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STUDIES ON GENETIC CHARACTERISTICS OF PIGEON PEA AND DETERMINATION OF SELECTION CRITERIA WITH PATH CO-EFFICIENT ANALYSIS

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ABSTRACT: Genetic analysis and association studies were conducted in 128 germplasm lines of pigeon pea received from NBPGR for yield and yield attributing characters. Higher amount of variation was observed for seed yield per plant followed by number of pods per plant and plant height. High heritability with high genetic advance as percentage of mean were obtained for seed yield and number of pods per plant indicated the presence of additive gene action influencing the inheritance of these characters. Significant positive correlations were observed for 100 seed weight, number of primary branches per plant, number of pods per plant and plant height on seed yield per plant were high and positive. Selection for higher seed weight, days to maturity, primary branches, pods per plant and plant height would be the best criteria for increasing the seed yield per plant in pigeon pea.

Key words : Pigeon pea, variability, heritability, genetic advance, correlations, path analysis

INTRODUCTION

Pigeon pea (Cajanus cajan (L.) Millsp.) is one of the major grain legume (pulse) crops grown in about 50 countries in the tropics and subtropics. It is the second important pulse crop of India which has diversified uses as food, feed, fodder and fuel. It has been recognized as a valuable source of protein for the vegetarians in their daily diet. In India, pigeonpea is grown in an area of 4.09 million hectares with a production of 3.27 million tonnes (Anonymous 2011). The Indian sub continent alone contributes nearly 92 per cent of the total pigeonpea production in the world. Although India leads the world both in area and production of pigeonpea, its productivity is lower (671 kg/ha) than the world average (742 kg/ha) (FAOSTAT 2010). One of the factors responsible for the poor productivity of pigenpea are the lack of improved cultivars. Research for genetic improvement of this crop to raise yield levels effectively has to be strengthened countering biotic stresses, through widening genetic base. To accomplish this task, an insight into the extent of variability, heritability and genetic advance to identify the factors responsible for high yield is essential. Further, seed yield is a character with complex gene action. In order to study it properly, different factors affecting the yield must be considered and evaluated with regard to their contribution to yield. Study of character association and path analysis helps the breeder in fixing the selection criteria for higher grain yield, so that selection will be effective in isolating the genotypes with desirable combination of characters. Accordingly, the present study was carried out to estimate the extent of variability, relationship between yield and its component characters and to assess the indirect influence of the various components on yield.

MATERIALS AND METHODS

The experimental material consisting of 128 germplasm lines of NBPGR with a flowering duration range of 150-180 days were sown in randomized block design with a row of 4m each with two replications at Agricultural Research Station, Warangal, ANGRAU during 2006-07 kharif with a spacing of 90x20 cm². All recommended package of practices were followed to raise a good crop. Observations were recorded on five randomly selected plants in each replication for days to fifty percent flowering, number of primary branches, number of pods per plant, seeds per pod, pod length (cm), plant height (cm), days to maturity, 100-seed weight (g) and seed yield per plant (g).

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Phenotypic and genotypic correlation co-efficients and path co-efficients were worked out as per Dewey and Lu (1959) and Wright (1921). Genotypic and phenotypic co-efficients of variation (Burton, 1952), Heritability in narrow sense, Genetic advance, genetic advance as percentage of mean (Johnson *et al* 1955) were estimated.

RESULTS AND DISCUSSION

Genotypes showed a wide range of variability for all the characters except for primary branches per plant, number of seeds per plant, pod length and 100 seed weight (Table1). Widest range of variability was recorded by number of pods per plant followed by plant height and days to maturity. The estimates of phenotypic co-efficient of variation (PCV) were higher than those of genotypic co-efficient of variation (GCV) for all the traits as was also reported earlier (Linge et al, 2010) indicating the greater effect of environment on expression of these characters.

The difference between PCV and GCV was relatively high for primary branches and seeds per pod which indicated that these characters were highly influenced by the environment. Higher amount of variation was observed for seed yield per plant followed by number of pods per plant, plant height and seed weight hence, may be considered as potential traits for improvement of seed yield. While, it was low in case of days to 50% flowering and days to maturity. Similar trend was reported by Suresh kumar and Reddy (1983), Sharma et al (1994), Rahman et al (1999), Linge et al (2010) and Bhadru (2011). Estimates of heritability in broad sense indicates the extent of genetic control of a given trait and thus reflects the efficiency of selection for that trait. The heritability estimates were highest for 100 seed weight, number of plants per plant, plant height, days to maturity, days to 50% flowering, pod length and seed yield per plant. Whereas, Number of primary branches per plant and number of pods per plant recorded low estimates of heritability. These results confirms that of Baskaran and Muthaiah (2006) except for 100 seed weight and seed yield per plant. Johnson (1955) suggested that for realistic conclusion and effective selection, the genetic parameters, heritability and genetic advance should be considered together. In the present study, high heritability estimates coupled with high genetic advance as percentage of mean (Table-1) were obtained for pods per plant and plant height.

