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Analysis of Path Coefficient and Genetic Divergence for Yield and its Components in Pigeon Pea [*Cajanus cajan* (L.) Millsp.] Genotypes

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ABSTRACT

The present investigation was conducted during August, 2021–April, 2022 at Oilseed Research Farm, Kalyanpur, C. S. Azad University of Agriculture and Technology, Kanpur, U.P., India, to work out the character relationship among yield and contributing traits and to know the direct and indirect effect of different character on seed yield plant^{-1} through path coefficient analysis. Path coefficient analysis was done by using seed yield as dependent variable and ten other quantitative characters as independent variables, The analysis of path emphasized that the characters viz., plant height, days to 50% flowering, days to maturity, number of secondary branches, number of pods plant^{-1}, biological yield, harvest index and 100 seed weight showed positive and direct effect on seed yield at genotypic level and phenotypic level, should be taken into consideration for formulating selection breeding programme in order to bring about improvement in the populations. The genetic divergence by Tocher's method for seed yield and it's component traits in pigeon pea genotypes. On the basis of genetic divergence under study, it was suggested that the crosses between cluster IV and cluster V, cluster II and cluster III be used for effective in hybridization breeding programme. The contribution of contribution of various characters towards the expression of genetic divergence were days to 50% flowering, days to maturity, number of branches per plant and 100 seed weight together contributed for about 95.44% of the total divergence.

KEYWORDS: Genetic divergence, path coefficient, pigeon pea, quantitative traits

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1. INTRODUCTION

Pigeonpea (*Cajanus cajan* [L.] Millsp.) is a climate-resilient crop that plays a pivotal role in sustainable agriculture and food security, particularly in tropical regions (Varshney et al., 2014; Upadhyaya et al., 2022). In India, it occupies the second-largest area among pulse crops and serves as a crucial component in pulse-based cropping systems (Odeny et al., 2023). Recent advances in genomics-assisted breeding have significantly enhanced pigeonpea improvement programs (Saxena et al., 2020; Bohra et al., 2020). The genus *Cajanus* has 32 species, most of them being distributed in India and Australia. About 17 *Cajanus* species including the most probable progenitor of pigeon pea [*C. cajanifolius* (Haines) Maesen] occur in India. There are several local names of *Cajanus cajan* in different parts of the world. Among these "Pigeon pea" is the globally popular name, coined by Plunket in Barbados, where the crop was grown in barren lands for feeding its seeds to pigeons (Varshney et al. 2014; Van der Maesen, 2022). Pigeonpea demonstrates a robust perennial growth habit, with modern cultivars like ICPL 20338 showing 82% survival after 4 years in semi-arid conditions (Saxena et al., 2021; Sharma et al., 2023). Pigeon pea possesses cleistogamous flowers which favour self-pollination. However, 14–20% natural outcrossing was observed in pigeon pea (Saxena et al., 2020). The rate of out crossing varies from place to place depending on the extent of pollinator bees and climatic conditions. Out crossing ranged from 20 to 70% at various locations (Saxena et al., 2019; Mula et al., 2021). Most important pollinators are Apis spp. (*A. dorsata*, *A. laboriosa*, *A. florae* and *A. cerana*), Megachilespp. (*M. lanata* and *M. flavipes*) and Xylocopa spp. (Bohra et al., 2022). Pigeonpea serves as an affordable source of high-quality plant protein (18-26%), vitamins, and essential minerals, addressing protein malnutrition in developing countries (Singh et al., 2022; Ntundu et al., 2022). Its cultivation not only provides nutritional security but also improves soil health through nitrogen fixation (Chauhan et al., 2025; Gopalakrishnan et al., 2023). The crop's economic viability in rainfed systems further enhances its importance (Singh et al., 2023). The cultivation of pigeonpea has gained additional importance due to its remarkable adaptability to climate change. Studies have identified several stress-tolerant genotypes that maintain stable yields under drought conditions (Choudhary et al., 2023; Sinha et al., 2023), making it a climate-smart crop choice for future agricultural systems. The per capita availability of pulses in India is 38g day^{-1}, against WHO recommendation of 80g day^{-1} and consequently malnutrition is the most serious problem among the poor vegetarian people, who avoid the animal protein. Path coefficient analysis proposed by Wright (1921) and first applied to plant selection by Dewey and Lu in (1959), modern applications in pigeonpea breeding have demonstrated its effectiveness in identifying key yield-contributing traits (Tiwari et al., 2021; Gangwar et al., 2022). Path analysis unfolds the nature of the association between component traits and yield, it reveals whether the association is due to their direct effect on yield or is a consequence of their indirect effect via some other character (Chauhan et al., 2021). Recent studies utilizing genetic divergence analysis have revealed substantial variability among pigeonpea genotypes, enabling targeted breeding programs (Bohra et al., 2022; Muniswamy et al., 2023; Suresh et al., 2023). Keeping the above facts in view, the present investigation was, therefore, undertaken to estimate association among different morphological traits and to assess their direct and indirect effects on seed yield of pigeon pea to develop suitable selection criteria for future pigeon pea breeding programme.

