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*Research Article*

# Estimation of Genetic Parameters, Correlation and Path Analysisin Advance Lines of Pigeonpea [*Cajanus cajan* (L.) Millspaugh.]

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**ABSTRACT**

*An experiment comprising of fifteen genotypes of pigeonpea was conducted during kharif 2019 to study the genetic variability, correlation and path coefficient analysis. The highest GCV was recorded for the number of pods/plant followed by seed yield/plant. High Heritability was observed for 100-seed weight (96.88%) followed by Days to flowering (91.07%) and days to maturity (90.28%). High estimates of genetic advance as percent of mean was recorded for number of pods/plant and 100-seed weight. Correlation studies revealed Pods/plant, Branches/plant are positively and significantly correlated with yield/plant. The path coefficient analysis indicated that characters viz. Days to maturity, pods/plant and 100-seed weight have direct effect on seed yield. Hence branches/plant, pods/plant, 100-seed weight should be considered during selection in yield improvement programme.*

***Keywords:*** *Pigeonpea, Correlation, Genetic advance, Heritability.*

## INTRODUCTION

Pigeonpea is often cross pollinated crop (20-70%), it belong to Family *Fabaceae*, Genus *Cajanus* and species *Cajan*. Pigeonpea is an important pulse crop of India after chickpea. It accounts for about 15% of total pulses produced in the country. India is the major pigeonpea producing country, contributing almost 80% of total production and area in the world. Pigeonpea [*Cajanus cajan* L. Millspaugh.] ranks sixth in global grain legume production and it is cultivated in about 6.99 m ha area worldwide with an annual production of 5.96 Mt and a mean productivity of 852 kg/ha (FAO, 2018). India ranks first in annual pigeonpea production with 4.25 Mt production in area of 4.43Mha at a productivity level of 960 kg/ha (DAC&FW, GOI, 2018-19). It is high in protein content (22%) and can play an important role in food security. The different parts of the pigeon pea plant reportedly have 39 different medicinal and cosmetic uses in 13 countries (Upadhyaya et al., 2006).

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The recognition of 2016 as the "International Year of Pulses" by United Nations was the right step towards generating global awareness. Pigeonpea can play a significant role because of its ability to grow well under diverse cropping systems and marginal soils. Despite these advantages the area and production of pigeonpea is not increasing in India. There may be a number of limiting factors but lack of high yielding cultivars with stable performance is considered as key factor.

The research programme on plant breeding focused on development of early, dwarf and high yielding varieties having resistance to major biotic stresses. Yield is a complex trait influenced by a number of components, thus for yield improvement selection of superior genotypes possessing better heritability for yield attributing characters is essential prerequisite. The present investigation was carried out with the objectives to estimate the extent of genetic variability, heritability, genetic advance and correlation for yield and yield attributing traits in pigeonpea genotypes.

## MATERIALS AND METHODS

The experimental material used in present investigation consisted of 11 advance breeding lines of pigeonpea and 4 check varieties *viz*. Paras, Manak, PAU881 and Pusa992. These genotypes were sown in a randomized block design (RBD) with three replications at field area of Pulses section of Dept. of Genetics and Plant Breeding CCS HAU, Hisar. Each genotype was sown in three replications; each plot consists of 8 rows of 4m length with 45 cm row to row spacing.

Five randomly competitive plants were selected for taking the observations of each genotype from each replication. Data were recorded for seven different characters viz., days to 50% flowering, Days to maturity, number of branches/plant, plant height(cm), number of pods/plant, 100 seed weight and seed yield/plot.

The mean values for each character were subjected to Analysis of Variances (ANOVA), given by Fisher (1920). The Phenotypic and genotypic coefficient of variations were calculated as performula given by Burton (1952). Heritability and genetic advance were calculated for all the traits by the method described by Allard (1960). Phenotypic and genotypic correlation coefficient for yield and yield attributing characters were calculated as suggested by Searle (1961). Path coefficient analysis to study direct and indirect effects of various characters on seed yield were estimated as suggested by Wright (1921) and Dewey and Lu (1959).

