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**Research Note**

# Genetic diversity and path coefficient analysis in Pigeonpea [*Cajanus cajan* (L.) Millsp.] germplasm accessions of Bastar origin

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**Abstract**

Forty five pigeonpea germplasms were studied for path coefficient and genetic divergence. The path coefficient analysis revealed that, the number of pod clusters plant $^{-1}$ had the highest direct effect on seed yield. Whereas, the characters namely number of pods plant$^{-1}$ and days to maturity had the highest indirect effect on seed yield via the characters number of pods plant$^{-1}$ and days to 50% flowering respectively. Cluster analysis showed existence of considerable diversity in pigeonpea germplasm accessions. The maximum inter cluster distance was observed between cluster I and IV. Hence, genotypes of cluster IV may be crossed with the genotypes of to cluster I to obtain high heterotic response and desirable segregants.

**Key words**

Divergence analysis, germplasm, path analysis, pigeonpea

Pigeonpea [*Cajanus cajan* (L.) Millsp.] is a leguminous crop grown in about 50 countries in the tropics and subtropics. It is the fourth most important pulse crop in the world where in, India alone accounts for 85 per cent of the world supply (Fattepurkar *et al.*, 2004). Pigeonpea is cultivated throughout tropical, sub tropical and in the warm temperate regions. On the basis of wide range of diversity present in India, pigeonpea is considered to be of Indian origin (Vavilov, 1951). Later on, De (1974) and Van der Maesen (1990) on the basis of abundance of *Cajanus cajan* and its wild relatives in the evergreen forest area of Western Ghat and Malabar Coast of India concluded its origin in India and reported that with the migration of Indian population, it spread over to other parts of the world. Pigeonpea root exudates have been found to contain phenolic compounds (e.g. piscidic acid), which chelate Fe to free P in Fe bound P in soils for crop uptake (Anonymous, 1999).

Globally, pigeonpea is grown on an area spanning 4.50 million ha with a grain output of 3.48 million tonne. The major pigeonpea producing countries are India followed by Myanmar, Malawi, Uganda, Kenya, Tanzania, Dominican Republic, Nepal. In Asia, pigeonpea is grown on 4.00 million ha, but its cultivation is largely restricted to South Asian countries, mainly India which accounts for 84.3 per cent of Asia's total pigeonpea area and contributes 65.2 per cent to total production (Anonymous, 2009).

An experiment was conducted during the *kharif*-season of 2010-11 at the experimental area of department of Genetics & Plant Breeding at Research cum Instructional Farm, Indira Gandhi Krishi Viswavidyalaya, Raipur to evaluate genetic variability and correlation of 45 pigeonpea germplasm accessions obtained from ICRISAT. Genotypes are: UPAS-120, ICPL-6994, ICPL-6996, ICPL-6999, ICPL-7000, ICPL-7359, ICPL-7364, ICPL-7409, ICPL-7429, ICPL-6992, ICPL-7001, ICPL-7003,ICPL-7004,ICPL-7005,ICPL-7358,ICPL-7362,ICPL-7363,ICPL-7366,ICPL-7367,ICPL-7374,ICPL-7389,ICPL-7391,ICPL-7397,ICPL-7404,ICPL-7420, ICPL-87119,BDN-2,ICPL-6992,ICPL-6997,ICPL-7002,ICPL-7349,ICPL-7376,ICPL-7379,ICPL-7382,ICPL-7392,ICPL-7393,ICPL-7406, ICPL-7373,ICPL-7384,ICPL-7385,ICPL-7388,ICPL-7398,ICPL-7405 and ICPL-7430.

Raipur is situated in Eastern Central part of Chhattisgarh at latitudes of $21^{0}.16^{'}$ N, longitude of $81^{0}.36^{'}$ E and an altitude 289.5 m above Mean Sea Level. The general climatic condition of Raipur is classified as sub-humid with hot summer and cold winter. The average annual rainfall of the region is 1200-1400 mm, most of the rainfall (85%) occurs from

June to September. At Raipur the average maximum and minimum temperatures during crop period was 35.7$^0$C and 7.3$^0$C, respectively while, the hottest and coldest months are May and December, respectively.