2. MATERIALS AND METHODS

The present investigation was carried out during during August, 2021–April, 2022 at Crop Experimental Research Farm, Chandra Shekhar Azad University of Agriculture and Technology, at Oilseed Research Farm, CSAUA&T, Kanpur (26.5°N, 80.3°E) using 34 genotypes of pigeon pea. The experiment was laid out in Randomized Block Design (RBD), spacing 75 cm×25 cm. All the recommended agronomic practices were followed to raise a good crop of pigeon pea. The study employed path coefficient analysis, a statistical technique originally developed by Wright (1921, 1934) and later adapted for agricultural research by Dewey and Lu (1959), to quantify the direct and indirect effects of various morphological traits on seed yield. This analysis was performed using OPSTAT software (version 1.0), with results presented in tabular form showing the path coefficients, direct and indirect effects, and residual values. Path coefficients were obtained by solving the simultaneous equation which expresses the basic relationship between correlation and path coefficient. The equation is as follows:

$$ry_1 = Py_1 + Py_1 r1_2 + Py_3 r1_3 + \ldots\ldots\ldots\ldots\ldots\ldots Pynr_{1n}$$

$$ry_2 = Py_2 + Py_1 r_{21} + Py_3 r_{23} + \ldots\ldots\ldots\ldots\ldots\ldots Pynr_{2n}$$

$$ry_n = Py_n + Py_1 r_{n1} + Py_n r_{n2} + \ldots\ldots\ldots\ldots\ldots\ldots Py_n r_{n(n-1)}$$

Where,

ry_1, ry_2…………… ry_n are the correlation coefficient of dependent variable (y) with various independent variables (1, 2,...... n).

Py_1, Py_2…………. Py_n are the direct path effects of independent variables (1, 2,...........n) on dependable variable (y).

r_{12}, r_{13}……………… r_{1n}…………. $r_{n(n-1)}$ are the correlation coefficient between various independent variables (1, 2,……..n).

Residual factor which measures the contribution of rest on the characters of causal scheme was obtained as given below:

$P_{xy}=\sqrt{1-R^{2}}$

Where, $R^{2}=\sum i=1P_{iy}\ r_{iy}$

Where R_{iy} denotes correlation between all possible combinations of independent character Y and the correlation is r_{12} to $r_{11\ 12}$

P= direct effect of ith character on Y.

r_{iy}= coefficient correlation between ith and y factor.

Genetic diversity among the pigeonpea genotypes was assessed using Mahalanobis D^{2} statistics, a multivariate analysis technique first proposed by C.R. Rao (1952).

$D^{2}=\lambda^{Ij}\ di\ dj$

Where,

λ^{Ij}= reciprocal matrix to the common dispersion matrix.

d_{i}=Difference between the mean values of the two populations for Ith character and

d_{j}=Difference between the mean values of the two populations for J^{th} character.

The parameter D^{2} can be estimated as D^{2} static (Rao, 1952).

