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Assessment of genetic diversity and path coefficient analysis for grain yield in pigeon pea (*Cajanus cajan* L. Millsp.)

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Abstract

An experiment has been conducted at the Agricultural Research Field of Department of Genetics and Plant Breeding, Rama University, Kanpur during kharif 2023-24 to estimate the extent of combining ability through the investigation. Twenty pigeonpea genotypes were assessed for genetic variability, heritability, and genetic advance across various traits. Observations were recorded on several parameters including days to flower initiation, days to 50% flowering, days to maturity, primary and secondary branches per plant, plant height, pods per plant, pod clusters per plant, pod characteristics, seed attributes, and seed yield per plant. Analysis of variance indicated significant variability among the genotypes for all traits studied. Notably, the number of pods per cluster exhibited the highest genetic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) among yield-related traits, suggesting substantial genetic diversity within the pigeonpea germplasm. Additionally, traits such as secondary branches per plant, number of pod clusters per plant, pods per plant, and seed yield per plant displayed high heritability and genetic advance, indicating the influence of additive gene action in their expression.

Keywords: Genotype, variability, heritability, genetic advance etc.

Introduction

Pigeonpea (*Cajanus cajan* L.) commonly known as red gram, thrives in semi-arid tropical and subtropical regions globally, primarily in South Asia, Eastern Africa, and Central America. India leads production at 77%, followed by Malawi (11%), Myanmar (8%), Kenya, and Tanzania (2% each). Cultivated on 4.5 million hectares, it yields 3.68 million tons annually at 832 kg/ha. Despite extensive cultivation, productivity lags due to its complex polygenic traits. Pigeonpea ranks sixth globally in grain legume production, covering 6.36 million hectares and yielding 5.96 million tons yearly, with India leading at 5.58 million hectares and 4.29 million tons, nearly 80% of global production and cultivation area. According to the Food and Agriculture Organization's report (2023), India leads in pigeonpea cultivation, with an extensive area of 5.58 million hectares and a production of 4.29 million tons, accounting for nearly 80 percent of the total production and cultivation area of pigeonpea worldwide. Following India, Myanmar, Malawi, and Kenya are the next top producers of pigeonpea.

Pigeonpea ranks as the second most extensively cultivated pulse crop in India, following chickpea. Apart from providing nutritional benefits and contributing to food security, pigeonpea's adaptability to various agro-ecological settings makes it an essential component of sustainable agricultural systems, as highlighted by Mula and Saxena (2010). According to Varshney *et al.* (2010) [12], the deposition of pigeonpea plant leaves on the ground plays a critical role in supplying essential nutrients to subsequent crops and enriching the soil through symbiotic nitrogen fixation. Notwithstanding its capacity to thrive in various agro-ecological settings, the productivity of pigeonpea has remained comparatively inadequate, with an average range of 700–900 kg/ha. The reasons for this phenomenon can be attributed to various factors, including but not limited to the restricted genetic diversity of cultivated pigeonpea, protracted crop duration, and inadequate uptake of improved cultivars, as highlighted.

This analysis helps researchers understand the relationships between various traits and their contributions to the overall yield of pigeon pea plants. Studies on pigeon pea have utilized path coefficient analysis to identify the key traits that directly influence grain yield, such as yield per plant, plant height, days to flowering, days to 50% flowering, number of pods per plant, 100-seed weight, and harvest index. Pigeonpea's seed and pod husks serve as quality feed, while its dry branches and stems are used for domestic fuel. The plant's fallen leaves contribute essential nutrients to the soil, and it enriches soil through symbiotic nitrogen fixation (Varshney, 2010) [12]. However, global pigeonpea productivity remains low and stagnant compared to cereals due to various biotic and abiotic stresses. This low productivity is attributed to its limited harvest index, resulting from insufficient man-made selections (Varshney *et al.*, 2010; Ajay *et al.*, 2011) [12, 1].

In pigeon pea research, path coefficient analysis serves as a powerful tool to unravel the intricate relationships between different traits and their collective influence on grain yield. This method enables researchers to prioritize traits for breeding programs, select superior genotypes, and enhance crop productivity by focusing on the most influential characteristics identified through the analysis. Path coefficient analysis proposed by Wright (1921) and first applied to plant selection by Dewey and Lu in (1959) [4], could provide a better insight into the contributing characters and their association with yield. 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 (Gautam *et al.*, 2021). In this way, correlation and path analysis helps in identifying traits on which selection pressure ought to be given for enhancing yield.

