# GENE ACTION IN SHORT-DURATION PIGEONPEAS

**K.B. Saxena\*, D.E. Byth, E.S. Wallis and I.H. De Lacy**
Department of Agriculture,
University of Queensland, St. Lucia-4067, Australia

## ABSTRACT

A half-diallel of seven short-duration pigeonpea lines was evaluated in the F1 and F2 generations at the University of Queensland, Redland Bay Farm (27 S), Australia. The Fl trial was space planted and the F2 trial was grown in normal plant density. The results indicated that GCA variance predominated for all characters considered. SCA variance was significant for some characters but was small compared with GCA. There was a clear effect of method of evaluation on the expression of genetic parameters among the progenies. This paper discusses the implications of these results in relation to the accuracy and meaningfulness of genetic parameters estimated in this and other similar studies and those of other workers for breeding strategies.

*Additional index words*: Pigeonpea, *Cajanus cajan*, diallel, combining ability.

## INTRODUCTION

Most of the present day pigeonpea [*Cajanus cajan* (L.) Millsp.] cultivars are land races which are maintained by open-pollination. The national average yield of pigeonpea in India continue to be around 600 kg/ha and to date, imporement in yield through breeding has been limited (Singh, 1971). This may, to some extent, be related to the relatively poor genetic knowledge of important economic characters.

Information on genetic variability, gene action and breeding value for yield and yield components is of importance to breeders in developing strategies and methods for improving yield. Srivastava (1986), reviewing the limited genetic information available in this crop, mentioned that for yield both additive and nonadditive genetic variances are important, but the former seems to be more predominant. In pigeonpea the availability of genetic information is limited as well as conflicting and, therefore, the present study on gene action was undertaken.

## MATERIAL AND METHOD

A half-diallel of seven relatively early flowering lines was evaluated in the $F_1$ and $F_2$ generations at Redland Bay Farm of the University of Queensland, Australia (27°S). The parental material consisted of seven short-duration pigeonpea cultivars. Of these four (QPL 1, 2, 3, 4) were selected at the University of Queensland; UPAS 120 and Prabhat were introduced from India, and 3D8103 was introduced from IITA, Nigeria. The 21 Fls and F2s were evaluated separately in randomized complete block designs with three replications, and were sown on

\*Present address: Pigeonpea Breeder, ICRISAT, Patancheru 502 324, A.P., India.

December 20, 1979. Due to limited seed quantities the F1 crosses were space planted (1 m × 1 m) in two row plots 5 m long. The F2 trial had six-row plots 3 m long with a .5 m × .2 m spacing. The experimental site has a humid coastal environment with a deep, high clay oxisol (kranznozem) soil. Fertilizer was applied to provide 20 kg N and 45 kg $P_2O_5$ per hactare. Spray irrigation was used as necessary to avoid moisture stress. The crop was protected from weed competition and insect damage to ensure good growth.

Data were recorded on days to flower, pod number, seed size, seeds/pod, yield/plant, and plant height (only in F1). In the F1 test, observations were made on all the plants whereas in the F2 plots, ten competitive plants per plot were sampled at random. Days to flowering was recorded on a whole plot basis for the F2 trial, and a bulk harvest was done for the plot yield. Statistical analysis was done on plot means according to method 4, model 1 of Griffing (1956).

## RESULTS AND DISCUSSION

The coefficients of variation for each character was almost similar in both the generations inferring that the characters had similar precision of determination in these trials (Table 1). Substantial genetic variation existed for plant height, days to flower, and yield but the genetic coefficient of variation values were relatively low for seed size and seeds/pod. In the F1 generation significant differences were found among entries for all characters (Table 1). In the F2 test, significant differences existed among the populations only for days to flower, seed size, seeds/pod, and yield/plot.

