



## Genetic variability of pigeonpea germplasm for yield and its components in North Eastern Hill (NEH) Region

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### ABSTRACT

Pigeonpea, a crucial protein source, that thrives well in varied climatic conditions has huge scope of cultivation in North Eastern Hill (NEH) region of India. The present study examined seven pigeonpea genotypes to assess the components of genetic variation and association of yield and component traits. The experiment was conducted in Randomized Block Design (RBD) with three replications. Results showed significant variation ( $P \leq 0.001$ ) among the genotypes for yield component traits. Environmental influence was evident, as the phenotypic coefficient of variance (PCV) exceeded the genotypic coefficient of variation (GCV). Traits such as the percentage of chaffy pods, plant dry weight, root dry weight, and root volume demonstrated high heritability ( $>60\%$ ) coupled with high genetic advance ( $>20\%$ ) indicating genetic improvement through selection. Traits like plant height, root volume, plant dry weight, root dry weight, proline content, number of pods plant<sup>-1</sup>, aluminum content in root biomass, and test weight exhibited strong positive associations with yield ( $P \leq 0.05$ ) at both genotypic and phenotypic levels. Further, path analysis revealed positive direct effect of root traits, proline content, test weight, pods per plant on dependent variable yield per plant indicating heritable additive gene action. The study also identified two promising genotypes PA-291 and PA-640 which can be used as parental lines for future breeding programme.

### **1. Introduction**

Pigeonpea (*Cajanus cajan* (L.) Millspaugh) stands as the second most significant pulse crop, trailing only behind chickpea. India dominates global pigeonpea production, contributing to 90% of the world's supply (Patel *et al.*, 2024). Predominantly consumed as dry split dal, pigeonpea is noted for its high protein content, ranging between 21-25% (Jeevarathinam & Chelladurai, 2020). This crop is nutritionally rich, offering a blend of proteins, carbohydrates, B-complex vitamins, carotenes, and minerals such as iron, magnesium, and phosphorus, along with essential amino acids like lysine, leucine, glutamic acid, aspartic acid, and arginine (Akshaya *et al.*, 2023). Despite India's leading

position in pigeonpea cultivation, the country's average productivity lags behind the global average. This disparity underscores the need to develop high-yielding pigeonpea varieties by leveraging the genetic variability within the population (Ranjani *et al.*, 2023). Although the NEH region offers favorable climatic conditions for pigeonpea growth, the acidic soils and high rainfall contribute to aluminium (Al) toxicity, posing significant obstacles.

Pigeonpea, with its broad genetic diversity, serves as a crucial resource for developing genotypes suited to the NEH region. Prior research has highlighted significant variation in aluminum tolerance among different pigeonpea genotypes (Sharma *et al.*, 2012). It is essential to identify or

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develop genotypes that are better adapted based on morphological characteristics. This study focuses on assessing the genetic variability in various pigeonpea genotypes and examining the relationships between yield and yield-related traits. Correlation analysis plays a key role in identifying effective selection criteria for enhancing yield and pinpointing genotypes that perform well in acidic soils. However, genetic variability and correlation studies alone may not fully reveal the relative significance of direct and indirect effects of each trait on grain yield. In these cases, path coefficient analysis becomes a vital method for distinguishing the direct and indirect impacts of independent variables on the dependent variable. Thus, genetic variability, correlation, and path coefficient analyses are essential tools for breeders aiming to improve pigeonpea production and productivity (Yadav *et al.*, 2024). This contributes to the development of Al-tolerant pigeonpea varieties, promoting sustainable agriculture in the NEH region. The primary aim of this investigation is to evaluate genetic variability, character associations, and elucidate the direct and indirect effects of different yield component traits in pigeonpea genotypes.

