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**Research Note**

# Variability, character association and path analysis for yield and yield attributes in pigeonpea

**R. Rekha*, L. Prasanthi*, M. Reddi Sekhar and M. Shanti Priya**
Department of Genetics and Plant Breeding, S.V. Agricultural College, Tirupati-517502, AP.
Email: rekha.agri84@gmail.com

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**Abstract**
The present investigation was undertaken with an objective to study the variability, heritability, character association and path analysis in 49 genotypes of pigeonpea. Number of secondary branches per plant, number of pods per plant, seed yield per plant, phenol content, 100 seed weight and number of primary branches per plant showed higher estimates of phenotypic and genotypic coefficient of variation. High heritability with high genetic advance as per cent of mean recorded for all the characters except protein content, days to 50 per cent flowering and days to maturity. Character association studies revealed the strong positive association of seed yield with number of pods per plant, number of secondary branches per plant, number of primary branches per plant and plant height. Path analysis indicated high positive direct effect of pods per plant on seed yield.

**Key words:** Pigeonpea, Genetic variability, heritability, correlation, path analysis.

Pigeonpea [*Cajanus cajan (L.)* Millsp] popularly known as arhar or tur or redgram is the second most important pulse crop of India. It is grown for split dry beans called Dal, which is rich in proteins. Being a rainfed crop, it plays an important role in Indian agriculture and is cultivated in more than 25 tropical and sub-tropical countries either as sole crop or as intercrop. Yield is a complex character and depends on number of component characters which are quantitatively inherited. The knowledge of variability, heritability and nature of association of the yield and its attributes enable a plant breeder to plan an effective breeding progrmame. Correlation in combination with path analysis can provide a better insight into the cause and effect relationship between different pairs of characters. The present study was conducted to know the variability, extent of character association between yield and its components and direct and indirect effects on seed yield in pigeonpea.

The experimental material consisted of 49 pigeonpea genotypes grown in a randomized block design with three replications during late *kharif*, 2008-2009 at Dry Land Farm of S.V. Agricultural College, Tirupati. Each genotype was sown in two rows of 3 m length with a recommended spacing of 90 x 20 cm. Observations were recorded on five randomly selected plants in each genotype for 12 characters. For statistical analysis INDOSTAT software was used. Heritability was estimated as per Allard (1960), Genetic Advance was computed as per Johnson *et al.* (1955), Correlation coefficients between yield and yield contributing characters were estimated as suggested by Burton (1952) and path analysis was carried out following Dewey and Lu (1959).

The analysis of variance revealed significant differences among genotypes for all the characters indicating the presence of adequate variability among the genotypes. The estimates of mean, range, phenotypic and genotypic coefficients of variation (PCV and GCV), heritability in broad sense ($h^2$) and genetic advance presented in Table 1 revealed that PCV estimates of all characters were slightly more than that of GCV indicating the less influence of environment. The GCV was higher for secondary branches per plant followed by pods per plant, seed yield per plant, phenol content, 100-seed weight and primary branches per plant indicating that these traits can be effectively selected for improvement. The estimates of heritability were higher for all the characters. High heritability coupled with high genetic advance as per cent of mean (>20%) was observed with nine yield components *viz.*, number of secondary branches per plant, pods per plant, seed yield per plant, phenol content, 100-seed weight, number of primary branches per plant, plant height, pod length and number of seeds per pod. Similar results were reported by Dahat *et al.* (1997) for primary branches per plant, secondary branches per plant, number of pods per plant, seed yield per plant and plant height; Kingshlin and Subbaraman (1999) for pod length, seeds per pod and Basavarajaiah *et al.* (1999) for 100-seed weight.

The genotypic and phenotypic correlation between different characters are given in Table 2. Seed yield was positively correlated with pods per plant, secondary branches per plant and plant height, both at phenotypic and genotypic levels. Further, a significant positive association was observed among these individual components. Such correlations indicate the possibility of selection of genotypes with higher number of pods per plant, primary and secondary branches per plant and plant height may help in crop improvement. These results are in accordance with the reports of Dahat *et al.* (1997), Deshmukh *et al.* (2000) and Anuradha *et al.* (2007). Hence, simultaneous selection based on these characters could be suggested for improvement in yield. On the other hand the characters days to 50 per cent flowering, days to maturity and phenol content recorded non-significant association with seed yield.

