



ISSN (E): 2277-7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2023; 12(5): 3008-3013
© 2023 TPI

www.thepharmajournal.com

Received: 08-02-2023

Accepted: 11-03-2023

KG Baria

Ph.D. Student, Department of Genetics and Plant Breeding, B. A. College of Agriculture, Anand Agricultural University, Anand, Gujarat, India

SS Patil

Assistant Professor, Department of Genetics and Plant Breeding, College of Agriculture, Navsari Agricultural University, Navsari, Gujarat, India

HD Pandya

Ph.D. Student, Department of Genetics and Plant Breeding, College of Agriculture, Navsari Agricultural University, Navsari, Gujarat, India

SM Bhargav

M.Sc. Student, Department of Genetics and Plant Breeding, College of Agriculture, Junagadh Agricultural University, Junagadh, Gujarat, India

Corresponding Author:

KG Baria

Ph.D. Student, Department of Genetics and Plant Breeding, B. A. College of Agriculture, Anand Agricultural University, Anand, Gujarat, India

Genetic variability, correlation and path analysis studies in pigeon pea [*Cajanus cajan* (L.) Millsp.]

KG Baria, SS Patil, HD Pandya and SM Bhargav

Abstract

A set of 20 genotypes of pigeon pea [*Cajanus cajan* (L.) Millsp.] grown in a randomized block design with three replications during *kharif*, 2021-22 at College of Agriculture, Navsari Agricultural University, Campus Bharuch to assess their variability. Wide range of variability was observed for different traits indicating the scope for selection of suitable breeding material for further improvement. Based on the mean performance of genotypes for yield BP-16-201, GT-104, GNP-2 and GT-105 were identified as elite genotypes for improving yield along with good quality. Character association studies indicated that seed yield per plant in desirable direction at both genotypic and phenotypic levels was observed for plant height and pods per plant were strongly associated with seed yield per plant. Path coefficient analysis revealed that the high positive direct effect on seed yield per plant was recorded by pod length followed by 100 seed weight, days to maturity and protein content.

Keywords: Genetic variability, heritability, correlation, path coefficient analysis, pigeon pea

Introduction

Pigeon pea [*Cajanus cajan* (L.) Millsp.] is a versatile food legume, serving as a lifeline to resource poor farmers in tropical and subtropical regions of Asia, Africa and Latin America. It belongs to the family 'Fabaceae' and is also known as 'Arhar' or 'Tur', generally used in preparing 'Dal' which is rich in protein (24-25%) and minerals and eaten by majority of Indian vegetarian population (Sodavadiya *et al.*, 2009) [21]. Pigeon pea is drought resistant, so can be grown in areas with less than 650 mm annual rainfall. It contains 22.3% protein, 1.7% fat, 3.5% minerals, 1.5% fibre, 57.6gm carbohydrate, 73 mg Ca and 0.5 mg Fe, respectively as per 100 g of pigeon pea (Subramani *et al.*, 2020) [22]. Its foliage is used as fodder and milling by products are used as feed for domestic animals. In India, pigeon pea occupies an area of 4.82 million ha with the production of 3.88 million tonnes and 804 kg/ha productivity (Anon., 2021) [2]. The area under pigeon pea cultivation in Gujarat is about 230350 ha with the production of 254.35 MT and 1104.18 kg/ha productivity (Anon., 2020) [1].

A successful breeding programme for yield improvement through phenotypic selection is mainly dependent on the nature and magnitude of variation in the available material and part played by the environment in the expression of the plant characters. Genotypic correlation coefficients provide a measure of genotypic conjugation between characters. The method of partitioning the correlation into direct and indirect effects by path-coefficient analysis suggested by Wright (1921) [26] provides useful information on the relative merit of the traits in the selection criterion.

Thus, present study was carried out to assess the genotypic variability, correlation and path coefficient analysis. This information may be utilized in development of high yielding varieties of pigeon pea that are suited to under rainfed conditions.

Materials and Methods

The present investigation was carried out at College of Agriculture, Navsari Agricultural University, Campus Bharuch during the *kharif* season of 2021-22. The experimental material consisted of 20 genotypes of pigeon pea. The genotypes were planted in Randomized block design. Each entry was presented by a single-row plot of fifteen plants, spaced at 90 x 20 cm. The morphological characters were studied by visual observation of individual plants or plant parts or by single observation of a group of plants in the plot depends upon the character under observation. The data for quantitative traits *viz.*, days to 50 percent 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, seed yield per plant and protein content (%)

was recorded on five random plants in each row.