## RESULTS AND DISCUSSION

Studies on genetic parameters provide information regarding genetic makeup of the population, based on such studies elite genotypes are selected. Analysis of variance revealed that significant differences existed among pigeonpea genotypes for the characters studied. The mean performance of total 15 pigeonpea genotypes is depicted in Table 1. Days to 50% flowering, days to maturity, number of branches per plant and plant height varied between 79-93 days, 127-148 days, 7-13 and 225-258 cm, respectively. Pods per plant, 100 seed weight and seed yield per plant varied between 127-315, 7.47-10.17 and 26-48g, respectively. Highest variability was observed for Days to maturity, branches per plant and number of pods per plant followed by seed yield per plant and plant height. Thus a good range of variability was observed in pigeonpea genotypes. The genetic parameters like genotypic and phenotypic coefficient of variations (GCV and PCV), heritability and genetic advance as per cent of means are shown in Table 2.The PCV was relatively high compared to GCV for all the character studied indicating environmental influence. PCV observed was moderate for characters like no. of pods per plant (30.06), seed yield per plant (21.16) and branches per plant (21.00) whereas 100 seed weight (9.85), days to 50% flowering (5.27), plant height (5.35) and days to maturity (4.06) exhibited low PCV. The GCV ranged from 0.89-26.65 and maximum was observed for number of pods per plant (26.65) followed by seed yield per plant (18.93) and branches per plant (17.37). The highest PCV and GCV

were recorded for number of pods per plant, seed yield per plant and number of branches per plant providing an opportunity for genetic improvement. Similar reports were reported by Shunyu et al. (2013), Pushpvali et al. (2018) and Hemavathy et al. (2019). The selection efficiency and genetic gain not only depends on magnitude of genetic variability but also on the heritability and genetic advance of the characters. High heritability was observedfor 100 seed weight (96.88%), days to flowering (91.07) and days to maturity (90.28%), followed by seed yield per plant (80.00%) and number of pods per plant (78.59%). Highest genetic advance as percent of mean was observed for number of pods/plant (28.67) followed by seed yield/plant (34.87) and number of branches/plant (29.58). This indicates that selection will be helpful in improving these traits.Similar results were also reported by Vohra et al. (2015), Meena et al. (2017) and Deepak et al. (2018). High heritability for pods per plants and 100 seed weight was earlier reported by Sharma et al. (2014) and Pushpavalli et al. (2018).

Genotypic correlation provides the measure of genotypic associations among different traits and helps in selection for yield and yield contributing traits (Table3). Days to 50% flowering was found to be significantly and positively correlated with days to maturity (0.845) this indicates that the genotypes which flowered early, mature earlier. Days to flowering was also positively and significantly correlated with 100 seed weight (0.621). Days to maturity showed positive correlated with 100 seed weight (0.318). Number of branches per plant was significantly and positively correlated with pods per plant, 100 seed weight and yield per plant. Plant height showed positive and significant correlation with yield/plant (1.252). Pods per plant were significantly and positively correlated with yield per plant (0.714). Similar results were reported by Patel et al. (2018), Pushpvalli et al. (2018) and Hemavati et al. (2019)

Phenotypic correlation was estimated and it was found that days to maturity was significantly and positively correlated with days to 50% flowering and days to flowering was positively and significantly correlated with 100 seed weight. Branches per plant were positively and significantly correlated with pods per plant, 100 seed weight and seed yield per plant. There was significant and positive correlation between pods per plant and yield per plant. The results are in agreement with Thanki and Sawargaonkar (2010), Singh et al. (2016), Meena et al. (2017) and Deepak et al. (2018). Selection for the traits which are positively correlated with yield will be useful in breeding programme.

