GENETIC PARAMETERS AND MULTIVARIATE ANALYSIS OF EARLY MATURING PIGEON PEA (*CAJANUS CAJAN*, LINNAEUS AND MILLSPAUGH) GENOTYPES

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ABSTRACT

Pigeon pea *(Cajanus cajan* L. Millsp.*) is regarded as underutilised despite its nutritive values and enormous potential for food security. An adequate understanding of the genetics of its earliness in maturity will foster rapid progress in selection for early maturity. Hence, the study aimed to identify early maturing pigeon pea genotypes and further evaluate the genetic parameters. Early maturing pigeon peas (n = 22; days to 50% maturity (D50M) < 160 days) were identified among genotypes collected from ICRISAT, Niamey, Niger through evaluation for maturity. These were planted in polyethene pots containing 2 kg of soil after conducting viability tests in a randomised complete block design with three replications. The study examined 13 quantitative traits. Results revealed variation in traits evaluated among genotypes. Traits such as days to 50% flowering (D50F), pod length, pod number (PDN), plant height, D50M, and seeds per pod, contributed to the variations accounted for by the principal component analysis (PC1 = 41.88%). Environmental variations, a summation of genotype by environment interactions (GEI), specific and general environmental variances were higher than genotypic variations for D50F and D50M implying more environmental influence than genetics in these traits. Unsurprisingly, there was a strong and positive significant correlation between D50F and D50M genotypically (rg = 0.65, p < 0.01) and phenotypically (rp = 0.83, p < 0.01). Only PDN showed a strong and positive significant correlation with both D50F (rg = 0.37, rp = 0.95, p < 0.01) and D50M (rg = 0.96, rp = 0.48, p < 0.01). These traits can be harnessed for early-maturity identification in pigeon peas and improvement programmes in pigeon peas.*

Keywords: ***Flowering, Genetics, Maturity, Pigeon pea, Variation***

INTRODUCTION

Pigeon pea (*Cajanus cajan* L. Millsp.) is a nutritious legume with enormous potential for food security. It is a perennial legume that belongs to the family Fabaceae and is widely grown in tropical and subtropical regions of the world, including Africa, the Caribbean, South Asia, and Latin America (Sarkar *et al*., 2018). It is used for a variety of purposes, including food, animal feed, fuel, and green manure. Pigeon pea is a good source of protein, carbohydrates, dietary fibre, and essential vitamins and minerals such as folate, iron, and potassium (Rabia and Ying, 2018). It significantly enhances food and feed security across continents such as Africa, Asia, and South America (Martinez-Villaluengaa *et al*., 2010)

The annual production of pigeon peas varies by region and country. According to the Food and Agriculture Organisation of the United Nations (FAO, 2021), India, Myanmar, Malawi, Tanzania, and

Mozambique are the top five pigeon pea-producing countries. India is the largest producer of pigeon pea, accounting for more than 78.9% of the world's production (FAO, 2021). In 2020, the global production of pigeon peas was estimated to be around 5.8 million tonnes on a 7.03-million-hectare land area (FAOSTAT, 2020). Its production in Nigeria is not properly documented, however, available data estimate its production to be on an area of about 190,000 hectares of land (Egbe, 2005).

According to Kumawat *et al*. (2012), the average productivity of pigeon peas has been low and stagnant over the last fifty years. Productivity constraints such as low genetic potential, varieties with low harvest index, poor plant type, long crop duration etc. are factors leading to poor crop management (Odeny *et al*., 2007). In a study by Zavinon *et al*. (2018), the maturity cycle was one of the five preference criteria with variable importance used by farmers to adopt pigeon pea landraces. At the same time, Saxena *et al*. (2018) stated that the long duration of traditional pigeon pea cultivars has compelled farmers into intercropping it with short-aged cereals and other legumes. Potential targets for increasing pigeon pea productivity per unit area and time will involve the exploitation of hybrid vigour, restructuring of plant type and early maturity (Saxena, 2008; Kumawat *et al*. 2012).

Pigeon pea is commonly cultivated in association with other short-duration crops such as sorghum, maize, millet, cotton, groundnut, and even other pulses like mung bean and urad bean (Singh *et al*., 2018). When it is intercropped with a crop of a shorter duration, the other crop can be sowed with a density almost as high as a sole crop and can be harvested before the pigeon pea plants grow too big (Mula and Saxena, 2010). Pigeon pea plants can quickly grow to their full size with a canopy once the other short-duration crop is harvested. Reports are indicating that intercropping pigeon peas with such short-duration crops reduces their yield because of the low planting density (Saxena *et al*., 2018).

