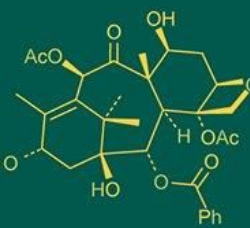
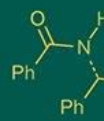
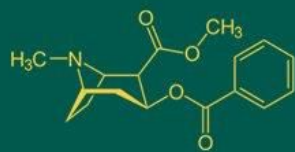


International Journal of Advanced Biochemistry Research



ISSN Print: 2617-4693
ISSN Online: 2617-4707
NAAS Rating (2026): 5.29
IJABR 2026; SP-10(4): 110-118
www.biochemjournal.com
Received: 04-02-2026
Accepted: 06-03-2026

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Unveiling variability in F₃ pigeonpea populations for crop improvement

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DOI: <https://www.doi.org/10.33545/26174693.2026.v10.i4Sb.8066>

Abstract

Pigeonpea (*Cajanus cajan*), a hardy and climate-resilient legume of global importance, occupies a pivotal position in Indian agriculture. Its adaptability to diverse environments and contribution to food and nutritional security make it a prime focus for genetic improvement. To explore its variability, an F₃ population was evaluated during the 2023 cropping season at Nagaland University using 16 breeding lines and two checks in a randomized block design. Significant genetic variability was observed across qualitative traits (stem, flower, pod, seed, and leaflet characteristics) and quantitative traits (flowering, maturity, plant height, branching, pod and seed attributes, and yield). High heritability coupled with high genetic advance was recorded for traits such as secondary branches, pods per plant, yield, and flowering duration, indicating additive gene action and suitability for direct selection. Correlation and path coefficient analyses identified pod bearing length, number of pods per plant, and seeds per pod as the most important yield-contributing traits, both directly and indirectly. Among the genotypes, NUPPC 30A emerged as the best performer, followed by NUPPC 32C and NUPPC 29C, while NUPPC 31C showed earliness in flowering and maturity. The study underscores the potential of exploiting genetic variability to develop superior, high-yielding pigeonpea cultivars, thereby strengthening India's long-term pulse productivity and agricultural resilience.

Keywords: Correlation, path coefficient, nuppc, maturity

Introduction

Pigeon pea (*Cajanus cajan*) is the sixth most important edible legume crop worldwide, valued for its adaptability, rapid growth, and resilience in semi-arid tropical regions (Abebe, 2022; Emefiene *et al.*, 2014) ^[1, 11]. It is a short-lived perennial, often cultivated as an annual, with a deep root system that enhances drought tolerance and soil stability. Globally, India is the largest producer, accounting for nearly 70% of the cultivated area, followed by Myanmar, Malawi, Tanzania, and Kenya (Emefiene *et al.*, 2014) ^[11].

In India, red gram (pigeon pea) covered 40.42 lakh hectares in 2023-24, slightly lower than 40.68 lakh hectares in 2022-23. The major producing states include Karnataka (13.37 lakh ha), Maharashtra (11.11 lakh ha), Uttar Pradesh (3.50 lakh ha), Andhra Pradesh (2.32 lakh ha), Gujarat (2.27 lakh ha), and Jharkhand (1.85 lakh ha). National production during 2023-24 was projected at 33.85 lakh tonnes (ANGRAU, 2023-24) ^[2]. These figures highlight the crop's central role in Indian agriculture, particularly in semi-arid zones.

It is rich in protein (22.3%), carbohydrates (57.6%), minerals (3.5%), fiber (1.5%), and energy (335 kcal/100 g), with key micronutrients like Ca (73 mg), P (304 mg), and Fe (5.8 mg/100 g), making it vital in protein-deficient regions (DPD, n.d.; Abebe, 2022) ^[1]. Entire plants are used for food, fodder, fuelwood, and green manure, while improving soil fertility through nitrogen fixation and erosion control (Rana & Kaushik, 2018; CGIAR, 2019; Choudhary *et al.*, 2011; Vartapetian & Jackson, 1997) ^[6, 8, 20, 30]. Economically, it supports flour, noodles, biscuits, and bread industries (Fatokimi & Tanimonure, 2021) ^[12], and medicinally it is linked to anti-inflammatory, antibacterial, antioxidant, anticarcinogenic, and antidiabetic properties in traditional systems (Emefiene *et al.*, 2014; Abebe, 2022) ^[1, 11].