## 2. Material and Method

The present investigation was carried out in randomized block design with three replications during the period of July to December, 2022 at the Department of Genetics and Plant Breeding, School of Agricultural Sciences (SAS), Medziphema Campus; Nagaland University (NU) with a total of seven (07) pigeon pea genotypes collected from AICRP-Pigeonpea, NU; SAS, Medziphema. Details of the collected genotypes along with code numbers, description, native place of growing and places of collection are given in Table 1. The observations were recorded on five randomly sampled plants in each plot. The observations included plant height plant<sup>-1</sup> in cm (PH), number of branches plant<sup>-1</sup> (NOB), Root volume plant<sup>-1</sup> (cm<sup>3</sup>) (RV), number of flowers plant<sup>-1</sup> (NOF), Plant dry weight plant<sup>-1</sup> (g) (PDW), Dry weight of shoot (g) (DWS), Dry weight of root (g) (DWR), Nitrate reductase Activity (mM) (NR) (Hageman and Hucklesby, 1971), Proline content (nmol mg<sup>-1</sup>) (PR) (Bates *et al.* (1973), Numbers of pods plant<sup>-1</sup> (NPP), Chaffy pods percentage (%) (cpp), Aluminium content in root biomass ( $\mu$ M) (Al), Test Weight (g) (TW) and seed yield per plant (g) (SYP).

The analysis of variance for all traits was conducted following the guidelines of Panse and Sukhathme (1967). The genotypic and phenotypic coefficients of variation were calculated according to the methods described by Burton (1952). Heritability and genetic advance were estimated using the methodologies of Lush (1940) and Johnson *et al.* (1955), respectively. Correlation coefficients were determined based on Pearson's (1897) procedure, and

path analysis was performed as outlined by Dewey and Lu (1959). The multivariate principal component analysis (PCA) method was calculated according to Hotelling (1933).

## 3. Results and Discussion

The success of a breeding program fundamentally depends on the presence of genetic variability. Thus, estimating the components of genetic variations is essential to assess the genetic potential for breeding programs.

The analysis of variance revealed significant differences among genotypes for all fourteen traits studied. Table 2 presents the mean yield component traits for various pigeonpea genotypes. Among the genotypes, PA-291 exhibited the highest responses for yield component and biochemical traits. Plant height (PH) ranged from 90.33 cm in PA-406 to 154.70 cm in PA-291, followed by PA-640. Number of branches plant<sup>-1</sup> (NOB) varied from 69.67 in PA-406 to 75.00 in PA-291. Root volume (RV) ranged from 6.64 in PA-406 to 12.87 in PA-291, while plant dry weight plant<sup>-1</sup> (PDW) varied from 13.41 in GT-101 to 24.73 in PA-291. Dry weight of shoot (DWS) ranged from 7.26 in PA-291 to 9.70 in PA-406, followed by PA-3. Nitrate reductase Activity (NR) varied from 2.45 in PA-406 to 2.95 in PA-291, followed by 2.93 in PA-640. Proline content (PR) ranged from 133.39 in PA-406 to 166.43 in PA-291, followed by PA-640. Seed yield plant<sup>-1</sup> (SYP) ranged from 21.33 in PA-414 to 30.78 in PA-291, followed by 21.74 in GT-101 (Table 2). The highest values for number of flowers plant<sup>-1</sup> (NOF, 150.33), Proline content (PR, 157.15), and number of pods plant<sup>-1</sup> (NPP, 129.33) were observed in PA-640. Conversely, the highest value for chaffy pods plant<sup>-1</sup> (CPP) was observed in PA-3 (5.55), and the highest test weight (TW) was in GT-101 (80.67). The lowest aluminium content was found in GT-101 (0.56) and PA-291 (0.57).

A wide range of phenotypic and genotypic coefficients of variation was observed for nearly all traits (Table 3). The higher value of phenotypic coefficient of variation (PCV) than the genotypic coefficient of variation (GCV) indicates environmental influence on trait expression. However, the small differences between PCV and GCV suggest that these traits are largely controlled by genetic factors with minimal environmental influence. Similar results were reported by Shruthi *et al.* (2019). GCV ranged from 2.35% (number of branches) to 34.75% (chaffy pods percentage), while PCV ranged from 2.64% (number of branches) to 36.85% (chaffy pods percentage). According to Johnson *et al.* (1955), PCV and GCV are classified as low (0-10%), medium (10-20%), and high (>20%).

