 (Bold figures = Direct effects)
**Significant at 1%level *significant at 5% level

Table 6: Distribution of 30 genotypes of pigeon pea in different Cluster as per the Tochers method:

Cluster	No. of genotypes	Genotypes include
I	18	PE-23-63, PE-23-67, PE-23-69, PE-23-70, PE-23-71, PE-23-73, PE-23-74, PE-23-77, PE-23-82, PE-23-84, PE-23-85, PE-23-86, PME-23-116, PME-23-129, PME-23-130, BP-18-184, UPAS-120, GT-105
II	4	PE-23-68, PE-23-78, PE-23-87, PME-23-123
III	2	PE-23-64, PE-23-83
IV	2	PE-23-79, PE-23-81
V	2	PE-23-65, PE-23-76
VI	1	PE-23-88
VII	1	PME-23-134

Table 7: Mean of Cluster by Tocher for 11 morphological characters among the 30 genotypes in pigeon pea

Sr. No.	Characters	Mean of Cluster						
		I	II	III	IV	V	VI	VII
1.	Days to 50% flowering	113.66	116.66	112.66	120.16	118.41	136.66	114.33
2.	Days to maturity	157.55	163.33	156.83	164.83	162.16	178.66	158.33
3.	Plant height	151.46	158.16	123.16	155.13	160.41	187.66	143.20
4.	Primary branches per plant	12.37	15.33	11.33	15.00	12.41	13.33	11.00
5.	Secondary branches per plant	25.61	30.16	22.16	30.16	26.75	32.00	21.66
6.	Pods per plant	234.03	309.33	181.66	272.83	260.08	267.33	178.33
7.	Pod length	6.05	5.81	7.36	6.86	6.32	7.53	5.33
8.	Seeds per pod	3.98	4.00	4.33	4.50	4.33	4.00	4.00
9.	100 seed weight	60.88	78.66	54.50	55.16	86.50	68.33	69.66
10.	Seed yield per plant	8.36	9.11	8.71	10.11	11.12	12.53	10.36
11.	Protein content	22.33	22.43	21.66	22.95	22.11	24.66	21.36

Table 8: Intra and inter-Cluster distances amongst genotypes of pigeon pea

Cluster	I	II	III	IV	V	VI	VII
I	**57.01**	95.70	104.95	111.43	96.26	161.13	81.77
II		**51.86**	102.03	96.57	140.37	95.45	76.90
III			**43.76**	79.60	227.37	135.04	194.64
IV				**62.25**	163.53	78.84	166.60
V					**66.18**	224.85	78.50
VI						**0**	184.03
VII							**0**

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References

Akshaya, M., Geetha, K., Nirmalakumari, A., Sharavanan, P. T., Sivakumar, C. and Parasuraman, P. (2024). Genetic variability, correlation and principal component analysis for yield related traits in pigeon pea (*Cajanus cajan* [L.] Millsp.). *Legume Research,* **47**(7), 1094–1098.

Alaka, T., Ashutosh, Bhanu, A. N., Singh, M. N., Kumar, S. and Swarnmala, S. (2020). Genetic variability, correlation and path analysis for yield and its attributes in long duration pigeon pea (*Cajanus cajan* [L.] Millsp.) genotypes. *International Journal of Current Microbiology and Applied Sciences,* **9**(3), 2808–2818.

Allard, R. W. (1960). *Principles of plant breeding*. John Wiley & Sons.

Anonymous. (2024a). *Agricultural statistics at a glance 2023*. Directorate of Economics and Statistics. https://desagri.gov.in

Anonymous. (2024b). *District-wise area, production and yield of important food and non-food crops in Gujarat (2023–24).* Directorate of Agriculture, Government of Gujarat. https://dag.gujarat.gov.in/Home/AreaProductionAndYield

Anuradha, N. and Patro, T. S. (2019). Genetic variability, heritability and correlation in advanced red gram genotypes. *International Journal of Chemical Studies,* **7**(3), 2964–2966.

Baria, K. G., Patil, S. S., Pandya, H. D. and Bhargav, S. M. (2023). Genetic variability, correlation and path analysis studies in pigeon pea (*Cajanus cajan* [L.] Millsp.). *The Pharma Innovation Journal,* **12**(5), 3008–3013.

Bhagat, P., Kumar, S., Kumar, K., Tiwari, J. K. and Sinha, S. K. (2022). Genetic variability and association studies for seed yield and related traits in pigeon pea (*Cajanus cajan* [L.] Millsp.). *The Pharma Innovation Journal,* **11**(9), 2963–2966.

Bhatt, A., Verma, S. K., Panwar, R. K., Yadav, H., Pragati, K., Kumawat, S. and Naresh, T. (2024). Assessment of genetic variability, correlation and path coefficient for yield and its contributing traits in pigeon pea (*Cajanus cajan* [L.] Millsp.). *Journal of Experimental Agriculture International,* **46**(8), 125–134.

Burhade, S. T., Palshetkar, M. G., Pethe, U. B., Mahadik, S. G., Rathod, R. R., Misal, S. S. and Shinde, P. S. (2023). Investigation of genetic variability in pigeon pea for yield and its attributing traits (*Cajanus cajan* [L.] Millsp.). *The Pharma Innovation Journal,* **12**(11), 2384–2386.

Burton, G. W. (1952). Quantitative inheritance in grasses. *Proceedings of the 6th International Grassland Congress,* **1**, 227–283.

Chaudhary, L., Yadav, R., Kumar, S. and Devi, U. (2022). Correlation and path analysis for yield and yield attributing traits in extra-early pigeon pea genotypes. *The Pharma Innovation Journal,* **11**(12), 4618–4621.

