Research Article

GENE ACTION OF YIELD AND YIELD CONTRIBUTING TRAITS OF STABLE CMS BASED HYBRIDS IN PIGEONPEA [*Cajanus cajan* (L.) Millspaugh.]

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Abstract: For enhancing biological yield in pigeonpea to gain economic benefits, basic information on genetics, inheritance of yield and its component characters are essential to determine the most efficient breeding approaches. The genetic components of ten yield related traits were studied by generation mean analysis, using six generations P_1, P_2, F_1, F_2, B_1 and B_2 of five crosses. Through additive-dominance model for the inheritance of characters, "Scaling" and "Joint scaling test" were found significant for most the characters. Frequencies of positive and negative alleles were distributed among parents. For most of the traits studied Dominance × Dominance (l) inter-allelic interactions were found more prominent than Additive × Additive (i) type, suggested that the performance of recurrent selection could be effective. Duplicate gene action was observed among many traits with few exhibiting complementary gene actions. Heritability and genetic advance both were indicated that a large proportion of the phenotypic variance was due to non-genetic effects. The observed dominance effects along with additive effects could be effective in selection of high yielding transgressive segregants in breeding program.

Keywords: *Pigeonpea, Epistasis, Heritability, Genetic advance, Gene action*

Academic Editor / Reviewer: Dr R. S. Umakanth

Introduction

Pigeonpea is an important food legume cultivated as annual crop in semi-arid tropics and subtropical regions of the world. Worldwide, it covers 6.9 million ha arable land with an annual production of 5.9 million tons and productivity of 852 kg/ha. In India, its total production is 4.2 metric tons with the mean productivity of 768 kg/hectare, which occupies 5.5 million hectares cultivated area [1]. Comparative productivity of pigeonpea against cereals is very low due to less harvest index. Several studies are required for enhancing biological and economic yield in pigeonpea [2]. Moreover, for the effective breeding approaches to improve pigeonpea crop, some preliminary information on genetics, inheritance of yield and its component characters are prerequisite [3,4]. Pigeonpea is an often-cross-pollinated diploid (2n = 2x = 22) crop with cross pollination probability of 5 to 70% [3]. Earlier selections were done for single plant or pedigree basis by considering it as a self-pollinated crop, but these methods have their own limitations [5]. Gene action of quantitative characters is a decisive factor to choose perfect breeding method. For the better genetic information, estimation of effect of several individual genes simultaneously is needed by using robust statistical method. Information on nature and magnitude of inter-allelic interactions are common but as far as possible these should be estimated for formulating a successful breeding program for the improvement of quantitative characters in pigeonpea [6].

Yield and its component characters are quantitative characters and may have additive, dominance and additive × dominance interaction [3]. Hence, for estimating main gene effects (additive and dominance) and their di-genic (additive × additive, additive × dominance, and dominance × dominance) interactions responsible for inheritance of quantitative traits, generation mean analysis is a useful technique. It gives us idea about breeding procedures to be adopted for the improvement of quantitative characters like yield. Therefore, the current investigation was carried to study number of genes, gene effects, heritability and genetic advance controlling yield and its quantitative characters through six parameter models in pigeonpea to suggest a breeding strategy for selection of plants for yield and yield contributing component traits, which may improve the yield significantly. Also, accelerated to threeline breeding system and helpful to identification of good restorers through marker assisted breeding as well as exploitation of cytoplasmic male sterile lines with the hybrid breeding program [2].

Materials and methods

Plant material and location of experiment

Five CMS based hybrids Cross-I (ICPA 2043 × Asha), Cross-II (ICPA 2043 × Azad), Cross-III (ICPA 2092 × Asha), Cross-IV (ICPA 2092 × Azad) and Cross-V (ICPA 2043 × MAL 13) were tested over two consecutive crop seasons (2009-10 and 2010-11). In second season, fresh F_{1s} and B_1 and B_2 populations were generated. The final experiments comprising of six populations P_1, P_2, F_1, F_2, B_1 and B_2 were conducted at Agricultural Research Farm, Institute of Agricultural Sciences, Banaras Hindu University Varanasi, India (25º18'N lat., 83º03' E long. and 75 m.a.s.l.) during crop season 2011-2012. The F_1 hybrids and parents were planted in one row each plot; while B_1 and B_2 were planted in two rows each plot, whereas F_2 was planted in 5 rows each plot per replication. All the crosses along with their parents were grown in compact family block design with three replications in entomophilous proof nylon net to avoid out crossing by following all necessary agronomical practices in each generation. Each plot consisted of one row of 4 meters length each with inter and intra row spacing of 75 × 25 cm, respectively. The observations were recorded on ten agronomic traits viz., days to 50% flowering (DF), days to maturity (DM), plant height (PH), primary and secondary branches (PB & SB) or Branches per plant (BPP), pods per plant(PPP),pod length (PL), seeds per pod (SPP), 100 seed weight (100SW) and seed yield per plant (SYP).

