Genetic variability and character association in pigeonpea \( [Cajanus cajan (L.) \text{ Millsp.}] \) core collection

A. Thanga Hemavathy*, J.R. Kannan Bapu and M. Priyadharshini

Department of Pulses, Tamil Nadu Agricultural University, Coimbatore-641 003, Tamil Nadu, India.

Received: 07-09-2018  Accepted: 27-03-2019  DOI: 10.18805/IJARe.A-5123

ABSTRACT
An experiment was conducted in fifty seven pigeonpea genotypes to study the variability, correlation and path coefficient in pigeonpea at Department of Pulses, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore during kharif, 2015. The highest GCV was recorded for number of secondary branches/plant (111.73) followed by number of pods/plant (40.73). Heritability in broad sense ranged from 94.66 (pod size) to 99.93 (number of pods per plant). High genetic advance were observed for number of secondary branches/plant (230.00), number of pods per plant (83.88), single plant yield (80.89) and number of racemes (60.41) indicating the prevalence of additive gene action for inheritance of these traits. Character association studies indicated that number of racemes, number of secondary branches, number of primary branches per plant, clusters per plant, pods per plant, pod length, seeds per pod, and 100 seed weight were strongly associated with seed yield. Path coefficient analysis revealed that days to 50 per cent flowering and number of pods per plant had high positive direct effect on seed yield. Pod size had moderate direct effect on seed yield. Hence due emphasis should be given on number of pods per plant for improvement of seed yield in pigeonpea.

Key words: Correlation, Path analysis, Pigeonpea, Yield.

INTRODUCTION
Pigeonpea \( [Cajanus cajan (L.) \text{ Millsp.}] \) (2n=22) is the most important pulse crop in the world. It contains 21% protein. Pigeonpea is widely grown in the semi-arid tropics, particularly in the Indian subcontinent where it accounts for over 70% of the production and covering 74% of the area. Although India leads the world both in area and production of pigeonpea, its productivity is lower than the world average. Therefore, there is a need to enhance the productivity potential of pigeonpea by evolving high yielding genotypes, which depends on the availability of variability for yield and its component traits in the population. Keeping these views in mind the present study was undertaken to assess the nature and magnitude of genetic variability present in different genotypes of pigeon pea. However scanty information is available on character association in pigeonpea. This is essential for planned heterosis breeding programme to give due weightage to the characters responsible for increased seed yield of hybrids. Correlation and path analysis thus help in identifying suitable selection criteria for improving the yield. The present investigation was undertaken to assess the genetic variability, correlation and the direct and indirect effects of different influencing characters on seed yield in pigeonpea.

MATERIALS AND METHODS
The experiment for the present study was conducted during kharif, 2015 at Department of Pulses, Tamil Nadu Agricultural University, Coimbatore. The experimental material comprised of 57 genotypes of pigeonpea entries and it was laid out in randomised block design with three replications. In each replication five plants were selected randomly for each genotypes and the following twelve quantitative characters viz., days to 50 per cent flowering, plant height (cm), seeds per primary branches per plant, secondary branches per plant, clusters per plant, pods per cluster, pod length (cm), seeds per pod, pods per plant, 100-seed weight (g), single plant yield (g) and days to maturity were observed for estimating genetic diversity. Standard statistical procedures were used for the analysis of variance, genotypic and phenotypic coefficients of variation (Burton, 1952), heritability (Lush, 1940), genetic advance and correlation (Johnson et al., 1955) and path analysis (Dewey and Lu, 1959).