With a view to know the direct and indirect effects of these traits seed yield correlations were further partitioned into direct and indirect effects through path coefficient analysis. The residual effect of 0.56 indicates that some more traits related to seed yield need to be included (Table 3). The results revealed that number of pods per plant exerted highest positive direct effect on seed yield. These results are in conformity with the reports of Jogendra Singh *et al.* (2008). The characters *viz.*, primary branches per plant and 100-seed weight had moderate and low positive direct effects on seed yield, respectively whereas plant height, seeds per pod and protein content had negative direct effects on seed yield. Number of pods per plant also had high indirect effect on seed yield via plant height, number of secondary branches per plant and number of primary branches per plant.

Based on the foregoing discussion on character association and path analysis, it can be concluded that number of pods per plant had strong positive correlation as well as high magnitude of positive direct effect on seed yield. Hence it may be a criteria in the selection of superior genotypes for seed yield.

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**Table 1. Variability and genetic parameters for twelve characters in pigeonpea**

| Character | Mean | Genotypic Coefficient of Variation (%) | Phenotypic Coefficient of Variation (%) | Heritability (Broad sense) (%) | Genetic advance (GA) | Genetic Advance as per cent of mean (%) |
|---|---|---|---|---|---|---|
| Days to 50% flowering | 97.89 | 4.71 | 4.75 | 98.42 | 9.42 | 9.62 |
| Days to maturity | 148.66 | 3.08 | 3.10 | 98.35 | 9.34 | 6.29 |
| Plant height (cm) | 154.61 | 14.65 | 14.68 | 99.51 | 46.54 | 30.10 |
| No. of primary branches per plant | 16.35 | 22.11 | 22.71 | 99.74 | 7.25 | 44.32 |
| No. of secondary branches per plant | 27.71 | 47.90 | 48.03 | 99.46 | 27.28 | 98.41 |
| No. of pods per plant | 377.13 | 32.96 | 32.97 | 99.90 | 255.89 | 67.85 |
| Pod length (cm) | 5.14 | 11.02 | 11.02 | 99.91 | 1.17 | 22.69 |
| No. of seeds per pod | 3.78 | 10.64 | 10.70 | 99.88 | 0.82 | 21.80 |
| 100-seed weight (g) | 9.97 | 23.93 | 23.93 | 99.96 | 4.92 | 49.28 |
| Protein content (%) | 24.96 | 5.74 | 5.75 | 99.72 | 2.95 | 11.80 |
| Phenol content (%) | 5.38 | 26.93 | 26.93 | 99.98 | 2.99 | 55.47 |
| Seed yield per plant (g) | 114.94 | 31.25 | 31.31 | 99.67 | 73.88 | 64.28 |