For yield/plant and pod number the genotypes differed significantly only in the F1, but not in the F2. It seems that the expression of genetic variability for these characters was influenced by the differences in inter-plant competition in the two trials. In the F2 test, the use of higher plant density perhaps resulted in greater competition and this suppressed the expression of the genetic potential for these characters. In contrast in the space-planted F1 trial, plants were virtually non-competitive which possibly resulted in the full expression of growth potential. This resulted in much larger plants in some crosses, particularly those involving the later flowering parents, and thus in the realization of a relatively higher variance components (Table 1). Consequently, the expression of genetic differences was confounded with the nature of the test environment in these trials. Yermanos and and Allard (1961) also reported influence of environment on the expression of genes in flax.

Most of the SCA effects for the characters studied in the F1 and F2 generations were not significantly different from zero. However, for cross UPAS 120 × 3D 8103, there was a significant negative SCA effect for days to flower (F1 and F2) and for plant height (F1), indicating a significant contribution of non-additive gene action in the expression of these traits in this cross. None of the

**Table 1.** Mean squares and statistics from analysis of combining abiility of various characters in the $F_1$ and $F_2$ from a $7 \times 7$ diallel

| Source | Days to flower | | Plant Height $P_1$ | Pod Number | | Seed Size | | Seeds/pod | | Yield/plant | | Yield/plot $F_2$ |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | $F_1$ | $F_2$ | $P_1$ | $F_1$ | $F_2$ | $F_1$ | $F_2$ | $F_1$ | $F_2$ | $F_1$ | $F_2$ | $F_2$ |
| Entries | 573.9** | 348.4** | 4072.3** | 87122** | 2465 | .365** | .529** | .126** | .109** | 6444** | 96.21 | 432500** |
| GCA | 610.1** | 354.8** | 4359.9** | 59864** | 1154 | .374** | .490** | .103** | .039 | 4982** | 57.31 | 336341** |
| SCA | 11.9** | 13 8** | 70.6** | 15831 | 679 | .014 | .042 | .016 | .035 | 934 | 21.25 | 61806* |
| [1]$\sigma^2$GCA | 121.64 | 70 03 | 869.93 | 9755.85 | | .073 | .092 | .018 | | 833.12 | | 62067 |
| [2]$\sigma^2$SCA | 10.03 | 9.18 | 60 42 | 4746.14 | | .003 | .013 | .004 | | 367.12 | | 35801 |
| [3]GCV(%) | 20.36 | 16.43 | 32.31 | 14.11 | 9.83 | 4.47 | 5.25 | 6.13 | 4 82 | 20.37 | 9.34 | 26.47 |
| [4]CV(%) | 3.50 | 5.82 | 4.88 | 19 20 | 22.49 | 3.19 | 4 06 | 6 59 | 8.57 | 21.22 | 22.49 | 21.51 |
| $\bar{X}$ | 67.6 | 64.3 | 113 6 | 949 6 | 176 0 | 7.2 | 7.3 | 2.8 | 2.8 | 195.2 | 35.4 | 1298 7 |

[1], [2]Mean square of GCA and SCA effects respectively.  [3]Genetic coefficient of variation.  [4]Coefficient of variation.

crosses involving Prabhat or QPL lines had a significant SCA effect for days to flower. This probably reflects the relatively narrow genetic base for genes influencing flowering in these parents and suggested that the prospects for selecting recombinants earlier than the parents are low.

For seed yield, the data showed a marked difference in GCA effect between yield/plant in the F1 and yield per plot in the F2. Parents 3D8103, UPAS 120, and Prabhat conditioned high seed yield/plant in the F1, but 3D 8103 was inferior in GCA to the other two lines for yield/plot in the F2. Further, QPL lines had similar negative GCA effects for yield/plant in the F1, but QPL 3 and 4 had large positive GCA effects for yield per plot in the F2. These differences reflect the effects of differential inter-plant competition. This suggests that evaluation of mating designs should be in cultural conditions simulating normal practice, at least as far as plant density is concerned.