Scaling, joint scaling test and six parameter model

Each of five crosses were analyzed separately for components of means, variance, heritability and genetic advance as per cent mean (GAM). The presence or absence epistasis was detected by using A, B, C and D scaling tests proposed by [7] and [8]. Joint scaling test based on three parameter model m(mean of F_2 generation), d (pooled additive effects) and h(pooled dominance effects)was estimated from six generations using weighted minimum square method as proposed by Cavalli (1952) [9]. The χ² test was applied to test the goodness of fit observed with expected generation means. If the χ² test was significant, then estimated other gene effects like i (additive × additive), j(additive × dominance) and l (dominance × dominance) epistatic effects in addition to m, d and h. The six-parameter model was estimated by following formulas [10].

Variance analysis

Heritable (D), non-heritable (H) and environment (E) components of variance was calculated individually for each cross according to formula [11].

Heritability

Broad sense heritability (h_b^2) as well as real sense (h_r^2) was estimated by [12] formulas:

$$H_b^2 = [V_{F_2} - (V_{P_1} + V_{P_2} + V_{F_1})/3]/V_{F_2}$$
$$H_r^2 = [2V_{F_2} - (V_{B_1} + V_{B_2})]/V_{F_2}$$

Genetic advance

The GAM was calculated through given formula as below

$$GA\% = [(h_b^2 \times \sigma_p \times k)/\bar{X}] \times 100$$

Where, K is the selection differential at 5% level of selection σ_P is the standard deviation of phenotypic variance of F_2, $\bar{X}$ is the grand mean for respective character.

Results and discussions

The mean values for ten yield contributing traits of six populations P_1, P_2, F_1, F_2, B_1 and B_2 [Table-1] showed that hybrid means for number of pods/plant and seed yield/plant in all five crosses were higher than either of the highest parent. These results were indicated the accumulation of genes from parents to their progenies which improved genetic or enhanced genetic diversity as earlier experienced in pigeonpea [13] and [14]. Scaling and joint scaling test, both were significant for most of the traits in all the five crosses studied [Table-2]. Significance of χ² value of joint scaling test confirmed presence of di-genic interactions and linkages.

The estimation of nature of gene action for different traits among five crosses is illustrated in [Table-3]. For DF both additive (d) and dominance (h) type of gene action had significant influence in the crosses Cross-I, Cross-II and Cross-V while in cross Cross-III only (d) was significant. For DM (d), (h), additive × additive (i) and dominance × dominance (l) type of gene actions was significant in all the crosses except in cross Cross-III where only (d) was non-significant. For PH (d), (h), (i) and (l) type of gene actions were significant in five crosses except in both the crosses Cross-IV and Cross-V where (d) was non-significant. Dominance component was predominant in all crosses, and additive component was significant in three crosses namely, Cross-I, Cross-IV and Cross-V for a PB. In addition, additive × additive and dominance × dominance type epistatic gene action was also significant in all the crosses. In case of SB, (d) and (h), (i) and (l) genetic components were predominant in the three crosses except in the cross Cross-I and Cross-V where (h), (i), (j) and (i) and (j) were non-significant. In the inheritance of PPP (d), (h), (i) and (l) were significant in cross Cross-II, Cross-I, Cross-III and Cross-V, whereas in the cross Cross-IV where (h) component was non-significant. For PL, (h), (i) and (l) component were significant in three crosses Cross I, Cross II and Cross V, while (i) and (l) was non-significant in cross Cross-IV and Cross-III, whereas, genetic component (d) was significant in three crosses Cross-III, Cross-IV and Cross-V. SPP were inherited mainly by (d) and (h) in all the five crosses were shown significant except in cross Cross-V where (d) was not significant. Epistatic gene interactions like (i) and (l) were prominent in the inheritance of SPP in three crosses Cross-III, Cross-IV and Cross-V, except for Cross-II where only dominance × dominance was significant and for Cross-I where (l) was not significant. In case of 100SW (d), (h), (i) and (l) were more predominant

