Table 3. Specific combining ability effects and mean performance of crosses for six traits in sorghum

| Crosses | Plant Height (cm) | | Stem girth (cm) | | Leaf area (cm²) | | Paniele length (cm) | | Panicle girth . (cm) | | Yield per plant (g) | |
|-------------------|----------------------|---------|-----------------|--------|-----------------|---------|------------------------|-------|-------------------------|-------|------------------------|---------|
| | 11. 10 | 5.03 | mean | gca | mean | gca | mean | gca | mean | gca | mean | gca |
| SPV - 462XSPV 472 | 183.5 | 715 | 1.6 | 0.04 | 420.6 | 5.62 | 24.2 | -0.16 | 13.4 | -0.40 | 48.4 | 0.75 |
| SPV 46XSPV 913 | 195.4 | 12 | *.5 | 0.08 | 415.3 | 24,56 | 22.4 | 2.14 | 12.3 | 0,43 | 40.3 | -1.85 |
| SPV 462X M35-1 | 205.2 | 21.68** | w | | 425.8 | 55.54 | 24.0 | 1.83 | 14.4 | 0.75 | 50.6 | 6.83* |
| SPV 462 X Moti · | 182.3 | -1.95 | 1.4 | -0.00 | 390.4 | 56.06 | 23.8 | 0.28 | 13.0 | -0.20 | 34.0 | -3.09 |
| SPV 472 X SPV 913 | 190.3 | 18.71* | 1.6 | 0.13* | 415.3 | 66.51 | 21.3 | 1.67 | 12.2 | 0.40 | 41.2 | 6.09 |
| SPV 472 X M35-1 | 186.6 | 7.38 | 1.4 | -0.07 | 405.7 | -0.45 | 20.5 | -0.14 | 14.6 | 0.25 | 43.4 | 2.16 |
| SPV 472 X Moti | 182.7 | 6.35 | 1.8 | -0.06 | 420.4 | - 44.95 | 23.4 | 0.14 | 11.3 | 0.24 | 48.5 | 11.56** |
| SPV 913 X M 35-1 | 202.4 | -12.97 | 1.7 | 0.15** | 430.2 | - 24.63 | 19.0 | -0.21 | 12.8 | -0.23 | 38.0 | 7.27* |
| SPV 913 X Moti | 192.3 | 4.00 | 1.4 | -0.01 | 395.4 | 8.76 | 21.3 | -0.01 | 11.4 | -0.10 | 40.0 | -0.45 |
| M 35 -1 X Moti | 195.6 | 6.28 | 1.6 | -0.13 | 428.6 | - 28.99 | 23.4 | -0.11 | 15.3 | 0.48 | 42.3 | 8.02* |
| SEM (Sij - Sik) | 7-72-23-67 | 11.77 | | 0.08 | 4 | 54.84 | | 1.68 | | 0.48 | | 4.63 |
| SEM (sij - Skl) | | 10.74 | | 0.07 | - | 57.06 | | 1.54 | | 0.44 | .7 | 4.23 |

^{*} and ** Significant at 0.05 and 0.01 levels of probability, respectively

parent with low gca indicating the expression of yield is the result of non-additive interallelic interaction. Hence, these association could provide valuable guidelines for the development of varieties as well as hybrids for future breeding programme for rabi sorghum.

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(Received: November 1995 Revised: September 1996)

Madras Agric, J., 83(9): 575-578 September 1996 https://doi.org/10.29321/MAL10.A01058

NATURE OF GENE ACTION FOR YIELD AND YIELD COMPONENTS IN PIGEONPEA

G.VALARMATHI AND J.N.GOVIL

Regional Agricultural Research Station Pattambi 679 306 Kerala

ABSTRACT

Study on nature of gene action in pigeonpea for quantitative characters in sets of two crosses revealed the presence of additive gene action for all the characters except number of secondary branches in one cross. Among the interaction effects, additive x additive and additive x dominance interactions were found to play a major role than dominance x dominance interaction. Duplicate type of epistasis was observed for all the traits except for number of secondary branches and days to 50 per cent maturity. Varying nature of gene action from cross to cross indicated that reciprocal recurrent selection will be the suitable breeding programme for further improvement.