There was a close association between the GCA effects of the parents and their performance in the F1 (Table 2); that is, parental performance *per se* was a good predictor of breeding value for most of the characters. Thus the earliest flowering parents conditioned relatively early flowering, short plants, low pod number and low yield per plant, whereas the progenies of the later flowering 3D 8103 tended to be relatively late flowering and taller with large pod number, small seed size and high yield/plant in the F1 trial. On the other hand in the F2 a significant positive association between GCA effect and parental performance was observed only for days to flower.

The results emphasize the need to restrict parentage of mating design to a relatively narrow range of phenology, otherwise, it may prejudice the accuracy and meaningfulness of the genetic parameters.

Table 2. GCA effects in a seven-parent diallel in $F_1$ and $F_2$.

| Parent | Days to flower $F_1$ | Days to flower $F_2$ | Plant Height $F_1$ | Pod Number $F_1$ | Seed size $F_1$ | Seed size $F_2$ | Seeds/Pod $F_1$ | Yield/Plant $F_1$ | Yield/Plot $F_2$ |
|---|---|---|---|---|---|---|---|---|---|
| Prabhat | 0.39 | 0.04 | 0.48 | 71.26 | −0.17 | −0.02 | 0.27 | 28.69 | 79.70 |
| UPAS-120 | 9.23 | 8.64 | 20.20 | 61.10 | 0.56 | 0.41 | 0.04 | 30.20 | 177.62 |
| 3D-8103 | 20.42 | 14.64 | 57.47 | 187.34 | 0.08 | −0.49 | −0.08 | 40.24 | −553.89 |
| QPL-2 | −6.05 | −4.96 | −15.82 | −40.71 | −0.07 | −0.19 | −0.11 | −17.34 | −13.21 |
| QPL-1 | −8.26 | −5.96 | −21.71 | −103.53 | −0.18 | 0.17 | −0.03 | −26.83 | −29.84 |
| QPL-4 | −8.68 | −6.23 | −22.39 | −78.79 | 0.02 | 0.29 | −0.09 | −20.65 | 179.37 |
| QPL-3 | −7.04 | −6.16 | −17.27 | −96.67 | −0.24 | −0.18 | −0.15 | −34.31 | 160.25 |
| $LSD_{G_iG_j}$ | 1.73 | 2.76 | 4.09 | 134.51 | 0.13 | 0.22 | 0.14 | 30.41 | 206.02 |
| $\bar{X}$ | 67.6 | 64.3 | 113.6 | 949.6 | 7.2 | 7.3 | 2.8 | 195.2 | 1298.7 |
| $rGCA, \bar{X}_p$[a] | 0.99** | 0.97** | 0.99** | 0.64 | 0.94** | −0.45 | 0.92** | 0.81** | 0.27 |

[a] Correlation of GCA effect of a parent with its mean performance.

To understand the potential influence of the parental phenology on the estimates of genetic parameters, the diallel set was reanalyzed eliminating the latest flowering parent 3D 8103 (Table 3). The elimination of 3D 8103 crosses had no influence on the significance of differences among the progenies (Table 1, 3), but SCA variance for days to flower and SCA and GCA variances for yield/plot were not significant in $6 \times 6$ diallel. For most of the characters, there was a substantial reduction in the size of GCA and SCA components. As in the $7 \times 7$ analysis, GCA variance dominated all characters but the ratio of the GCA to SCA component was greater in $6 \times 6$ analysis.

In the present study GCA variance predominated for all characters studied (Table 1) both in F1 and F2 generations. SCA variance was significant for some characters, but was small relative to GCA. These results are similar to those of **Sharma** *et al.* (1972), **Sharma** *et al.* (1973), and **Dahiya** and **Brar** (1977) in pigeonpea. On the other hand, **Reddy** *et al.* (1977) and **Reddy** *et al.* (1979 a, b) reported predominance of SCA variance for all characters studied, including days to flower, plant height and seed yield and its components. The cause of this total difference between these studies is not known, but it may be related to the genetic material used in the study. Plant height and seed size are known to be highly heritable characters in pigeonpea (**Munoz** and **Abrams**, 1971; **Khan** and **Rachie**, 1972; **Sharma** *et al.*, 1972, **Sharma** *et al.*, 1973), and this is in disagreement with estimates indicating a preponderance of SCA variance for such traits (**Reddy** *et al.*, 1977, **Reddy** *et al* , 1979 a, b). Estimates of the form of genetic variation have quite fundamental influence of the definition of breeding strategies and methods.