Traditional pigeon peas are more like their wild species (*C. cajanifolius*), maturing in 170-180 days or more (Varshney *et al*., 2017). Landraces in many centres of origin have similar flowering/maturity durations as the wild progenitor (Saxena *et al.*, 2018). The longer growth cycle has the advantage of being adapted to certain agroecological conditions, such as regions with extended growing seasons. However, it can also be a drawback in terms of agricultural productivity and commercial viability (Kumawat *et al*., 2012). Extended growth cycles may limit the number of crops that can be cultivated in a year and delay the availability of harvest, potentially affecting market demands and farmer's income (Kumawat *et al.*, 2012).

The few breeding works on pigeon peas have centred on the production of varieties that are resistant to diseases and have shorter growth durations. Additionally, various varieties have been developed to cater to diverse agroclimatic conditions, crop seasons, and durations, whether for intercropping or sole cropping (Singh *et al.*, 2016). However, these varieties are not widespread, so researchers in different regions are trying to produce more varieties better adapted to diverse environmental conditions. There is also the challenge of variation in the timing of pod maturation. Asynchrony of pod maturity poses a major challenge in identifying pigeon pea genotypes that mature early (Saxena *et al*., 2018).

In Nigeria, as in most other African countries that produce pigeon peas, farmers cultivate their local varieties, which take a long time to mature. Ayenan *et al*. (2017) observed that the majority of farmers store their seeds for subsequent seasons, are given seeds as gifts, or buy them from the local markets. This means that the long-duration seeds which are mostly low-yielding are planted season after season. The implication of this is that the traditional farmers will leave the crop for other crops that mature early with a better return on investment. Although regarded as underutilised, identifying and understanding the genetics of early maturity in pigeon peas will foster improvement programmes especially where there are no improved varieties in a country like Nigeria. Hence, the study was aimed at identifying early-maturing genotypes and evaluating for factors such as days to 50% flowering, days to 50% maturity, number of pods, seeds per pod, seed weight, pod length, and overall plant yield.

MATERIALS AND METHODS

Samples Collection and Planting

A total of 44 pigeon pea accessions (Table 1) collected from the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Niamey, Niger and a local check (making a total of 45 accessions) were evaluated for early maturity, from which only 22 were early maturing genotypes that were analysed in the study (Figure 1). After conducting viability tests, sample seeds from these 45 genotypes were planted in 2 kg polyethene pots laid out in a randomised complete block design with three replications. Plants were thinned down to one per pot two weeks after germination and standard agronomic practices such as watering, weeding, and fumigating were carried out appropriately. The crops were watered every other day during establishment, and later, they were watered once a week. Weeds were removed three times before flowering, and fumigation was carried out using dedevap (Sniper) at 0.5ml/l and endosulfan when insect infestations were noticed.

Phenotypic Evaluation

The study examined 13 quantitative traits according to the International Plant Genetic Resources Institute (IPGRI) and International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) (IPGRI & ICRISAT, 1993). These traits include leaflet length, leaflet width, days to 50% flowering, pod length, pod number, seeds per pod, plant height, primary branches, secondary branches, tertiary branches, days to 50% maturity, 100 seed weight, and seed yield per plant (Table 2).

Analysis of data

The statistical analysis of the morphological data collected from the screen-house evaluation was conducted using R 4.2.1 and RStudio (R Core Team, 2022). Analysis of variance (ANOVA) was employed to test the differences in accession performance. Traits contribution among early-maturing genotypes was assessed using Principal Component Analysis (PCA) and traits with high factor loading (factor loading close to 1 or -1) were used to construct a path analysis for early maturity using the Ωnyx software (von Oertzen *et al*., 2015). In factor analysis, researchers commonly use an approach focused on the highest factor loading with a predetermined cutoff for item inclusion. Items with factor loadings surpassing a specified cutoff value are retained. The cutoff choice, such as 0.40 for leniency or 0.60–0.70 for stringency, determines item inclusion on a liberal-to-conservative scale (Matsunaga, 2010). Another method involves assessing both the highest and second-highest factor loadings for a more thorough analysis (Matsunaga, 2010). Genetic parameters were evaluated

according to Amusa *et al*. (2022) as stated below;