Devi, O. P., Sharma, M. B., Seyie, K. and Ozukum, C. (2020). Correlation and path analysis studies in pigeon pea genotypes under foothill conditions of Nagaland. *International Journal of Bio-Resource and Stress Management,* **11**(3), 311–314.

Dewey, D. R. and Lu, K. H. (1959). A correlation and path analysis of components of crested wheat grass seed production. *Agronomy Journal,* **51**, 515–518.

Gaur, A. K., Verma, S. K. and Panwar, R. K. (2020). Estimation of genetic variability and character association for development of selection criteria in pigeon pea. *International Journal of Chemical Studies,* **8**(2), 391–394.

Hemavathy, A. T., Bapu, J. R. K. and Priyadharshini, M. (2019). Genetic variability and character association in pigeon pea core collection. *Indian Journal of Agricultural Research,* **53**(3), 362–365.

Johnson, H. W., Robinson, H. F. and Comstock, R. E. (1955). Estimates of genetic and environmental variability in soybean. *Agronomy Journal,* **47**, 314–318.

Kaur, H., Singh, I., Sethi, S., Bhatia, D. and Singh, S. (2023). Genetic analysis and association studies for devising efficient selection in pigeon pea. *Agricultural Research Journal,* **60**(3), 348–354.

Kesha, R., Saxena, K., Shrimali, T. and Bisnoi, G. (2016). Genetic variability, correlation and path analysis in pigeon pea (*Cajanus cajan* L.). *International Journal of Agricultural Sciences,* **8**(51), 2287–2289.

Kumar, A., Kamaluddin, Sharma, V., Singh, H. C., Kumar, H., Mourya, A. K. and Kumar, A. (2023). Genetic variability and character association for yield and its components in pigeon pea (*Cajanus cajan* [L.] Millsp.). *Journal of Food Legumes,* **36**(1), 16–22.

Mahalanobis, P. C. (1936). On the generalized distance in statistics. *Proceedings of the National Institute of Sciences of India,* **2**, 49–55.

Meena, S. S., Verma, S. K., Choudhary, R., Panwar, R. K. and Singh, J. P. (2017). Genetic variability and inter-relationship among yield contributing characters in advanced pigeon pea lines. *Chemical Science Review and Letters,* **6**(22), 1120–1128.

Miller, P. A., Williams, J. C., Robinson, H. F. and Comstock, R. E. (1958). Estimates of genotypic and environmental variances in upland cotton. *Agronomy Journal,* **50**, 126–131.

Panse, V. G. and Sukhatme, P. V. (1985). *Statistical methods for agricultural workers*. ICAR.

Parmar, M. J., Monpara, B. A., Chovatiya, N. C., Dudhat, H., Chhodavadiya, R. J., Patel, H. and Vardhini, T. R. (2023). Character association and causal relationship of seed yield in pigeon pea. *The Pharma Innovation Journal,* **12**(12), 2939–2943.

Pashwan, V. R., Chaurasia, A. K., Rao, D., Spandana, R., Rajkumar, M. and Surender, V. (2021). Genetic variability for quantitative traits in pigeon pea. *The Pharma Innovation Journal,* **10**(11), 269–275.

Ranjani, M. S., Vanniarajan, C. V., Kumar, C. V. S., Saxena, R. K., Sudhagar, R. and Hingane, A. J. (2018). Genetic variability and association studies in super-early pigeon pea. *Electronic Journal of Plant Breeding,* **9**(2), 682–691.

Rao, C. R. (1952). *Advanced statistical methods in biometrical research*. John Wiley & Sons.

Rao, V. T. and Rao, P. J. M. (2020). Genetic variability and character association in pigeon pea. *International Journal of Chemical Studies,* **8**(4), 1051–1053.

Rathore, T., Srivastava, A. K., Kushwaha, C. and Kumar, B. (2020). Genetic variability and character association in pigeon pea under central plain agroclimatic region. *International Journal of Current Microbiology and Applied Sciences,* **11**(5), 3297–3308.

Sahu, J. K. and Ekka, R. E. (2020). Genetic variability in pigeon pea germplasm. *Journal of Pharmacognosy and Phytochemistry*, *Special Issue* **6**, 377–379.

Sarkar, S., Mishra, S. P., Tripathi, D., Patidar, B., Soni, M. and Mishra, S. (2020). Genetic variability, heritability and genetic advance in pigeon pea. *International Journal of Current Microbiology and Applied Sciences,* **9**(10), 2319–2326.

Saxena, K. B. (2006). *Seed production system in pigeon pea.* ICRISAT.

Sharma, S. C., Kumar, R., Gautam, C. and Aarif, M. (2021). Direct selection parameters for seed yield in pigeon pea. *International Journal of Current Microbiology and Applied Sciences,* **10**(3), 1943–1947.

Tharageshwari, L. M. and Hemavathy, A. T. (2020). Correlation and path analysis in pigeon pea. *International Journal of Current Microbiology and Applied Sciences,* **9**(1), 80–86.

Van der Maesen, L. J. G. (1983). *World distribution of pigeon pea* (Information Bulletin No. 14). ICRISAT.

Vanniarajan, C., Magudeeswari, P., Gowthami, R., Indhu, S. M., Ramya, K. R., Monisha, K., Pillai, M. A., Verma, N., Yasin, J. K. and Jayapradhachandran. (2023). Genetic variability and trait association in pigeon pea germplasm. *Legume Research,* **46**(10), 1280–1287.

Verma, S. K., Bisht, C., Gaur, A. K. and Chandra, D. (2018). Genetic parameters for yield traits in pigeon pea. *Chemical Science Review and Letters,* **7**(25), 70–76.

Wright, S. (1921). Correlation and causation. *Journal of Agricultural Research,* **20**, 257–287.