India is not self-sufficient in pigeon pea because its domestic demand consistently exceeds national production, creating a persistent reliance on imports to meet consumption needs, as highlighted by Legume Research, which notes that "although India is the largest producer of pulses in the world, its domestic demand outstrips domestic production and the shortfall

is met from imports” (Singh *et al.*, 2022) [28]. This continual supply deficit underscores the urgent need to develop high-yielding and stable pigeon pea varieties to enhance productivity and move the country toward long-term self-reliance. Given the crop’s cross-pollinated nature (20-70%) and its diploid chromosome number ($2n = 22$), pigeon pea possesses substantial genetic diversity that can be effectively exploited in breeding programs (Mallikarjuna *et al.*, 2014) [16]. In this context, the present study on variability in the F_3 population aims to assess the extent of variability among segregating lines, analyze the association between yield and key yield-attributing traits, and identify promising lines that can be advanced for the development of superior, high-yielding cultivars.

Materials and Methods

The present study on Variability studies in F_3 population of Pigeon pea [*Cajanus cajan* (L.) Millspaugh] was conducted during the 2023 cropping season at the Department of Genetics and Plant Breeding experimental farm, Nagaland University, SAS, Medziphema Campus, located at 305 m above sea level under subtropical climatic conditions. Sixteen breeding lines along with two check varieties from the AICRP (Pigeonpea) program were evaluated in a randomized block design with two replications, maintaining 60 cm × 20 cm spacing. Standard land preparation and sowing practices were followed, and intercultural operations were carried out as per recommended guidelines. Observations were recorded on five randomly selected plants per replication for quantitative traits such as plant height, number of branches, flowering and maturity duration, pod and seed attributes, and seed yield, along with qualitative traits including stem colour, growth habit, flower colour, pod form, seed shape, and seed coat characteristics. The plot means were subjected to analysis of variance, estimation of genetic parameters, correlation studies, and path coefficient analysis to assess variability and trait associations with yield. During the crop period, temperatures ranged from a maximum of 36.9°C to a minimum of 8.2°C, relative humidity varied between 97% and 42%, and rainfall fluctuated from 123.6 mm to negligible levels. Meteorological data were obtained from ICAR, Jharnapani.

Results and discussions

The results and discussion section provides a detailed account of the variability, heritability, genetic advance,

correlation, and path coefficient effects observed among the pigeon pea genotypes studied.

Qualitative traits

Eleven qualitative traits were studied across breeding lines and check varieties. Stem colour was predominantly green, with NUPPC-29D showing minor segregation (11% purple). All lines exhibited erect growth habit and indeterminate flowering. Base flower colour showed wide segregation, ranging from uniform yellow in checks (PA-291, UPAS-120, NUPPC-32D) to mixtures of yellow, red, ivory, and light yellow in breeding lines. Pod colour was largely mixed, though several lines segregated into purple and green types. Pod form was mostly cylindrical, with varying proportions of flat pods in segregating lines. Seed shape ranged from oval (uniform in checks) to square, globular, and elongate in breeding lines. Base seed colour was predominantly light brown, with cream variants in some lines and dark purple restricted to NUPPC-29D. Seed colour pattern varied from plain (uniform in checks) to mottled and speckled in segregating lines. Leaflet shape was lanceolate in checks, while breeding lines showed segregation into broad and narrow elliptical forms. Overall, check varieties remained uniform, whereas breeding lines exhibited segregation for most qualitative traits, confirming variability within the F_3 population.