Results and Discussion

The presence of genetic variability for economically important traits is major factor for improving local varieties with regard to specific traits. Present study was thus undertaken to study variability, heritability, genetic advance, correlation and path analysis. The data obtained were subjected to statistical analysis to find out mean, variance, genetic parameters, correlation and path coefficients among the different characters under study. Range, mean, genotypic, phenotypic and environmental variance, phenotypic and genotypic coefficient of variation, heritability and expected genetic advance as percentage of mean for eleven traits are presented in Table 1(a) and Table 1(b).

All the eleven characters had a wide range of variability. Among the evaluated 20 genotypes, BP-16-261, GT-104, GNP-2 and GT-105 were observed most potential high yielding genotypes. Moderate to high estimates of genotypic and phenotypic variances were observed for days to maturity, plant height, secondary branches per plant, pods per plant and seed yield per plant. Similar result was observed by Bhadru (2011) [3] for plant height and pods per plant, Birhan *et al.* (2013) [4] for pods per plant and seed yield per plant, Galian *et al.* (2016) [8] for days to maturity, plant height and primary branches per plant, Mallesh *et al.* (2017) [13] pods per plant, Hussain *et al.* (2021) for plant height, secondary branches per plant and pods per plant. Low estimates of genotypic and phenotypic variance were observed for the traits *viz.*, primary branches per plant, pod length, seeds per pod, 100 seed weight and protein content. Similar result was observed by Bhadru *et al.* (2011) [3] for primary branches per plant, pod length, seeds per pod and 100 seed weight, Galian *et al.* (2016) [8] for seeds per pod, Mallesh *et al.* (2017) [13] for protein content and Fousiya *et al.* (2021) [7] for seeds per pod and protein content in pigeon pea. The moderate to high genotypic and phenotypic coefficient of variances were observed for plant height followed by secondary branches per plant, pods per plant and seed yield per plant. Similar results were also obtained by Mallesh *et al.* (2017) [13] for pods per plant, Galian *et al.* (2016) [8] for plant height, secondary branches per plant and pods per plant, Shruthi *et al.* (2019) [20] for plant height, pods per plant and seed yield per plant and Vannirajan *et al.* (2021) [23] for plant height.

The estimates of heritability in broad sense [h^2 (bs)] for all the characters under study are presented in Table 2. High estimates of heritability were recorded by plant height (99.17%), secondary branches per plant (95.49%), primary branches per plant (84.21%), pod length (80.53%), seed yield per plant (72.88%) and pods per plant (69.67%). whereas, moderate amount of heritability was recorded by 100 seed weight (50.01%), days to 50% flowering (44.14%), days to maturity (39.83%), protein content (38.78%) and seeds per pod (36.15%). The high genetic advance expressed as percent of mean was obtained for plant height (67.61%) and pods per plant (48.46%) and seed yield per plant (13.50%) reported moderate genetic advance expressed as percent of mean. High heritability coupled with high genetic advance as percent of mean were observed for plant height and pods per plant. Similar findings were earlier reported by Ranjani *et al.* (2018) [14] for plant height, Hemavathy *et al.* (2019) plant height and pods per plant, Sahu and Ekka (2020) for pods per plant, Gaur *et al.* (2020) [9] for pods per plant, Hussain *et al.* (2021) [11] for

pods per plant and plant height in pigeon pea.

The characters seed yield per plant showed high heritability coupled with moderate genetic advance as percent of mean. High heritability accompanied with moderate genetic advance as percent of mean indicated that the genotypes under study were diverse with immense genetic potential and further improvement in these traits were possible by practicing simple selection technique. Moderate heritability coupled with low genetic advance as percent of mean was observed for the characters days to 50% flowering, days to maturity, seeds per pod and protein content (%). It showed the predominance of non-additive variance in the expression of this trait. Hence, breeder should use suitable methodology to use additive or non-additive gene action simultaneously for significant improvement.