| Character | Mean | Range | PCV | GCV | $h^2_{BS(\%)}$ | GA | GAM |
|------------------------|----------------------|----------------|--------|--------|----------------|-------|-------|
| Days to 50% flowering | 50% flowering 155.98 | | 4.448 | 4.331 | 94.8 | 13.55 | 8.68 |
| Primary Branches 12.63 | | 9-18 | 19.21 | 9.254 | 23.2 | 1.16 | 9.18 |
| Pods / plant. 139.07 | | 25-280 | 28.967 | 28.915 | 99.6 | 82.68 | 59.45 |
| Seeds / Pod | 4.01 | 3-5 | 12.269 | 4.334 | 12.5 | 0.13 | 3.15 |
| Pod length (cm) | 4.82 (cm) | 3.78-5.73 (cm) | 12.728 | 12.358 | 94.3 | 1.19 | 4.72 |
| Plant height (cm) | 61.44 (cm) | 117-262 (cm) | 13.556 | 13.495 | 99.1 | 44.68 | 27.67 |
| Days to maturity | 205.95 | 128-237 | 8.114 | 7.993 | 97.0 | 33.40 | 16.22 |
| 100 Seed Weight (g) | 9.16 (g) | 4-11.9 (g) | 13.365 | 12.767 | 91.3 | 2.30 | 5.12 |
| Seed yield/ Plant | 23.71 (g) | 1.86-61.43 (g) | 48.568 | 48.483 | 99.6 | 23.64 | 19.69 |

Table 1. Estimates of genetic parameters for yield and yield traits of pigeon pea

PCV= Phenotypic coefficient of variation

GCV= Genotypic coefficient of variation

h2 BS=broad sense heritability

GA = Genetic advancement at 5%

GAM= genetic advance as percent of mean at 5 percent level.

This indicated the preponderance of additive gene action with less environmental influence in the inheritance of these characters and selection for these traits would be more effective. High heritability with moderate genetic advance as per cent of mean in case of seed yield per plant and days to maturity indicated the importance of both additive and non-additive gene action. Virdi *et al* (2004) reported similar results. In the present investigation, the genotypic correlation co-efficients, in general were higher than phenotypic correlations (Table-2) which indicated that, though there is strong inherent association between the genotype and phenotype, the phenotypic expression of the characters decreased under the influence of environment.

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Further insight revealed that, the seed yield per plant was positively correlated with 100-seed weight, primary branches per plant, days to maturity and plant height at genotypic and phenotypic level. Hence, can be considered important for selection in breeding programmes targeted for high yield in pigeon pea. Similar observations were also reported by Bhaskaran and Muthiah 2007.

| Character | | Primary Branches | Pods / plant. | Seeds / Pod | Pod length | Plant height | Days to maturity | Seed Weight | Seed yield/ Plant |
|--------------------------|----------------|---------------------|------------------|-------------|------------|-----------------|---------------------|----------------|----------------------|
| Days to 50% flowering | rg | 0.0937 | -0.0063 | 0.1390* | -0.0396 | -0.2965 ** | 0.0712 | -0.3794** | -0.1965** |
| | r _p | 0.0289 | -0.0072 | 0.0547 | -0.0361 | -0.2889 ** | 0.0678 | -0.3496 ** | -0.1913** |
| Primary | r _g | | 0.4043** | -0.3723** | 0.4647 ** | 0.1434 * | -0.1394* | 0.0026 | 0.2241** |
| Branches | r _p | | 0.1927 ** | -0.0525 | 0.1857 ** | 0.0683 | -0.0656 | 0.007 | 0.1166 |
| Pods / plant. | r _g | | | 0.1734 ** | -0.0387 | 0.1268* | -0.052 | -0.0987 | 0.1074 |
| | r _p | | | 0.0605 | -0.039 | 0.1266 * | -0.0514 | -0.0924 | 0.1073 |
| Seeds / Pod | r _g | | | | -0.0512 | -0.2847** | 0.1531* | -0.2664** | -0.2033** |
| | r _p | | | | -0.0027 | -0.0986 | 0.0615 | -0.0831 | -0.0786 |
| Pod length | r _g | | | | | 0.1831** | -0.0812 | 0.0133 | 0.0373 |
| | r _p | | | | | 0.1745 ** | -0.0839 | 0.0198 | 0.0379 |
| Plant height | r _g | | | | | | -0.0748 | 0.2349** | 0.1711** |
| | r _p | | | | | | -0.0705 | 0.2210 ** | 0.1697** |
| Days to maturity | r _g | | | | | | | -0.1269 * | 0.1307* |
| | r _p | | | | | | | -0.1205 | 0.1276* |
| Seed Weight | r _g | | | | | | | | 0.2061** |
| | r _p | | | | | | | | 0.1974** |

Table 2. Estimates of correlation coefficients at genotypic (r_g) and phenotypic (r_p) levels