ANOVA

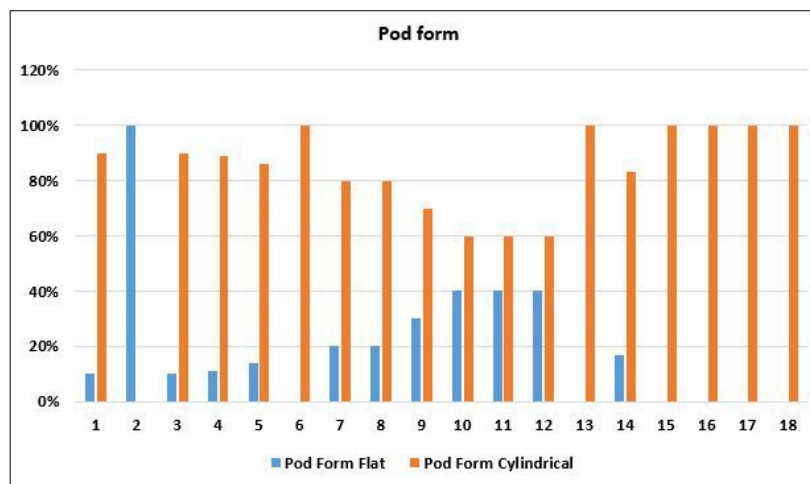
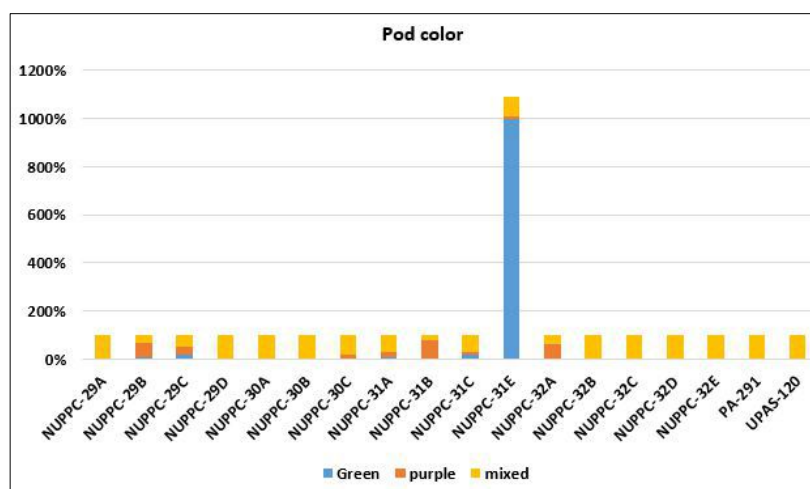
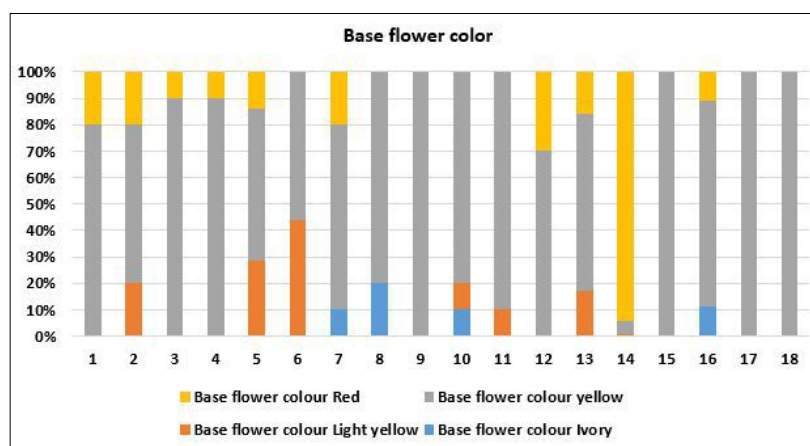
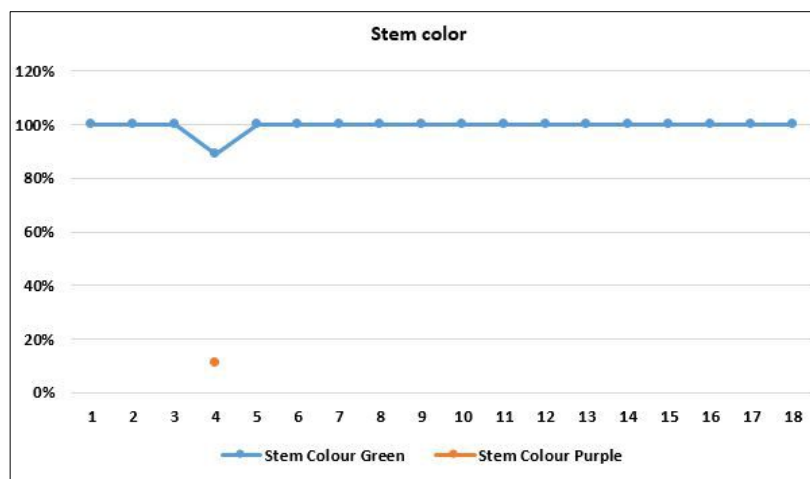
The analysis of variance showed clear and significant differences across all quantitative traits, confirming wide genetic variability in the F_3 pigeonpea population. Days to 50% flowering ranged from 98 to 149 days, while days to maturity varied between 151 and 271 days, indicating both early and late maturing types. Plant height ranged from 207 cm to 337 cm, reflecting variation in plant stature.