$D^{2}=\sum\sum\ d_{ij},\ d_{i}\ d_{j}$= Sample estimate of X_{ij}

Where,

d_{ij}=Sample estimates of X^{ij}

d_{i}=Sample estimates of d_{i}

d_{j}=Sample estimates of d_{j}

The analysis involved computation of pairwise genetic distances (D^{2} values) and subsequent grouping of genotypes into clusters based on Ward's minimum variance method using Orange software (version 3.36.0). While the cluster analysis provided valuable information about genetic relationships among the genotypes, the results were presented solely in tabular format without accompanying dendrograms or other visual representations. The tables included detailed information on cluster compositions, inter and intra-cluster distances. All trait measurements were subjected to comprehensive statistical analysis including

Table 1: Genotypic path coefficient analysis for 11 characters in pigeon pea

Characters	Plant height (cm)	Days to 50% flowering	Days to maturity	No. of primary branches	No. of secondary branches	No. of pods plant^{-1}	No. of seeds pod^{-1}	Biological yield (g)	HI (%)	100 seed weight (g)	R with seed yield plant^{-1} (g)
Plant height	0.0849	0.0865	0.0297	0.0248	-0.0170	-0.0078	-0.0015	0.1444	-0.0569	-0.0852	0.202^{*}
Days to 50% flowering	0.0535	0.1373	0.0372	0.0182	-0.0172	-0.0074	-0.0007	0.0292	0.0784	-0.1066	0.222^{*}
Days to maturity	0.0491	0.0994	0.0514	0.0161	-0.0158	-0.0080	-0.0016	0.1116	0.3183	-0.1165	0.504^{**}
No. of primary branches	0.0444	0.0527	0.0175	0.0474	-0.0209	-0.0067	-0.0043	0.0189	-0.1103	-0.0476	-0.009
No. of secondary branches	0.0498	0.0812	0.0279	0.0341	-0.0290	-0.0071	-0.0030	0.0971	-0.0649	-0.0724	0.114
No. of pods plant^{-1}	0.0584	0.0907	0.0367	0.0283	-0.0182	-0.0113	-0.0022	0.0794	0.2609	-0.1048	0.418^{**}
No. of seeds pod^{-1}	0.0207	0.0151	0.0130	0.0326	-0.0139	-0.0040	-0.0063	0.0086	-0.0688	-0.0083	-0.011
Biological yield (g)	0.0250	0.0082	0.0117	0.0018	-0.0057	-0.0018	-0.0001	0.4912	-0.0202	-0.0204	0.489^{**}
Harvest index	-0.0055	0.0122	0.0186	-0.0059	0.0021	-0.0033	0.0005	-0.0113	0.8807	-0.0569	0.831^{**}
100 Seed weight (g)	0.0487	0.0986	0.0403	0.0152	-0.0142	-0.0080	-0.0004	0.0675	0.3379	-0.1484	0.437^{**}
Seed yield plant^{-1} (g)	0.0849	0.0865	0.0297	0.0248	-0.0170	-0.0078	-0.0015	0.1444	-0.0569	-0.0852	0.202^{*}

Residual effect: 0.0274

computation of path coefficients with results systematically organized in tables to facilitate interpretation (Table 1).

2.1. Observations recoded

Observations were recorded on yield and yield attributing characters. All the observations were taken from each plot, on randomly five selected plants from each genotype. The data were recorded for the following characters:

plant height (X_1), Days to 50% flowering (X_2), days to maturity (X_3), Number of primary branches plant^{-1} (X_4), Number of secondary branches plant^{-1} (X_5), Number of pods pod^{-1}(X_6), Number of seeds plant^{-1} (X_7), biological yield (X_8), Harvest index (X_9),100 Seed Weight (X_{10}), Seed yield plant^{-1} (X_{11}).

3. RESULTS AND DISCUSSION

3.1. Path coefficient analysis

In the present study path coefficient analysis was carried out considering the seed yield as the dependent character and yield attributes as the independent characters. The results (Table 2) revealed thatout of eleven characters, eight were showed positive and direct effect on seed yield at both genotypic level and phenotypic. At the genotypic level, eight traits exhibited positive and direct effects on seed yield, with the highest contributions *viz*, harvest index (0.831), followed by days to maturity (0.504), biological yield (0.489), and 100-seed weight (0.437), days to 50% flowering (0.222), plant height (0.202), number of pods per plant (0.418), and number of secondary branches (0.114). Conversely, two traits showed negative effects: number of primary branches (-0.009) and number of seeds per pod (-0.011), though their impact was minimal. At the phenotypic level, a similar trend was observed, with harvest index (0.828) remaining the strongest positive contributor, followed closely by biological yield (0.485) and days to maturity (0.492), 100-seed weight (0.425), number of pods plant^{-1} (0.388), days to 50% flowering (0.218), plant height (0.198), and number of secondary branches (0.109)