Correlation coefficient provides information about nature and extent of association of different characters. For breeders, yield is the ultimate interest for any crop, so the knowledge of traits associated with yield help breeders to make the breeding program easy to some extent by direct selection of traits which are positively associated with yield. When two traits are positively correlated, selection of one trait will automatically affect selection of others trait. Whenever traits are negatively associated, it would be very difficult to get desirable combination, for this according to breeding objective, priority should be fixed. The genotypic (r_g) and phenotypic (r_p) correlation coefficients of eleven characters are presented in Table 3. In present investigation, Values of genotypic correlation coefficients were higher than those of their respective phenotypic correlation coefficients in most of the cases. In some cases, however, the phenotypic correlation was slightly higher than their genotypic counterpart, which implied that the non-genetic causes inflated the value of genotypic correlation because of the influence of environmental factors. Similar findings were reported by Satyanarayana *et al.* (2018) [17] and Verma *et al.* (2018) [24] in pigeon pea. Significant association of seed yield per plant in desirable direction at both genotypic and phenotypic levels was observed for various traits *viz.*, plant height and pods per plant, while, days to 50% flowering, 100 seed weight and protein content show significant and positive association at genotypic level only, indicating that these attributes were mainly influencing the seed yield in pigeon pea. Similar results were also reported by Sawant *et al.* (2007) [18] for protein content, Saroj *et al.* (2013) [16] for plant height, Birhan *et al.* (2013) [4] for pods per plant, Verma *et al.* (2018) for 100 seed weight and Devi *et al.* (2020) [6] for days to 50% flowering. Hence, these characters should be given due consideration while selecting for increasing yield.

Path coefficient analysis could provide a more realistic picture of the interrelationship, as it considers direct as well as indirect effects of the variables by partitioning the correlation coefficient. In the present study, all the 10 characters were considered as causal variables of seed yield per plant. The results obtained for direct and indirect effects of different characters on seed yield per plant are presented in Table 4. In the present investigation, highest positive direct effect on seed yield per plant was recorded for pod length followed by 100 seed weight, days to maturity and protein content. This result is in accordance with Sawant *et al.* (2007) [18] for protein content, Saroj *et al.* (2013) [16] for 100 seed weight, Ranjani *et al.* (2018) [14] for pod length, Devi *et al.* (2020) [6] for days to maturity. Negative direct effects on seed yield per plant were

unveiled by days to 50% flowering, plant height, primary branches per plant and pods per plant. Comparable outcomes were revealed by Saroj *et al.* (2013) ^[16] for plant height, Vijayalakshmi *et al.* (2013) ^[25] for pods per plant, Ranjani *et al.* (2018) ^[14] for days to 50% flowering, Sharma *et al.* (2021) ^[19] for primary branches per plant. An important consideration for formulating the path diagram is that all the important causal factors affecting the seed yield per plant are included.

In present study, the residual effect at genotypic level was 0.451 which suggested that there might be few component traits responsible to influence the seed yield per plant than those studied. The overall picture of path analysis revealed that for improving yield in pigeon pea, selection advantage should be given to pod length, 100 seed weight, days to maturity and protein content as they recorded high positive direct effect on seed yield per plant.

Table 1 a: Descriptive statistics of eleven traits in pigeon pea

Sr. no.	Characters	Range		Mean
		Min.	Max.	
1.	Days to 50% flowering	93.67	105.33	100.17
2.	Days to maturity	142.33	161.67	153.58
3.	Plant height (cm)	137	238.47	174.99
4.	Primary branches per plant	11.73	16.40	14.19
5.	Secondary branches per plant	18.87	32.27	24.72
6.	Pods per plant	121.67	230.13	180.47
7.	Pod length (cm)	4.12	6.13	5.44
8.	Seeds per pod	3.47	4.27	3.86
9.	100 seed weight (g)	7.34	10.93	9.08
10.	Seed yield per plant (g)	42.73	72.11	58.46
11.	Protein content (%)	23.57	26.10	24.70

Table 1 b: Descriptive statistics of eleven traits in pigeon pea

Sr. no.	Characters	Variance		
		Genotypic	Phenotypic	Environmental
1.	Days to 50% flowering	7.19	16.30	9.10
2.	Days to maturity	16.83	42.24	25.41
3.	Plant height (cm)	1086.01	1095.01	9.00
4.	Primary branches per plant	1.33	1.58	0.25
5.	Secondary branches per plant	16.19	16.95	0.76
6.	Pods per plant	794.28	1140.05	345.77
7.	Pod length (cm)	0.21	0.26	0.05
8.	Seeds per pod	0.03	0.09	0.06
9.	100 seed weight (g)	0.46	0.93	0.46
10.	Seed yield per plant (g)	58.94	80.87	21.93
11.	Protein content (%)	0.36	0.94	0.58