KEY WORDS: Pigeonpea, Yield, Yield Components, Gene Action

Pigeonpea [Cajanus cajan (L.Millp.)] is one of the most important legumes, cultivated in a wide range of tropical and subtropical environments.

hybridisation and recombination in pigeonpea needs top priority. A good understanding of inheritance of the genetic systems determining the quantitative character is essential for successful breeding programmes. The present study was undertaken to determine the nature of gene action for important quantitative characters in pigeonpea.

MATERIALS AND METHODS

Six generations viz., P1, P2, F1, F2, BC1, BC2, of two crosses viz., Pusa 33 x Prabhat DT (cross I) and High branch x ICPL-4 (cross-II) were studied during 1990-1991. The F1 s of the crosses were selfed to produce F2 seeds and backcrossed with respective recurrent parents to produce BC1 and BC2 generations. The six generations were raised during kharif season 1991, in a randomised block design with two replications at the farm attached to the Indian Agricultural Research Institute (IARI), New Delhi. Parental lines, F1, BC1, BC2 were raised in plots of two rows of four m length and F2 s were raised in four rows for both the crosses with a spacing of 30 x 30 cm.

Two rows of border lines were sown around the entries to aviod any border effects and to standardise the precise estimation of various statistical parameters. Five plants from P1, P2, F1, BC1, BC2, and 20 plants from F2 were randomly selected and data were recorded on 10 yield contributing quantitative traits viz., plant height, days to 50 per cent flowering, days to 50 per cent maturity, number of primary branches per plant, number of secondary branches per plant, seed per pod, hundred seed weight, number of grains per plant and yield per plant. Gene effects were estimated by six parameter model proposed by Hayman (1958)

RESULTS AND DISCUSSION

Generation means of 10 characters in pigeonpea are presented in Table 1. Scaling test (A,B,C,D) given by Mather (1949) was used to test the presence of gene interaction for all the characters studied. In both the crosses, atleast one scale was significant for all the characters indicating the presence of non allelic interaction. The estimates of gene effects with their standard

Table 1. Generation mean and the standard error of the mean of 10 characters of the two crosses cross I 'Pusa 33 x Prakhat DT' and cross II 'High Branch x ICPL-4'