* Significant at 5 percent level; ** significant at 1 percent level

| Character | | Days to 50% flowering | Primary Branches | Pods / plant. | Seeds / Pod | Pod length | Plant height | Days to maturity | Seed Weight | Correlation with Seed yield/ Plant |
|-----------------------|---|-----------------------------|---------------------|------------------|----------------|---------------|-----------------|---------------------|----------------|--|
| Days to 50% flowering | G | <u>-0.1576</u> | -0.0148 | 0.001 | -0.0219 | 0.0062 | 0.0467 | -0.0112 | 0.0598 | -0.1965** |
| | Р | <u>-0.121</u> | -0.0035 | 0.0009 | -0.0066 | 0.0044 | 0.035 | -0.0082 | 0.0423 | -0.1913** |
| Primary Branches | G | 0.025 | <u>0.2669</u> | 0.1079 | -0.0994 | 0.124 | 0.0383 | -0.0372 | 0.0007 | 0.2241** |
| | Р | 0.0028 | <u>0.0984</u> | 0.0189 | -0.0052 | 0.0183 | 0.0067 | -0.0065 | 0.0007 | 0.1166 |
| Pods / plant. | G | -0.0001 | 0.0094 | 0.0232 | 0.004 | -0.0009 | 0.0029 | -0.0012 | -0.0023 | 0.1074 |
| | Р | -0.0008 | 0.0203 | 0.1056 | 0.0064 | -0.0041 | 0.0134 | -0.0054 | -0.0098 | 0.1073 |
| Seeds / Pod P | G | -0.0092 | 0.0247 | -0.0115 | <u>-0.0663</u> | 0.0034 | 0.0189 | -0.0101 | 0.0177 | -0.2033** |
| | Р | -0.0034 | 0.0033 | -0.0038 | <u>-0.0625</u> | 0.0002 | 0.0062 | -0.0038 | 0.0052 | -0.0786 |
| Pod length | G | 0.0037 | -0.0429 | 0.0036 | 0.0047 | -0.0922 | -0.0169 | 0.0075 | -0.0012 | 0.0373 |
| | Р | -0.0006 | 0.0031 | -0.0006 | 0.0000 | 0.0166 | 0.0029 | -0.0014 | 0.0003 | 0.0379 |
| Plant height P | G | -0.0187 | 0.009 | 0.008 | -0.0179 | 0.0115 | <u>0.063</u> | -0.0047 | 0.0148 | 0.1711** |
| | Р | -0.0238 | 0.0056 | 0.0104 | -0.0081 | 0.0144 | 0.0824 | -0.0058 | 0.0182 | 0.1697** |
| Days to maturity | G | 0.0147 | -0.0287 | -0.0107 | 0.0315 | -0.0167 | -0.0154 | 0.2058 | -0.0261 | 0.1307* |
| | Р | 0.0121 | -0.0117 | -0.0092 | 0.011 | -0.015 | -0.0126 | <u>0.1782</u> | -0.0215 | 0.1276* |
| Seed Weight | G | -0.0542 | 0.0004 | -0.0141 | -0.038 | 0.0019 | 0.0335 | -0.0181 | <u>0.1427</u> | 0.2061** |
| | Р | -0.0566 | 0.0011 | -0.015 | -0.0135 | 0.0032 | 0.0358 | -0.0195 | 0.162 | 0.1974** |

Bold underlined values are direct effects

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However, days to 50% flowering recorded negative correlation with seed yield per plant. In contrary to this, positive association of days to 50% flowering was reported by Anuradha et al.,2007. The Negative association of days to 50% flowering and positive correlation of days to maturity with seed yield per plant indicated that the prolonged flowering duration in pigeon pea might have helped in realising higher number of pods which resulted ultimately in higher seed yield. As yield is influenced by many factors, selection based on correlations without considering the interaction between important yield contributing characters could be misleading. Therefore, the correlation co-efficients were partitioned into direct and indirect effects (Table-3). Path co-efficient analysis revealed that seed weight, days to maturity, number of primary branches, number of pods per plant and plant height had exhibited positive direct effects and positive association with seed yield per plant at genotypic and phenotypic levels. These results clearly gave an indication that the selection based on these characters would directly improve the seed yield in pigeon pea. Maximum direct effect of primary branches on seed yield besides its indirect effect via number of pods per plant, pod length, plant height and 100 seed weight indicated that it was the most important yield contributing trait among all. Days to 50% flowering although exhibited negative association and negative direct effect on seed yield, its indirect contribution though seed weight, plant height, pod length and number of pods per plant was positive. These results are in conformity with the findings of Dahiya and Singh (1994), Lal et al (2002), Virdi et al (2004) and Sree Lakshmi et al (2011).

Based on the critical analysis of these genetic parameters, selection for higher seed weight, days to maturity, primary branches, pods per plant and plant height would be the best criteria for increasing the seed yield per plant in Pigeonpea.

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