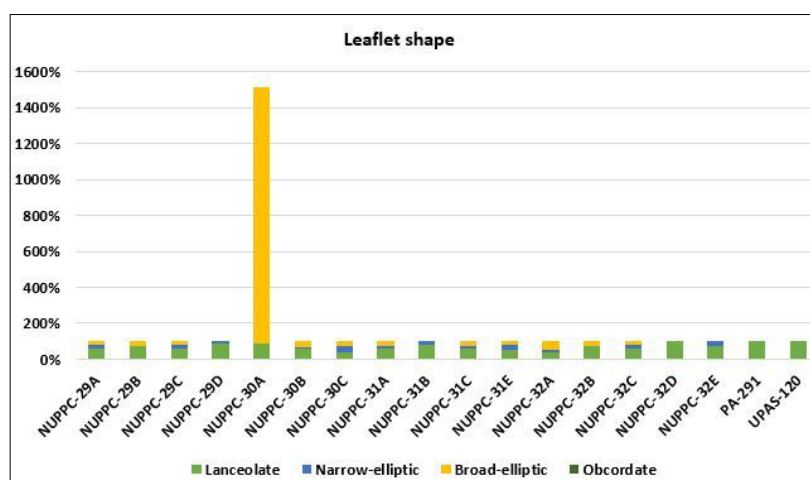
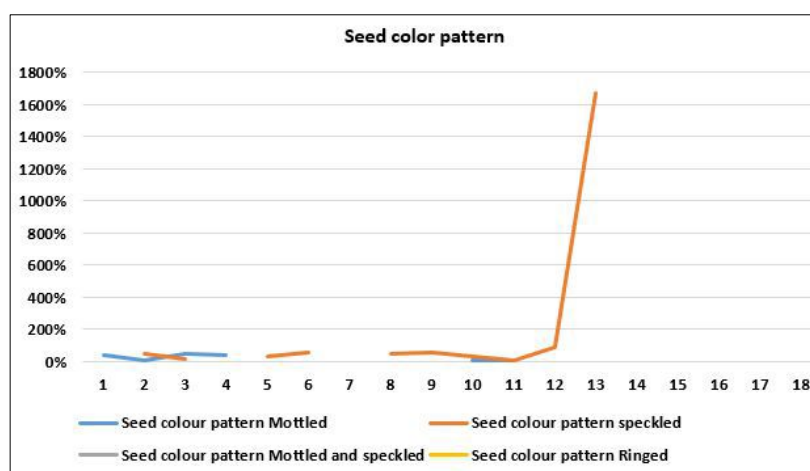
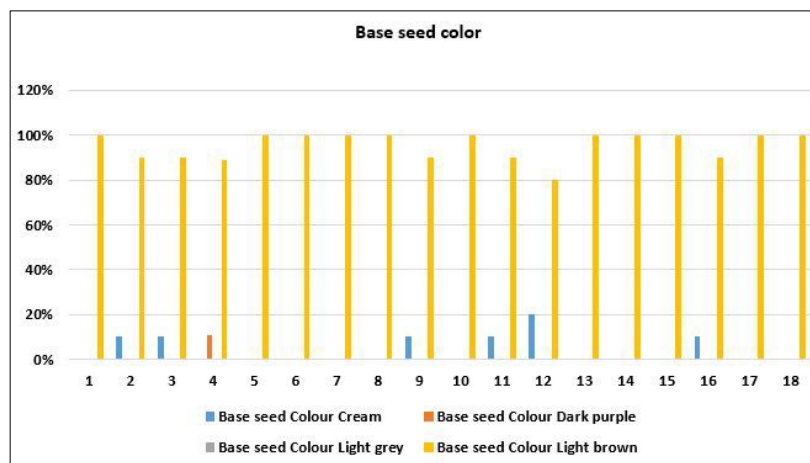
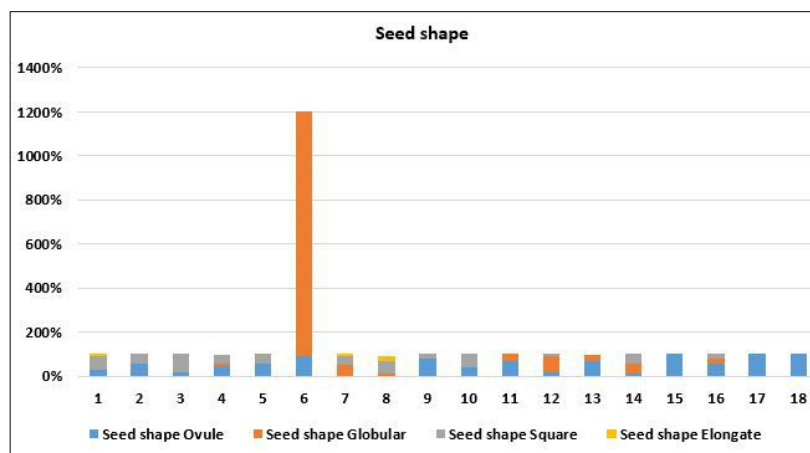
Branching traits also showed diversity, with primary branches per plant ranging from 12 to 29 and secondary branches per plant from 4 to 59. Pod bearing length varied between 71 cm and 154 cm, while pods per cluster ranged from 2.2 to 3.7. The number of pods per plant ranged from 127 to 363, and seeds per pod varied between 4.2 and 5.3.