Materials and Methods

Kanpur, located in the central part of Uttar Pradesh, sits at an elevation of 126.49 meters above mean sea level in the Gangetic plain. It lies between latitude and longitude coordinates of 26°33'0" north and 80°13'28" east, respectively. The region experiences a subtropical climate with intermittent winter showers. Meteorological data recorded at the Rama University Mandhana Kanpur U.P. laboratory during the crop period indicate hot and dry summers, with May and June being the hottest months. December and January are cooler, with maximum temperatures reaching 34.4 °C in summer and minimums dropping to 4.6 °C in winter. The experimental material for this investigation comprised 20 genotypes, including checks. Sourced from germplasm materials at the Department of Genetics and Plant Breeding, Rama University, Mandhana, Kanpur. The experiment followed a randomized block design with three replications in the experimental field. Each plot consisted of two rows spaced 2.5 m apart, with plants spaced 60 cm apart within rows and 20 cm between rows. These accessions were raised following recommended practices during the *Kharif season 2023-24* to ensure a healthy crop.

Observations recorded

Observations were recorded on 10 quantitative characters, including days to 50% flowering, days to maturity, Days to Maturity, Number of Branches per Plant, Pod-bearing

Length of Plant (cm), Number of Pods per Plant, Length of Pod (cm), Number of Seeds per Pod, Seed Yield per Plant (g) Harvest index (%). These observations were used to estimate genetic variability, heritability, and genetic advance. The experimental data collected for 12 characters across 20 pigeonpea genotypes and 2 checks were compiled by averaging the values of selected plants in each plot. These data were then subjected to the following statistical analyses: Analysis of variance (Panse and Shukhatme, 1988) [6] Analysis of variance of RBD field experiment (Panse and Sukhatme, 1967) [6]. Correlation coefficient analysis (Searle, 1961) [11] and Path coefficient analysis (Dewey and Lu, 1959) [4].

Results and Discussion

Days to 50% flowering exhibited considerable variation among the genotypes, ranging from 59.667 days for Pusa Amber-16 to 111.333 days for VCA-1, indicating diversity in flowering time. On average, the genotypes showed a flowering time of 81.317 days, with some genotypes flowering earlier in the season while others flowered later. Plant height varied significantly across the genotypes, with measurements ranging from 122.000 cm for Pusa Amber-16 to 269.667 units for VCA-1. This trait, crucial for overall plant development, represents the total biomass produced by the plants and is indicative of their growth vigor. Taller plants, such as VCA-1, may offer advantages such as increased light interception and potentially higher yield. However, taller plants are also susceptible to lodging, which can impact yield and harvest efficiency.

The Primary branch measurements ranged from 9.000 units for Pusa Amber-16 to 18.500 units for Pusa-992, reflecting differences in the overall biomass production capacity of the genotypes. A higher number of Primary branches is often associated with better resource capture and utilization, contributing to enhanced crop productivity. Additionally, the Secondary branches showed variation in biomass, ranging from 19.833 grams for Pusa Amber-16 to 28.833 grams for VPAS-120 among the genotypes. This trait represents the biomass specifically allocated, which is critical for grain development and ultimately influences yield potential. Understanding these variations in branch development and biomass among the genotypes is crucial for identifying high-yielding varieties and optimizing management practices for improved crop productivity.

Pod length varied from 4.450 cm for AL-201 to 6.750 cm for ICPL-151 among the genotypes. Pod length is a crucial yield component as it determines the length of plant and, consequently, the potential grain yield per plant. Seed yield per pod exhibited significant diversity among the different genotypes. CORG-9701 displayed the highest seed yield per pod, averaging 5.667 seeds per pod, while genotypes AL-201, GT-100, and GT-101 recorded the lowest seed yield per pod, averaging 3.333 seeds per pod. This variability highlights genetic differences in pod development and seed production potential among these chickpea genotypes. Biomass per plant ranged from 137.667 grams for ICPL-151 to 274.500 grams for Pusa-992 among the genotypes. This trait reflects the total above-ground biomass produced by individual wheat plants and serves as a key indicator of their growth and productivity. Seed yield per plot varied from 32.137 grams for Pusa Amber-16 to 104.807 grams for Pusa-992 across the genotypes. Seed yield is the ultimate goal of wheat cultivation and is influenced by various

agronomic traits such as biomass accumulation, spike characteristics, and harvest index. Harvest index ranged from 21.203% for Pusa Amber-16 to 47.430% for Pusa-992 among the genotypes. This trait represents the proportion of total biomass allocated to the grain and is an important indicator of the efficiency of resource utilization for grain production. Higher harvest index values indicate better

partitioning of assimilates towards grain formation. Similar results were also reported by Sawant *et al.* (2007) [10], for protein content, Saroj *et al.* (2013) [9] for plant height, Birhan *et al.* (2013) [12], for pods per plant for 100 seed weight and Devi *et al.* (2020) [13], for days to 50% flowering. Hence, these characters should be given due consideration while selecting for increasing yield.

