Journal of Pharmacognosy and Phytochemistry

Available online at www.phytojournal.com

E-ISSN: 2278-4136
P-ISSN: 2349-8234
www.phytojournal.com
JPP 2020; 9(4): 1629-1632
Received: 04-05-2020
Accepted: 06-06-2020

KG Kandarkar
Department of Agricultural Botany, PGI, MPKV, Rahuri, Maharashtra, India

NS Kute
Principal scientist, Pulses Improvement Project, MPKV, Rahuri, Maharashtra, India

SA Tajane
Department of Agricultural Botany, PGI, MPKV, Rahuri, Maharashtra, India

AU Ingle
Assistant Professor, Department of Agricultural Botany, PGI, MPKV, Rahuri, Maharashtra, India

Corresponding Author:
KG Kandarkar
Department of Agricultural Botany, PGI, MPKV, Rahuri, Maharashtra, India

Correlation and path analysis for yield and its Contributing traits in pigeonpea [*Cajanus cajan* (L.) Mill Sp]

KG Kandarkar, NS Kute, SA Tajane and AU Ingle

Abstract
A field experiment of twenty-seven genotypes of pigeonpea had done with an aim to study correlation and association analysis for grain yield and its yield contributing characters so as to identify genotypes with desirable attributes for utilization in the crop improvement program during *Kharif- 2017*. Association studies revealed that seed yield Kg per ha showed the highest significant positive correlation with the number of pods per plant (0.8671) followed by plant spread (0.8046) number of branches per plant (0.7098) and number of seeds per pod (r= 0.5023). Direct selection fornumber of pods per plant (0.392), number of branches per plant (0.358) and plant spread (0.35) may be advantageous for selecting the high yielding genotypes in pigeonpea. Indirect effects of the number of branches per plant on seed yield via the number of pods per plant(0.308) and plant spread (0.223). Hence, this character seems to be an important contributor to seed yield and must be considered in the selection for high seed yield.

Keywords: Pigeonpea, correlation, path analysis, association.

Introduction
Pigeonpea is the second most important pulse crop next to chickpea in India. Out of the total production of the pulse (239.5 lakh tonnes), 16.78 percent share (40.2 lakh tonnes) is from pigeonpea (Directorate of Economics and Statistics, 2017 a 2nd advance estimate). It plays an important role in food security, balanced diet and alleviation of poverty because of its diverse usages as food, fodder and fuel (Rao *et al*. 2002) [13].

Yield, is a complex character, is composed of several components some of which affect the yield directly, while, others affect indirectly. However, the inheritance of quantitative characters is often influenced by variation in other characters which may be due to pleiotropy or genetic linkage. Hence, knowledge of the association between yield and its components helps in formulating selection program. Correlation studies would provide estimates of the degree of association between grain yield and its various components and also among the components. While path co-efficient analysis further elucidates the intrinsic nature of the association of component traits by determining the direct or indirect contribution of these traits to yield.

Character association and path coefficients among the yield and yield component traits studied in a set of 29 new pigeonpea genotypes and a local variety for genetic variability, revealed high phenotypic coefficient of variability and genotypic coefficient of variability were relatively high for number of pods per plant, dry pod weight, dry grain yield and number of primary branches (Vange and Moses, 2009) [18]. Pandey *et al*., (2016) [12] evaluated twenty-three pigeonpea genotypes and found correlation analysis biological yield/plant, pods/plant, 100-seed weight, harvest index, and secondary branches/plant had a highly significant positive correlation with seed yield. Ram *et al*., (2016) [14] studied thirty varieties of pigeon pea and found that correlation and path coefficient analysis (genotypic and phenotypic) revealed that pods/plant, 100 -seed weight, days to 50% flowering, primary branches and secondary branches had maximum direct effect resulted in significantly positive correlation with grain yield/plant. These traits can be used to improve the grain yield of pigeon pea.

Yield is a complex character and is influenced by genotype, environment, and genotype x environment interaction. Increased yield of crops is one of the prime concerns of the breeders in any crop breeding program. Considering this fact present investigation was carried out to study the association of different yield attributing traits and their relative level of correlation with a yield that facilitates breeder to select superior high yielding genotype.