| Generation | Cross . | Plant height | Days to 50% flowering | Days to- 50% maturity | No. of primary branches | No. of secondary branches | Pods/ plant | Seed per pod | 100 seed weight | Grains per plant | Yield per plant |
|------------|---------|-----------------|-----------------------------|-----------------------------|-------------------------------|---------------------------------|----------------|-----------------|--------------------|---------------------|--------------------|
| PI | 1 | 189.80 | 102.80 | 142.60 | 14.20 | 8.80 | 165.7 | 3.76 | 7.42 | 307.5 | 22,71 |
| | - | +2.67 | +0.44 | +0.61 | +0.34 | +0.22 | +4.40 | +0.05 | +0.07 | +4.21 | +0.34 |
| | 11 | 205.50 | 102.80 | 293.00 | 38.90 | 13.60 | 474.4 | 3.38 | 6.59 | 637.6 | 43.81 |
| | | +3.89 | +0.44 | +0.48 | +0.69 | +0.33 | +4.38 | +0.01 | +0.04 | +6.56 | +0.46 |
| P2 | 1 | 146.50 | 109.40 | 153.60 | 8.70 | 5.80 | 129.7 | 2.97 | 6.50 | 318.4 | 20.42 |
| | | +2.33 | +0.24 | +0.46 | +0.33 | +0.20 | +2.55 | +0.09 | +0.03 | +1.13 | +0.35 |
| | 11 | 131.50 | 105.40 | 144,40 | 14.40 | 4.50 | 112.0 | 3.62 | 8.27 | 247.5+ | 18.87 |
| | +1.30 | +0.24 | +0.39 | +0.42 | +0.27 | +1.17 | +0.03 | +0.03 | 3.03 | +1.83 | |
| Fl | 1 | 193.00 | 103.90 | 144.60 | 18.30 | 6.00 | 183.6 | 4.22 | 7.08 | 323.8 | 22.52 |
| * * | | +1.93 | +0.42 | +9.61 | +0.50 | +0.28 | +2.31 | +0.09 | +0.02 | +6.60 | +0.28 |
| | 11 | 193.10 | 103.90 | 231.70 | 19.40 | 9.00 | 340.I | 3.72 | 6.49 | 437.5 | 31.46 |
| | | +2.60 | +0.42 | +0.63 | +0.50 | +0.23 | +2.91 | +0.03 | +0.64 | +5.29 | - +0.31 |
| F2 | 1. | 193.45 | 114.85 | 157.30 | 16.65 | 0.70 | 187.9 | 4.19 | 7.12 | 319.2 | 22.68 |
| • • | | +2.61 | +0.41 | +0.40 | +0.40 | +0.29 | +2.23 | +0.07 | +0.05 | +3.15 | +0.22 |
| | 11 | 176.60 | 128.45 | 173.10 | 18.95 | 7.55 | 349.5 | 3.70 | 6.42 | 501.9 | 32.09 |
| | | +0.90 | +0.46 | +0.41 | +0.40 | +0.19 | +1.79 | +0.04 | +0.02 | +4.39 | +0.24 |
| ECI | I | 208.5 | 103.40 | 152.30 | 22.50 | 7.30 | 250.7 | 4.16 | 7.49 | 370.80 | 27.75 |
| DC1 | | +3.43 | +0.33 | +0.49 | +0.85 | +0.30 | +5.87 | +0.05 | +0.08 | +12.80 | +0.96 |
| | n | 174.20 | 205.50 | 270.00 | 31.70 | 14.30 | 340.5 | 3.52 | 6.78 | 453.40 | 30.83 |
| 1 | , ,,, | +2.27 | +0.50 | +0.35 | +1.07 | +0,32 | +1.95 | +0.06 | +0.04 | +2,15 | +0.63 |
| BC2 | | 184.90 | 114,40 | 158.30 | 17.20 | 6.70 | 157.3 | 4.19 | 6.29 | 320,70 | 21.14 |
| DCI | | +4.76 | +0.51 | +0.44 | +0.50 | +0.30 | +3.89 | +0.07 | +0.30 | +3.74 | +0.19 |
| | п | 141.70 | 118.00 | 160.60 | 17.50 | 5.80 | 217.6 | 3.93 | 7.19 | 294.10 | 20.91 |
| | | +1 60 | +0.67 | +0.62 | +0.35 | +0.22 | +2.54 | +0.03 | +0.02 | +4.83 | +0 16 |

Table 2. Estimates of gene effects with their standard errors for the yield and yield contributing characters of the cross 'Pusa 33 x Prakhat DT'