Table 1: Analysis of variance different pigeon pea genotype

Genotypes name	DF	DM	PH	PB	SB	PL	SP	BP	SY	HI
ICPL-84031	77.333	137.000	159.833	13.500	24.833	6.400	4.167	187.000	57.543	31.107
AL-15	74.000	143.000	158.333	11.167	21.833	4.767	3.500	191.500	58.000	31.410
ICPL-151	94.000	141.000	158.667	11.333	21.333	6.750	5.000	137.667	38.927	28.323
ICPL-87	96.000	145.000	150.000	11.500	21.500	5.900	4.167	166.167	43.720	26.427
Pusa Amber-16	59.667	122.000	112.000	9.000	19.833	5.333	3.833	152.000	32.137	21.203
Pusa-33	96.333	146.667	244.667	14.833	25.500	6.133	5.167	242.000	95.470	39.467
Pusa-991	99.000	147.000	230.667	15.833	26.333	5.100	3.500	193.000	89.827	47.430
Pusa-992	73.333	143.667	254.000	18.500	28.500	5.933	4.500	274.500	104.807	38.400
PA-291	74.667	140.333	250.167	14.833	24.833	6.150	4.333	164.167	52.133	32.110
AL-201	78.667	142.000	191.667	11.833	24.167	4.450	3.333	161.167	56.050	34.900
Pusa-84	77.000	134.667	255.667	17.667	27.667	5.417	4.000	154.167	46.610	30.047
Paras	78.000	136.333	232.333	10.167	20.500	5.883	4.333	196.833	67.350	33.900
AL-1992	66.333	123.333	197.667	13.667	25.833	5.450	3.667	138.333	39.833	28.490
Manak	76.000	134.667	263.333	13.500	23.500	5.783	4.000	218.500	71.030	32.897
CORG-9701	74.333	139.333	230.333	15.000	25.000	6.267	5.667	177.500	68.990	40.013
VPAS-120	74.667	142.000	246.333	16.333	28.833	6.350	5.000	235.833	83.783	35.700
PAU-881	87.333	142.000	159.000	10.333	20.333	5.017	4.000	143.167	42.947	30.153
GT-100	79.333	140.667	223.000	14.833	25.333	5.467	3.667	170.333	57.017	33.603
GT-101	79.000	136.667	184.167	13.167	23.167	5.333	3.667	180.000	69.577	38.840
VCA-1	111.333	149.667	269.667	14.000	25.000	5.883	4.000	172.500	70.813	41.140
Mean	81.317	139.350	208.575	13.550	24.192	5.688	4.175	182.817	62.328	33.778
Min.	59.667	122.000	112.000	9.000	19.833	4.450	3.333	137.667	32.137	21.203
Max	111.333	149.667	269.667	18.500	28.833	6.750	5.667	274.500	104.807	47.430
C.D.	4.057	4.647	28.836	3.436	3.203	0.603	0.972	30.661	12.235	6.86
SE(m)	1.412	1.617	10.033	1.196	1.115	0.21	0.338	10.668	4.257	2.387
SE(d)	1.996	2.287	14.189	1.691	1.576	0.297	0.478	15.087	6.021	3.376
C.V.	3.007	2.01	8.332	15.282	7.98	6.386	14.027	10.135	11.83	12.24

Table 2: Estimates of PCV, GCV, heritability, and genetic advance in 20 germplasm of pigeonpea

Character	Min.	Max.	Mean	h ² (%)	GCV (%)	PCV (%)	GV	GA % means	% Contribution
DF	59.667	111.333	81.317	96.17	15.066	15.363	24.75	30.436	13.23
DM	122.00	149.667	139.350	85.553	4.891	5.287	12.985	9.318	11.77
PH	112.00	269.667	208.575	87.145	21.693	23.238	87.011	41.717	11.99
PB	9.00	18.50	13.550	53.808	16.494	22.485	3.377	24.924	7.40
SB	19.833	28.833	24.192	61.06	9.992	12.788	3.891	16.085	8.40
PL	4.450	6.750	5.66	69.752	9.699	11.613	0.949	16.686	9.60
SP	3.333	5.667	4.175	44.322	12.515	18.799	0.717	17.164	6.10
BP	137.667	274.500	182.81	77.741	19.01	21.56	63.122	34.528	10.70
SY	32.137	104.807	62.32	87.44	31.215	33.382	37.478	60.13	12.03
HI	21.203	47.430	33.78	63.654	16.198	20.303	8.992	26.622	8.76

