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# Multivariate and Association Studies in Short Duration Pigeonpea [*Cajanus cajan* (L.) Millsp.] Genotypes

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## ABSTRACT

**Background:** Absolute understanding of the relationship between yield and yield attributing traits contributing to variance is predominant in a breeding programme. To study the multivariate analysis and interrelationship among the yield and yield attributing traits in the pigeonpea, 68 genotypes were subjected to principal component analysis and association studies.

**Methods:** The 68 pigeonpea genotypes were raised during two seasons *viz*., *rabi*, 2019-2020 and *rabi*, 2020-2021 in a randomized complete block design with two replications. The two-season data was pooled and utilized for multivariate and association studies.

**Result:** The total variance was split into 12 principal components. Four principal components were found to have eigen values more than one and explained 78.75 per cent of the total variance. The correlation studies revealed that, the single plant yield was highly correlated with the traits *viz.,* days to 50 per cent flowering ($r_g$=0.213, P<0.05), days to maturity ($r_g$=0.347, P<0.01), plant height ($r_g$=0.536,P<0.01), number of branches per plant ($r_g$=0.331, P<0.01), number of clusters per plant ($r_g$=0.705, P<0.01), number of pods per plant ($r_g$=0.805,P<0.01), pod length ($r_g$=0.481, P<0.01), number of seeds per pod ($r_g$=0.231, P<0.05) and hundred seed weight ($r_g$=0.505, P<0.01). Selection for these traits will improve single plant yield. Path analysis showed that the traits *viz.,* number of pods per plant (0.871), shelling percentage (0.391) and hundred seed weight (0.744) had high positive direct effect on single plant yield, whereas the high indirect effect on single plant yield possessed by number of pods per plant through traits *viz.,* days to maturity (0.316), plant height (0.421), pod bearing length (0.454) and number of clusters per plant (0.706).


**Key words:** Correlation, Path analysis, Principal component analysis, Short duration pigeonpea.

## INTRODUCTION

Pigeonpea [*Cajanus cajan* (L.) Millsp.] is a unique pulse crop suitable for the rainfed system adopting to the varying climatic conditions and cropping systems (Kumar *et al.,* 2016). India is the largest producer (3.38 million tonnes) and consumer of pigeonpea in the world. The pigeonpea or Arhar is the major protein supplement especially in the vegetarian diet with the protein content of 20-22%. The pigeonpea can be grown as an intercrop with various crops *viz*., greengram, blackgram, soybean, wheat, groundnut *etc*., with groundnut and pigeonpea intercropping leading to the highest benefit cost ratio (Kumawat *et al.,* 2017). This versatile crop provides 40-60 kg/ha nitrogen to the subsequent crop (Sarkar *et al.,* 2020). The short duration pigeonpea genotypes which mature within 120-130 days are highly recommended for intercropping with other crops owing to its photo-insensitivity and compact plant stature. The study of pigeonpea genotypes in the short duration group and their evaluation will help in the improvement of yield and development of hybrids. Multivariate analysis was carried out to understand the genotypes better and to recognize the quantitative characters contributing to the genetic divergence. The pigeonpea genotypes were also subjected to correlation and path analysis to study the interrelationship among the yield and yield attributing traits in the pigeonpea genotypes.

## MATERIALS AND METHODS

The study was conducted using 68 pigeonpea genotypes of short duration (120-130 days) group including the local check variety Co (Rg) 7. The experiment was conducted at the Department of Pulses, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Tamil Nadu, India during *rabi*, 2019-2020 (October, 2019 to January, 2020) and *rabi*, 2020-2021 (October, 2020 to January, 2021). The pigeonpea genotypes were raised in a 4 m with a row to row spacing of 90 cm and plant to plant spacing of 30 cm. The randomized complete block design (RCBD) was employed with two replications. The standard field operations and agronomical practices were performed as per recommendation. Twelve quantitative traits *viz.,* days to 50 per cent flowering, days to maturity, plant height (cm), number of branches per plant, pod bearing length (cm), number of clusters per plant, number of pods per plant, pod length (cm), number of seeds per pod, shelling per cent, hundred seed weight (g) and single plant yield (g) were