High values of PCV and GCV detected for traits such as chaffy pods percentage, plant dry weight, dry weight of roots, and root volume in our study was in consistent with

earlier reports (Sinha *et al.*, 2024; Akshaya *et al.*, 2023; Yadav *et al.*, 2024). Moderate PCV and GCV estimates were recorded for dry weight of roots, plant height, and seed yield per plant. Patel *et al.* (2021) also found moderate GCV values for the number of pods per plant, primary branches per plant, secondary branches per plant, and plant height. Conversely, low GCV and PCV estimates were observed for the number of branches, test weight, and nitrate reductase, indicating less variability for these traits, making them more suitable for selection. Similar results were reported by Patel *et al.* (2021) and Galian *et al.* (2016) for plant height, days to 50% flowering, days to maturity, and 100-seed weight.

Heritability and genetic advance are key aspects of genetic variability and essential tools for selecting traits in crop improvement. Heritability measures the extent to which a trait is inherited, influenced by both genetic and environmental factors, while genetic advance (GA) quantifies the improvement achieved through phenotypic selection. According to Johnson *et al.* (1955), heritability is categorized as high (>60%), moderate (30-60%), and low (<30%), and genetic advance as a percentage of the mean is classified as low (0-10%), moderate (10-20%), and high (>20%). Broad-sense heritability ( $h^2$ ) ranged from 79.78% for the number of branches to 99.81% for plant height. Since heritability is also influenced by the environment, estimates of heritability alone is not sufficient for selecting superior genotypes. Estimates of heritability combined with genetic advance as a percentage of the mean are more useful for selecting the best genotypes (Tiwari *et al.*, 2015). The highest GA was observed for chaffy pods percentage (67.51%), followed by plant dry weight (57.44%), dry weight of roots (54.05%), and root volume (52.90%). Traits such as chaffy pods percentage, plant dry weight, dry weight of roots, and root volume showed high heritability coupled with high genetic advance, indicating the predominance of additive gene effects. These findings are consistent with those of Pandey *et al.* (2021), Phom *et al.* (2022), Sandeep *et al.* (2022), and Parre *et al.* (2022).

### Correlation analysis

Correlation coefficient analysis is a crucial statistical tool for evaluating the interrelationships among various traits, facilitating effective phenotypic selection for yield enhancement. This analysis helps pinpoint traits or trait combinations that can act as indicators for identifying high-yielding genotypes. The correlation coefficient for all quantitative traits with yield and inter-trait relationships was calculated at both phenotypic and genotypic levels (Tables 4 and 5). In this study, seed yield per plant exhibited a positive and significant correlation with several traits at both the genotypic and phenotypic levels (Khulbe *et al.*, 2020). These traits include plant height (PH) in cm (0.88), number of

branches per plant (NOB) (0.84), root volume per plant in  $\text{cm}^3$  (RV) (0.91), number of flowers per plant (NOF) (0.79), plant dry weight per plant in grams (PDW) (0.89), shoot dry weight in grams (DWS) (0.85), root dry weight in grams (DWR) (0.89), nitrate reductase activity in mM (NR) (0.62), proline content in  $\text{nmol mg}^{-1}$  (PR) (0.69), and number of pods per plant (NPP) (0.59). However, the correlation with chaffy pods percentage (CPP) was non-significant. Additionally, negative correlations were observed with aluminium content in root biomass ( $\mu\text{M}$ ) (Al) and test weight in grams (TW). These findings are consistent with those of Gaur *et al.* (2020) and Ranjani *et al.* (2018) regarding days to fifty percent flowering and days to maturity. Hussain *et al.* (2021) similarly reported significant correlations for plant height, number of primary branches per plant, and number of pods per plant, while Rao *et al.* (2020) noted similar results for hundred seed weight. The highest positive significant correlation was found between days to fifty percent flowering and days to maturity. Hence, these traits can be used alone or in combination to enhance the yield potential of pigeonpea.