Estimates of Phenotypic Coefficient of Variation (PCV) were determined for various traits across 20 germplasm of pigeonpea. The PCV values ranged from 15.363% to 33.382%, indicating the extent of variability present in the traits under study. Traits such as seed yield (SY) exhibited relatively higher PCV (33.382%), suggesting considerable phenotypic variation among the germplasm for this trait. On the other hand, traits like pod length (PL) showed lower PCV (11.613%), indicating comparatively lesser phenotypic variability. These PCV estimates provide valuable insights into the range of variation present in different traits within the pigeonpea germplasm, aiding in the selection of desirable genotypes for breeding programs and crop improvement initiatives.

The Genotypic Coefficient of Variation (GCV) was assessed across 20 germplasm of pigeonpea to evaluate the extent of genetic variability present in various traits. The GCV values ranged from 4.891% to 31.215%, reflecting the genetic diversity observed within the traits under investigation. Traits such as seed yield (SY) exhibited higher GCV (31.215%), indicating significant genetic variation among the germplasm for this trait. Conversely, traits like pod length (PL) showed lower GCV (9.699%), suggesting relatively lesser genetic variability. These GCV estimates offer valuable insights into the genetic diversity existing within the pigeonpea germplasm, aiding in the selection of promising genotypes for breeding endeavors and crop enhancement strategies.

The Heritability (h^2) was calculated across 20 germplasm of pigeonpea to determine the proportion of phenotypic variation attributable to genetic factors for each trait. The heritability values ranged from 44.322% to 96.17%, indicating the degree to which genetic factors contribute to the expression of these traits. Traits such as days to 50% flowering (DFF) exhibited higher heritability (96.17%), suggesting strong genetic control over this trait. Conversely, traits like seed per pod (SP) showed lower heritability (44.322%), indicating a relatively higher influence of environmental factors on the phenotypic expression. These heritability estimates provide valuable insights into the genetic basis of trait variability within the pigeonpea germplasm, essential for informed breeding decisions and selection of superior genotypes.

Genetic advance as a percentage of the mean (5%) was calculated across 20 germplasm of pigeonpea to assess the potential improvement achievable through selection for each trait. The genetic advance values ranged from 9.318% to 60.13% of the mean, indicating the magnitude of improvement that can be attained through selection within the population. Traits such as seed yield (SY) exhibited higher genetic advance (60.13% of the mean), suggesting substantial scope for improvement through breeding efforts. Conversely, traits like pod length (PL) showed lower genetic advance (16.686% of the mean), indicating relatively limited potential for improvement through selection. These genetic advance estimates provide valuable guidance for breeders in prioritizing traits for selection and breeding strategies to enhance pigeonpea productivity and quality.

The percent contribution was calculated across 20 germplasm of pigeonpea to determine the relative importance of each trait towards overall variation. The percent contribution values ranged from 6.10% to 13.23%, indicating the proportion of trait variation contributed by each trait. Traits such as days to 50% flowering (DFF) exhibited higher percent contribution (13.23%), suggesting a significant impact on overall trait variability. Conversely, traits like seed per pod (SP) showed lower percent contribution (6.10%), indicating a relatively lesser influence on overall trait variation. These percent contribution estimates offer insights into the relative importance of each trait in contributing to the overall variability within the pigeonpea germplasm, aiding breeders in prioritizing traits for selection and breeding program. The difference in magnitude between Genetic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) was minimal for all traits, indicating a reduced influence of environmental factors on trait expression. Several studies, including those conducted by Ranjani *et al.* (2021)^[8], have reported minimal variation between GCV and PCV for various characteristics in pigeonpea. According to Burton (1952), this suggests that the observed variability in the traits is predominantly due to genetic factors rather than environmental influences.

Conclusion

The trait seed yield per plant exhibited high heritability alongside moderate genetic advance as a percentage of the mean, suggesting considerable genetic diversity and potential among the studied genotypes. Percent contribution across 20 pigeonpea germplasms revealed varying importance of traits in overall variation, ranging from 6.10%

to 13.23%. Traits like days to 50% flowering (DFF) showed higher contribution (13.23%), while seed per pod (SP) displayed lower contribution (6.10%). Minimal disparity between Genetic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) suggests limited environmental influence on trait expression. Notably, there was a significant positive correlation between seed yield per plant and both plant height and pods per plant at both genotypic and phenotypic levels. Consequently, directly selecting for these traits could prove beneficial for further enhancing seed yield in pigeon pea.

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