The experiment was laid out in Randomized Complete Block Design (RCBD) in two replications. Experimental site has heavy soil. A fertilizer dose of 20N: 50P: 20K kg / ha was applied by broadcasting. Each entry was sown in paired rows of four meter length keeping a distance 60 cm between row is and 15 cm between plants. All the recommended package of practices were adopted to raise a good crop. The following data were collected: days to flower initiation, days to 50% flowering, days to physical maturity, plant height, number of primary branches plant$^{-1}$, number of pods plant$^{-1}$, pod length, number of pods cluster$^{-1}$, number of pod clusters plant$^{-1}$, number of seeds pod$^{-1}$, 100 seed weight, seed yield plant$^{-1}$. All data collected were analyzed using GENSTAT, following Standard Analysis of Variance procedures. Randomized block design experiment were analyzed statistically as per the procedure given by Dewey and Lu (1959). The Divergence analysis was calculated as per procedure developed by Mahalanobis in 1928.

The results of present study presented in Table 1. revealed that number of pod cluster plant$^{-1}$ had the highest direct effect (0.557) on seed yield. Similar results were reported by Awatade *et al.* (1980) and Brar *et al.* (1991). It also had significant positive association with seed yield, coupled with high heritability and genetic advance. Hence, this character seems to be important contributor of seed yield and must be considered in selection for high seed yield. Other important characters having considerable direct effects were pod length (0.505), days to 50% flowering (0.483) and number of pods plant$^{-1}$ (0.331). Similar contribution of these characters was also reported by Chandirakala and Subbaraman (2010). The character number of pods plant$^{-1}$ also exhibited high positive association with seed yield having high heritability and genetic advance. Hence, direct selection for these traits may lead to the development of high yielding genotypes in pigeonpea. The number of pods plant$^{-1}$ showed significant correlation (r=0.643) and its direct effect on seed yield plant$^{-1}$ was (0.331) which is mainly due to the indirect effects *via* number of pod clusters plant$^{-1}$ (0.240) and days to maturity (0.138). Similarly, number of primary branches plant$^{-1}$ had positive correlation with seed yield plant$^{-1}$ (r=0.319) and its direct effect on seed yield plant$^{-1}$ was (0.124) which is mainly due to the indirect effects *via* number of pods plant$^{-1}$ (0.048), plant height (0.040), days to maturity (0.029), number of pod clusters plant$^{-1}$ (0.024) and pod length (0.023). Hence, indirect selection of these traits may increase more number of primary branches plant$^{-1}$ which ultimately lead to development of high yielding genotypes. Such finding was earlier reported by Thanki and Sawargaonkar (2010) for indirect contribution of the character number of pods plant$^{-1}$.

A set of 45 genotypes of pigeonpea were subjected to D$^2$ analysis for twelve characters. Based on D$^2$ values four clusters were formed (Table 2). This indicated that substantial diversity exists in the available gene pool of pigeonpea. Results of cluster analysis revealed that the cluster II was the largest which consisted of (16 accessions) followed by cluster III (12 accessions), I (9 accessions) and IV (8 accessions). From the clustering pattern, it was found that the pigeonpea germplasm accessions received from ICRISAT of Bastar origin were genetically diverse to each other. Hence, the genotypes studied are reliable enough for hybridization and selection.

The maximum inter cluster distance was observed in between cluster I and VI (4.904) followed by between cluster II and IV (4.048) and cluster III and IV (3.599). This suggested that the hybridization programme involving parents from these clusters is expected to give higher frequency of better segregates or desirable combination for development of useful genetic stocks or varieties. The minimum inter cluster distance was observed in between II and III (2.125) followed by cluster I and II (2.518) and cluster I and III (3.178) indicating minimal diversity (differences) for the genotypes under study.

The maximum intra cluster distance was observed in cluster IV (3.674) followed by cluster I (2.818), cluster III (2.634) and cluster II (2.364). The cluster mean values of twelve characters presented in Table 3 revealed that cluster I was found to be better for earliest days to flower initiation (100.50 days), earliest days to 50% flowering (122.72 days), earliest days to maturity (169.33 days) and number of seeds pod$^{-1}$ (4.83) whereas, cluster III exhibited the highest 100 seed weight (10.17 g). Similarly, cluster IV has better genotypes for more number of primary branches (16.38), number of pods plant$^{-1}$ (375.75), number pods cluster$^{-1}$ (3.12), number of pod clusters plant$^{-1}$ (102.56), pod length (5.58 cm) and high seed yield plant$^{-1}$ (45.06 g).