### Path coefficient analysis

Correlation analysis identifies the relationship between two variables, whereas path coefficient analysis separates direct and indirect effects through other traits by partitioning the correlation. Thus, combining correlation and path analysis offers a better understanding of trait relationships. Table 6 illustrated the direct and indirect effects of various independent variables on dependent variable seed yield per plant. Trait like plant height, root volume, plant dry weight, root dry weight, proline content, number of pods per plant, aluminium content in root biomass, and test weight exhibits positive direct effects on seed yield per plant. This suggests the presence of heritable and additive gene action. In analogue to our findings, the positive direct effects of traits on yield were previously reported by Ranjaniet *al.* (2018) for days to maturity and Sharma *et al.* (2021) for the number of seeds per pod. Therefore, these traits can be used in selection programs to enhance the yield potential of pigeonpea.

### Principles component analysis

Principal component analysis (PCA) was performed using phenotypic variability based on morpho-physiological and biochemical traits from the 7 pigeonpea genotypes. The variance proportion and eigenvalues are presented in Table 7. The PCA results showed that the first four components explained 97% of the variability, with PC1 (66.81%) followed by PC2 (20.71%), PC3 (6.12%), and PC4 (3.35%). The eigenvectors of the first two principal components, which scaled more than 1, indicated maximum contribution to diversity. The high positive loading value

contributed by PC1, indicated by PH, RV, DWR, PDW, DWS, NOF, NOB, and SYP, accounted for 66.81% of the variation. The negatively loaded characters were AI and TW (Table 7). Additionally, PC2 accounted for positive loading traits NPP, CPP, AI, PH, NOF, DWS, and DWR, with 20.71% of variability. Similar studies in pigeonpea revealed that three significant principal components accounted for 81.24% of phenotypic variation among the studied genotypes (Akshaya *et al.*, 2023).

#### 4. Conclusion

In conclusion, our detailed analysis of pigeonpea genotypes revealed notable variability in the traits studied. The phenotypic coefficient of variation (PCV) was generally higher than the genotypic coefficient of variation (GCV), indicating an environmental influence on trait expression. Traits such as plant dry weight, root dry weight, and root volume demonstrated high heritability coupled with high genetic advance, suggesting the predominance of additive gene effects and the potential for improvement through direct selection. Correlation and path analysis indicated that selecting for plant height, root volume, plant dry weight, root dry weight, proline content, and the number of pods per plant would be more promising for improving seed yield per plant. Genotypes such as PA-291 and PA-640 could be selected for yield improvement in future breeding programs.

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**Table 1.** Description of the pigeonpea genotypes used for the study

Genotype code	Name of Genotypes	Description of the genotypes	Source of Collection	Native place of growing
G1	PA-3	A promising pigeonpea genotype known for its resilience to aluminium stress and high yield.	AICRP-Pigeonpea, NU; SAS, Medziphema.	NEH Region, India
G2	PA-291	Pigeonpea genotype known for its resilience and productivity under aluminium stress conditions	AICRP-Pigeonpea, NU; SAS, Medziphema.	NEH Region, India
G3	PA-406	Aluminium-tolerant, high-yielding, drought-resistant, and suitable for acidic soils in NEH India	AICRP-Pigeonpea, NU; SAS, Medziphema.	NEH Region, India
G4	PA-414	High yield, aluminum-tolerant, with strong root growth and good disease resistance.	AICRP-Pigeonpea, NU; SAS, Medziphema.	NEH Region, India
G5	PA-421	High-yielding pigeonpea genotype with robust resistance to aluminium toxicity in acidic soils.	AICRP-Pigeonpea, NU; SAS, Medziphema.	Maharashtra, India.
G6	GT-101	Promising pigeonpea genotype studied for aluminium stress tolerance in acidic soils of Northeastern India.	AICRP-Pigeonpea, NU; SAS, Medziphema.	NEH Region, India
G7	PA-640	Exhibits robust growth and tolerance to aluminium stress in acidic soils	AICRP-Pigeonpea, NU; SAS, Medziphema.	Maharashtra, Madhya Pradesh, Karnataka, and Uttar Pradesh.