RESULTS AND DISCUSSION
Genetic variability studies provide basic information regarding the genetic properties of the population based on which breeding methods are formulated for further improvement of the crop. In the present investigation, values of phenotypic coefficient of variation were greater than genotypic coefficient of variation for all the traits studied (Table 1). It implied that apparent variation was not only due to genotype but also due to the influence of environment. The values for phenotypic coefficient of variation obtained for various yield and yield attributing characters ranged from 111.80 to 3.56
The highest PCV and GCV were recorded for number of secondary branches (111.73%) followed by number of pods per plant (40.73%), single plant yield (39.48%) and number of racemes (29.36%). Moderate PCV was observed for plant height (12.57%), pod bearing length (12.42%) and number of primary branches (12.36%). The values for genotypic coefficient of variation obtained for various yield and yield attributing characters ranged from 5.56 to 111.73 per cent. The highest GCV were observed for number of secondary branches (111.80%) followed by number of pods per plant (40.75%), single plant yield (39.70%) and number of racemes (29.39%). This indicated high variability for this character among the accessions and hence there is a great scope for improvement of these characters by direct selection among the genotypes. Moderate PCV was observed for plant height (12.57%), pod bearing length (12.42%) and number of primary branches (12.36%). The values for genotypic coefficient of variation obtained for various yield and yield attributing characters ranged from 5.56 to 230.01 per cent. Number of secondary branches (230.01) followed by number of pods per plant (83.88), single plant yield (80.89), number of racemes (60.41) plant height (25.44), pod bearing length and number of primary branches (25.12) and 100 seed weight (24.11).

High heritability linked with high genetic advance indicates predominance of additive gene effects and effectiveness of selection for that trait. High heritability along with high genetic advance as per cent of mean were recorded for number of pod per plant, single plant yield, number of racemes, plant height, pod bearing length, number of primary branches and 100 seed weight. Similar observation was reported by Ram, (2016) for number of branches per plant, number of pods per plant and seed yield per plant, Mittal et al., 2010 and Patel and Acharya (2011) for number of branches per plant and number of pods per plant. Thus, selection of these traits is likely to accumulate more additive genes leading to further improvement of their performance and these traits may be used as selection criteria in pigeon pea breeding program.

Correlation coefficient for different quantitative characters was presented in Table 2. Single plant yield was highly significant and positively correlated with number of pods per plant, number of secondary branches, number of racemes, days to 50% flowering, days to maturity, pod bearing length, number of seeds per pod and pod size however hundred seed weight was non significantly correlated with single plant yield. Regarding intercorrelation, days to 50% flowering had positive significant correlation with plant height, number of racemes, number of primary branches, number of secondary branches, number of pods per plant and days to maturity (Table 2). Hence selection of these traits will be useful for future breeding.

Table 1. Variability studies in pigeonpea germplasm.

| Traits                        | PCV  | GCV  | Heritability (%) | GA as per cent of mean |
|-------------------------------|------|------|------------------|------------------------|
| Days to 50% flowering         | 5.61 | 5.56 | 98.06            | 11.34                  |
| Plant height (cm)             | 12.57| 12.46| 98.24            | 25.44                  |
| Pod bearing length (cm)       | 12.42| 12.31| 98.16            | 25.12                  |
| Pod size (cm)                 | 10.86| 10.56| 94.66            | 21.17                  |
| Seeds per pod                 | 8.73 | 8.61 | 97.25            | 17.50                  |
| No. of racemes                | 29.39| 29.36| 99.77            | 60.41                  |
| No. of primary branches       | 12.36| 12.28| 98.65            | 25.12                  |
| No. of secondary branches     | 111.80|111.73|99.87            |230.01                  |
| No. of pods per plant         | 40.75| 40.73| 99.93            | 83.88                  |
| 100 seed weight (g)           | 11.93| 11.82| 98.10            | 24.11                  |
| Days to maturity              | 3.56 | 3.53 | 98.24            | 7.21                   |
| Single plant yield (g)        | 39.70| 39.48| 98.90            | 80.89                  |
programme. The results are in agreement with Singh (1999) and Bainiwal et al. (1981).

Path coefficient analysis considers direct as well as indirect effects of the variables by partitioning the correlation coefficients. Path coefficient analysis in the present study revealed that days to 50% flowering and number of pods per plant had high positive direct effect on seed yield per plant. Pod size had moderate direct effect and number of pods per plant had high positive direct effect on seed yield. Hence, seed yield can be improved in pigeonpea through selection of this character.

REFERENCES

Bainiwal C.R., Mehrotra N. and Jatasa R.S. (1981). Studies on variability and correlation in pigeon pea. Indian J. Agric. Res., 15: 161-165.