Seed traits showed further variability, with 100-seed weight ranging from 10.7 g to 14 g, and seed yield per plant ranging from 21 g to 103 g. Overall, the presence of such variation across flowering, maturity, plant stature, branching, pod traits, seed size, and yield highlights the importance of these characters in selection and breeding programs aimed at developing high-yielding pigeonpea varieties.

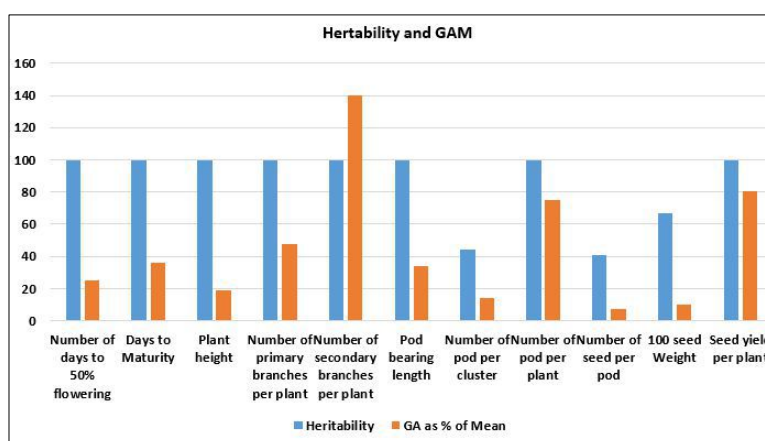
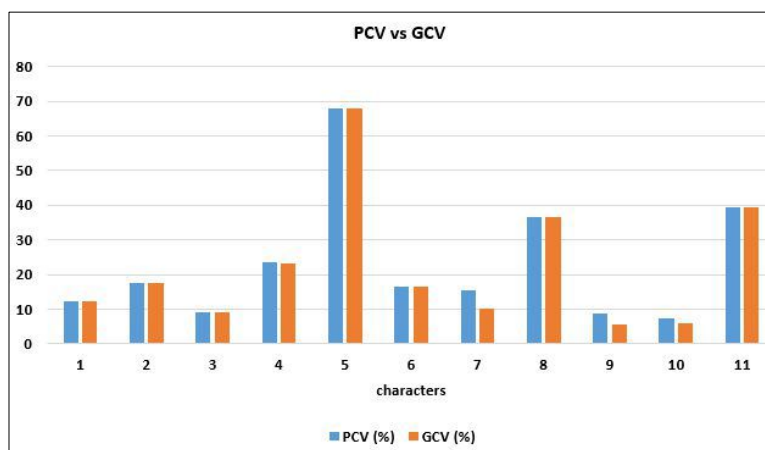
Table 1: Analysis of variance for 11 characters in pigeonpea lines

Sources of variations	Degree of freedom	Number of days to 50% flowering	Days to maturity	Plant height	Number of primary branches per plant	Number of secondary branches per plant	Pod bearing length	Number of pods per cluster	Number of Pods per plant	Number of seeds per pod	100 seed weight (g)	Yield Per plant
Replication	1	39.564	41.796	46.535	22.468	28.891	31.491	8.604	7.887	11.583	33.120	20.839
Genotypes	17	428.970**	3095.656**	1414.362*	48.240*	353.088*	737.648*	0.273*	8606.459*	0.231*	1.331*	929.903**
Error	17	0.166	0.180	0.096	0.137	0.121	0.148	0.106	0.189	0.098	0.264	0.180
CD (%)		0.858	0.894	0.653	0.782	0.733	0.810	0.687	0.917	0.660	1.084	0.896
CV		0.336	0.189	0.107	1.762	1.781	0.332	11.417	0.242	6.647	4.251	0.773