**Table 2. Phenotypic ($r_p$) and genotypic ($r_g$) correlation coefficients among twelve characters in pigeonpea**

| Character | | Days to Maturity | Plant height (cm) | No. of primary branches / plant | No. of secondary branches / plant | No. of Pods/ plant | Pod Length (cm) | No. of Seeds/ Pod | 100-seed Weight (g) | Protein content (%) | Phenol content (%) | Seed yield/ plant (g) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Days to 50% | $r_p$ | 0.7194** | 0.0999 | 0.0030 | 0.3160** | 0.0530 | -0.1089 | -0.2228** | -0.1359 | -0.0098 | -0.0494 | 0.1093 |
| Flowering | $r_g$ | 0.7305** | 0.1018 | -0.0003 | 0.3193** | 0.0535 | -0.1098 | -0.2269** | -0.1370 | -0.0091 | -0.0502 | 0.1118 |
| Days to Maturity | $r_p$ | | 0.2001* | -0.0609 | 0.2969** | 0.1518 | -0.2705** | -0.2705** | -0.3501** | -0.0458 | 0.0975 | 0.1133 |
| | $r_g$ | | 0.2031* | -0.0663 | 0.3005** | 0.1533 | -0.2724** | -0.2762** | -0.3533** | -0.0462 | 0.0983 | 0.1151 |
| Plant height (cm) | $r_p$ | | | 0.4579** | 0.5988** | 0.7167** | -0.2175** | -0.0645 | -0.2796** | 0.0008 | 0.2091* | 0.5621** |
| | $r_g$ | | | 0.4701** | 0.6019** | 0.7185** | -0.2182** | -0.0651 | -0.2803** | 0.0001 | 0.2096* | 0.5638** |
| No. of primary | $r_p$ | | | | 0.6007** | 0.4902** | 0.0753 | -0.0787 | -0.2013* | -0.1642* | -0.0914 | 0.5715** |
| branches/ plant | $r_g$ | | | | 0.6137** | 0.5045** | 0.0783 | -0.0804 | -0.2062* | -0.1670* | -0.0945 | 0.5885** |
| No. of secondary | $r_p$ | | | | | 0.6630** | -0.1362 | -0.2765** | -0.4004** | -0.0058 | -0.0122 | 0.6124** |
| branches/ plant | $r_g$ | | | | | 0.6657** | -0.1367 | -0.2786** | -0.4014** | -0.0059 | -0.0122 | 0.6153** |
| No. of pods/ plant | $r_p$ | | | | | | -0.2704** | -0.3105** | -0.5286** | 0.0729 | 0.2064* | 0.7589** |
| | $r_g$ | | | | | | -0.2707** | -0.3122** | -0.5290** | 0.0728 | 0.2065* | 0.7604** |
| Pod length (cm) | $r_p$ | | | | | | | 0.6596** | 0.5574** | -0.2623** | -0.1875* | -0.0201 |
| | $r_g$ | | | | | | | 0.6632** | 0.5577** | -0.2631** | -0.1876* | -0.0198 |
| No. of seeds/ pod | $r_p$ | | | | | | | | 0.3929** | -0.2181** | -0.1157 | -0.2004* |
| | $r_g$ | | | | | | | | 0.3952** | -0.2187** | -0.1164 | -0.2012* |
| 100-seed weight | $r_p$ | | | | | | | | | 0.0038 | -0.2113* | -0.2558** |
| (g) | $r_g$ | | | | | | | | | 0.0038 | -0.2113* | -0.2562** |
| Protein content | $r_p$ | | | | | | | | | | 0.2051* | -0.0758 |
| (%) | $r_g$ | | | | | | | | | | 0.2055* | -0.0756 |
| Phenol content | $r_p$ | | | | | | | | | | | 0.0771 |
| (%) | $r_g$ | | | | | | | | | | | 0.0773 |