and significant in four crosses with the exception of Cross-I where (h) and (i) were non-significant. Similarly, for SYP, significant (d) and (h) were observed in five crosses in inheritance of this trait. Epistatic interactions like (i) and (l) were significant of all the five cross combinations. The Cross-I recorded duplicate type of gene action in six traits i.e. DF, PH, PB, PPP, PL and SYP except days to maturity where complimentary type of gene action was reported. In Cross-II duplicate type of gene action for all the ten traits was observed. Cross-III assessed duplicate type of gene action in three traits namely, DM, SPP and 100SW, however, PH, PB and SB, PPP and SYP were exhibited complementary type of gene action. Complimentary type of gene action was observed for DF, PB & SB and SPP while duplicate type of gene action was recorded for the DM, PH, PPP, PL, 100SW and SYP in Cross-IV. Eight traits were observed duplicate gene action while complementary gene action was recorded in two traits primary and secondary branches for Cross-V. The dominance gene effect was higher than additive gene effect for all studied traits in the five crosses indicating predominant role of dominant component of gene action in inheritance of these traits, so the selection for these traits should be delayed to later generation when dominant effect is diminished. In a study, [15] observed h was significant for maximum traits like PH, BPP, PPP, 100 SW and SYP, while [16] advocated h was more prominent with PPP and SYP and SPP for d. In this study, h indicates the heterozygosity is high and homozygosity is low in the population. Selection should be avoided until heterozygosity is reduced in the population [16].

Average degree of dominance [$\sqrt{H/D}$] was greater than one for seed yield/plant in all crosses indicating the over-dominance gene action for this trait. Remaining traits were affected either by over-dominance effects or partial dominance. The ratio of $F/\sqrt{H \times D}$ for all the traits of five crosses were close to zero, hence results showed that heritable and non-heritable genes are had cumulative effect for all the traits of five crosses. Among epistasis (i), (j) and (l), (l) was more prominent than (i) type for most of the traits among five crosses. Dominance × dominance (1) interaction was reported significant for biological yield per plant and 100 SW as earlier also reported by [17]. In similar study, [16] also observed significant (l) interactions for most of the yield contributing traits. Although, scaling test was significant for all the traits studied among all five crosses with significant non-allelic interactions. This indicates that such traits are governed by higher order interactions or under the control of complex genetic control, or they have less environmental variance. The higher order epistasis among more than two loci play crucial role in genetic interactions and earlier reported in pigeonpea [16] and [18]. With the gain in (h) there will be a simultaneous loss in (l) interaction [19]. Therefore, opposite signs of (h) and (l) cancel each other leading to reduced heterosis [6]. The presence of duplicate epistasis indicates that variability in segregating generation may be reduced which hinders the selection process [20] hence it is difficult to utilize them in breeding program [15]. Population improvement must be effective in these Cross-I, Cross-II, Cross-IV and Cross-V. The presence of complementary gene action in Cross-III for most traits suggested that parents selected for crossing were diverse and approving [21] strategy, which agreed that if parents selected for crossing are complementary for traits then it potential to raise genetic gain in a breeding program. Hence, in the present study genotypes, ICPA 2092 and Asha were identified as best parents since their respective crosses showed complementary gene action for a number of pods and seed yield.

Both broad and real sense (narrow sense) heritability estimated along with genetic advance for ten different characters among five crosses presented in [Table-4]. Broad sense heritability was higher in all traits among all the crosses. Percentage of GAM in broad sense was also scored high for traits among five crosses. While, real-sense heritability scored high values for the all traits except SP in Cross-I, DF in Cross-II and PP in Cross- III. While, Cross-IV and Cross-V shown very low real sense heritability for SYP. Percentages of GAM of broad sense were variable in five crosses of ten traits, in which seed yield per plant showed high values in five crosses. The expected genetic advances calculated for the remaining characters were high, hence, for these characters early generation selection would be effective. Similar results were indicating that selection might be effective for these traits to increase yield [22]. [23] also observed high heritability with high genetic advance for SYP, [24] for SYP, SPP and 100SW, [16] for BPP, PH, PPP and SYP.