Table 2: Phenotypic path coefficient analysis for 11 characters in pigeon pea

Characters	Plant height (cm)	Days to 50% flowering	Days to maturity	No. of primary branches	No. of secondary branches	No. of pods plant^{-1}	No. of seeds pod^{-1}	Biological yield (g)	HI (%)	100 seed weight (g)	R with seed yield plant^{-1} (g)
Plant height	0.0669	0.0742	0.0297	0.0095	-0.0184	0.0089	0.0027	0.1397	-0.0526	-0.0628	0.198*
Days to 50% flowering	0.0421	0.1179	0.0371	0.0070	-0.0185	0.0085	0.0012	0.0279	0.0730	-0.0785	0.218*
Days to maturity	0.0387	0.0852	0.0513	0.0062	-0.0170	0.0093	0.0028	0.1078	0.2937	-0.0858	0.492**
No. of primary branches	0.0347	0.0448	0.0173	0.0183	-0.0224	0.0076	0.0075	0.0177	-0.0967	-0.0347	-0.006
No. of secondary branches	0.0392	0.0695	0.0278	0.0130	-0.0314	0.0081	0.0052	0.0934	-0.0624	-0.0534	0.109
No. of pods plant^{-1}	0.0441	0.0742	0.0351	0.0102	-0.0188	0.0135	0.0033	0.0761	0.2244	-0.0738	0.388**
No. of seeds pod^{-1}	0.0132	0.0102	0.0104	0.0100	-0.0120	0.0033	0.0137	0.0056	-0.0513	-0.0054	-0.002
Biological yield (g)	0.0195	0.0069	0.0115	0.0007	-0.0061	0.0022	0.0002	0.4797	-0.0143	-0.0148	0.485**
Harvest index	-0.0042	0.0101	0.0178	-0.0021	0.0023	0.0036	-0.0008	-0.0081	0.8487	-0.0396	0.828**
100 seed weight (g)	0.0384	0.0845	0.0402	0.0058	-0.0153	0.0091	0.0007	0.0648	0.3067	-0.1095	0.425**
Seed yield plant^{-1} (g)	0.0669	0.0742	0.0297	0.0095	-0.0184	0.0089	0.0027	0.1397	-0.0526	-0.0628	0.198*

Residual effect: 0.0453

whereas two traits viz, number of primary branches plant^{-1} (-0.006) and number of seeds per pod (-0.002 showed slight negative effects, though weaker than at the genotypic level. The positive nature and magnitude of association of seed yield with major agronomic characters viz., plant height (cm), days to 50% flowering, days to maturity, number of branches plant^{-1}, number of pods plant^{-1} and 100 seed weight (g). These results were consistent with the findings of Bhatt et al. (2024), who identified harvest index (HI) and pod number per plant as key determinants of yield in pigeon pea under drought stress. A negative direct effect on seed yield plant^{-1} was observed for the number of primary branches plant^{-1} and number of seed pod^{-1}. These findings corroborated the work of Devi et al. (2020) and Pushpavalli et al. (2017) highlighted the predominant role of secondary branches and 100-seed weight in yield stability across diverse environments. Note: genotypic path coefficients demonstrated greater reliability than phenotypic values for trait selection.This reinforced the importance of prioritizing genotypic-level analysis in breeding programs.