Environmental variance (Ve)

$$\text{Ve} = \text{Residual mean Square}$$

Genotypic variance (Vg)

$$\text{Vg} = \frac{\text{Genotype mean square} - \text{Residual mean sqaure}}{\text{Number of replicates (r)}}$$

Phenotypic variance (Vp)

$$\text{Vp} = \text{Vg} + \frac{\text{Ve}}{\text{r}}$$

Environmental Coefficient of Variance (GCV)

$$\text{ECV} = \sqrt{\frac{\text{Ve}}{\text{Mean}}} \times 100$$

Genotypic Coefficient of Variance (GCV)

$$\text{GCV} = \sqrt{\frac{\text{Vg}}{\text{Mean}}} \times 100$$

Phenotypic Coefficient of Variance (PCV)

$$\text{PCV} = \sqrt{\frac{\text{Vp}}{\text{Mean}}} \times 100$$

Heritability (H^2)

$$\text{H}^2 = \frac{\text{Vg}}{\text{Vp}}$$

Genetic Advance

$$\text{GA} = \text{K}\sqrt{\text{Vg}}\text{H}^2$$

Genetic Advance as a percentage of mean (GA%)

$$\text{GA}(\%) = \frac{\text{GA}}{\text{Mean}} \times 100$$

Phenotypic and genotypic correlations were estimated according to Blanco-Fuentes *et al*. (2022) while path analysis was done for early maturity using the variability package in R (Popat *et al*., 2021)

Phenotypic correlation (rp)

$$\text{rp} = \frac{\text{COVp}_{(\text{xy})}}{[\sigma^2{}_{(x)}\ \sigma^2{}_{(y)}]^{½}}$$

Genotypic correlation (rg)

$$\text{rg} = \frac{\text{COVg}_{(\text{xy})}}{[\sigma^2{}_{(x)}\ \sigma^2{}_{(y)}]^{½}}$$

Where rp, rg and $\text{COV}_{(\text{xy})}$ are the phenotypic and genotypic correlations and covariances between traits *x* and *y*, respectively; $\sigma^2{}_{(x)}$ and $\sigma^2{}_{(y)}$ are the phenotypic and genotypic variances of *x* and *y*, respectively, and K-constant = 2.06 at 5% selection intensity.

Table 1: List of selected pigeon pea accessions collected from ICRISAT and a White local check

Accessions	Accessions	Accessions	Accessions	Accessions
ISC-141	WHITE*	ISC-61	ISC-22	ISC-175
ISC-46	ISC-91	ISC-180	ISC-184	ISC-48
ISC-41	ISC-115	ISC-100	ISC-174	ISC-186
ISC-178	ISC-155	ISC-123	ISC-1	ISC-11
ISC-118	ISC-203	ISC-37	ISC-30	ISC-189
ISC-172	ISC-24	ISC-197	ISC-124	ISC-20
ISC-176	ISC-198	ISC-185	ISC-90	ISC-40
ISC-36	ISC-84	ISC-5	ISC-200	ISC-32
ISC-202	ISC-74	ISC-140	ISC-179	ISC-157

*White is a local landrace from Nigeria included in the study

Table 2: Morphological traits recorded for the early maturing pigeon pea accessions

S/N	Trait Designation	Code	Trait Description
1	Leaflet Length (cm)	LLT	Mean length of 10 randomly selected terminal leaflets/stand at maturity
2	Leaflet Width (cm)	LWT	Mean breadth of 10 randomly selected terminal leaflets/stand at maturity
3	Days to 50% Flowering (days)	D50F	Number of days after planting in which 50% of the plants had at least one open flower
4	Pod Length (cm)	PDL	Mean length of 10 randomly selected pods/stand at maturity
5	Number of Pods	PDN	Number of pods borne on a plant at maturity
6	Seeds per Pod	SD_PD	Number of seeds per pod selected from 10 random pods per stand at maturity
7	Plant Height (cm)	PHT	Length measured from the base of a plant to the tip of the plant/stand
8	Primary Branches	PBR	Total number of main branches that originate from the central stem per stand
9	Secondary Branches	SBR	Total number of branches that grow from the primary branches per plant
10	Tertiary Branches	TBR	Total number of small branches that grow from the secondary branches per stand
11	Days to 50% Maturity (days)	D50M	Number of days from planting to the time when 50% of the plant in a plot has reached maturity or ready for harvest
12	100 Seed Weight (g)	SDWT	Weight of air-dried 100 seeds per stand
13	Seed Yield per Plant (g)	SD_PLT	Weight of seeds produced per plant stand