Material and Methods

The experiment was conducted in Randomized Block Design (RBD) with three replications. Each genotype consisted of four rows with a plant to plant distance of 25 cm. The rows were spaced 90 cm apart. The experiment was carried out in *kharif* 2017 at Pulses Improvement Project, MPKV, Rahuri. The recommended package of practices was followed to raise a good crop. Observations on metric traits were recorded on a single plant basis from five randomly selected competitive plants from each genotype in each replication separately. Observations on flowering and maturity were recorded on a plot basis. Total nine characters were studied which are days to 50% flowering, days to maturity, plant height (cm), plant spread (cm), number of branches per plant, number of pods per plant, number of seeds per pod, 100 seed weight (g) and Seed yield (kg per ha).To understand the association among the characters, genotypic correlation coefficients were worked out by adopting the method described by Singh and Chaudhary (1977) [16]. The data were subjected to a standard regression analysis known as path analysis to unravel whether the association of different traits with yield is due to their direct effect or it is a consequence of their indirect effect via some other traits. The procedure was adopted from Wright (1921) [19], Dewey and Lu (1959) [7]. All the statistical calculations were done with the help of INDOSTAT-Statistical software.

Result and Discussion

Correlation of attributing characters with seed yield

In plant breeding, correlation coefficient analysis measures the mutual relationship between various characters and determines the component characters on which selection can be based for genetic improvement. Association studies revealed that seed yield Kg/ha showed the highest significant positive correlation with the number of pods per plant (r= 0.8671) followed by plant spread (r= 0.8046) number of branches per plant (r=0.7098), number of seeds per pod (r= 0.5023). However, days to 50% flowering (r= -0.0245), days to maturity (r= -0.1357) and 100 seed weight (r= -0.0678) shows non-significant negative correlation. Moreover, days to maturity shows a significant positive correlation with days to 50% flowering (r= 0.802). Number of branches per plant showed significant positive correlation with number of pods per plant (r= 0.785) followed by plant spread (r= 0.6282), number seeds per pod (r= 0.326), plant height (r= 0.249) and days to maturity (r=0.2377). The number of pods per plant showed a significant positive correlation with a number of branches per plant (r= 0.7847) followed by plant spread (r= 0.7557) and plant height (r= 0.294). The number of seeds per pod showed a significant positive correlation with plant spread (r= 0.393) followed by number of pods per plant (r= 0.356).

Somewhat similar results for phenotypic correlation coefficient recorded where seed yield kg per ha shows significant positive correlation with number of pods per plant (rp= 0.804) followed by plant spread (rp= 0.733), number of branches per plant (rp=0.674) and number of seeds per pod (rp= 0.412). Similar results obtained and were reported by Francis (2003) [8], Mahajan *et. al*., (2007) [11], Bhadru (2010) [5] and Bal *et. al*., (2018) [4].

The results of the present study, which revealed a comparative higher degree of genotypic correlation coefficients than their phenotypic counterparts in all the characters, indicated that the higher degree of association between two characters was genotypic; their phenotypic association was lessened due to the influence of environment. Hence, direct selection for seed yield kg per ha, plant spread, number of branches per plant, number of pods per plant, number of seeds per pod may be advantageous for selecting the high yielding genotypes in pigeon pea from the available genotypes.

Direct and indirect effect of attributes on seed yield

Path coefficient analysis is simply a standardized partial regression coefficient, which splits the correlation coefficient into direct and indirect effects. In order to achieve a clear picture of the interrelationship of various component traits with yield, direct and indirect effects were calculated using path analysis at the genotypic level. In present study, number of pods per plant (0.392) exhibited maximum positive direct effect on seed yield followed by number of branches per plant (0.358), plant spread (0.35) and days to 50% flowering (0.21) whereas days to maturity (-0.454), plant height (-0.26), 100 seed weight and number seeds per pods (-0.016) of had negative but direct effect on seed yield.

Days to 50% flowering had maximum positive indirect effect on seed yield via., number of pods per plant (0.084) followed by number of branches per plant (0.06), 100 seed weight (0.009), number of seeds per pod (0.004) and plant spread (0.002) whereas negative indirect effect on seed yield via., days to maturity (-0.364) and plant height (-0.027). Days to maturity had maximum positive indirect effect on seed yield via., days to 50% flowering (0.17) followed by number of branches per plant (0.085), number of pods per plant (0.054), 100 seed weight (0.012), number of seeds per pod (0.007) and plant height (0.009) whereas negative indirect effect on seed yield via., plant spread (-0.018).

In the present investigation, the highest positive direct effect on grain yield was recorded the number of pods per plant followed by a number of branches per plant. Similar results have been reported by Kumar *et al*. (2014) [9, 10], Vanisree and Sreedhar (2014) [17].

The high negative direct effects on grain yield were exhibited by plant height and days to 50 percent flowering, while, 100-seed weight, number of pods per plant, days to maturity and number of seeds per pod showed low negative direct effects on grain yield per plant. Such negative direct effects were also reported by Mittal *et al*. (2010), Arbad *et al*. (2014) [3], Kumar *et al*. (2014) [9, 10], Chandana et.al. (2014) [6] and Rekha *et al*. (2013) [15] for plant height and number of seeds per pod.