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observed in three randomly selected plants in each genotype/ replication and seasons. The data from the two seasons were pooled to carry out the analysis. The principal component analysis (PCA) was first formulated by Pearson (1901). The PCA analysis was carried out with the data collected from the plants according to the guidelines contributed by Jackson and Edward (1991). The genotypic correlation coefficient ($r_g$) was calculated according to Robinson and Comstock (1950). The significance of genotypic correlation coefficient was tested by referring to the standard table given by Snedecor and Cochran (1967) at n-2 degrees of freedom. Path coefficient analysis was carried out as suggested by Dewey and Lu (1959). The direct and indirect effects were ranked according to the classification by Lenka and Mishra (1973). The principal component analysis was done utilizing R package version 3.3.2 and R studio 1.0.136 (R 2016). The correlation was performed using the statistical package STAR version 2.0.1 developed by IRRI (STAR, 2014). Path analysis was done with the help of TNAUSTAT software package (Manivannan, 2014).

## RESULTS AND DISCUSSION

The principal component analysis helps in identification of trends in undetermined multidimensional data set and to eliminate its redundancy without losing the information (Jolliffe and Cadima, 2016). In the present study, 68 genotypes of pigeonpea were assessed based on twelve quantitative characters. The total variation was divided into twelve principal components. The eigen values, variance per cent towards divergence and cumulative per cent variance towards divergence are presented in Table 1. The eminent principal components were those with eigen values more than one. Out of the twelve principal components, the first four principal components *viz.,* PC1 (λ=4.85), PC2 (λ=1.96), PC3 (λ=1.48) and PC4 (λ=1.17) had eigen values more than one. PC1 represented 40.38 per cent of total variance followed by PC2, PC3 and PC4 explaining 16.34, 12.30 and 9.73 per cent of total variance, respectively. The first four principal components represented a cumulative variance of 78.75 per cent. The scree plot showing contribution of each principal component towards total variance is given in Fig 1. Similar results were observed by Hemavathy *et al.* (2017) and reported four principal components with eigen values more than one and explaining about 80.57 per cent of the total variance using 58 pigeonpea genotypes. The biplot showing 68 pigeonpea genotypes along with the twelve quantitative characters constructed utilizing first two principal components is given in Fig 2. The biplot depicts the fact that, the genotypes in proximity to the origin are close to the average value and those away from the origin are the extreme observations or the outliers (Hartmann *et al.,* 2018). It is also reported that, when the genotypes are close to each other and overlapping on the loading plot are similar and they are found in proximity to the origin (Walle *et al.,* 2019). The genotypes ICPL 85010, CO 9R, ICPL 19011 and Co (Rg) 7 were placed in four different quadrants indicating that, they are genetically diverse from each other. However, the genotypes *viz.,* ICPL 19008, ICPL19016, ICPL 19040 and ICPL19042 are close to each other depicting their genetic similarity.

**Table1:** Eigen values and contribution of twelve quantitative characters towards divergence.

| Principal components | Eigenvalue λ | Variance per cent towards divergence | Cumulative per cent variance towards divergence |
|---|---|---|---|
| PC1 | 4.85 | 40.38 | 40.38 |
| PC2 | 1.96 | 16.34 | 56.73 |
| PC3 | 1.48 | 12.30 | 69.02 |
| PC4 | 1.17 | 9.73 | 78.75 |
| PC5 | 0.85 | 7.06 | 85.82 |
| PC6 | 0.50 | 4.13 | 89.94 |
| PC7 | 0.44 | 3.68 | 93.62 |
| PC8 | 0.28 | 2.37 | 96.00 |
| PC9 | 0.20 | 1.70 | 97.69 |
| PC10 | 0.15 | 1.22 | 98.92 |
| PC11 | 0.08 | 0.70 | 99.62 |
| PC12 | 0.05 | 0.38 | 100.00 |