| - | | | | | · | | |
|------------------|------------|------------|------------|------------|------------|------------|-----------|
| Characters | m | d: | h | | J. | 1 | Epístasis |
| plant | 193.45 | 23.60 | 37.85 | 13.00 | 1.95 | -77,40 | D |
| height (cm) | +2.6075** | +5.8681** | +15.7012 | +6.1299 | +26.2296** | | |
| Days to 50% | 114.85 | -3.00 | -16.99 | -19.79 | 6.29 | 10.19 | D |
| flowering | -+0.4086** | +0.6083** | +2.0952** | +0.0374** | +0.6585 | +8.0897 | |
| Days to 50% | 157.30 | -6.00 | -11.85 - | -8.00 | -0.45 | -28.70 | C |
| maturity | +0.3993** | +0.6557** | +2.1889** | +2.0667** | +0.7523 | +3.3928** | 7.7 |
| No.of | 16.65 | 5.30 | 19.65 | 2.55 | 2,55 | -32,70 | D |
| primary branches | +0.4017** | +0.9874** | +2.6057** | +1.0161** | +1.0161 | +4.4059** | 4 |
| No. of secondary | 6.70 | 0.60 | -0.09 | 1.20 | -0.89 | -2.60 | С |
| branches | +0.2934** | +0.4243 | +1.4833 | +1.4484 | +0.4500 | +2.1605 | |
| Pods/plant | 187.90 | . 93.40 | 100.30 | 64.40 | 75.40 | -217.80 | D |
| 44 | +2.2267** | +7.0402** | +16.9898** | +16.6611** | +7.4348** | +30.2757** | , " |
| Sees/pod | 4.19 | -3.00 | 0.28 | -0.079 | - 0.075 | 0.45 | D |
| | +0.0741** | +0.0892** | +0.3482** | +0.3334 | +0.1028 | +0.4970 | |
| 100-seed | 7.12 | 1.20 | -0.82 | -0.94 | 0.74 | 1.46 | D |
| weight (g) | +0.0501** | +0.3143** | 0.6614 | +0.6598 | +0.3170 | +1.2765 | c# |
| Grains/plant | 319.20 | 50.10 | 116.85 | 106.20 | 55.55 | -216.10 | D |
| . . | +3.1469** | +13.3402** | +30.3082** | +29,5006* | +45.5599** | 4 | -1 |
| Grain | . 22.66 | 6.61 | 8.03 | 7.07 | 5.47 | -16.68 | D |
| yield/plant | +6.2431** | +0.9821** | +2.1890** | +2.1574** | +1.0119** | +4.0962** | |

^{*} Significant at 5% level; ** Significant at 1% level

errors for all the characters are given in Tables 2 and 3 for the cross I and cross II respectively. In both the crosses, F1 mean values were towards the parental mean in most of the characters except seed per pod, where it exceeded the better parent, indicating the presence of partial dominance for genes controlling yield characters except seed per pod. The high F1 mean for seed per pod indicated that this character may be influenced by complete dominance. Mohamed et al. (1985) reported similar results. Perusal of data in respect of BC I of both the crosses showed the trend towards the recurrent parent except seed per pod and hundred seed weight, where it was higher. It is expected as the frequency of desired homozyte is much higher in backcrossing than selfing. Analysis of generation mean revealed the role of additive gene effect in all the characters in both the crosses except number of secondary branches in the cross I confirming the assumption of partial dominance of genes controlling this character. Preponderance of additive gene effect was observed earlier for seed size and agronomic characters.

Dominance effect significantly contributed to yield contributing trait in both the crosses except number of secondary branches, seed per pod and hundred seed weight, in the cross I indicating the role of non additive gene action. Similar reports were given by Patel et al. (1987) for grain yield, Mehra et al. (1986) for plant height, Sardhana et al. (1987) for pods per plant. The significance of dominance was possibly depended on the order of parent used in the crossing. High branch in the cross II resulted in the positive significance of the maturity character. From the result, both additive and dominance gene effect are thus found to be important for yield and yield traits. Partioning of epistasis interaction indicated that additive x additive and dominance x dominance effect were more important that additive x dominance effect. These results are in accordance with the findings of Sardhana et al. (1987).