An important consideration for formulating the path diagram is that all the important causal factors affecting the grain yield per plant are included. Since yield is a very complex character being affected by so many factors; 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 the present study, the residual effect at the genotypic level was 0.283 which suggested that there might be few more component traits responsible to influence the grain yield per plant than those studied. For the improvement of grain yield, emphasis should be made on all yield contributing characters that are influencing it directly or indirectly. In the present study, the overall picture of a path analysis revealed that for improving yield in pigeonpea, weightage in selection should be given to branches per plant, plant spread and the number of pods per plant.

Table 1: Genotypic and phenotypic correlation coefficient for different nine characters in Pigeon pea

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	Plant spread (cm)	No. branches /plant	No. pods/ plant	No. seeds / pod	100 seed wt. (gm)	Yield (kg/ha)
	1	2	3	4	5	6	7	8	9
1	1.00	0.80**	0.1	0.005	0.16	0.21	-0.23**	-0.04	-0.02
2	0.782 **	1.00	-0.03	-0.05	0.24**	0.14	-0.44**	-0.05	-0.13
3	0.089	-0.025	1.00	0.19	0.25**	0.29**	0.14	-0.2	0.09
4	0.005	-0.044	0.121	1.00	0.63**	0.75**	0.39**	0.18	0.8**
5	0.148	0.221*	0.160	0.5388 **	1.00	0.74**	0.33**	0.16	0.71**
6	0.201	0.13	0.204	0.64 **	0.7 **	1.00	0.35**	-0.12	0.87**
7	-0.171	-0.324 **	-0.022	0.23*	0.241 *	0.2886 **	1.00	-0.04	0.50**
8	-0.039	-0.033	-0.138	0.14	0.13	-0.101	0.041	1.00	-0.07
9	-0.019	-0.126	0.073	0.733	0.67	0.804	0.412	-0.050	1.00

** Significant at 1% probability * Significant at 5% probability

Above diagonal values for genotypic correlation coefficient while below diagonal are of phenotypic correlation coefficient

Table 2: Direct and indirect genotypic path effects of different characters with yield

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	Plant spread (cm)	No. branches / plant	No. pods/ plant	No. seeds / pod	100 seed wt. (gm)	Correlation Yield (kg/ha)
	1	2	3	4	5	6	7	8	9
1	0.21	-0.364	-0.027	0.002	0.06	0.084	0.004	0.009	-0.025
2	0.17	-0.454	0.009	-0.0018	0.085	0.054	0.007	0.012	-0.136
3	0.022	0.015	-0.26	0.068	0.09	0.11	-0.002	0.0043	0.089
4	0.001	0.023	-0.05	0.35	0.22	0.29	-0.006	-0.04	0.805
5	0.03	-0.108	-0.065	0.223	0.358	0.308	-0.005	-0.03	0.71
6	0.045	-0.062	-0.077	0.27	0.28	0.392	-0.006	0.02	0.867
7	-0.049	0.198	-0.036	0.14	0.117	0.139	-0.016	0.009	0.502
8	-0.009	0.025	0.052	0.066	0.057	-0.046	0.0007	-0.214	-0.0678

Residual Effect=0.283

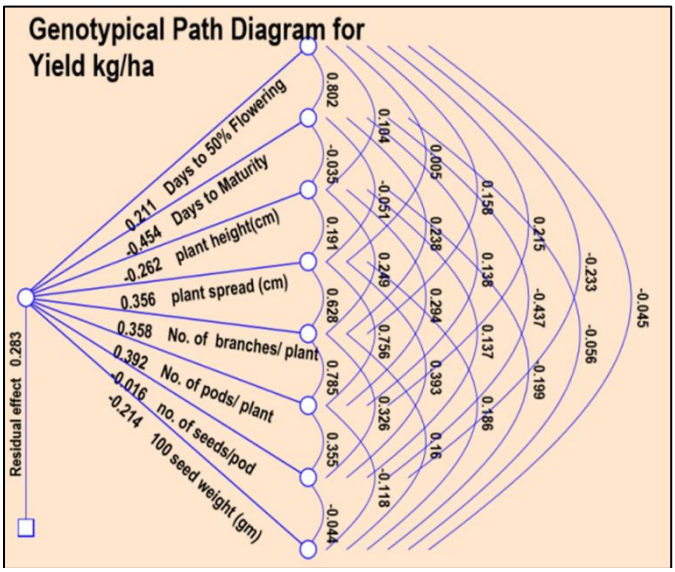

Fig 1: Genotypic path diagram showing the direct and indirect effect of different yield contributing characters on yield kg/ha along with residual effect.