**Table 2.** Mean of yield component traits of pigeonpea genotypes

Genotypes	PH	NOB	RV	NOF	PDW	DWS	DWR	NR	PR	NPP	cpp	Al	TW	SYP
<b>G1</b>	140.17	71.33	10.40	132.67	20.85	14.60	6.25	2.62	136.10	121.00	5.55	0.68	71.47	24.23
<b>G2</b>	154.70	75.00	12.87	142.67	24.73	16.45	7.26	2.95	166.43	112.67	2.77	0.57	72.02	30.78
<b>G3</b>	90.33	69.67	6.64	121.67	10.99	9.70	3.54	2.45	133.39	104.67	2.95	0.76	72.00	21.40
<b>G4</b>	104.67	71.00	7.43	129.00	14.07	10.51	4.22	2.78	155.15	107.67	3.20	0.58	70.33	21.33
<b>G5</b>	113.90	71.33	8.91	127.00	17.15	12.25	4.90	2.81	146.10	109.00	2.85	0.63	70.75	22.42
<b>G6</b>	96.00	70.67	7.34	112.67	13.41	9.81	3.93	2.78	144.00	94.67	2.28	0.56	80.67	21.74
<b>G7</b>	147.47	73.00	12.32	150.33	20.81	14.33	6.48	2.93	157.15	129.33	5.02	0.72	69.73	27.40
<b>LSD (0.05)</b>	2.03	1.51	1.01	8.74	1.20	1.37	0.68	0.02	1.22	6.62	0.76	0.02	0.78	1.62

PH= Plant Height (cm), NOB=Number of Branches, RV=Root Volume, NOF=Number of Flowers, PDW=Plant Dry Weight, DWS=Dry weight of Shoot, DWR=Dry weight of Root, NR=Nitrate reductase, PR=Proline, NPP=Number of pods plant<sup>-1</sup>, cpp=chaffy pods %, Al= Al content in root biomass, TW=Test Weight, SYP=Seed Yield plant<sup>-1</sup>

**Table No.3.** Genetic variability of different pigeonpea genotypes

Characters	General mean±SE	GV	PV	GCV	PCV	h <sup>2</sup> (%)	GA	GA (% of mean)
PH	121.03	689.91	680.60	21.56	21.58	99.81	53.69	44.36
NOB	71.71	3.57	2.84	2.35	2.64	79.78	3.11	4.33
RV	9.42	6.47	6.15	26.35	27.03	95.00	4.98	52.90
NOF	130.86	175.38	151.24	9.40	10.12	86.24	23.53	17.98
PDW	17.43	24.52	24.06	28.15	28.42	98.13	10.01	57.44
DWS	12.52	7.47	6.88	20.95	21.84	92.07	5.19	41.42
DWR	5.23	2.16	2.01	27.18	28.16	93.17	2.83	54.05
NR	2.76	0.03	0.03	6.31	6.32	99.58	0.36	12.97
PR	148.33	141.69	141.21	8.01	8.03	99.66	24.44	16.48
NPP	111.29	135.96	122.09	9.93	10.48	89.80	21.57	19.38
cpp	3.52	1.67	1.49	34.75	36.85	88.94	2.37	67.51
AI	0.64	0.006	0.006	12.05	12.14	98.57	0.16	24.64
TW	72.42	14.06	13.87	5.14	5.18	98.62	7.62	10.52
SYP	24.19	13.68	12.85	14.82	15.30	93.89	7.16	29.59