Duplicate type of epistasis was found to exist for all the characters, except days to 50 per cent maturity and number of secondary branches in the cross I where complementary type of epistasis was observed. In the cross I, the character day to 50 per cent maturity showing additive component and complementary type of epistasis, has reinforcing effect and could be exploited for developing fixed lines. Presence of additive gene action and absence of heterosis for 100 seed weight in the cross II suggested the improvement by simple selection. Yield and yield components were influenced by all the three types of gene action viz., additive, dominance and epistasis. Hence, reciprocal

fable 3. Estimates of gene effects with their standard errors for the yield and yield contributing characters of the cross 'High branch x ICPL-4'

| Characters | m | ď | h | i | j | I | Epistasis |
|-----------------|-------------|-----------|------------|------------|-----------|-------------|-----------|
| Plant | 176.70+ | 32.50 | -50.40 | -75.00 | -4.50 | 166.40 | D |
| beight (cm) | 0.8991** | +2.8364** | +7.4879** | +6.7160** | +3.5000 | +13.6189** | |
| Days to 50% | 128.45 | 87.50 | 146.90 | 133.20 | 24.50 | -113.60 | D |
| flowering | +0.4622** | +0.7937** | +2.5417** | +2.4367** | +0.8381** | +3.9481** | |
| Days to 50% | 173.10 | 109.20 | 182.20 | 169.20 . | 34.90 | -130.00 | Ď |
| maturity | +0.4150** | +0.7176** | +2.3045** | +2.1944** | +0.7810** | +3.6022** | |
| No. of | 18.95 | 14.20 | 22.60 | 22,60 | 1.95 | -28.90 | D |
| primary branche | s +0,3976** | +1.1269** | +2.7584** | +2.7584** | +1.1969 | +4.9496** | |
| No of secondary | 7.55 - | 9.00 | 0.95 | 11.00 | 4.45 | -16.10 | D |
| branches | +0.1893** | +0.3873** | +1.1290** | +1.0832** | +0.4430** | : +1.8380** | |
| pods/plant | 349.50 | 122.90** | -234.90 | -281.80 | 50.30 | 432.20 | D |
| and the second | +1.7921** | +3.2023 | +10.2976** | +9.6128** | +3.9248** | +16.4317** | |
| Seeds/pod | 3.70 | -0.41 | 0.32 | 0.09 | -0.29 | -0.56 | ,D |
| *.* | +0.3756** | +0.0663** | +0.2045 | +0.2004 | +0.0713** | +0.3155** | |
| 100-Seed | 6.42 | -0.42 | 1.30 | 2.24 | 0.43 | -2.32 | D |
| weight (g) | +0.0247** | +0.0479** | +0.6595** | +0.1375** | +0.0541** | +1.3079 | |
| Grains/plant | 501.90 | 159.30 | -517.65 | 512.60 | -35.75 | 777.70 | D. |
| * A | +4.3595** | +5.2853** | +21.3740** | +20.3919** | +6.4031** | +30,2511** | |
| Grain yield / | 32.09 | 9.92 | -24.76 | -24,89 | -2.55 | 47.02 | D |
| plant (g) | +0.2374** | +0.6514** | +1.8945** | +1.6123** | +1.1480* | +3.4133** | |

Significant at 5% level; ** Significant at 1% level

ecurrent selection procedure seems to be best uited method of breeding for improvement in this crop. Effort should be made to pool up the genotypes having predominance of additive genetic variation and complementary epistasis, for further improvement at yield level.

ACKNOWLEDGEMENT

This paper forms a part of M.Sc thesis of the senior author submitted to IARI, New Delhi in 1991. The author is greatful to the director IARI for the financial assistance in the form of IARI Junior fellowship and for providing necessary facilities for the study.

Madras Agric. J., 83(9): 578-581 September 1996

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(Received: December 1995 Revised: August 1996)

HETEROSIS IN EIGHT PARENT DIALLEL CROSS IN GARDEN PEA

P.K. PANDA. K.P. SINGH AND R.M.KAR

Department of Horticulture Institute of Agricultural Sciences Banaras Hindu University Varanasi 221 005

ABSTRACT

Diallel analysis was carried out by using eight parents of garden pea (Pisum sativum L.) along with 28 hybrids. These were evaluated for heterosis. Analysis of variance revealed significant difference for all the characters except length of pod indicating the presence of genetic diversity in the studied material. The amount of heterosis was high for number of pods per plant and green pod yield per plant, moderate for days to 50 per cent flowering, plant height, number of primary branches