Table-1 *Means and standard errors of the ten characters of the five crosses for P_1, P_2, F_1, F_2, B_1 and B_2 populations*

Crosses and their generations	DF	DM	PH	PB	SB	PPP	PL	SPP	100 SW	SYP
Cross-I (ICPA 2043 × Asha)										
P_1	108.41±0.43	237.40±0.36	131.73±1.06	7.94±0.57	6.62±0.44	165.61±1.54	4.51±0.07	3.19±0.03	11.33±0.07	35.54±0.60
P_2	110.05±0.44	238.48±0.86	154.75±1.87	17.93±0.97	24.08±1.54	179.19±1.68	4.20±0.02	3.29±0.01	10.40±0.08	36.18±0.16
F_1	109.00±0.30	229.00±0.26	162.17±0.82	4.75±0.21	15.07±0.56	255.47±0.93	4.33±0.06	3.25±0.01	11.05±0.02	50.97±0.16
F_2	111.27±0.21	243.77±0.14	133.99±1.27	8.66±0.09	19.73±0.16	213.52±1.69	4.31±0.02	3.09±0.01	10.30±0.01	40.51±0.36
B_1	111.41±0.38	244.30±0.33	180.89±2.40	16.35±0.55	21.17±0.44	157.17±0.63	4.47±0.09	3.22±0.00	10.19±0.01	30.81±0.06
B_2	103.78±0.21	240.44±0.19	167.58±2.69	14.82±0.29	17.57±0.43	174.12±1.80	4.58±0.01	3.17±0.02	10.34±0.06	35.15±0.37
Cross-II (ICPA 2043 × Azad)										
P_1	108.41±0.43	237.40±0.35	131.73±1.06	7.94±0.57	6.62±0.44	165.61±1.53	4.51±0.07	3.19±0.03	11.33±0.07	35.54±0.60
P_2	109.33±0.67	237.75±0.34	143.00±0.86	11.58±0.71	9.04±0.51	174.13±0.91	5.22±0.04	3.65±0.00	10.39±0.03	36.20±0.09
F_1	103.33±0.09	230.71±0.39	156.88±3.85	11.22±0.11	4.73±0.25	293.79±0.69	5.09±0.02	3.18±0.00	10.31±0.02	54.83±0.22
F_2	108.87±0.17	237.89±0.17	152.14±0.90	10.54±0.10	5.45±0.14	230.32±0.26	4.58±0.03	3.09±0.00	10.85±0.00	44.53±0.06
B_1	107.24±0.62	237.12±0.29	147.31±6.83	9.57±0.35	7.05±0.15	150.05±2.28	4.34±0.05	3.19±0.03	10.10±0.01	30.42±0.72
B_2	104.33±0.23	231.67±0.18	176.75±2.28	8.12±0.72	13.06±0.41	213.71±1.14	4.44±0.04	3.04±0.01	10.20±0.04	37.52±0.36
Cross-III (ICPA 2092 × Asha)										
P_1	108.67±0.33	235.33±0.83	143.83±2.07	10.00±0.47	9.84±0.89	177.68±4.93	4.53±0.06	3.19±0.01	9.72±0.04	33.36±0.63
P_2	110.05±0.44	238.48±0.86	154.75±1.87	17.93±0.97	24.08±1.54	179.19±1.68	4.20±0.02	3.29±0.01	10.40±0.07	36.19±0.16
F_1	102.15±0.20	234.29±0.45	211.52±2.24	25.64±1.28	25.30±1.33	259.30±1.83	4.31±0.01	3.23±0.02	10.21±0.02	47.44±0.44
F_2	103.77±0.09	236.35±0.13	137.02±1.07	7.50±0.11	7.73±0.10	154.48±0.71	4.14±0.01	3.20±0.03	10.02±0.00	30.97±0.11
B_1	105.00±0.36	239.29±0.32	140.67±3.61	10.15±0.61	7.64±0.64	171.09±0.63	4.18±0.02	3.20±0.04	9.61±0.05	32.74±0.36
B_2	105.98±0.25	239.99±0.23	162.08±0.48	10.57±0.28	12.65±0.31	124.90±1.63	4.29±0.00	3.06±0.01	9.82±0.04	24.38±0.28
Cross-IV (ICPA 2092 × Azad)										
P_1	108.67±0.33	235.33±0.83	143.83±2.07	10.00±0.47	9.84±0.89	177.68±4.93	4.53±0.06	3.19±0.01	9.72±0.04	33.36±0.63
P_2	109.33±0.67	237.75±0.34	143.00±0.86	11.58±0.71	9.04±0.51	174.13±0.91	5.22±0.04	3.65±0.00	10.39±0.03	36.20±0.09
F_1	109.85±0.69	234.07±0.30	196.56±2.60	17.45±0.95	23.99±0.23	237.85±1.86	4.52±0.03	3.35±0.04	9.88±0.01	43.32±0.41
F_2	107.14±0.29	237.51±0.25	114.42±0.69	8.97±0.13	7.35±0.08	181.98±0.47	4.15±0.01	2.96±0.01	10.62±0.02	33.62±0.23
B_1	107.32±0.18	233.22±0.44	158.08±5.14	7.67±0.32	11.11±0.37	146.52±3.11	4.01±0.07	3.05±0.01	10.27±0.00	28.01±0.41
B_2	107.67±0.23	235.45±0.49	161.90±1.68	12.64±0.47	9.25±0.34	180.86±2.38	4.19±0.01	3.10±0.01	9.65±0.02	32.93±0.32
Cross-V (ICPA 2043 × MAL 13)										
P_1	108.41±0.43	237.40±0.36	131.73±1.06	7.94±0.57	6.62±0.44	165.99±1.54	4.51±0.07	3.19±0.03	11.33±0.07	35.54±0.60
P_2	107.18±1.38	237.00±1.22	154.43±1.14	9.56±0.41	11.60±0.30	199.90±4.89	5.72±0.04	3.16±0.02	11.46±0.07	42.29±0.77
F_1	102.47±0.33	236.74±0.24	150.87±0.87	12.59±0.44	17.40±0.62	235.25±0.54	5.18±0.03	3.17±0.01	10.43±0.03	43.62±0.19
F_2	106.27±0.06	236.62±0.11	140.77±0.33	10.21±0.06	8.96±0.12	194.22±0.58	5.01±0.01	3.19±0.00	10.32±0.02	37.13±0.15
B_1	104.85±0.19	236.76±0.26	148.52±2.34	10.90±0.32	8.08±0.30	141.25±0.81	5.18±0.01	3.09±0.01	10.31±0.02	27.44±0.25
B_2	101.51±0.25	234.81±0.18	149.52±0.78	8.90±0.09	9.41±0.08	132.25±1.00	5.08±0.01	3.09±0.01	10.15±0.02	26.86±0.18

