

Genetic variability studies in pigeon pea [*Cajanus cajan* (L.) Millsp.]

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SUMMARY

The present investigation was undertaken with the objective to evaluate the variation among the population consisting of eight parents and twelve F₂'s of pigeon pea. The variability was studied in terms of genotypic and phenotypic variance, coefficient of genotypic and phenotypic variation, heritability and genetic advance. The wide range of variability was exhibited by number of pods per plant, plant height and seed yield per plant. High heritability was exhibited by days to maturity, number of pods per plant, 100 seed weight, days to 50% flowering and seed yield per plant. However, moderate to low heritability estimates were displayed by number of secondary branches per plant and number of primary branches per plant, respectively. High genetic advance coupled with high heritability estimates were observed for number of pods per plant, seed yield per plant, plant height and days to maturity.

Key words : Genotypic variance, Heritability, Genetic advance, Variability, Pigeon pea.

Pigeon pea (*Cajanus cajan* (L.) Millsp) is the second most widely grown legume in India. It is very important component of farming system in India because of its ability to fix atmospheric nitrogen in to the soil. Beside that it has multiple uses as a source of food, feed, fuel and fertilizer. Breeding strategy of any crop involves collection, evaluation and selection of superior genotypes. The important consideration in each of the above needs the detailed study of genetic variability. The estimates of heritable and non heritable variances give a clue on improvement for the character under study. Hence, the present investigation was undertaken with object to evaluate the variation among the material, consisted of 10 parents and 12 F₂'s of pigeon pea genotypes.

MATERIALS AND METHODS

The experiment was conducted during *kharif*, 2003 at experimental farm of College of Agriculture, Latur. The experimental material for the present investigation was comprised of 10 parents and 12 F₂ crosses, respectively. The 22 treatments were grown in Randomized Block Design with three replications. The spacing between row to row and plant to plant was kept 60 cm and 30 cm, respectively. Five plants were selected from each parent and twenty plants were selected from each F₂ crosses randomly for recording observations. Average value of each character was determined from these observational plants.

The observations were recorded on eight characters namely days to 50% flowering, days to maturity, plant height (cm), number of primary branches, number of secondary branches, number of pods per plant, 100 seed

weight (g) and grain yield per plant.

The coefficients of variation were estimated by using the method suggested by Burton (1952). Heritability in broad sense was calculated according to the method suggested by Allard *et al.* (1960) while genetic advance under selection was estimated by using the formula of Johnson *et al.* (1955).

RESULTS AND DISCUSSION

The results revealed presence of wide range of variability among the parents and F₂ population for yield and its contributing characters. The estimates of mean, range, phenotypic and genotypic coefficient of variance, heritability, genetic advance and expected genetic advance to all the characters are presented in the Table 1.

The relative contribution of genotype and environment could be judged by computing phenotypic and genotypic coefficient of variation. In general, the phenotypic variances were higher than genotypic ones for almost all characters under study. The genotypic coefficient of variation was observed to be high for number of pods per plant (27.29%) followed by seed yield per plant (26.43%), number of secondary branches per plant (25.23%), number of primary branches per plant (18.29%) and 100 seed weight (11.47%). For rest of the characters, the genotypic coefficient was ranged from 4.36 % to 6.73%. In case of most of the characters under study the magnitude of genotypic coefficient of variation was closer to the phenotypic coefficient of variation. This indicated that greater role was played by genotype rather than environment. The characters having high genotypic coefficient of variation possessed better potential for

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