Table 2: Genotypic and phenotypic coefficient of variation, heritability, genetic advance and genetic advance as percent of mean for eleven traits of pigeon pea

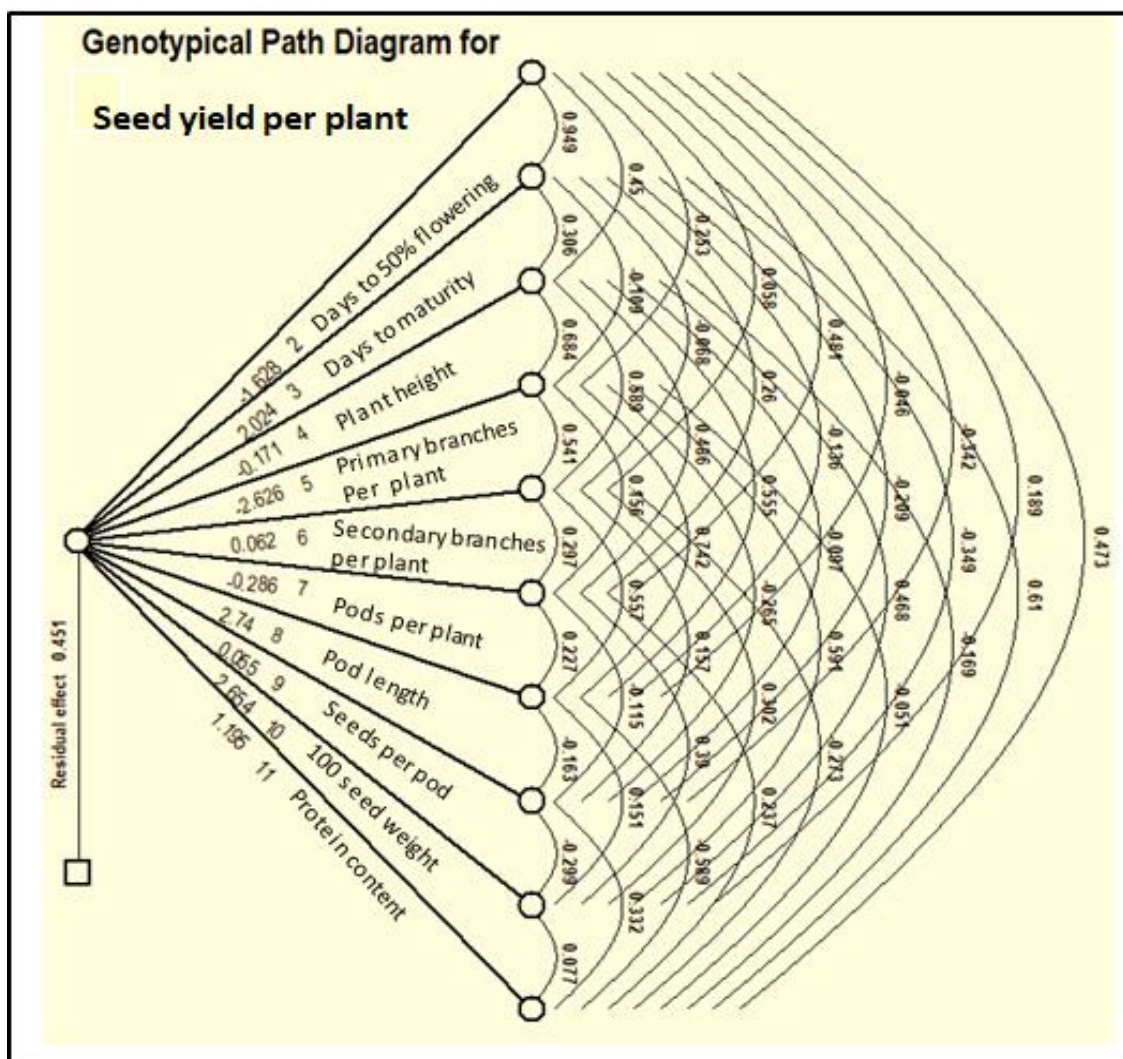
Sr. No.	Characters	GCV %	PCV %	Heritability Broad Sense (%)	Genetic Advance	Genetic Advance (% of mean)
1.	Days to 50% flowering	2.68	4.03	44.14	3.67	3.66
2.	Days to maturity	2.67	4.23	39.83	5.33	3.47
3.	Plant height	18.83	18.91	99.17	67.61	38.64
4.	Primary branches per plant	8.13	8.85	84.21	2.18	15.36
5.	Secondary branches per plant	16.28	16.65	95.49	8.10	32.76
6.	Pods per plant	15.62	18.71	69.67	48.46	26.85
7.	Pod length	8.34	9.29	80.53	0.84	15.42
8.	Seeds per pod	4.64	7.72	36.15	0.22	5.75
9.	100 seed weight	7.50	10.61	50.01	0.99	10.93
10.	Seed yield per plant	13.13	15.38	72.88	13.50	23.10
11.	Protein content	2.45	3.93	38.78	0.77	3.14