PC-Principal component

The per cent contribution of the twelve quantitative characters towards each principal component is represented in Table 2. The quantitative trait with more absolute value in a principal component contributes more to the total variability in the particular principal component. All the traits contributed positively to PC1 except shelling percentage, which showed negative contribution towards PC1. The PC1 explained 40.38 per cent of the total variation and the highest contribution to PC1 was offered by the trait plant height (0.866) followed by other traits. The traits *viz.,* hundred seed weight (0.702), pod length (0.688), number of seeds per pod (0.520) and number of branches per plant (0.304) contributed more to the PC2 which represented 16.34 per cent of the total variation. A total of 12.30 per cent of the total variation was accounted by PC3 and the traits *viz.,* shelling percentage (0.609) and single plant yield (0.579) contributed more to the PC3. PC4 exhibited 9.73 per cent of the total variation and it was contributed by the number of seeds per pod (0.417) followed by shelling percentage (0.343), days to maturity (0.342), pod bearing length (0.340) and plant height (0.260). The remaining principal components (PC5-PC12) accounted a total variation of 21.25 per cent and had eigen values less than one. Yohane *et al.* (2020) estimated principal components for 81 pigeonpea genotypes involving 25 phenotypic traits in which, three principal components were found to have eigen values above one and explaining 98 per cent of the total variance. Upadhyaya *et al.* (2007) reported five principal components with eigen values accounting for the cumulative variance of 69.9 per cent in entire core collection of different maturity groups of pigeonpea based on various quantitative and qualitative characters.

**Table 2:** Per cent contribution of twelve quantitative characters towards principal components.

| Variables | PC1 | PC2 | PC3 | PC4 | PC5 | PC6 | PC7 | PC8 | PC9 | PC10 | PC11 | PC12 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Days to fifty per cent flowering | 0.588 | 0.062 | -0.537 | 0.120 | 0.424 | 0.262 | 0.133 | -0.227 | 0.170 | 0.026 | -0.001 | 0.006 |
| Days to maturity | 0.736 | 0.039 | -0.367 | 0.342 | 0.083 | 0.210 | 0.058 | 0.330 | -0.204 | 0.026 | 0.003 | -0.004 |
| Plant height | 0.866 | -0.124 | -0.084 | 0.260 | -0.245 | -0.229 | 0.092 | -0.116 | -0.009 | -0.042 | 0.032 | -0.152 |
| Number of branches per plant | 0.512 | 0.304 | -0.050 | -0.657 | 0.177 | -0.182 | 0.350 | 0.072 | -0.050 | -0.127 | 0.012 | 0.015 |
| Pod bearing length | 0.794 | -0.312 | -0.029 | 0.340 | -0.299 | -0.146 | 0.066 | -0.099 | -0.006 | -0.100 | 0.015 | 0.144 |
| Number of clusters per plant | 0.766 | -0.467 | 0.175 | -0.171 | 0.048 | -0.179 | 0.057 | 0.117 | 0.124 | 0.243 | -0.100 | 0.012 |
| Number of pods per plant | 0.690 | -0.467 | 0.283 | -0.210 | 0.233 | 0.074 | -0.268 | 0.086 | 0.078 | -0.065 | 0.178 | -0.006 |
| Pod length | 0.555 | 0.688 | 0.229 | 0.124 | -0.147 | 0.076 | -0.124 | 0.164 | 0.245 | -0.119 | -0.086 | -0.008 |
| Number of seeds per pod | 0.133 | 0.520 | 0.362 | 0.417 | 0.536 | -0.322 | -0.073 | -0.048 | -0.081 | 0.040 | 0.015 | 0.018 |
| Shelling percentage | -0.474 | -0.238 | 0.609 | 0.343 | 0.047 | 0.166 | 0.429 | 0.075 | 0.091 | -0.013 | 0.054 | -0.012 |
| Hundred seed weight | 0.500 | 0.702 | 0.203 | -0.145 | -0.329 | 0.148 | 0.050 | -0.095 | -0.041 | 0.189 | 0.123 | 0.021 |
| Single plant yield | 0.673 | -0.149 | 0.579 | -0.140 | 0.070 | 0.282 | -0.052 | -0.175 | -0.181 | -0.053 | -0.125 | -0.014 |

PC- Principal component.

