

GENETIC ANALYSIS FOR YIELD AND ITS COMPONENTS IN PIGEONPEA (*CAJANUS CAJAN* (L.) MILL SP)

P. Jagan Mohan Rao and V.Thirumala Rao*

Regional Agricultural Research Station, Warangal

Professor Jayashankar Telangana State Agricultural University, Rajendranagar, Hyderabad-500 0030, India

*Scientist (PI Br), RARS, Mulugu Road, Warangal, -506 007, Telangana State, India (Present Address)

ABSTRACT: Study was carried out for genetic variability, heritability and genetic advance of eight characters in fifty four germplasm lines. Analysis of variance revealed significant difference among genotypes for all the nine characters studied. The magnitude of PCV and GCV was moderate to high for pods per plant, seed yield and primary branches per plant. High heritability was recorded for days to 50% flowering, seed yield per plant, number of pods per plant, test weight and plant height. High heritability combined with high genetic advance was recorded for number of pods per plant and seed yield per plant indicating that these characters are controlled by additive gene effect and phenotypic selection of these characters would be effective for further breeding purpose.

Key words: Genetic variability, Heritability and Pigeonpea

INTRODUCTION

Pigeonpea is the second important pulse crop after chickpea in India. It plays an important role in subsistence agriculture because, it produces protein rich food with fewer inputs and can be grown in diverse cropping systems. India has the largest pigeonpea area (3.5 m.ha) with an estimated production of 2.5 m. tons. To meet the protein needs of population, it is essential to increase the production of pulses. Development and adaption of high yielding varieties have been instrumental in increasing the yield and production. Success of crop improvement programme in pigeonpea depends upon the extent of genetic variability, choice of parents for hybridization and selection procedure adopted. The seed yield of Pigeonpea (*Cajanus cajan* (L.) Mill sp) is a complex character, which is highly influenced by environmental variations. Information on nature and magnitude of variability present in a population due to genetic and non genetic causes is an important prerequisite for systematic breeding programme. An attempt was made in the present investigation to assess the variability, heritability and genetic advance of some quantitative characters in a set of genotypes.

MATERIALS AND METHODS

Fifty four pigeonpea genotypes were grown in 2 rows of 4m length in randomized block design with three replications during kharif 2013-14. Row to row and plant to plant spacing were maintained at 120 and 20 cm, respectively. Observations were recorded for eight traits including days to 50% flowering, days to maturity, plant height, primary branches per plant, secondary branches per plant, number of pods per plant, test weight and seed yield per plant. The data were collected on five randomly selected plants from each replication. The coefficient of variation was calculated as per Burton (1952). Heritability in broad sense and genetic advance were calculated as per Johnson *et al.*, (1955).

RESULTS AND DISCUSSION

The success of any breeding programme depends upon the extent of genetic variability in base population and it is essential to subject a population for selection for achieve improvement in a particular trait. In the present study the analysis of variation shown highly significant differences among the genotypes for all the characters studied *viz.*, days to 50% flowering, days to maturity, plant height, primary branches per plant, secondary branches per plant, number of pods per plant, test weight and seed yield, indicating the existence of considerable genetic variation in the experimental material. This variability can be utilized effectively to develop high yielding cultivars through hybridization followed by selection.

Perusal the components of variance revealed that the phenotypic coefficient of variation (PCV) were higher than Genotypic coefficient of variation (GCV) for all the characters studied indicating the role of environmental variance in the total variance. Magnitude of PCV and GCV was moderate to high for number of pods per plant (35.7&31.3), seed yield per plant (28.2&29.6) and primary branches per plant (24.1&18.1). These results were in conformity with that of Satish Kumar *et al.*, (2006); Firoz mahamad *et al.*, (2006) and Badru, 2011. Although GCV is indicative of the presence of high degree of genetic variation, the amount of heritable portion can only be determined with the help of heritability estimates and genetic gain. Heritability in broad sense was high in most of the characters *viz.*, days to 50% flowering (93%), seed yield per plant (90.7%), number of pods per plant (76.9%), test weight (75.9%) and plant height (70.2%). Similar results were reported by Patel and Patel (1998); Baskaran and Muthaiah, (2006) and Sreelakshmi *et al.*, (2010). Though high heritability indicates the effectiveness of selection on the basis of phenotypic performance, it does not show any indication of the amount of genetic progress for selecting the best individuals. According to Johnson *et al.*, (1955), heritability estimates along with the genetic gain are usually more useful. High heritability coupled with high genetic advance as percent of mean was more for number of pods per plant and seed yield per plant indicating the role of additive gene in expressing these traits, suggesting better scope for improvement of these traits through direct selection.

Table.1 Estimates of variability, heritability and genetic advance in pigeonpea

Character	Mean	Range	GCV (%)	PCV (%)	Heritability in Broad sense(H ²)	Genetic advance	GA as percent of mean
Days to 50% flowering	117.3	88-144.3	12.8	13.2	93.0	29.8	25.4
Days to maturity	163.5	139.3-188	8.4	10.2	68.8	23.5	14.4
Plant height	172.7	126.6-210	10.2	12.2	70.2	30.4	17.6
Primary branches per plant	14.2	9-22.3	18.9	24.1	61.3	4.3	30.5
Secondary branches per plant	17.7	11.6-26.6	14.7	26.4	31.0	3.0	16.9
Number of pods per plant	256.1	132-571	31.3	35.7	76.9	144.7	56.5
Test weight	8.1	5.7-9.5	10.3	11.8	75.9	1.5	18.4
Seed yield per plant	57.1	24-107.2	28.2	29.6	90.7	31.6	55.4

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