The mean length of 10 randomly selected terminal leaflets/stand at maturity

RESULTS

Agronomic traits among the Pigeon pea Accessions

Days to 50% maturity was used to categorise the pigeon pea accessions into two major clusters – early and late-maturing genotypes (Fig. 1). Two major clusters were observed categorising the accessions that are early-maturing and late-maturing. Cluster 1 (early maturing genotypes) comprised of 22

accessions grouped in two sub-clusters. The first sub-cluster within Cluster 1 comprises 16 accessions: ISC-84, ISC-91, ISC-5, ISC-46, and ISC-90, ISC-123, ISC-184, ISC-11, ISC-30, ISC-176, ISC-140, ISC-40, ISC-178, ISC-179, ISC-115, and ISC-172 while the second subcluster had 6 accessions which include ISC-48, ISC-118, ISC-196, ISC-124, ISC-174, and ISC-185. The remaining 23 accessions were considered late maturing accessions as they had D50M > 160 days during the early maturity screening evaluation.

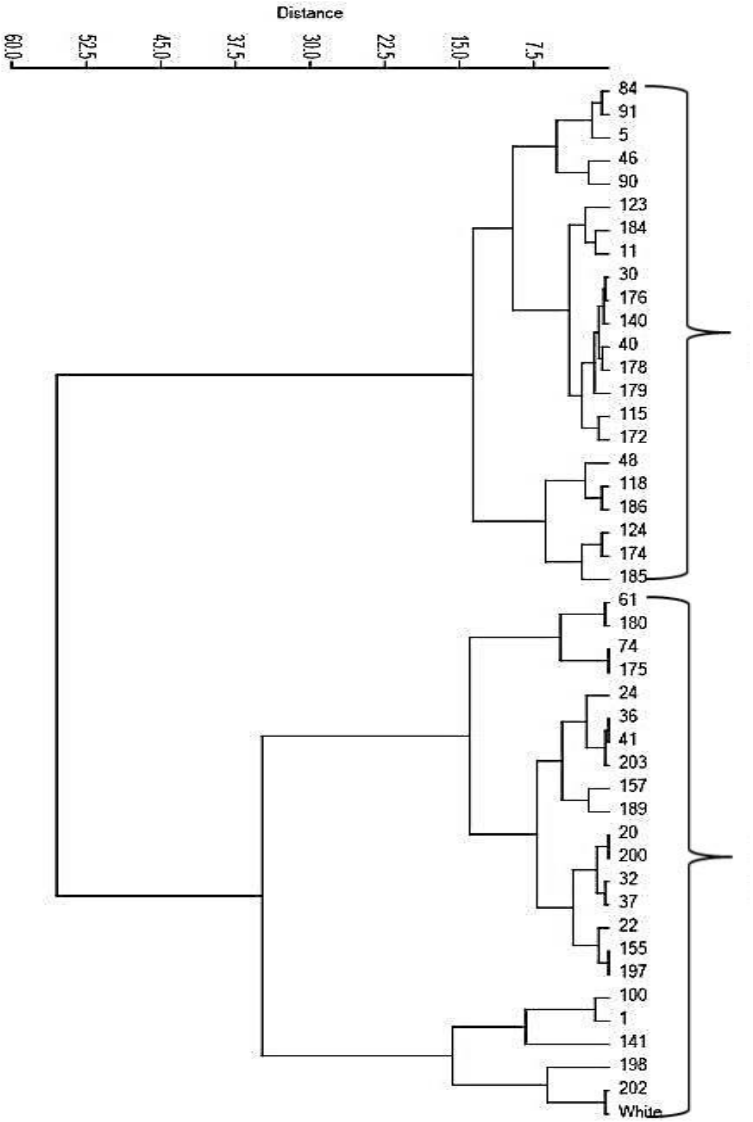

Fig. 1: Genotype grouping based on days to maturity

Evaluation of the Genetic Parameters among Early Maturing Genotypes

The genetic parameters among early-maturing genotypes were evaluated and the results are presented in Table 4. Except for Days to 50% Flowering (D50F), all traits showed a strong significant difference in genotype performance. The number of pods (PDN) showed the highest environmental variance (Ve = 255.43), genetic variance (Vg = 2814.63), and phenotypic variance (Vp = 3070.05), while Pod Length (PDL)