Table 3: Genotypic and phenotypic correlations of seed yield per plant with other characters in eleven genotypes of pigeon pea

Characters		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)	Protein content (%)
Seed yield per plant (g)	r _g	0.335**	0.052 ^{NS}	0.372**	0.139 ^{NS}	0.235 ^{NS}	0.915**	0.155 ^{NS}	0.102 ^{NS}	0.404**	0.345**
	r _p	0.137 ^{NS}	-0.053 ^{NS}	0.312*	0.118 ^{NS}	0.208 ^{NS}	0.657**	0.076 ^{NS}	0.025 ^{NS}	0.184 ^{NS}	0.229 ^{NS}
Days to 50% flowering	r _g	1	0.949**	0.450**	0.253 ^{NS}	0.058 ^{NS}	0.481**	-0.046 ^{NS}	-0.342**	0.189 ^{NS}	0.473**
	r _p	1	0.459**	0.307*	0.182 ^{NS}	-0.021 ^{NS}	0.274*	-0.039 ^{NS}	-0.091 ^{NS}	0.021 ^{NS}	0.077 ^{NS}
Days to maturity	r _g		1	0.306*	-0.109 ^{NS}	-0.068 ^{NS}	0.260*	-0.136 ^{NS}	-0.209 ^{NS}	-0.349**	0.610**
	r _p		1	0.169 ^{NS}	0.007 ^{NS}	-0.019 ^{NS}	0.255*	-0.191 ^{NS}	-0.107 ^{NS}	-0.041 ^{NS}	0.174 ^{NS}
Plant height (cm)	r _g			1	0.684**	0.589**	0.486**	0.555**	-0.097 ^{NS}	0.468**	-0.169 ^{NS}
	r _p			1	0.624**	0.572**	0.401**	0.501**	-0.071 ^{NS}	0.330*	-0.095 ^{NS}
Primary branches per plant	r _g				1	0.541**	0.156 ^{NS}	0.742**	-0.265*	0.591**	-0.051 ^{NS}
	r _p				1	0.484**	0.173 ^{NS}	0.608**	-0.172 ^{NS}	0.417**	-0.102 ^{NS}
Secondary branches per plant	r _g					1	0.297*	0.557**	0.157 ^{NS}	0.302*	-0.273*
	r _p					1	0.257*	0.479**	0.095 ^{NS}	0.212 ^{NS}	-0.129 ^{NS}
Pods per plant	r _g						1	0.227 ^{NS}	-0.115 ^{NS}	0.390**	0.237 ^{NS}
	r _p						1	0.102 ^{NS}	-0.070 ^{NS}	0.234 ^{NS}	-0.068 ^{NS}
Pod length (cm)	r _g							1	-0.163 ^{NS}	0.151 ^{NS}	-0.589**
	r _p							1	-0.058 ^{NS}	0.152 ^{NS}	-0.253 ^{NS}
Seeds per pod	r _g								1	-0.299**	0.332**
	r _p								1	-0.112 ^{NS}	0.181 ^{NS}
100 seed weight (g)	r _g									1	0.077 ^{NS}
	r _p									1	0.095 ^{NS}
Protein content (%)	r _g										1
	r _p										1