Table-2 *Scaling and Joint scaling test (χ^2) for yield contributing traits in five pigeonpea crosses*

Scaling test factors	DF	DM	PH	PB	SB	PPP	PL	SPP	100 SW	SYP
Cross-I (ICPA 2043 × Asha)										
A	5.41**	22.21**	67.88**	20.01**	20.65**	-106.73**	0.10	-0.01	-1.99**	-24.89**
B	-11.5**	13.41**	18.23**	6.96**	-4.02*	-86.41**	0.64**	-0.21**	-0.78**	-16.85**
C	8.60**	41.20**	-74.84**	-0.73	18.07**	-1.65	-0.13	-0.61**	-2.65**	-11.6**
D	7.35**	2.79**	-80.48**	-13.85**	0.72	95.74**	-0.43**	-0.2**	0.06	15.07**
χ^2	605.40**	1762.69**	412.90**	464.33**	468.52**	2873.01**	177.06**	450.84**	821.71**	2030.10**
Cross-II (ICPA 2043 × Azad)										
A	2.74*	6.13**	6.02	-0.03	2.75**	-159.3**	-0.91**	0.01	-1.44	-29.53**
B	-4 .00**	-5.13**	53.62**	-6.56**	12.35**	-40.5**	-1.42**	-0.75**	-0.29**	-18.6**
C	11.07**	14.99**	20.07**	0.20	-3.31**	-6.04*	-1.58**	-0.84**	1.08**	-5.89**
D	6.16**	7.0**	-19.78**	3.39**	-9.21**	96.88**	0.37**	-0.05	1.41**	21.12**
χ^2	256.65**	570.36**	91.66**	19.68**	317.56**	1420.45**	376.73**	1705.23**	4766.29**	932.77**
Cross-III (ICPA 2092 × Asha)										
A	-0.82	8.96**	-74.00**	-15.34**	-19.85**	-94.79**	-0.49**	-0.03	-0.71**	-15.32**
B	-0.24	7.22**	-42.11**	-22.44**	-24.08**	-188.68**	0.07**	-0.41**	-0.98**	-34.86**
C	-7.95**	3.03	-173.6**	-49.22**	-53.58**	-257.52**	-0.78**	-0.12	-0.46**	-40.56**
D	-3.44**	-6.58**	-28.72**	-5.72**	-4.82**	12.97**	-0.18**	0.16*	0.61**	4.81**
χ^2	151.70**	215.49**	673.21**	364.22**	333.16**	2872.67**	160.02**	211.73**	118.09**	2496.08**
Cross-IV (ICPA 2092 × Azad)										
A	-3.87**	-2.96*	-24.24*	-12.11**	-11.6**	-122.49**	-1.02**	-0.43**	0.94**	-20.67**
B	-3.85**	-0.92	-15.76**	-3.74*	-14.53**	-50.27**	-1.35**	-0.79**	-0.97**	-16.26**
C	-9.15**	8.81**	-222.3**	-20.58**	-37.44**	-99.58**	-2.18**	-1.7**	2.62**	-24.31**
D	-0.71	6.34**	-91.15**	-2.36**	-5.65**	36.59**	0.10	-0.24**	1.32**	6.31**
χ^2	26.74**	75.39**	1593.42**	140.55**	1213.47**	336.38**	848.10**	558.04**	1527.02**	684.83**
Cross-V (ICPA 2043 × MAL 13)										
A	-1.18	-0.62	14.44**	1.26	-7.86**	-118.35**	0.66**	-0.18**	-1.13**	-24.28**
B	-6.64**	-4.12**	-6.27**	-4.36**	-10.18**	-170.64**	-0.74**	-0.17**	-1.59**	-32.19**
C	4.56	-1.39	-24.82	-1.84	-17.16	-59.13	-0.54	0.08	-2.39	-16.57
D	6.16	1.67	-16.49	0.63	0.44	114.93	-0.23	0.20	0.17	19.95
χ^2	357.78**	27.85**	114.18**	80.48**	207.28**	5786.99**	534.66**	165.06**	484.29**	3155.36**