showed a low value of environmental variance (Ve = 0.01), genetic variance (Vg = 0.07), and phenotypic variance (Vp = 0.08). Tertiary Branching had the highest environmental coefficient of variation (ECV = 61.32), phenotypic coefficient of variation (PCV = 235.58), and genotypic coefficient of variation (GCV = 227.46) among traits evaluated. Pod length had the lowest value of Environmental Coefficient of variation (ECV = 1.66) and phenotypic coefficient of variation value (PCV = 5.89). Days to 50% maturity (D50M) had the lowest genotypic coefficient of variation (GCV = 4.53). The highest heritability was observed in plant Height (H^2 = 0.98), while the lowest heritability was seen in Days to 50% Flowering (H^2 = 0.20). The percentage of genetic advance (GA%) ranged from 5.04% in D50M to 452.41% in Tertiary Branching. Pod Number (PDN) has the highest genetic advance (GA = 104.64) followed by plant height (GA = 84.35).

Genotypic and Phenotypic Correlation of Evaluated Traits

In this study, the phenotypic and genotypic associations among the traits of the early-maturing accessions were found to vary (Table 5). For the genotypic correlation, a positive and significant relationship was observed between Leaflet Length and Leaflet Width, indicating a strong genotypic correlation (rg = 0.81, $p < 0.01$), Leaflet Length and 100 seed weight (rg = 0.61, $p < 0.01$), and Leaflet Length and Days to 50% Maturity (rg = 0.40, $p < 0.01$). Leaflet Width and Days to 50% Maturity also show a positive correlation (rg = 0.35, $p < 0.01$). Additionally, Days to 50% Flowering displayed a strong and positive association with Number of Pods (rg = 0.95, $p < 0.01$), Seed yield per Plant (rg = 0.54, $p < 0.01$), and Days to 50% Maturity (rg = 0.65, $p < 0.01$). Pod Length and Plant Height are positively correlated (rg = 0.35, $p < 0.01$), while Seeds per Plant is positively correlated with Number of Pods (rg = 0.37, $p < 0.01$), Plant Height (rg = 0.38, $p < 0.01$) and Seed Weight (rg = 0.37, $p < 0.01$). Similarly, a significantly strong positive relationship was observed between Number of Pods and Days to 50% Maturity (rg = 0.96, $p < 0.01$), Number of Pods and Plant Height (rg = 0.62, $p < 0.01$), Seed Weight and Days to 50% Maturity (rg = 0.39, $p < 0.01$). Similarly, Pod Length showed a considerably strong correlation with 100 Seed Weight (rg = 0.63, $p < 0.01$). Tertiary Branching and Pod Number had a negative correlation (rg = -0.28, $p < 0.05$), while there was no significant correlation between Seeds per Pod and any trait.

The phenotypic correlation was also assessed for each trait of the early-maturing accessions (Table 5). Leaflet Length and Leaflet Width exhibited a strong and positively significant relationship (rp = 0.77, $p < 0.01$). Seed Weight displayed a significantly weak and positive relationship with Seed Yield per Plant (rp = 0.33, $p < 0.01$). The number of pods and Days to 50% Maturity showed a significantly positive relationship (rp = 0.48, $p < 0.01$), whereas Days to 50% Maturity exhibited a positive and significantly strong relationship with D50F (rp = 0.83, $p < 0.01$). There was no significant correlation between Seeds per Pod and any trait.