**Table 4.** Genotypic Correlation yield component traits

	PH	NOB	RV	NOF	PDW	DWS	DWR	NR	PR	NPP	cpp	AI	TW	SYP
<b>NOB</b>	0.914**													
<b>RV</b>	0.992**	0.969**												
<b>NOF</b>	0.903**	0.862**	0.926**											
<b>PDW</b>	0.984**	0.941**	0.978**	0.817**										
<b>DWS</b>	0.997**	0.922**	0.984**	0.868**	1.006**									
<b>DWR</b>	1.007**	0.934**	0.998**	0.880**	1.001**	1.011**								
<b>NR</b>	0.605**	0.826**	0.676**	0.591**	0.645**	0.555**	0.615**							
<b>PR</b>	0.581**	0.882**	0.648**	0.660**	0.604**	0.546*	0.595**	0.895**						
<b>NPP</b>	0.811**	0.543*	0.783**	0.915**	0.688**	0.754**	0.763**	0.310NS	0.275NS					
<b>cpp</b>	0.582**	0.140NS	0.479*	0.622**	0.461*	0.514*	0.532*	-0.044NS	-0.136NS	0.911**				
<b>AI</b>	-0.006NS	-0.319NS	-0.009NS	0.227NS	-0.149NS	-0.028NS	-0.053NS	-0.548*	-0.508*	0.490*	0.543*			
<b>TW</b>	-0.429NS	-0.272NS	-0.380NS	-0.704**	-0.346NS	-0.427NS	-0.398NS	-0.061NS	-0.223NS	-0.730**	-0.514*	-0.462*		
<b>SYP</b>	0.914**	1.031**	0.966**	0.822**	0.913**	0.939**	0.936**	0.653**	0.720**	0.566**	0.257 <sup>NS</sup>	-0.093	-0.266	

\* and \*\* indicate significance at 5% and 1% levels, respectively.

**Table 5.** Phenotypic Correlation yield component traits

	PH	NOB	RV	NOF	PDW	DWS	DWR	NR	PR	NPP	cpp	AI	TW	SYP
PH														
NOB	0.809**													
RV	0.966**	0.826**												
NOF	0.844**	0.644**	0.818**											
PDW	0.974**	0.842**	0.945**	0.766**										
DWS	0.955**	0.801**	0.925**	0.738**	0.961**									
DWR	0.976**	0.828**	0.954**	0.798**	0.975**	0.958**								
NR	0.602**	0.747**	0.662**	0.530*	0.635**	0.532*	0.591**							
PR	0.578**	0.796**	0.623**	0.601**	0.597**	0.527*	0.569**	0.892**						
NPP	0.770**	0.407 <sup>NS</sup>	0.710**	0.863**	0.668**	0.667**	0.718**	0.280 <sup>NS</sup>	0.260 <sup>NS</sup>					
cpp	0.554**	0.098 <sup>NS</sup>	0.467*	0.512*	0.418 <sup>NS</sup>	0.449*	0.483*	-0.034 <sup>NS</sup>	-0.130 <sup>NS</sup>	0.781**				
AI	-0.002 <sup>NS</sup>	-0.293 <sup>NS</sup>	-0.008 <sup>NS</sup>	0.225 <sup>NS</sup>	-0.147 <sup>NS</sup>	-0.045 <sup>NS</sup>	-0.044 <sup>NS</sup>	-0.544*	-0.507*	0.463*	0.521*			
TW	-0.425 <sup>NS</sup>	-0.226 <sup>NS</sup>	-0.369 <sup>NS</sup>	-0.660**	-0.347 <sup>NS</sup>	-0.403 <sup>NS</sup>	-0.374 <sup>NS</sup>	-0.060 <sup>NS</sup>	-0.221 <sup>NS</sup>	-0.697**	-0.466*	-0.455*		
SYP	0.888**	0.843**	0.910**	0.793**	0.892**	0.850**	0.894**	0.622**	0.694**	0.595**	0.226 <sup>NS</sup>	-0.085	-0.260	

\*and\*\* indicate significance at 5% and 1% levels, respectively.