On the basis of their estimates of gene action, **Sharma** *et al.* (1973) suggested the development of composite varieties; **Dahaya** and **Brar** (1977) preferred the use of the bulk population improvement over pedigree methods, and **Reddy** *et al.* (1979 b) suggested the exploitation of non-additive gene action through hybrids. **Khan** (1973) and **Frey** (1975) advocated population breeding using natural out crossing in the crop. Interestingly, the reproductive biology of pigeonpea permits both options. Varietal hybrids based on genetic male sterility and natural out crossing have exhibited considerable heterosis for seed yield (**Saxena** *et al.*, 1986). Also, pedigree or bulk breeding methods directed towards pure lines have been used sucessfully in pigeonpeas (**Gupta** and **Saxena**, 1985). **Byth** *et al.* (1981) reported a modification of floral morphology which enforces self-pollination is pigeonpea, and purposed its use in breeding scheme aimed for the production of both improved pure lines and populations.

In view of the conflicting and limited literature on gene action, in pigeonpea it is not possible to define breeding strategies directed exclusively at the exploitation of additive versus non-additive genetic variance. However, the present results and those of **Sharma** *et al.* (1972), **Sharma** *et al.* (1973) and **Dahiya** and **Brar** (1977) suggest that for the improvement of pigeonpea the additive genetic variation should be exploited through appropriate breeding procedure.

**Table 3.** Mean squares and statistics from analysis of combining ability for various characters in the $F_1$ and $F_2$ from a 6×6 diallel.

| Source | Days to flower | | Plant Height | | Pod Number | | Seed Size | | Seeds/pod | | Yield/plant | | Yield/plot $F_2$ |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | $F_1$ | $F_2$ | $F_1$ | $F_2$ | $F_1$ | $F_2$ | $F_1$ | $F_2$ | $F_1$ | $F_2$ | $F_1$ | $F_2$ | |
| Entries | 288.9** | 218.8** | 1528.1** | 1864.1** | 63101* | 1156.6 | .431** | .377** | .166** | .029** | 5992.6** | 94.59 | 773946** |
| GCA | 263.0** | 192.6** | 1359.6** | 1680.4** | 42776** | 347.7 | .392** | .301** | .130** | .021 | 4723.5** | 48.45 | 42392 |
| SCA | 3.7 | 6.1 | 37.3** | 32.9 | 8954 | 406.5 | .012 | .029 | .011 | .003 | 482.8 | 22.13 | 16579 |
| $^{1}\sigma^{2}$GCA | 65.29 | 47.04 | 338.52 | 404 06 | 8479 | | .094 | .069 | .030 | | 1051.7 | | |
| $^{2}\sigma^{2}$SCA | 1.86 | 1.59 | 31 82 | 0.00 | 97.95 | | .004 | .004 | .003 | | 0.0 | | |
| $^{3}$GCV(%) | 15.99 | 13.89 | 23.75 | 19.85 | 12.44 | 5 36 | 5.02 | 4.28 | 7.58 | 0.00 | 21.16 | 9.95 | 32.49 |
| $^{4}$CV(%) | 3.86 | 6.23 | 4.30 | 7.20 | 18.37 | 17.73 | 2.78 | 3.54 | 6.16 | 8.75 | 21.66 | 20 62 | 18.73 |
| $\bar{X}$ | 60.8 | 59.4 | 94.5 | 118 9 | 887.1 | 170.0 | 7.2 | 7.5 | 2.8 | 2.8 | 181.8 | 36.2 | 1483.4 |

[1,2]Mean square of GCA and SCA effect respectively.    [3]Genetic coefficient of variation.    [4]Coefficient of variation.

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