The loading plot represents the relationship of the quantitative trait with the principal components considered and the correlation between the traits (Hartmann *et al.,* 2018). The loading plot for first two principal components is given in Fig 3. The orientation of the vector with the principal component axis explains its contribution to the principal component. The traits *viz.,* days to 50 per cent flowering, days to maturity, plant height, single plant yield, pod bearing length, number of clusters per plant, number pods per plant are oriented with the axes of PC1, indicating their higher contribution to PC1 than PC2. The traits *viz.,* seeds per pod, hundred seed weight and pod length were directed towards axes of PC2, hence contributed more to PC2 than PC1. Longer the vector in the loading plot, higher variability of the variables is explained by the two principal components. The shorter vectors are explained better in other dimensions. The quantitative traits *viz.,* plant height, pod bearing length, number of clusters per plant, number of pods per plant, pod length and hundred seed weight were contributed more to the variability of PC1 and PC2. The traits with smaller angles between them are positively correlated and those with opposite angles are said to have negative correlation. The traits which are at right angle to each other are negatively related. The traits in the same quadrant are closely related and distantly related with those in the different quadrant. The traits *viz.,* days to 50 per cent flowering, days to maturity, number of branches per plant are highly correlated with each other and negatively correlated with the traits in the IV quadrant. All the traits were negatively correlated with shelling percentage which is at right angle to rest of the traits. Vijayakumar *et al.* (2020) reported similar results in cowpea.

Plant breeding program aims in increasing the yield which is a complex trait and influenced by other yield contributing attributes. The study of magnitude and direction of association between the yield contributing traits and yield helps in formulating a plant ideotype which contribute to enhance yield. The correlation studies indicate only the association between the characters, whereas the path analysis specify the direction of association and measures its magnitude. The genotypic correlation between the 12 quantitative traits is presented in Table 3. The single plant yield was observed to have positive and significant correlation with the quantitative traits *viz.,* days to 50 per cent flowering ($r_g$=0.213, P<0.05), days to maturity ($r_g$=0.347, P<0.01), plant height ($r_g$=0.536, P<0.01), number of branches per plant ($r_g$=0.331, P<0.01), number of clusters per plant ($r_g$=0.705, P<0.01), number of pods per plant ($r_g$=0.805, P<0.01), pod length ($r_g$=0.481, P<0.01), number of seeds per pod ($r_g$=0.231, P<0.05) and hundred seed weight ($r_g$=0.505, P<0.01). The trait shelling percentage ($r_g$=-0.066) showed non- significant correlation with the single plant yield. The positive and significantly correlated traits have impact on the single plant yield and their improvement will aid in increasing the yield. Most of the other traits had positive and significant correlation with other traits implying that every trait had interrelationship with yield. However, shelling percentage had negative significant correlation with all the traits except number of seeds per pod ($r_g$=0.307, P<0.01). The shelling percentage