The pattern of distribution of pigeonpea genotypes in various clusters revealed existence of considerable diversity present in the material (Table 4). The highest intra cluster distance was observed for the cluster IV. Hence, genotypes belonging to this cluster *viz.*, ICPL-7373, ICPL-7384, ICPL-7430 and ICPL-7405 may be utilized as parents in future breeding programmes with the genotypes belonging to cluster I *i.e.*, UPAS-120, ICPL-6994, ICPL-6996 and ICPL-7409 as the maximum inter cluster distance was noted between the cluster I and Cluster IV. The experimental findings of cluster analysis are in general agreement with the findings of Sarma and Roy (1994), Nandan *et al.* (1996), Basawarajaiah *et al.* (2000), Gohil (2006), Mahamad *et al.* (2006).

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### Table 1. Genotypic path coefficient of various characters influencing seed yield plant$^{-1}$

| Character | Days to flower initiation | Days to 50% flowering | Days to maturity | Plant height (cm) | No. of primary branches plant$^{-1}$ | No. of pods plant$^{-1}$ | No. of pod clusters plant$^{-1}$ | Pod length (cm) | No. of seeds pod$^{-1}$ | 100 seed weight (g) | Genotypic Correlation Coefficient with seed yield |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Days to flower initiation | **-0.558** | -0.433 | -0.279 | 0.057 | -0.084 | -0.119 | -0.167 | -0.107 | 0.065 | 0.053 | -0.110 |
| Days to 50% flowering | 0.375 | **0.483** | 0.342 | -0.039 | 0.062 | 0.110 | 0.109 | 0.009 | -0.093 | 0.019 | -0.088 |
| Days to maturity | -0.294 | -0.417 | **-0.589** | -0.097 | -0.139 | -0.246 | -0.243 | -0.180 | 0.126 | -0.081 | 0.059 |
| Plant height (cm) | 0.016 | 0.012 | -0.025 | **-0.154** | -0.049 | -0.040 | -0.021 | -0.022 | 0.010 | -0.001 | 0.078 |
| No. of primary branches plant$^{-1}$ | 0.019 | 0.016 | 0.029 | 0.040 | **0.124** | 0.048 | 0.024 | 0.023 | -0.030 | 0.018 | 0.319* |
| No. of pods plant$^{-1}$ | 0.071 | 0.076 | 0.138 | 0.085 | 0.127 | **0.331** | 0.240 | 0.073 | -0.008 | 0.036 | 0.643** |
| No. of pod clusters plant$^{-1}$ | 0.166 | 0.125 | 0.230 | 0.075 | 0.105 | 0.405 | **0.557** | 0.051 | 0.022 | -0.041 | 0.546** |
| Pod length (cm) | 0.097 | 0.010 | 0.155 | 0.072 | 0.095 | 0.111 | 0.046 | **0.505** | 0.082 | 0.160 | 0.340* |
| No. of seeds pod$^{-1}$ | 0.023 | 0.038 | 0.042 | 0.013 | 0.048 | 0.005 | -0.008 | -0.032 | **-0.199** | -0.007 | -0.006 |
| 100 seed weight (g) | -0.004 | 0.002 | 0.006 | 0.000 | 0.006 | 0.005 | -0.003 | 0.014 | 0.002 | **0.043** | 0.224 |

Diagonal values are direct effects, other values are indirect effects. Residual effect = 0.3128.
* and ** significant at 5% and 1% respectively.