*A, B, C and D Mather's Scaling test, *,** Significant at $P \leq 0.05$ and $P \leq 0.01$, respectively*

Table-3 *Estimates of gene effects and epistasis for ten characters in five pigeonpea crosses*

Gene action	DF	DM	PH	PB	SB	PPP	PL	SPP	100 SW	SYP
Cross-I (ICPA 2043 × Asha)										
m	111.26**	243.77**	133.99**	8.66**	19.73**	213.52**	4.31**	3.09**	10.29**	40.51**
d	7.63**	3.86**	13.31**	1.52*	3.60**	-16.95**	-0.11	0.05*	-0.15*	-4.34**
h	-14.93**	-14.53**	179.88**	19.51**	-1.72	-108.42**	0.84**	0.40**	0.07	-15.04**
F	9.57	4.73	-6.52	-5.75	18.62	2.52	12.99	-19.97	20.01	-10.10
$\sqrt{H/D}$	0.93	0.87	1.04	1.06	0.96	1.07	0.91	0.95	0.87	1.29
$F/\sqrt{D \times H}$	0.11	0.07	-0.07	-0.06	0.20	0.03	0.14	-0.25	0.25	-0.13
i	-14.69**	-5.59**	160.95**	27.70**	-1.44	-191.49**	0.87**	0.39**	-0.12	-30.14**
j	8.46	4.40	24.82	6.52	12.33	-10.16	-0.27	0.10	-0.61	-4.02
l	20.78**	-30.03**	-247.06**	-54.67**	-15.19**	384.62**	-1.61**	-0.18	2.89**	71.88**
epistasis	D	C	D	D	-	D	D	-	-	D
Cross-II (ICPA 2043 × Azad)										
m	108.87**	237.89**	152.14**	10.54**	5.45**	230.32**	4.58**	3.09**	10.85**	44.53**
d	2.91**	5.45**	-29.44**	1.45	-6.01**	-63.66**	-0.1	0.15**	-0.11*	-7.1**
h	-17.86**	-20.86**	59.08**	-5.32**	15.32**	-69.84**	-0.52**	-0.14*	-3.36**	-24.57**
F	2.10	0.09	14.00	2.03	2.32	0.97	6.00	16.47	1.00	5.04
$\sqrt{H/D}$	2.04	0.92	1.12	0.61	0.74	0.83	0.89	0.70	0.60	1.67
$F/\sqrt{D \times H}$	0.04	0.00	0.18	0.03	0.03	0.01	0.08	0.18	0.04	0.10
i	-12.33**	-13.99**	39.57**	-6.79**	18.41**	-193.75**	-0.75**	0.10	-2.81**	-42.23**
j	3.37	5.63	-23.8	3.27	-4.80	-59.40	0.25	0.38	-0.58	-5.46
l	13.58**	12.99**	-99.2**	13.37**	-33.52**	393.55**	3.07**	0.64**	4.55**	90.36**
epistasis	D	D	D	D	D	D	D	D	D	D
Cross-III (ICPA 2092 × Asha)										
m	103.77**	236.35**	137.02**	7.50**	7.73**	154.48**	4.14**	3.21**	10.02**	30.97**
d	-0.98*	-0.70	-21.41**	-0.42	-5.01**	46.19**	-0.12**	0.14**	-0.21**	8.36**
h	-0.32	10.53**	119.68**	23.11**	17.98**	54.92**	0.31**	-0.33*	-1.08**	3.05**
F	-5.75	1.50	-11.82	-10.04	4.03	11.18	-32.98	-3.08	11.01	2.98
$\sqrt{H/D}$	0.72	0.88	1.02	1.16	1.20	1.31	0.74	0.87	0.94	1.05
$F/\sqrt{D \times H}$	-0.07	0.02	-0.13	-0.14	0.05	0.13	-0.44	-0.04	0.14	0.03
i	6.89**	13.15**	57.45**	11.43**	9.65**	-25.95**	0.37**	-0.32*	-1.23**	-9.62**
j	-0.29	0.87	-15.95	3.55	2.11	46.95	-0.28	0.19	0.13	9.77
l	-5.83**	-29.33**	58.66**	26.35**	34.29**	309.42**	0.05	0.76**	2.91**	59.80**