Table 4 – Estimation of the genetic parameters of early-maturing genotypes

SoV (df)	LLT	LWT	D50F	PDL	PDN	SD_PD	PHT	SDWT	SD_PLT	PBR	SBR	TBR	D50M
Rep (2)	0.21	0.03	118.23	0.24**	2150.17**	0.05*	445.74**	2.47**	317.80**	0.16	0.02	7.92	1.41
Gen (21)	2.26**	0.35**	180.60	0.22**	8699.31**	0.264**	5195.42**	1.47**	155.60**	26.11**	131.50**	176.63**	184.112*
Residual (42)	0.15	0.04	103.42	0.01	255.43	0.01	42.08	0.26	14.93	1.20	2.33	4.18	82.11
Maximum	10.50	3.80	117.00	5.17	229.80	4.50	187.00	10.99	49.35	15.00	27.00	32.00	157.00
Minimum	5.90	2.20	56.00	4.10	27.00	3.20	54.00	6.42	8.45	3.00	4.00	0.00	96.00
Mean	8.34	2.97	83.50	4.70	118.86	3.81	131.53	8.41	24.40	10.54	11.71	3.33	128.86
SEM	0.23	0.11	5.87	0.05	9.23	0.06	3.75	0.29	2.23	0.63	0.88	1.18	5.23
Ve	0.15	0.04	103.42	0.01	255.43	0.01	42.08	0.26	14.93	1.20	2.33	4.18	82.11
Vg	0.70	0.10	25.73	0.07	2814.63	0.08	1717.78	0.40	46.89	8.30	43.06	57.49	34.00
Vp	0.86	0.14	129.14	0.08	3070.05	0.10	1759.86	0.66	61.82	9.51	45.39	61.66	116.11
ECV	4.72	6.67	12.18	1.66	13.45	2.83	4.93	6.04	15.84	10.41	13.04	61.32	7.03
GCV	10.04	10.84	6.07	5.65	44.64	7.62	31.51	7.55	28.06	27.34	56.03	227.46	4.53
PCV	11.09	12.73	13.61	5.89	46.62	8.13	31.89	9.67	32.22	29.26	57.52	235.58	8.36
H^2	0.82	0.73	0.20	0.92	0.92	0.88	0.98	0.61	0.76	0.87	0.95	0.93	0.29
GA	1.56	0.57	4.66	0.53	104.64	0.56	84.35	1.02	12.28	5.55	13.17	15.08	6.50
GA%	18.72	19.01	5.58	11.17	88.04	14.72	64.13	12.15	50.34	52.64	112.41	452.41	5.04

*, ** Significant at $p < 0.05$ and $p < 0.01$; SoV: Source of Variation; df: degree of freedom; Rep: Replicate; Gen: General; Max: Maximum; Min: Minimum; SEM: Standard Error of Mean; Vg: Genetic variance; Ve: Environmental variance; Vp: Phenotypic variance; GCV: Genotypic coefficient of variation; PCV: Phenotypic coefficient of variation; ECV: Environmental coefficient of variation; H^2: Heritability; GA: Genetic advance; GA(%): Genetic advance percentage; LLT: Leaf length; LWT: Leaflet width; D50F: Days to 50% Flowering; PDL: Pod Length; PDN: Pod Number; SD_PD: Seed Per Pod; PHT: Plant Height; SDWT: 100 Seed Weight; SD_PLT: Seed Yield Per Plant; PBR: Primary Branches; SBR: Secondary Branches; TBR: Tertiary Branches; D50M: Days of 50% Maturity

Principal Component Analysis of Early-Maturing Genotypes

The degree of variations in early maturity was explained by five principal components (Table 3) accounting for 75.77% of the variability explained. PC1 exhibited the highest variation, contributing 23.86% with an Eigenvalue of 3.10. This component was primarily influenced by the traits – number of pods, plant height and hundred seeds weight, which contributed 0.77, 0.67, and 0.67, respectively. Additionally, PC2 accounted for variations associated with LLT and LWT, with values of 0.77 and 0.87, respectively.

Path Analysis of Evaluated Days to Maturity

The study utilised path analysis to examine the direct and indirect impacts of the traits with high factor loading in the PCA on D50M (Figure 2). The direct effect was highest with D50F (β = 0.74) and was significant (Z = 10.49). So also, PDN had a significant direct effect (β =0.27, Z = 3.15). However, PHT showed a non-significant negative direct effect (β = -0.07, Z = 0.84). The model fit was acceptable with $\chi 2$ = 118.09, $p < 0.01$; CFI > 0.90; TLI > 0.95; RMSEA < 0.08 and SRMR < 0.08.

Table 6 – Genotypic and phenotypic correlation of the evaluated traits among the early-maturity genotypes