**Table 2. Genotypes of pigeonpea included in different clusters**

| Cluster number | Number of genotypes included | Names of genotypes |
|---|---|---|
| I | 9 | UPAS-120, ICPL-6994, ICPL-6996,ICPL-6999, ICPL-7000,ICPL-7359,ICPL-7364,ICPL-7409,ICPL-7429 |
| II | 16 | ICPL-6992,ICPL-7001,ICPL-7003,ICPL-7004,ICPL-7005,ICPL-7358,ICPL-7362,ICPL-7363,ICPL-7366,ICPL-7367,ICPL-7374,ICPL-7389,ICPL-7391,ICPL-7397,ICPL-7404,ICPL-7420 |
| II | 12 | ICPL-87119,BDN-2,ICPL-6995,ICPL-6997,ICPL-7002,ICPL-7349,ICPL-7376,ICPL-7379,ICPL-7382,ICPL-7392,ICPL-7393,ICPL-7406 |
| IV | 8 | ICPL-7373,ICPL-7384,ICPL-7385,ICPL-7388,ICPL-7398,ICPL-7405,ICPL-7430 |

**Table 3. Inter and Intra cluster distance of genotypes in pigeonpea**

| **Cluster** | **I** | **II** | **III** | **IV** |
|---|---|---|---|---|
| **I** | **2.818** | 2.518 | 3.178 | 4.904 |
| **II** | | **2.364** | 2.125 | 4.048 |
| **III** | | | **2.624** | 3.599 |
| **IV** | | | | **3.674** |

**Table 4. Mean performance of genotypes in individual cluster for different yield traits**

| Clusters | Characters | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | Entries | Days to flower initiation | Days to 50% flowering | Days to maturity | Plant height (cm) | Number of branches Plant$^{-1}$ | No. of pods plant$^{-1}$ | No. of pods Cluster$^{-1}$ | No. of pod clusters Plant$^{-1}$ | Pod length (cm) | No. of seeds pod$^{-1}$ | 100 seed weight (g) | Seed yield plant$^{-1}$ (g) |
| I | 9 | 100.50 | 122.72 | 169.33 | 184.85 | 13.28 | 251.00 | 2.67 | 60.39 | 5.30 | 4.83 | 8.58 | 28.13 |
| II | 16 | 102.31 | 127.72 | 175.56 | 193.70 | 15.06 | 242.31 | 2.75 | 55.31 | 5.27 | 4.00 | 7.76 | 30.74 |
| III | 12 | 106.29 | 132.83 | 182.00 | 179.34 | 14.83 | 260.67 | 2.79 | 55.25 | 5.30 | 4.00 | 10.17 | 35.40 |
| IV | 8 | 112.12 | 134.88 | 196.19 | 203.16 | 16.38 | 375.75 | 3.12 | 102.56 | 5.58 | 4.25 | 8.70 | 45.06 |

**Table 5. Desirable genotypes based on cluster performance**

| Characters | Clusters | | | |
|---|---|---|---|---|
| | I | II | III | IV |
| Days to flower initiation | UPAS- 120 | ICPL-6992 | ICPL-6995 | ICPL- 7373 |
| Days to 50% flowering | UPAS-120 | ICPL-6992 | ICPL-6997 | ICPL-7373 |
| Days to maturity | UPAS-120 | ICPL-6992 | ICPL-7392 | ICPL-7373 |
| Plant height (cm) | ICPL-6994 | ICPL-7005 | ICPL-7349 | ICPL-7384 |
| No. of primary branches plant $^{-1}$ | ICPL- 6999 | ICPL-7366 | ICPL-87119 | ICPL-7384 |
| No. of pods plant$^{-1}$ | ICPL-7409 | ICPL-6992 | ICPL-7392 | ICPL- 7430 |
| Number of pods cluster$^{-1}$ | UPAS-120 | ICPL-7389 | ICPL-87119 | ICPL-7385 |
| No. of pod clusters plant$^{-1}$ | UPAS-120 | ICPL-7366 | ICPL-7392 | ICPL- 7405 |
| Pod length (cm) | UPAS- 120 | ICPL- 7003 | ICPL- 6997 | ICPL-7373 |
| No. of seeds pod$^{-1}$ | ICPL-6996 | ICPL-6992 | ICPL-87119 | ICPL-7373 |
| 100 seed weight (g) | ICPL-7000 | ICPL-7389 | ICPL-7382 | ICPL-7385 |
| Seed yield plant$^{-1}$ | UPAS-120 | ICPL-7363 | ICPL-7392 | ICPL-7373 |