Path coefficient is used to study the cause and effect relationship by portioning the correlation coefficient into direct and indirect effects. Path coefficient analysis using phenotypic correlations as shown in table 5, revealed that pods per plant had maximum direct effect (0.687) followed by days to maturity (0.280) and 100 seed weight on seed yield per plot (0.110). Thus no. of pods per plant has been identified as an important yield component as it had highest direct effect towards yield per plot. Dahiya and Singh (1994), Thanki et al. (2010), Bhadru et al. (2011), Hemvati et al. (2019) also obtained similar results. Number of branches per plants is contributing towards yield indirectly through no. of pods per plant (0.445) indicating its importance in plant selection. Days to 50% flowering showed negative direct effect on yield (-0.559) but effecting yield via no. of pods per plant (0.142). the residual effect was 0.574 in path analysis, this showed that other contributing characters were also important and may play role in pigeonpea breeding. The present investigation suggested that estimates of genetic variability, correlation and path analysis are important for the identification of superior genotypes for yield and yield attributing traits. High heritability coupled with high genetic advance was observed for100 seed weight, Days to flowering, Days to maturity and seed yield/plant which indicates that there is opportunity for improvement by selection in these traits. Correlation studies revealed that number of branches/plant, number of pods/plant and seed yield/plant is positively

and significantly correlated and should consider in selection of high yielding genotypes. The genotypes AH 17-13, AH17-17, AH17-28 and AH15-20 were found high yielding above best check among all the 11 genotypes. These genotypes can be used in breeding programme for the development of the high yielding variety.

**Table 1: Mean performance for different characters of pigeonpea genotypes**

| Genotype | Days to 50% flowering | Days to maturity | Branches/ plant | Plant height (cm) | Pods/plant | 100-seed weight(g) | Seed yield/ plant(g) |
|---|---|---|---|---|---|---|---|
| AH 17-01 | 87.00 | 135 | 8 | 225.33 | 297 | 10.17 | 33.91 |
| AH 17-12 | 90.67 | 139 | 10 | 242.33 | 295 | 9.36 | 32.8 |
| AH 17-13 | 83.67 | 134 | 10 | 249.67 | 255 | 8.91 | 48.24 |
| AH 17-17 | 83.00 | 136 | 13 | 240.67 | 315 | 8.69 | 39.54 |
| AH 17-18 | 91.00 | 141 | 12 | 237.33 | 237 | 9.51 | 26.19 |
| AH 17-28 | 86.33 | 140 | 10 | 250.00 | 280 | 7.61 | 39.1 |
| AH 16-02 | 82.67 | 135 | 10 | 243.67 | 208 | 9.34 | 33.06 |
| AH 16-07 | 81.33 | 138 | 7 | 240.33 | 127 | 8.15 | 31.38 |
| AH 16-21 | 91.33 | 143 | 9 | 243.33 | 137 | 10.07 | 23.84 |
| AH 15-07 | 92.67 | 148 | 9 | 244.00 | 232 | 8.71 | 32.74 |
| AH 15-20 | 85.00 | 131 | 11 | 256.00 | 288 | 9.02 | 40.27 |
| Paras (C ) | 86.33 | 138 | 7 | 249.00 | 163 | 8.27 | 29.06 |
| Manak(C ) | 81.67 | 136 | 8 | 244.33 | 174 | 7.47 | 26.2 |
| PAU881(C ) | 79.00 | 127 | 7 | 246.33 | 155 | 7.70 | 27 |
| Pusa 992(C ) | 92.00 | 146 | 10 | 257.67 | 223 | 9.60 | 34.7 |
| Mean | 86.24 | 137.82 | 9.37 | 244.67 | 226 | 8.84 | 33.20 |
| Range | 79.00-92.67 | 127-148 | 7-13 | 225-258 | 127-315 | 7.47-10.17 | 26.2-48.24 |
| CV% | 1.575 | 1.266 | 12.15 | 5.27 | 13.91 | 1.739 | 9.601 |