Traits		LLT	LWT	D50F	PDL	PDN	SD_PD	PHT	SDWT	SD_PLT	PBR	SBR	TBR
LWT	rg	0.81**	1.00										
	rp	0.77**	1.00										
D50F	rg	0.24	0.35**	1.00									
	rp	-0.02	-0.05	1.00									
PDL	rg	0.26	0.04	-0.04	1.00								
	rp	0.22	0.02	0.02	1.00								
PDN	rg	0.12	0.06	0.95**	0.16	1.00							
	rp	0.11	0.05	0.37**	0.16	1.00							
SD_PD	rg	-0.39	-0.50*	-0.24	0.25	0.03	1.00						
	rp	-0.31*	-0.38**	0.00	0.24	-0.02	1.00						
PHT	rg	0.06	-0.08	0.25	0.35**	0.62**	0.17	1.00					
	rp	0.05	-0.09	0.14	0.35**	0.61**	0.17	1.00					
SDWT	rg	0.61**	0.13	0.16	0.63**	0.33	-0.20	0.52*	1.00				
	rp	0.46**	0.06	0.13	0.49**	0.29 *	-0.09	0.44**	1.00				
SD_PLT	rg	0.11	-0.01	0.54**	0.46*	0.37**	0.22	0.38**	0.37**	1.00			
	rp	0.13	0.05	0.21	0.43**	0.37**	0.18	0.37**	0.33**	1.00			
PBR	rg	0.02	-0.04	-0.24	-0.01	0.22	0.13	0.23	0.11	-0.34	1.00		
	rp	-0.02	-0.09	0.09	0.02	0.20	0.13	0.24	0.10	-0.28*	1.00		
SBR	rg	0.30	0.52*	0.27	0.09	0.25	-0.10	0.13	-0.01	-0.07	0.51*	1.00	
	rp	0.26*	0.43**	0.14	0.09	0.24	-0.07	0.13	0.04	-0.10	0.48**	1.00	
TBR	rg	0.03	0.26	-0.07	0.11	-0.29	-0.28	-0.11	-0.15	-0.05	-0.06	0.45*	1.00
	rp	0.02	0.19	-0.07	0.11	-0.28*	-0.24	-0.10	-0.09	-0.04	-0.04	0.42**	1.00
D50M	rg	0.40**	0.30	0.65**	0.16	0.96**	-0.03	0.34	0.39**	0.30	0.15	0.19	-0.30
	rp	0.04	-0.08	0.83**	0.15	0.48**	0.05	0.21	0.25	0.14	0.21	0.12	-0.16

*, ** Significant at $p < 0.05$ and $p < 0.01$ LLT: Leaf length; LLT: Leaflet width; D50F: Days to 50% Flowering; PDL: Pod Length; PDN: Pod Number; SD_PD: Seed per Pod; PHT: Plant Height; SDWT: 100 Seed Weight; SD_PLT: Seed Yield Per Plant; PBR: Primary Branches; SBR: Secondary Branches; TBR: Tertiary Branches; D50M: Days of 50% Maturity

DISCUSSION

This study set out to compare the phenotypic variations in early-maturing pigeon pea accessions using the measured quantitative traits. The study revealed significant variations among all 13 measured traits. Among them, pod number, plant height, days to 50% maturity, 100 seed weight, leaflet length, and leaflet width contributed the most to the observed variations, as shown in the principal component analysis table. Specifically, leaflet width, leaflet length, pod number, plant height, and 100 seed weight had the most pronounced effects on variations in early-maturing pigeon pea accessions.

This study showed that considerable variability was observed in phenotypic traits such as the number of pods and days to 50% flowering, an indication that they are mostly influenced by the environment. They are affected by the presence of environmental promoters of growth as reported by Georfoy *et al.* (2020). The Environmental coefficient of variation varied from 1.66 in pod length - 61.66 in tertiary branching. This indicates that the environment had a substantial

influence on the tertiary branches. The environmental influence was minimal in pod length.

Table 3 – Principal component analysis of agronomic and yield components traits of early maturing pigeon pea genotypes

PC	1	2	3	4	5
LLT	0.31	0.77	0.22	0.21	0.25
LWT	0.09	0.87	0.06	0.18	0.10
D50F	0.50	0.12	0.56	0.44	0.35
PDL	0.56	0.01	0.51	0.30	0.29
PDN	0.77	0.08	0.15	0.07	0.23
SD_PD	0.14	0.59	0.12	0.40	0.05
PH	0.67	0.14	0.05	0.26	0.22
D50M	0.67	0.12	0.40	0.02	0.10
SDWT	0.56	0.14	0.54	0.11	0.28
SD_PLT	0.27	0.02	0.54	0.60	0.31
PBR	0.29	0.57	0.43	0.49	0.14
Eigen Value	3.10	2.34	1.83	1.45	1.13
% Variance	23.86	18.01	14.11	11.13	8.66
Cumulative %	23.86	41.88	55.99	67.12	75.77

LLT: Leaflet length; LWT: Leaflet width; D50F: Days to 50% Flowering; PDL: Pod Length; PDN: Pod Number; SD_PD: Seed per Pod; PHT: Plant Height; SDWT: 100 Seed Weight; SD_PLT: Seed Yield per Plant; PBR: Primary Branches; SBR: Secondary Branches; TBR: Tertiary Branches; D50M: Days of 50% Maturity.