Conclusion

Overall observations on correlation coefficient and path coefficients for seed yield and its attributes in pigeonpea genotypes indicated the presence of ample variability for most of the traits.Correlation studies revealed that yield showed the highest significant positive correlation with the number of pods per plant followed by plant spread, number of branches per plant and number seeds per pod.The results of path coefficient analysis indicated that the characters like the number of branches per plant, numbers of pods per plant and plant spread should be considered essential for developing high yielding genotypes as they had high positive direct effects on grain yield per plant.

Acknowledgements

This is part of research work of M.Sc. thesis carried out by Kuldeep Kandarkar and submitted to Mahtma Phule Krishi Vidyapeeth, Rahuri. The authors grateful to the Department of Agricultural Botany and Pulses Improvement Project, MPKV, Rahuri (MS) for the facilities provided and supply of seed material of Pigeonpea genotypes for present study.

References

1. Aonymous. 2nd Advance estimate for Area, Production and Productivity of pulses and pigeonpea crop. Agricultural Statistics Division, Directorate of Economics and Ministry of Agriculture and Farmers Welfare, Govt. of IndiaM, 2017a.
2. Anonymous. 2nd Advance estimates Project Coordinator Pigeonpea annual report. ICAR-Indian Institute of Pulse Research, Kanpur, India, 2017b, 2-4.
3. Arbad SK. Deosarkar DB, Kothimbire SS. Correlation and path analysis for grain yield and its attributing traits in pigeonpea (*Cajanus cajan* (L.)Millsp.). Bionfolet. 2014; 11(1):237-241.
4. Bal CP, Bhave SG, Thaware BL, Desai SS. Correlation and path analysis studies in pigeon pea (*Cajanus cajan*). Global journal of Bio-sci. and Biotech. 2018; 7(1)70-73.
5. Bhadru, D. 2010. Correlation and path analysis for yield and its attributing traits in white coated pigeonpea [*Cajanus cajan* (L.) Millsp]. Indian journals Legume Res. 33(3):196-200.
6. Chandana KC, Prasanthi L, ReddiSekhar M, Reddy BV. Studied on correlation andpath analysis for yield and its attributes in rabi redgram. Indian J. Agric. Res. 2014; 48(1):47-51.
7. Dewey DR, Lu KH. A correlation and path co-efficient analysis of components of wheat grass seed production. Agron. J. 1959; 51: 515-518.

8. Francis K. Correlation and path analysis for yield and yield components in pigeonpea (*Cajanus cajan* L. Millsp.). Pakistan J. Bio. Sci. 2003; 6:1689- 1694.
9. 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.
10. Kumara BN, Dharmaraj PS, Wali VB. Genetic diversity and variability studied of advanced breeding lines of pigeonpea (*Cajanus cajan*. (L) Millsp.). International journal of advances in pharmacy, biology and chemistry. 2014; 3(2).
11. Mahajan V, Shukla SK, Tiwari V, Prasad SV, Gupta HS. Path analysis in pigeonpea. Indian Journal, Com. 2007; 34(1):56-58.
12. Pandey P, Kumar R, Pandey VR. Genetic association studies for yield and yield related traits in pigeonpea [*Cajanus cajan* (L.) Millsp.] Legume Research. 2016; 39(2):189-193.
13. Rao SC, Coleman SW, Mayeux HS. Forage production and nutritive value of selected pigeonpea ecotypes in southern Great Plains. Crop Sci. 2002; 42:12591263.
14. Ram K *et al*. A Study on Genetic Variability, Correlation and Path Analysis in Pigeon pea [*Cajanus cajan* L. Millspaugh]. International Journal of Agriculture Sciences, ISSN: 0975-3710 & E-ISSN: 0975-9107. 2016; 8(51):2287-2289.
15. 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. 2013; 4(4):1331-1335.
16. Singh RK, Chaudhary BD. Biometrical Methods in Quantitative Genetic Analysis. Kalyani Publishers, New Delhi, 1977; 39-68.
17. Vanisree S, Sreedhar M. Genetic analysis of yield and yield components and determination of selection criteria in pigeonpea germplasm. Journal of Food Legumes. 2014; 27(1):6870.
18. Vange T, Egbe Moses O. Studies on Genetic Characteristics of Pigeon Pea Germplasm at Otobi, Benue State of Nigeria. World J. Agril. Sci. 2009; 5(6):714719.
19. Wright S. Correlation and causation. Journal of Agricultural Research. 1921; 20:557.