**Table 3:** Genotypic correlation between twelve quantitative characters in 68 pigeonpea genotypes.

| | DFF | DM | PH | NBPP | PBL | CPP | PPP | PL | SPP | SP | HSW | SPY |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DFF | 1 | 0.674** | 0.459** | 0.331** | 0.384** | 0.304** | 0.295** | 0.205 | 0.035 | -0.596** | 0.140 | 0.213* |
| DM | | 1 | 0.668** | 0.223* | 0.635** | 0.428** | 0.363** | 0.417** | 0.091 | -0.504** | 0.271* | 0.347** |
| PH | | | 1 | 0.276* | 0.937** | 0.681** | 0.483** | 0.423** | 0.037 | -0.386** | 0.355** | 0.536** |
| NBPP | | | | 1 | 0.085 | 0.404** | 0.301** | 0.359** | -0.026 | -0.521** | 0.499** | 0.331** |
| PBL | | | | | 1 | 0.676** | 0.521** | 0.302** | -0.075 | -0.229* | 0.211* | 0.534** |
| CPP | | | | | | 1 | 0.811** | 0.139 | -0.138 | -0.226* | 0.105 | 0.705** |
| PPP | | | | | | | 1 | 0.139 | -0.077 | -0.258* | 0.036 | 0.805** |
| PL | | | | | | | | 1 | 0.444** | -0.299** | 0.815** | 0.481** |
| SPP | | | | | | | | | 1 | 0.307** | 0.236* | 0.231* |
| SP | | | | | | | | | | 1 | -0.339** | -0.066 |
| HSW | | | | | | | | | | | 1 | 0.505** |
| SPY | | | | | | | | | | | | 1 |

**, *: Significance at 1% and 5% probability level, respectively.

DFF- Days to 50 per cent flowering; DM- Days to maturity; PH- Plant height; NBPP- Number of branches per plant; PBL- Pod bearing length; CPP- Number of clusters per plant; PPP- Number of pods per plant; PL- Pod length; SPP- Number of seeds per pod; SP- Shelling percentage; HSW-Hundred seed weight; SPY- Single plant yield.

**Table 4:** Path coefficient analysis showing direct (diagonal) and indirect effect (out of diagonal) of eleven quantitative characters on single plant yield in 68 pigeonpea genotypes.

| | DFF | DM | PH | NBPP | PBL | CPP | PPP | PL | SPP | SP | HSW | SPY |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DFF | 0.133 | 0.002 | 0.060 | -0.043 | -0.051 | 0.015 | 0.256 | -0.033 | 0.002 | -0.233 | 0.104 | 0.213* |
| DM | 0.090 | 0.003 | 0.087 | -0.029 | -0.084 | 0.021 | 0.316 | -0.066 | 0.005 | -0.197 | 0.202 | 0.347** |
| PH | 0.061 | 0.002 | 0.130 | -0.036 | -0.124 | 0.034 | 0.421 | -0.067 | 0.002 | -0.151 | 0.264 | 0.536** |
| NBPP | 0.044 | 0.001 | 0.036 | -0.130 | -0.011 | 0.020 | 0.262 | -0.057 | -0.001 | -0.203 | 0.372 | 0.331** |
| PBL | 0.051 | 0.002 | 0.122 | -0.011 | -0.132 | 0.034 | 0.454 | -0.048 | -0.004 | -0.089 | 0.157 | 0.534** |
| CPP | 0.040 | 0.001 | 0.088 | -0.052 | -0.090 | 0.050 | 0.706 | -0.022 | -0.008 | -0.088 | 0.078 | 0.705** |
| PPP | 0.039 | 0.001 | 0.063 | -0.039 | -0.069 | 0.041 | 0.871 | -0.022 | -0.004 | -0.101 | 0.027 | 0.805** |
| PL | 0.027 | 0.001 | 0.055 | -0.047 | -0.040 | 0.007 | 0.121 | -0.159 | 0.025 | -0.117 | 0.607 | 0.481** |
| SPP | 0.005 | 0.000 | 0.005 | 0.003 | 0.010 | -0.007 | -0.067 | -0.071 | 0.057 | 0.120 | 0.175 | 0.231* |
| SP | -0.079 | -0.002 | -0.050 | 0.067 | 0.030 | -0.011 | -0.225 | 0.048 | 0.018 | 0.391 | -0.252 | -0.066 |
| HSW | 0.019 | 0.001 | 0.046 | -0.065 | -0.028 | 0.005 | 0.031 | -0.130 | 0.013 | -0.133 | 0.744 | 0.505** |

Residual effect = 0.0914.