3.2. Genetic divergence

Based on D^2 value, thirty four genotype of pigeon pea were grouped into five non-overlapping clusters. Cluster IV had maximum number of genotypes twelve followed by Cluster III and Cluster V with seven genotypes, Cluster I and Cluster II with four genotypes. The intra cluster distance were highest in Cluster I (2.357), followed by Cluster III (2.120), Cluster V (2.005), Cluster IV (1.884), and Cluster II (1.298), showing that Cluster I had the highest internal variability while Cluster II was the most genetically uniform. At the inter-cluster level, the greatest genetic divergence was observed between Cluster I and Cluster IV (5.981), followed by Cluster I and Cluster V (5.770), Cluster I and Cluster II (4.888), Cluster III and Cluster IV (4.256), Cluster III and Cluster V (4.260), Cluster II and Cluster III (4.361), Cluster IV and Cluster V (2.195), Cluster II and Cluster V (3.570) and Cluster II and Cluster IV (3.597) indicating closer genetic relationships among these clusters.Cluster I exhibited the maximum intra cluster distance (2.357), so genotypes grouped under these cluster are somewhat diverse while, the minimum was recorded in Cluster II (1.298) as they included four genotypes. This revealed the presence of moderate diverse genotypes with in cluster. The minimum inter cluster distance observed between Cluster II (3.570) and Cluster III (4.260) indicated less diversity between the genotypes belongs to these clusters. Whereas the maximum inter cluster distance was observed between Cluster IV (2.195) and Cluster V (5.770), indicating high diversity between the genotypes belongs to these clusters. It is desirable to select genotypes from these clusters with high inter cluster distance as one of the parent in recombination breeding programme for obtaining wide variability and desirable segregants for seed yield and its attributing characters. The percent contribution of seed yield and its contribution character in genetic divergence were reported maximum for days to maturity (47.95%), plant height (21.21%), number of secondary branches (13.54%), 100 seed weight (12.12%), days to 50% flowering (3.74%). The rest of the character had minute percent contribution in genetic divergence i.e. number of primary branches and biological yield showed same contribution (0.71%) while number of pods per plant, number of seed per pod showed no percent contribution. The contribution of various characters towards the expression of genetic divergence were days to 50% flowering, days to maturity, number of branches plant^{-1} and 100 seed weight together contributed for about 95.44% of the total divergence. Therefore, these traits should be emphasized during the selection. Yamini et al. (2018) and Chauhan et al. (2025) confirmed the predominance of phenological and architectural traits in genetic divergence, while Tuntun et al. (2022) and Sandeep et al. (2022) validated seed weight's crucial role (10–15% contribution). The observed cluster patterns mirror Nag

Table 3: Distribution of 34 genotypes of pigeon pea in five clusters

Cluster	No. of genotypes	Genotypes
I	4	Pusa Arhar-16 (PADT16), AL-15, Vipula, Pusa 33
II	4	KA-12-01, KA-12-03, KA-12-05, IPA-8-F
III	7	T-7, Type-17, Type-21, Manak, Upas-120, Pusa-9 AL-201
IV	12	KA-16-1, KA-16-5, KA-17-1, KA-18-1, Azad, NDA-1, NDA-2, MAL-6, IPA-9-F, IPA-203, Asha (ICPL-87119), Maruthi (ICPL-8863)
V	7	KA-17-3, KA-18-2, Amar, DA-11, Bahar, IPA-7-F

Table 4: Average intra and inter cluster D^2 values for five clusters in 34 pigeon pea genotypes

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	2.357	4.888	4.325	5.981	5.770
Cluster II		1.298	4.361	3.597	3.570
Cluster III			2.120	4.256	4.260
Cluster IV				1.884	2.195
Cluster V					2.005

et al. (2012) findings in heat-tolerant germplasm, where D²>5.0 identified promising crosses. Kaur et al. (2023), Muniswamy et al. (2023) and Borah et al. (2023) further substantiated our methodology, particularly regarding maturity duration's predictive value (45–50% contribution) and the effectiveness of D² analysis in identifying heterotic groups, collectively reinforcing our recommendations for trait-based selection in pigeon pea improvement programs.

4. CONCLUSION

The path analysis results underscored the importance of harvest index, number of pods plant^{-1} and seed weight in yield enhancement at both genotypic and phenotypic level, while the genetic divergence study highlighted maturity duration and plant height as key diversification traits. Crosses between genotypes from highly divergent cluster IV comprised of KA-16-1, KA-16-5, KA-17-1, KA-18-1, Azad, NDA-1, NDA-2, MAL-6, IPA-9-F, IPA-203, Asha (ICPL-87119), Maruthi (ICPL-8863) and cluster V constituted KA-17-3, KA-18-2, Amar, DA-11, Bahar, IPA-7-F were expected to generate transgressive segregants, offering opportunities for yield breakthroughs.

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