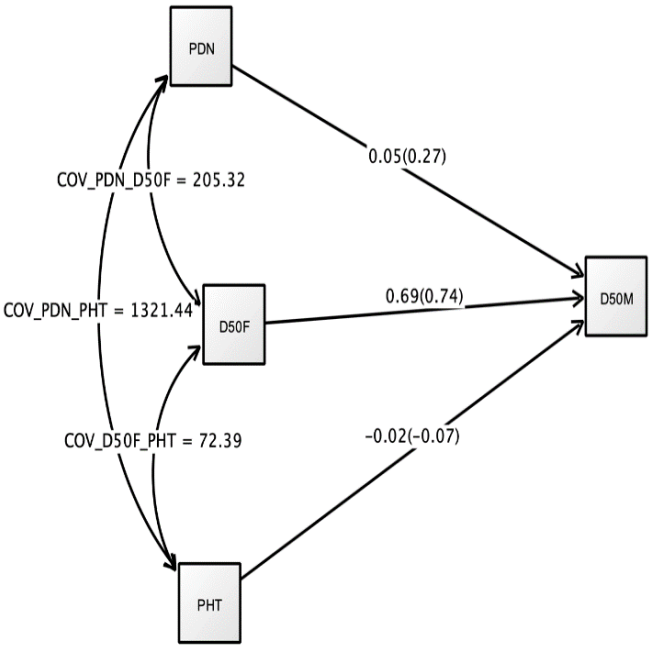

Fig. 2: Sequential path analysis indicating relationships between early maturity traits and predictor variables (days to 50% flowering, number of pods and plant height).

Pearson's bivariate analysis showed a correlation between days to 50% maturity with days to 50% flowering to have a strong and significant positive relationship. This formed the primary basis of the classification of pigeon pea into different categories of maturity, i.e. early, medium, or late maturing genotypes (Addeae-Frimpomaah *et al.*, 2021). Days to 50% flowering is strongly correlated to days to 50% maturity. This was also reported by several other researchers (Pushpavalli and Yamini, 2018; Addeae-Frimpomaah *et al.* (2021). There was a positive significant relationship between days to 50% maturity and plant height and primary branches. This agrees with the report of Pushpavalli and Yamini (2018). These traits were reported by Addeae-Frimpomaah *et al.* (2021) to be yield-related and thus, could be exploited to develop pigeon pea genotypes with great yield.

The studies of Amusa *et al.*, (2022) and Roychowdhury *et al*. (2012) suggest that the criteria for acceptable selection include high genetic advance with heritability, suggesting that addictive genes are present. They can be used in selecting superior crop varieties. Low to high heritability and genetic advances were recorded. The trait, pod number of the early and late-maturing genotypes which had a high heritability and high genetic advance shows that it experienced little to no environmental influence. Thus, additive genes are present. Days to 50% maturity displayed low heritability and genetic advance, indicating the absence of additive gene interaction.

Gore *et al*. (2023) in their study highlighted the important use of sequential path analysis in identifying and simplifying the relationships between influential traits on a trait of interest. The sequential path analysis revealed that days to 50% flowering had the highest direct effect on the number of pods and plant height, indicating its prominent role in early maturity in both types of analyses, while the number of pods also had a positive direct effect on plant height, although minor. Days to 50% maturity have been reported to positively influenced crop yield (Devi et al., 2020; Tharageshwari and Hemavathy, 2020). Hence, these trait predictors having significant direct effects on days to 50% maturity should be considered when breeding or selecting for early maturity pigeon peas.

CONCLUSION

The study was successful in examining the phenotypic variations in early-maturing pigeon pea genotypes. This was done by studying different genetic parameters and employing bivariate analysis. The quantitative traits analysed showed a strong correlation between the early-maturing pigeon pea traits. The genotypes showed genetic variations in the quantitative traits. The phenotypic path analysis of the correlation values showed that days to 50% flowering had a significant impact on the accession variations. This could be responsible for environmental variations observed in the grown population. This shows that in breeding programmes, days to 50% flowering should be evaluated as it has the potential to characterise a new line of pigeon peas. This new line will have the right length of maturity and be able to thrive in conditions favouring either type of maturation pattern for better survival. Multivariate analysis which is based on observation and analysis of more than one statistical outcome variable at a time, selecting traits for breeding will be much easier.

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