Quantitative traits



Genetic Parameters

The study revealed that phenotypic variance was consistently higher than genotypic variance, underscoring the role of environmental factors in trait expression. Traits such as number of pods per plant and secondary branches per plant showed the widest variability, a trend also emphasized by Rangare *et al.* (2013) and Rekha *et al.* (2013) [22, 24]. In contrast, number of seeds per pod exhibited

the least variability, reflecting the relative stability of this trait as noted by Saroj *et al.* (2013) and Singh *et al.* (2013) [25, 29]. This pattern highlights that while certain traits remain stable across environments, others such as branching and pod number provide greater scope for genetic improvement through selection, a conclusion further supported by Ram *et al.* (2016) and Hemavathy *et al.* (2019) [13, 18].

Table 2: Genetic parameters for 11 quantitative characters of pigeonpea

S.No	Traits	Range	MEAN $\pm$ Sem	Phenotypic variance	Genotypic variance	PCV (%)	GCV (%)	Heritability	GA as % of Mean
1	Number of days to 50% flowering	98.220-148.955	121.048 $\pm$ 0.29	21.222	21.317	12.101	12.096	99.923	24.909
2	Days to Maturity	111.295-270.730	224.19 $\pm$ 0.30	39.356	38.387	17.549	17.548	99.988	36.147
3	Plant height	207.465-337.090	287.96 $\pm$ 0.19	7.746	7.680	9.235	9.234	99.986	19.021
4	Number of primary branches per plant	12.525-26.940	21.02 $\pm$ 0.26	11.442	11.218	23.397	23.331	99.433	47.925
5	Number of secondary branches per plant	4.015-58.905	19.51 $\pm$ 0.25	174.272	174.675	68.130	68.106	99.932	140.251
6	Pod bearing length	70.510-153.590	115.73 $\pm$ 0.27	38.075	38.106	16.597	16.594	99.960	34.176
7	Number of pod per cluster	2.175-3.655	2.87 $\pm$ 0.21	0.183	0.1047	15.252	10.113	43.967	13.814
8	Number of	104.085-	179.92 $\pm$ 0.17	380.681	380.508	36.449	36.448	99.996	75.081

	pod per plant	362.660							
9	Number of seed per pod	4.155-5.255	4.70 ± 0.22	0.016	0.067	8.617	5.484	40.499	7.189
10	100 seed Weight	10.730-13.975	12.00 ± 0.30	0.079	0.537	7.391	6.046	66.924	10.190
11	Seed yield per plant	22.095-103.240	54.94 ± 0.31	466.029	465.256	39.243	39.236	99.961	80.810

The study revealed high GCV and PCV for traits like secondary branches per plant, seed yield, and number of pods per plant, suggesting strong genetic variability and potential for selection, as earlier emphasized by Bhadru (2010) [4]. Moderate values were observed for traits such as flowering time and pod-bearing length, consistent with the findings of Rangare *et al.* (2013) and Rekha *et al.* (2013) [22, 24]. In contrast, plant height, seeds per pod, and seed weight showed low variability, a pattern also noted by Meena *et al.* (2017) [17]. For several traits, GCV values were close to PCV values, indicating minimal environmental influence and high heritability, whereas traits with larger differences were more environmentally sensitive, a conclusion reinforced by Hemavathy *et al.* (2019) [13]. Collectively, these findings highlight the scope for exploiting genetic variability in crop improvement.

Broad sense heritability and Genetic advance

Heritability and genetic advance are important indicators for plant breeders, as they show how much of trait variation is genetic and how much improvement can be expected through selection. In this study, most traits showed high heritability (>60%), except pods per cluster (43.97%) and seeds per pod (40.50%). Heritability ranged from 40.50% (seeds per pod) to 99.99% (pods per plant). Genetic advance was highest for secondary branches per plant (140.13%), followed by yield per plant (80.81%) and pods per plant (75.08%), while seeds per pod recorded the lowest (7.19%). Traits such as secondary branches, pods per plant, yield, primary branches, days to maturity, and days to 50% flowering showed both high heritability and high genetic advance, indicating additive gene action and their suitability for direct selection. Similar results were reported by Kumara *et al.* (2013), Rangare *et al.* (2013), Sharma *et al.* (2014), Saroj *et al.* (2015), and Chethana *et al.* (2015) [7, 15, 22, 25, 27]. In contrast, plant height and test weight showed high heritability but low genetic advance, suggesting complex inheritance and non-additive gene effects, as also noted by Arshad *et al.* (2003) [3]. Overall, traits under additive control

can be effectively improved through selection, while traits with complex inheritance may require alternative breeding approaches.