**Table 6.** Path analysis for yield component traits of pigeon pea

Parameters	PH	NOB	RV	NOF	PDW	DWS	DWR	NR	PR	NPP	cpp	AI	TW	SYP
PH	<b>0.379</b>	-0.242	0.240	-0.136	0.952	-0.324	0.102	-0.320	0.522	0.119	-0.232	-0.003	-0.143	0.915
NOB	0.346	<b>-0.265</b>	0.235	-0.130	0.910	-0.300	0.095	-0.436	0.792	0.080	-0.056	-0.149	-0.091	1.031
RV	0.376	-0.257	<b>0.242</b>	-0.139	0.946	-0.320	0.102	-0.357	0.581	0.115	-0.191	-0.004	-0.127	0.967
NOF	0.342	-0.229	0.224	<b>-0.150</b>	0.791	-0.282	0.090	-0.312	0.593	0.135	-0.248	0.106	-0.235	0.822
PDW	0.372	-0.249	0.237	-0.123	<b>0.968</b>	-0.327	0.102	-0.341	0.543	0.101	-0.184	-0.070	-0.115	0.913
DWS	0.378	-0.244	0.238	-0.131	0.973	<b>-0.325</b>	0.103	-0.294	0.490	0.111	-0.205	-0.013	-0.142	0.939
DWR	0.381	-0.248	0.242	-0.132	0.969	-0.329	<b>0.102</b>	-0.325	0.534	0.112	-0.212	-0.025	-0.133	0.936



NR	0.229	-0.219	0.164	-0.089	0.625	-0.181	0.063	<b>-0.528</b>	0.803	0.046	0.017	-0.255	-0.020	0.653
PR	0.220	-0.234	0.157	-0.099	0.585	-0.178	0.061	-0.473	<b>0.898</b>	0.040	0.054	-0.237	-0.074	0.720
NPP	0.307	-0.144	0.189	-0.138	0.666	-0.245	0.078	-0.164	0.247	<b>0.147</b>	-0.363	0.229	-0.243	0.566
cpp	0.220	-0.037	0.116	-0.094	0.447	-0.167	0.054	0.023	-0.122	0.134	<b>-0.398</b>	0.253	-0.171	0.257
AI	-0.002	0.085	-0.002	-0.034	-0.144	0.009	-0.005	0.289	-0.456	0.072	-0.216	<b>0.466</b>	-0.154	-0.093
TW	-0.163	0.072	-0.092	0.106	-0.335	0.139	-0.041	0.032	-0.200	-0.107	0.205	-0.215	<b>0.333</b>	-0.266

Residual effect= 0.18

**Table 7.** Contribution of different traits towards total variance in pigeon pea

	PC 1	PC 2	PC 3	PC 4	PC 5	PC 6
PH	0.32	0.04	0.17	0.05	-0.07	0.03
NOB	0.30	-0.21	-0.02	-0.22	0.01	0.11
RV	0.32	-0.01	0.13	-0.07	0.14	-0.19
NOF	0.30	0.13	-0.28	-0.02	0.20	0.21
PDW	0.31	-0.04	0.23	0.01	-0.25	-0.21
DWS	0.31	0.02	0.22	-0.11	-0.29	-0.14
DWR	0.32	0.01	0.21	-0.02	-0.13	-0.03
NR	0.22	-0.34	-0.24	0.39	0.36	-0.58
PR	0.23	-0.33	-0.45	0.04	0.15	0.44
NPP	0.26	0.34	-0.11	0.25	0.17	-0.07
cpp	0.16	0.44	0.21	0.57	0.08	0.38
AI	-0.01	0.53	-0.05	-0.46	0.48	-0.25
TW	-0.16	-0.33	0.63	0.09	0.57	0.15
SYP	0.30	-0.10	0.12	-0.41	0.17	0.28
Eigenvalue	9.35	2.90	0.86	0.47	0.33	0.09
Total % variance	66.81	20.71	6.12	3.35	2.36	0.64