Bal.C.P. Bhave, S.G., Thaware, B.L. and Desai, S.S. 2018. Correlation and path analysis studies in pigeon pea (Cajanus cajan). Global Journal of Bioscience and Technology. 7: 70-73

Baskaram K. and Muthiah A.R. (2006). Variability studies in pigeon pea [Cajanus cajan (L.)Millsp.] Research on Crops, 7: 249-252.
Bhadru D. (2008). Genetic variability, heritability and genetic advance in pigeon pea \textit{[Cajanus cajan (L.) Millsp.]} \textit{Research on Crops}, \textbf{9}: 661- 662.

Burton G.W. (1952). Quantitative inheritance in grasses. \textit{Proc. 6th Int. Grassland Cong.}, \textbf{1}: 277-283.

Chandirakala, R. and N. Subbaraman. (2010). Character association and path analysis for yield attributes in full sib progenies in Pigeonpea \textit{[Cajanus cajan (L.) Mill Sp.]} \textit{Electronic Journal of Plant Breeding}, \textbf{1}: 824-827.

Dewey, D.R. and Lu, K.H. (1959). A correlation and path coefficient analysis of components of crested wheat grass production. \textit{Agron. J.}, \textbf{51}: 515-518.

Dhameliya, H.R. and Pathak. A.R. (1995). Path analysis in Pigeonpea. \textit{Gujarat Agric. Res. J.}, \textbf{20}: 160-163.

Firoz Mahamad, Gowda M. B. and Girish G. (2006). Genetic variability and association studies in vegetable pigeon pea. \textit{Environment and Ecology}, \textbf{24(4)}: 1124-1129.

Johnson, H.W., Robinson H.F. and Comstock R.E.. (1955). Estimation of genetic variability and environmental variability in soybean. \textit{Agron. J.}, \textbf{47}: 314 - 318.

Lush, J. L. (1940). Intra - sire correlation and regression of offspring on dams as a method of estimating heritability of characters. \textit{Proc. Amer. Soc. Animal Prod.}, \textbf{33}: 293 - 301.

Mittal VP, Singh P, Brar KS. (2010) Character association and path coefficient analysis for yield components in pigeonpea. \textit{Madras Agricultural Journal.} ; \textbf{97}:319- 20.

Patel, J. B. and Acharya S. (2011). Genetic divergence and character association in Indo-African derivatives of pigeonpea \textit{[Cajanus cajan (L.) Mill sp.]} \textit{Journal of Food Legumes}, \textbf{24}: 198-201.

Ram, K., Kanak, S., Shrimali, T.M. and Geeta, B. (2016). A study on genetic variability, correlation and path analysis in pigeon pea \textit{[Cajanus cajan (L.) Millspangh]} \textit{International Journal of Agriculture Sciences}, \textbf{8}: 2287- 2289.

Rao, P.J.M., Malathi, S, Reddy, D.V.V. and Upender, M. (2013). Genetic studies of association and path coefficient analysis of yield and its component traits in pigeonpea. \textit{Intl. J. of Scientific and Res. Publications}, \textbf{3}(8).

Sarsamkar, S.S., Borgaonkar S.B., Kalyankar S.V., Kadam B.P. and Kadam G. R. (2008). Genetic variability studies in pigeon pea \textit{[Cajanus cajan (L.) Millsp.]} \textit{International J. Plant Sci.}, \textbf{3(2)}: 502-503.

Shunyu,V., Chaturvedi H. P., Changkija S. and Singh J. (2013). Genetic variability in pigeon pea \textit{[Cajanus cajan (L) Millsp.]} genotypes of Nagaland. \textit{Indian Res. J. Genet. and Biotech.}, \textbf{5}: 165-171.

Singh J. 1999. Correlation coefficient analysis for seed yield in pigeon pea. \textit{Crop Res.}, \textbf{17}: 381-385.

Sodavadiya, M.S., Pithia, Savaliya J.J., Pansuriya A.G. and Korat V.P. (2009). Studies on characters association and path analysis for seed yield and its components in pigeonpea \textit{[Cajanus cajan (L.) Mill sp.]} \textit{Legume Research}, \textbf{32}: 203-205, 2009.

Thanki, H.P. and Sawargaonkar S.L. (2010). Path coefficient analysis in pigeonpea \textit{[Cajanus cajan L. Mill sp.]} \textit{Electronic Journal of Plant Breeding}, \textbf{1}: 936-939.

Wright, S. (1921). Systems of mating. \textit{Genetics}, \textbf{6}: 111-178.