Correlation studies

The analysis included computation of simple correlation coefficients at both phenotypic and genotypic levels for nine characters, with significance tested at the 5% and 1% levels. Seed yield per plant showed a significant positive association with pod bearing length, number of pods per plant, and number of seeds per pod, and the correlations were stronger at the genotypic level, suggesting that these traits are largely governed by genetic factors. Pod bearing length and number of pods per plant emerged as the most important yield-contributing traits, which agrees with the findings of Sawant *et al.* (2009) and Bhadru (2010) [4, 26], while the positive association of seeds per pod with yield was also reported by Jogendra (2018). These results indicate that selection for pod bearing length, pods per plant, and seeds per pod would be effective in developing high-yielding pigeon pea genotypes.

Path coefficient Analysis

Path coefficient analysis revealed that number of pods per plant exerted the highest positive direct effect on seed yield, followed by pod bearing length and seeds per pod, which agrees with earlier findings in pigeon pea by Saroj *et al.* (2013) and Ramesh *et al.* (2017) [19, 25]. Pods per cluster, days to maturity, primary branches per plant, and days to 50% flowering also showed positive direct contributions, consistent with reports by Devi *et al.* (2012) and Rao *et al.* (2013) [10, 23]. Positive indirect effects were mainly expressed through number of pods per plant, with pod bearing length and seeds per pod contributing substantially via this pathway, as observed by Birhan *et al.* (2013) [5]. Overall, the study highlights number of pods per plant and pod bearing length as the most important yield-contributing traits, both directly and indirectly, suggesting that selection for these characters would be effective in improving pigeon pea yield.

Table 3: Genotypic correlation coefficient of yield and its contributing characters

	Number of days to 50% flowering	Days to maturity	Plant height	Number of primary branches per plant	Number of secondary branches per plant	Pod bearing length	Number of pods per cluster	Number of Pods per plant	Number of seeds per pod	100 seed weight (g)	Yield per plant
Number of days to 50% flowering	1	0.402*	0.470**	-0.364*	0.597**	0.306	0.473**	0.278	0.358*	-0.360*	0.312
Days to Maturity		1	0.331*	0.227	0.116	0.137	0.31	0.091	-0.421*	-0.004	0.079
Plant height			1	0.141	0.540**	0.699**	0.710**	0.032	0.304	-0.086	0.083
Number of primary branches per plant				1	-0.327	-0.02	-0.247	-0.419*	-0.430**	0.021	-0.341
Number of					1	0.318	0.642**	0.204	0.778**	0.027	0.258

secondary branches per plant											
Pod bearing length						1	0.431**	0.236	0.318	0.047	0.334*
Number of pod per cluster							1	0.247	0.490**	0.041	0.306
Number of pod per plant								1	0.713**	-0.093	0.902**
Number of seed per pod									1	-0.176	0.664**
100 seed Weight										1	-0.165
Yield per plant											1

Table 4: Phenotypic correlation coefficient of yield and its contributing characters

	Number of days to 50% flowering	Days to maturity	Plant height	Number of primary branches per plant	Number of secondary branches per plant	Pod bearing length	Number of pods per cluster	Number of Pods per plant	Number of seeds per pod	100 seed weight (g)	Seed yield per plant
Number of days to 50% flowering	1	0.402*	0.470**	-0.364*	0.596**	0.306	0.311	0.278	0.226	-0.284	0.312
Days to Maturity		1	0.331*	0.226	0.116	0.137	0.202	0.091	-0.266	-0.003	0.079
Plant height			1	0.141	0.539**	0.699**	0.467**	0.032	0.191	-0.072	0.083
Number of primary branches per plant				1	-0.325	-0.021	-0.157	-0.418*	-0.269	0.008	-0.340
Number of secondary branches per plant					1	0.317	0.420*	0.204	0.496**	0.027	0.258
Pod bearing length						1	0.289	0.236	0.204	0.038	0.334*
Number of pod per cluster							1	0.165	0.344*	-0.072	0.202
Number of pod per plant								1	0.454**	-0.076	0.901**
Number of seed per pod									1	-0.12	0.427**
100 seed Weight										1	-0.13
Seed yield per plant											1

Table 5: Estimate of direct (diagonal) and indirect effects of yield component at genotypic level in pigeonpea