DFF- Days to 50 per cent flowering; DM- Days to maturity; PH- Plant height; NBPP-Number of branches per plant; PBL- Pod bearing length; CPP- Number of clusters per plant; PPP- Number of pods per plant; PL- Pod length; SPP- Number of seeds per pod; SP- Shelling percentage; HSW- Hundred seed weight; SPY- Single plant yield.

can be improved when number of seeds per pod increases. Birhan *et al.* (2013) reported significant negative correlation of shelling percentage with pods per plant in pigeonpea. Pushpavalli *et al.* (2017) reported that the traits *viz.,* days to 50 per cent flowering, plant height, number of secondary branches per plant, number of pods per plant, hundred seed weight and days to maturity had positive and significant association with single plant yield in pigeonpea. The quantitative traits *viz.,* number of pods per plant, number of seeds per plant, hundred seed weight, plant height and number of primary branches per plant showed positive significantly correlated with single plant yield in pigeonpea germplasm (Vanniarajan *et al.,* 2023).

The path coefficient analysis dissects the correlation coefficient into direct and indirect effects. The path coefficient analysis showing the direct and indirect effect of various traits on single plant yield are depicted in Table 4. The residual effect for path analysis is 0.0914, which is very low indicating that the considered quantitative traits are sufficient to study the partitioning. The traits *viz.,* number of pods per plant (0.871), shelling percentage (0.391) and hundred seed weight (0.744) had high positive direct effect on single plant yield. However, correlation between the shelling percentage and single plant yield was non-significant owing to the moderate negative indirect effect of traits *viz.*, number of pods per plant (-0.225) and hundred seed weight (-0.252) on single plant yield through shelling percentage. This depicts the importance of studying the direct and indirect effects before indulging in selection for a breeding programme. Therefore, direct selection for number of pods per plant and hundred seed weight can help in the improvement of yield. Days to 50 per cent flowering (0.133)