Table 4: Direct and Indirect effects of ten causal variables on seed yield per plant in twenty 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	-1.628	-1.544	-0.733	-0.412	-0.093	-0.783	0.075	0.556	-0.307	-0.769	0.335**
Days to maturity	1.919	2.024	0.619	-0.221	-0.136	0.526	-0.275	-0.423	-0.707	1.234	0.052 ^{NS}
Plant height (cm)	-0.077	-0.052	-0.171	-0.117	-0.100	-0.083	-0.095	0.016	-0.080	0.028	0.372**
Primary branches per plant	-0.664	0.287	-1.796	-2.626	-1.419	-0.410	-1.949	0.696	-1.552	0.132	0.139 ^{NS}
Secondary branches per plant	0.003	-0.004	0.036	0.033	0.061	0.018	0.034	0.009	0.018	-0.016	0.235 ^{NS}
Pods per plant	-0.137	-0.074	-0.139	-0.044	-0.084	-0.286	-0.065	0.032	-0.111	-0.067	0.915**
Pod length (cm)	-0.126	-0.372	1.520	2.033	1.526	0.621	2.739	-0.445	0.415	-1.612	0.155 ^{NS}
Seeds per pod	-0.018	-0.011	-0.005	-0.014	0.008	-0.006	-0.009	0.055	-0.016	0.018	0.102 ^{NS}
100 seed weight (g)	0.500	-0.927	1.243	1.569	0.800	1.034	0.402	-0.792	2.654	0.203	0.404**
Protein content (%)	0.564	0.728	-0.201	-0.060	-0.326	0.283	-0.703	0.396	0.091	1.194	0.345**



Genotypic path diagram based on the different morphological characters of pigeon pea

Conclusion

Sufficient genetic variability is observed in the experimental material studied, suggesting that there is ample scope to develop early maturing and high yielding genotypes. Based on the mean performance, BP-16-261, GT-104, GNP-2 and GT-105 were identified as elite genotypes for improving yield along with good quality. The trait seed yield per plant showed high heritability coupled with moderate genetic advance as percent of mean indicating that the genotypes, under study were diverse with immense genetic potential. Significant association of seed yield per plant in desirable direction at both genotypic and phenotypic levels was observed for plant height and pods per plant. The overall picture of path analysis revealed that for improving yield in pigeon pea, selection advantage should be given to pod length, 100 seed weight, days to maturity and protein content as they recorded high positive direct effect on seed yield per plant. However, consumer preference must be taken into consideration while the selection of the trait. Moreover, the traits protein content and 100 seed weight had the high positive direct effect along with highly significant correlation with seed yield per plant. Further, it is interesting to note that highly significant correlation of 100 seed weight and protein content 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.

References

1. Anonymous. Directorate of Agriculture, Government of Gujarat, 2020.
2. Anonymous. Agriculture Market Intelligence Centre, ANGRAU, 2021.
3. Bhadru D. Genetic studies in pigeon pea [*Cajanus cajan* (L.) Millsp.]. Elec. J Plant Breeding. 2011;2(1):132-134.
4. Birhan T, Zeleke H, Ayana A. Path coefficient analyses and correlation of seed yield and its contributing traits in pigeon pea [*Cajanus cajan* (L.) Millsp.]. Indian J Agric. Res. 2013;47(5):441-444.
5. Birhan T, Zeleke H, Ayana A, Tilahun A, Chemed A. Genetic variability, heritability and genetic advance in early maturing pigeon pea [*Cajanus cajan* (L.) Millsp.] genotypes. World J. Agric. Sci. 2013;1(7):241-247.
6. Devi OP, Sharma MB, Seyie K, Ozukum C. Correlation and path analysis studies in pigeon pea [*Cajanus cajan* (L.) Millsp.] genotypes under foothill conditions of Nagaland. Int. J. Bio-resource and Stress Management. 2020;11(3):311-314.
7. Fousiya A, Jayamani P, Uma D, Hemavathy AT. Genetic variability for vegetable traits in pigeon pea [*Cajanus cajan* (L.) Millsp.]. Elec. J. Plant Breeding. 2021;12(2):342-346.
8. Galian JK, Mohan N, Kumar CV, Mallesh P. Genetic variability studies in pigeon pea [*Cajanus cajan* (L.)