	Number of days to 50% flowering	Days to maturity	Plant height	Number of primary branches per plant	Number of secondary branches per plant	Pod bearing length	Number of pods per cluster	Number of Pods per plant	Number of seeds per pod	100 seed weight (g)	Seed yield per plant
Number of days to 50% flowering	1	0.402*	0.470**	-0.364*	0.596**	0.306	0.311	0.278	0.226	-0.284	0.312
Days to Maturity		1	0.331*	0.226	0.116	0.137	0.202	0.091	-0.266	-0.003	0.079
Plant height			1	0.141	0.539**	0.699**	0.467**	0.032	0.191	-0.072	0.083
Number of primary branches per plant				1	-0.325	-0.021	-0.157	-0.418*	-0.269	0.008	-0.340
Number of secondary branches per plant					1	0.317	0.420*	0.204	0.496**	0.027	0.258
Pod bearing length						1	0.289	0.236	0.204	0.038	0.334*
Number of pod per							1	0.165	0.344*	-0.072	0.202

cluster											
Number of pod per plant								1	0.454**	-0.076	0.901**
Number of seed per pod									1	-0.12	0.427**
100 seed Weight										1	-0.13
Seed yield per plant											1

Table 6: Mean performance in respect of 11 characters for F₃ lines of pigeonpea

	Seed yield per plant (g)	Number of days to 50% flowering	Days to maturity	Plant height	Number of primary branches per plant	Number of secondary branches per plant	Pod bearing length	Number of pods per cluster	Number of Pods per plant	Number of seeds per pod	100 seed weight (g)
NUPPC-29A	54.085	149	271	293.655	21.120	28.615	121.330	2.830	159.010	4.780	11.320
NUPPC-29B	37.310	104	239	278.715	26.940	9.895	88.595	2.435	148.680	4.350	11.345
NUPPC-29C	78.840	112	240	295.350	25.810	35.160	126.580	2.635	214.475	4.755	12.190
NUPPC-29D	69.060	107	211	275.615	16.570	24.685	120.650	3.220	175.645	4.685	12.200
NUPPC-30A	103.240	135	226	278.665	15.485	46.090	135.290	3.055	362.660	5.200	11.780
NUPPC-30B	65.895	131	231	284.305	22.320	14.035	126.71	2.365	186.100	4.350	11.515
NUPPC-30C	62.300	143	225	337.090	13.880	58.905	131.140	3.160	200.495	5.255	11.320
NUPPC-31A	44.360	133	190	295.895	21.415	6.425	114.330	2.790	153.625	5.000	10.730
NUPPC-31B	43.980	107	179	311.235	20.245	5.900	153.590	2.695	184.595	4.565	12.490
NUPPC-31C	38.575	98	151	207.465	14.805	4.990	70.510	2.175	143.055	4.795	12.325
NUPPC-31E	35.855	131	233	323.900	18.485	29.485	121.510	3.655	127.625	4.805	12.785
NUPPC-32A	42.925	123	253	285.275	25.680	7.420	100.255	3.215	113.385	4.155	10.965
NUPPC-32B	70.195	111	179	303.615	28.985	10.385	105.115	3.075	187.020	5.250	12.875
NUPPC-32C	86.005	135	254	273.585	12.525	43.250	135.3050	3.095	293.985	4.750	12.755
NUPPC-32D	20.740	119	254	289.960	25.095	24.020	98.280	2.535	125.505	4.255	13.975
NUPPC-32E	37.255	119	243	282.695	19.860	8.995	111.350	2.545	104.085	4.240	12.755
PA-291	66.410	111	254	295.010	23.440	4.015	113.100	2.990	233.055	4.805	11.720
UPAS-120	32.095	108	200	271.605	25.710	8.835	109.385	2.890	126.595	4.695	12.440
Overall Mean	54.951	121.048	224.189	287.980	21.021	19.506	115.724	2.853	179.977	4.705	12.083
CD(%)	0.896	0.858	0.894	0.653	0.733	0.810	0.687	0.917	0.660	0.660	1.084
CV	0.773	0.336	0.189	0.107	1.762	1.781	0.332	11.417	0.242	6.647	4.251

Conclusion

Significant variability was observed among the genotypes, with pod bearing length, number of pods per plant, and number of seeds per pod identified as the most important characters for yield improvement. Among the lines evaluated, NUPPC-30A was the best performer, showing high values in traits positively correlated with seed yield, followed by NUPPC-32C and NUPPC-29C, which also recorded high pod numbers, pod bearing length, and seed yield. NUPPC-31C exhibited the least days to 50% flowering and maturity, making it a potential genotype for use in breeding programs.

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