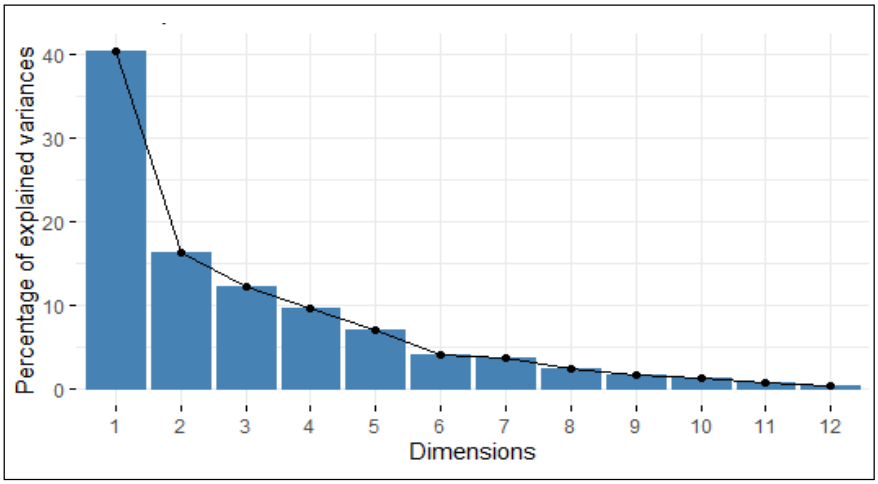


**Fig 1:** Screeplot showing contribution of various prinipal components towards divergence.

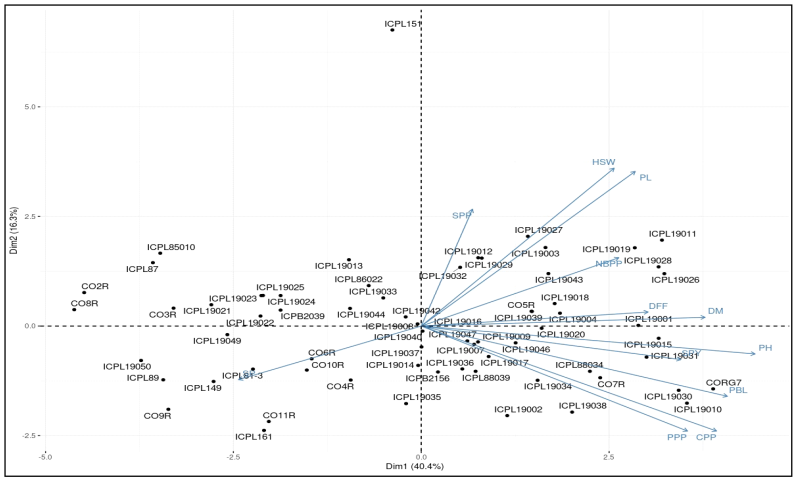


**Fig 2:** Biplot showing variation between PC1 and PC2 for twelve quantitative characters of 68 genotypes.

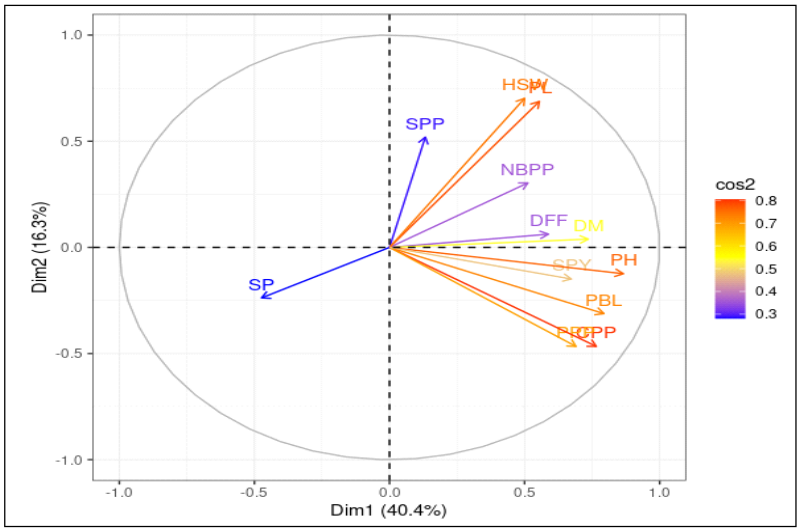


**Fig 3:** Loading plot of twelve quantitative characters based on PC1 and PC2.

and plant height had positive low direct effect on single plant yield, whereas number of branches per plant (-0.130), pod bearing length (-0.132) and pod length (-0.159) had negative low direct effect on single plant yield. The negligible direct effect on single plant yield was possessed by traits *viz.,* days to maturity (0.003), number of clusters per plant (0.050) and number of seeds per pod (0.057).

High positive indirect effect on single plant yield was imposed by number of pods per plant via traits *viz*., days to maturity (0.316), plant height (0.421), pod bearing length (0.454) and number of clusters per plant (0.706). The trait hundred seed weight had positive indirect effect on single plant yield through traits *viz.,* number of branches per plant (0.372) and pod length (0.607). All the other indirect effects on single plant yield were either low or negligible. The above results implied the fact that, the indirect effect of various traits should also be considered in a breeding programme involving improvement of yield. Satapathy *et al.* (2019) reported positive high direct effect of traits *viz*., plant height, number of seeds per pod, pod weight, root weight and biological yield per plant on single plant yield in pigeonpea. The same author also observed negative high direct effect of number of primary branches per plant on single plant. In pigeonpea, the number of pods per plant had high positive direct effect and high positive indirect effect through traits *viz.,* plant height, number of primary branches per plant and number of secondary branches per plant on single plant yield (Rekha *et al.,* 2013).

## CONCLUSION

The better understanding of interrelationship between yield and yield contributing traits and the contribution of each trait to the total variation aids in developing breeding strategies to improve the yield. The yield contributing traits *viz.,* number of clusters per plant, number of pods per plant and single plant yield showed high variability. The high variability for the above traits maximizes the opportunities for improvement of short duration pigeonpea through selection. The traits *viz.,* number of clusters per plant, number of pods per plant and hundred seed weight showed positive correlation with single plant yield. The selection for above traits will be useful in enhancing the yield and desirable seed size in short duration pigeonpea.

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### Conflict of interest

All authors declared that there is no conflict of interest.

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