epistasis	-	D	C	C	C	C	-	D	D	C
Cross-IV (ICPA 2092 × Azad)										
m	107.14**	237.51**	114.42**	8.97**	7.35**	181.98**	4.15**	2.96**	10.62**	33.62**
d	-0.34	-2.23**	-3.83	-4.98**	1.86**	-34.34**	-0.18*	-0.05**	0.62**	-4.92**
h	2.27	-15.16**	235.44**	11.38**	25.85**	-11.23	-0.55**	0.40 **	-2.81**	-5.38**
F	9.57	4.73	-6.52	-5.75	18.62	2.52	12.99	-19.97	20.01	-10.10
$\sqrt{H/D}$	0.93	0.87	1.04	1.06	0.96	1.07	0.91	0.95	0.87	1.29
$F/\sqrt{D \times H}$	0.11	0.07	-0.07	-0.06	0.20	0.03	0.14	-0.25	0.25	-0.13
i	1.42	-12.69**	182.29**	4.73**	11.30**	-73.18**	-0.19	0.47**	-2.64**	-12.62**
j	-0.01	-1.02	-4.24	-4.19	1.46	-36.11	0.17	0.18	0.96	-2.20
l	6.31**	16.56**	-142.3**	11.12**	14.84**	245.94**	2.57**	0.75**	2.66**	49.55**
epistasis	C	D	D	C	C	D	D	C	D	D
Cross-V (ICPA 2043 × MAL)										
m	106.273**	236.623**	140.773**	10.210**	8.963**	194.217**	5.013**	3.193**	10.317**	37.127**
d	3.343**	1.953**	-1.000	2.000**	-1.333**	9.000**	0.093**	-0.003	0.160**	0.577*
h	-17.702**	-3.803**	40.778**	2.593**	7.412**	-177.360**	0.535**	-0.408**	-1.295**	-35.190**
F	-10.90	-4.01	-7.90	-6.38	14.89	7.01	10.00	-5.69	3.89	4.93
$\sqrt{H/D}$	1.13	0.89	1.04	0.77	1.03	1.09	1.20	0.98	1.18	1.56
$F/\sqrt{D \times H}$	-0.17	-0.06	-0.08	-0.07	0.20	0.07	0.13	-0.07	0.05	0.07
i	-12.380**	-3.347**	32.987**	-1.253*	-0.880	-229.853**	0.467**	-0.407**	-0.333**	-39.900**
j	2.728	1.753	10.352	2.810	1.158	26.143	0.698	-0.018	0.228	3.953
l	20.203**	8.087**	-41.157**	4.347*	18.923**	518.840**	-0.390**	0.737**	3.057**	96.367**
epistasis	D	D	D	C	D	D	D	D	D	D

m= mean of the F2 generation, d= additive gene effects, h= dominance gene effects, i=additive× additive gene effect, j = additive ×dominance gene effect and l = dominance × dominance gene effects, C = complimentary gene action, D = duplicate gene action, F= correlation between D and H over all loci, Average degree of dominance [√(H/D)], Ratio of F/√(H×D), respectively.
(*,** Significant at P ≤ 0.05 and P ≤ 0.01, respectively).

Conclusion

Six-parameter model has exhibited that both intra (dominance gene action) and inter-allelic (epistasis) interaction play an important role in the inheritance studied of all the yield traits. Since, both additive and non-additive gene effects were involved in our study, bi-parental mating approach or reciprocal recurrent selection would be successful in utilizing both type of gene effects.