**Table 2: Estimation of Genetic parameters in different genotypes of pigeonpea**

| Character | Coefficient of variation | | Broad sense heritability % | Genetic advance | Genetic advance as mean (%) |
|---|---|---|---|---|---|
| | Genotypic | Phenotypic | | | |
| Days to flowering | 5.03 | 5.27 | 91.07 | 8.53 | 9.89 |
| Days to maturity | 3.86 | 4.06 | 90.28 | 10.41 | 7.55 |
| Branches/plant | 17.37 | 21.00 | 68.37 | 2.77 | 29.58 |
| Plant height (cm) | 0.89 | 5.35 | 2.79 | 0.75 | 0.308 |
| Pods/plant | 26.65 | 30.06 | 78.59 | 109.86 | 48.67 |
| 100-seed weight(g) | 9.69 | 9.85 | 96.88 | 1.73 | 19.65 |
| Seed yield/plot (kg/ha) | 18.93 | 21.16 | 80.01 | 617.53 | 34.87 |

**Table 3: Genotypic correlation coefficient among various characters in pigeonpea genotypes**

| | Days to flowering | Days to maturity | Branches/ plant | Plant height (cm) | Pods/ plant | 100-seed weight | Yield/ plant |
|---|---|---|---|---|---|---|---|
| **Days to flowering** | | | | | | | |
| **Days to maturity** | $0.845^{**}$ | | | | | | |
| **Branches/ plant** | $0.268^{NS}$ | $0.127^{NS}$ | | | | | |
| **Plant height(cm)** | $0.140^{NS}$ | $0.045^{NS}$ | $-0.018^{NS}$ | | | | |
| **Pods/plant** | $0.221^{NS}$ | $-0.043^{NS}$ | $0.778^{**}$ | $-0.589^{**}$ | | | |
| **100-seed weight** | $0.621^{**}$ | $0.318^{*}$ | $0.392^{**}$ | $-1.130^{**}$ | $0.277^{NS}$ | | |
| **Yield/plant** | $-0.147^{NS}$ | $-0.194^{NS}$ | $0.541^{**}$ | $1.252^{**}$ | $0.714^{**}$ | $-0.012^{NS}$ | |

*significant at 5% level **significant at 1% level

**Table 4: Phenotypic correlation coefficient among various characters in pigeonpea genotypes**

| | Days to flowering | Days to maturity | Branches/ plant | Plant height (cm) | Pods/ plant | 100-seed weight | Yield/ plant |
|---|---|---|---|---|---|---|---|
| **Days to flowering** | | | | | | | |
| **Days to maturity** | 0.796** | | | | | | |
| **Branches/plant** | 0.246NS | 0.112NS | | | | | |
| **Plant height(cm** | -0.026NS | 0.077NS | 0.126NS | | | | |
| **Pods/plant** | 0.207NS | -0.056NS | 0.647** | 0.014NS | | | |
| **100-seed weight** | 0.586** | 0.304* | 0.312* | -0.164NS | 0.257NS | | |
| **Yield/plant** | -0.139NS | -0.165NS | 0.358* | 0.125NS | 0.567** | 0.019NS | |

*significant at 5% level **significant at 1% level

**Table 5: Path coefficient analysis using phenotypic correlation showing direct (diagonal) and indirect effects of different characters on seed yield**

| | Days to flowering | Days to maturity | Branches/ plant | Plant height(cm) | Pods/ plant | 100-seed weight |
|---|---|---|---|---|---|---|
| **Days to flowering** | **-0.559** | 0.223 | -0.007 | -0.003 | 0.142 | 0.065 |
| **Days to maturity** | -0.445 | **0.280** | -0.003 | 0.008 | -0.038 | 0.033 |
| **Branches/plant** | -0.137 | 0.031 | **-0.028** | 0.013 | 0.445 | 0.034 |
| **Plant height(cm)** | 0.015 | 0.022 | -0.003 | **0.101** | 0.009 | -0.018 |
| **Pods/plant** | -0.115 | -0.016 | -0.018 | 0.001 | **0.687** | 0.028 |
| **100-seed weight** | -0.328 | 0.085 | -0.009 | -0.017 | 0.177 | **0.110** |

Residual effect: 0.574

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