- Millsp.]. J. Res. ANGRAU. 2016;43(3&4):1-7.
9. Gaur AK, Verma SK, Panwar RK. Estimation of genetic variability and character association for development of selection criteria in pigeon pea [*Cajanus cajan* (L.) Millsp.]. Int. J. Chem. Sci. 2020;8(2):391-394.
 10. Hemavathy AT, Bapu JR, Priyadharshini M. Genetic variability and character association in pigeon pea [*Cajanus cajan* (L.) Millsp.] core collection. Indian J Agric. Res. 2019;53(3):362-365.
 11. Hussain ME, Sharma S, Joel AJ, Rajasekaran R, Senthil N, Senthil A. Genetic variability of agronomic traits in extra-early maturing introgression lines of pigeon pea [*Cajanus cajan* (L.)]. Elec. J. Plant Breeding. 2021;12(2):507-514.
 12. Mahalanobis PC. On generalized distance in statistics. Proc. Nat. Ins. India. 1936;2:49-55.
 13. Mallesh P, Nanda HC, Durgaraju S, Kumar CV, Mohan N, Lee J. Variability, heritability and genetic advance for quantitative traits in pigeon pea [*Cajanus cajan* (L.) Millsp.]. Int. J Pure and App. Biosci. 2017;5(5):25-28.
 14. Ranjani MS, Vanniarajan C, Sameer Kumar CV, Saxena RK, Sudhagar R, Hingane AJ. Genetic variability and association studies for yield and its attributes in super-early pigeon pea [*Cajanus cajan* (L.) Millsp.] genotypes. Elec. J. Plant Breeding. 2018;9(2):682-691.
 15. Sahu JK, Ekka RE. Genetic variability studies in germplasm accession of pigeon pea [*Cajanus cajan* (L.) Millsp.]. J Pharmacognosy and Phytochemistry. 2020;6:377-379.
 16. Saroj SK, Singh MN, Kumar R, Singh R, Singh MK. Genetic variability, correlation and path analysis for yield attributes in pigeon pea. Bioscan. 2013;8(3):941-944.
 17. Satyanarayana N, Sreenivas G, Jagannadham J, Amarajyothi P, Rajasekhar Y, Swathi B. Genetic variability, correlation and path analysis for seed yield and its components in red gram [*Cajanus cajan* (L.) Millsp.]. Bull. Env. Pharmacology and Life Sci. 2018;7:53-57.
 18. Sawant NM, Sonane AH, Anarase SA. Character association, path coefficient analysis and genetic diversity in pigeon pea. J. Maharashtra Agric. Univ. 2007;34(2):134-137.
 19. Sharma P, Singh I, Khosla G, Singh G, Singh S, Dhaliwal SK, *et al.* Variability and association studies for yield and yield related traits in pigeon pea [*Cajanus cajan* (L.) Millsp.]. Leg. Res. 2021;1(6):4374.
 20. Shruthi HB, Hingane AJ, Sekhar MR, Kumar CV, Srivarsha J, Bhosle TM, *et al.* Genetic variability for yield, physiological and quality traits in novel super-early pigeon pea [*Cajanus cajan* (L.) Millsp.]. Indian J Pure and App. Biosci. 2019;7(6):378-385.
 21. Sodavadiya MS, Pithia JJ, Savaliya AG, Pansuriya KVK. Studies on characters association and path analysis for seed yield and its components in pigeon pea [*Cajanus cajan* (L.) Millsp.]. Leg. Res. 2009;32(3):203-205.
 22. Subramani T, Velmurugan A, Singh AK, Damodaran V. Influence of pigeon pea varieties and plant geometries on yield and economics in coconut plantation under island condition. J. Pharmacognosy and Phytochemistry. 2020;9(3):1188-1191.
 23. 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.] germplasms. Leg. Res. 2021;44(2):1-8.
 24. Verma SK, Bisht C, Gaur AK, Chandra D. Study on some genetic parameters for yield and related traits in pigeon pea [*Cajanus cajan* (L.) Millsp.] genotypes. Chem. Sci. Rev. and Lett. 2018;7(25):70-76.
 25. Vijayalakshmi P, Anuradha CH, Kumar PD, Srilakshmi A, Anuradha G. Path coefficient and correlation response for yield attributes in pigeon pea [*Cajanus cajan* (L.) Millsp.]. Int. J. Scientific and Res. Pub. 2013;3(4):2250-3153.
 26. Wright S. Correlation and causation. J. Agric. Res. 1921;20:257-287.