* Significant at 5% level ** Significant at 1% level

**Table 3. Phenotypic (P) and genotypic (G) path coefficients among seed yield and its components in pigeonpea**

| Character | | Days to 50% flowering | Days to Maturity | Plant height | No. of primary Branches / plant | No. of secondary branches/ plant | No. of pods/ Plant | Pod Length | No. of seeds/ Pod | 100-seed Weight | Protein Content | Phenol content | 'r' with seed yield/ plant |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Days to 50% Flowering | P | 0.0467 | 0.0264 | -0.0058 | 0.0006 | 0.0221 | 0.0402 | -0.0114 | 0.0167 | -0.0260 | 0.0009 | -0.0010 | 0.1093 |
| | G | 0.0500 | 0.0309 | -0.0069 | -0.0001 | 0.0193 | 0.0406 | -0.0107 | 0.0158 | -0.0268 | 0.0008 | -0.0012 | 0.1118 |
| Days to Maturity | P | 0.0336 | 0.0367 | -0.0117 | -0.0121 | 0.0208 | 0.1150 | -0.0283 | 0.0203 | -0.0670 | 0.0041 | 0.0020 | 0.1133 |
| | G | 0.0366 | 0.0424 | -0.0137 | -0.0144 | 0.0182 | 0.1164 | -0.0266 | 0.0192 | -0.0692 | 0.0040 | 0.0023 | 0.1151 |
| Plant height | P | 0.0047 | 0.0073 | -0.0585 | 0.0911 | 0.0419 | 0.5427 | -0.0228 | 0.0048 | -0.0535 | -0.0001 | 0.0043 | 0.5621** |
| | G | 0.0051 | 0.0086 | -0.0675 | 0.1024 | 0.0364 | 0.5456 | -0.0213 | 0.0045 | -0.0549 | 0.0000 | 0.0050 | 0.5638** |
| No. of primary branches/ plant | P | 0.0001 | -0.0022 | -0.0268 | 0.1990 | 0.0420 | 0.3712 | 0.0079 | 0.0059 | -0.0385 | 0.0147 | -0.0019 | 0.5715** |
| | G | 0.0000 | -0.0028 | -0.0317 | 0.2178 | 0.0371 | 0.3831 | 0.0077 | 0.0056 | -0.0404 | 0.0145 | -0.0022 | 0.5885** |
| No. of secondary branches/ plant | P | 0.0148 | 0.0109 | -0.0350 | 0.1195 | 0.0699 | 0.5021 | -0.0143 | 0.0208 | -0.0766 | 0.0005 | -0.0003 | 0.6124** |
| | G | 0.0160 | 0.0127 | -0.0406 | 0.1336 | 0.0605 | 0.5055 | -0.0134 | 0.0194 | -0.0786 | 0.0005 | -0.0003 | 0.6153** |
| No. of pods/ plant | P | 0.0025 | 0.0056 | -0.0419 | 0.0975 | 0.0464 | 0.7573 | -0.0283 | 0.0233 | -0.1011 | -0.0065 | 0.0042 | 0.7589** |
| | G | 0.0027 | 0.0065 | -0.0485 | 0.1099 | 0.0402 | 0.7594 | -0.0264 | 0.0217 | -0.1036 | -0.0063 | 0.0049 | 0.7604** |
| Pod length | P | -0.0051 | -0.0099 | 0.0127 | 0.0150 | -0.0095 | -0.2047 | 0.1048 | -0.0496 | 0.1066 | 0.0235 | -0.0038 | -0.0201 |
| | G | -0.0055 | -0.0115 | 0.0147 | 0.0171 | -0.0083 | -0.2056 | 0.0977 | -0.0461 | 0.1092 | 0.0229 | -0.0045 | -0.0198 |
| No. of seeds/ pod | P | -0.0104 | -0.0099 | 0.0038 | -0.0157 | -0.0193 | -0.2351 | 0.0691 | -0.0751 | 0.0751 | 0.0195 | -0.0024 | -0.2004* |
| | G | -0.0114 | -0.0117 | 0.0044 | -0.0175 | -0.0168 | -0.2371 | 0.0648 | -0.0695 | 0.0774 | 0.0190 | -0.0028 | -0.2012* |
| 100-seed weight | P | -0.0064 | -0.0128 | 0.0163 | -0.0401 | -0.0280 | -0.4003 | 0.0584 | -0.0295 | 0.1912 | -0.0003 | -0.0043 | -0.2558** |
| | G | -0.0069 | -0.0150 | 0.0189 | -0.0449 | -0.0243 | -0.4017 | 0.0545 | -0.0275 | 0.1959 | -0.0003 | -0.0050 | -0.2562** |
| Protein content | P | -0.0005 | -0.0017 | 0.0000 | -0.0327 | -0.0004 | 0.0552 | -0.0275 | 0.0164 | 0.0007 | -0.0896 | 0.0042 | -0.0758 |
| | G | -0.0005 | -0.0020 | 0.0000 | -0.0364 | -0.0004 | 0.0553 | -0.0257 | 0.0152 | 0.0007 | -0.0869 | 0.0049 | -0.0756 |
| Phenol content | P | -0.0023 | 0.0036 | -0.0122 | -0.0182 | -0.0009 | 0.1563 | -0.0196 | 0.0087 | -0.0404 | -0.0184 | 0.0205 | 0.0771 |
| | G | -0.0025 | 0.0042 | -0.0141 | -0.0206 | -0.0007 | 0.1568 | -0.0183 | 0.0081 | -0.0414 | -0.0179 | 0.0237 | 0.0773 |

Phenotypic residual effect : 0.5656 Genotypic residual effect : 0.5609

* Significant at 5% level ** Significant at 1% level