Pigeonpea being an often-cross-pollinated crop such an interaction effect between alleles can be exploited by selecting individuals based on their performance in recurrent selection. Yield performance of hybrids are higher than best performing parents. So that, these crosses have scope for varietal development or further breeding programmes.

Application of research

Study evaluated different cross combinations to identify best parental combination for better hybrid which maybe notify as a new hybrid variety in order to enhanced production and productivity of pigeonpea crops.

Research Category: CMS based hybrid in pigeonpea

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Table-4 *Broad (h^2_b) and real sense (h^2_r) heritability and GAM in broad sense (GAM % b) and real sense (GAM % r) for ten characters in five pigeonpea crosses*

Crosses	DF	DM	PH	PB	SB	PPP	PL	SPP	100 SW	SYP
Cross-I (CPA 2043 × Asha)										
h^2_b	98.35	95.49	96.79	97.34	99.13	99.29	98.19	81.17	98.55	98.69
h^2_r	94.03	63.98	54.36	67.84	66.57	72.32	46.33	19.28	45.88	64.27
GAM%(b)	13.14	3.26	9.05	129.75	84.36	8.14	210.25	120.99	96.90	32.13
GAM%(r)	12.57	2.18	5.08	90.43	56.65	5.93	99.20	28.73	45.11	20.93
Cross-II(ICPA 2043 × Azad)										
h^2_b	98.49	98.35	98.85	99.04	98.54	98.63	99.78	99.58	97.42	98.97
h^2_r	31.92	69.24	60.71	83.40	77.16	73.24	71.42	79.86	82.48	41.40
GAM%(b)	12.14	6.32	10.02	154.62	290.99	7.54	336.19	596.29	88.77	27.62
GAM%(r)	3.93	4.45	6.15	130.21	227.86	5.60	240.64	478.24	75.16	11.55
Cross-III (ICPA 2092 × Asha)										
h^2_b	98.93	98.89	97.39	96.42	98.73	96.98	99.96	99.99	99.94	99.33
h^2_r	78.37	71.43	63.92	57.51	57.22	52.23	78.44	72.34	69.26	64.13
GAM%(b)	16.70	7.00	12.30	191.30	207.09	10.28	400.96	518.43	162.00	54.79
GAM%(r)	13.23	5.05	8.07	114.10	120.02	5.54	314.61	375.07	112.27	35.38
Cross-IV(ICPA 2092 × Azad)										
h^2_b	97.37	97.02	98.27	99.15	97.53	96.30	99.96	99.98	99.98	99.84
h^2_r	68.17	70.40	63.88	63.57	66.61	61.21	70.68	68.93	72.65	54.60
GAM%(b)	15.84	6.14	15.03	194.60	233.87	9.26	421.95	545.30	154.66	45.42
GAM%(r)	11.09	4.45	9.77	124.78	159.71	5.89	298.37	375.98	112.39	24.84
Cross-V(ICPA 2043 × MAL 13)										
h^2_b	97.52	98.89	99.76	99.05	97.16	99.37	98.26	97.86	98.26	97.91
h^2_r	59.49	70.88	64.81	76.40	63.57	62.19	57.13	66.13	57.92	44.06
GAM%(b)	13.13	6.28	12.47	171.42	170.60	8.97	475.87	312.40	149.62	39.77
GAM%(r)	8.01	4.50	8.10	132.23	111.63	5.61	276.69	211.12	88.20	17.90

Abbreviations: Kg. – Kilogram, ha. – Hectare, P₁- Parent number one
P₂- Patent number two, F₁- F₁ Generation, F₂- F₂ Generation
B₁- Back cross with one parent, B₂ - Back cross with one parent
GMA- Generation means analysis, Cm.-Centimetre,
°C-Degree centigrade, °N – Degree North, °E-Degree East

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Author Contributions: All authors equally contributed

Author statement: All authors read, reviewed, agreed and approved the final manuscript. Note-All authors agreed that- Written informed consent was obtained from all participants prior to publish / enrolment

Study area / Sample Collection: All the research activity, experimental sites, CMS based hybrid evaluation/research materials were at Institute of Agricultural Sciences, Banaras Hindu University Varanasi, India.

Cultivar / Variety / Breed name: Two cytoplasmic male sterile lines viz; CMS ICPA 2043, CMS ICPA 2092 and three cultivars as Azad, Asha, MAL 13.

Conflict of Interest: None declared

Ethical approval: This article does not contain any studies with human participants or animals performed by any of the authors.
Ethical Committee Approval Number: Nil

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