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Genetic analysis for yield and its components in mustard (*Brassica* spp.)

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ABSTRACT

The nature of gene action in the inheritance of seed yield and its contributing traits in three crosses of mustard (Kranti x PC-6, ACN-9 x PC-6, and TAM 108-1 x PC-6) was studied using generation mean analysis. Six generations (P_1, P_2, F_1, F_2, BC_1, BC_2) in each cross were evaluated in a Randomized block design with three replications during 2022-23 Rabi season. For crop improvement it is necessary to know the gene action governing various yield contributing traits so appropriate breeding methods can be decided. Analysis of variance for six generations revealed significant differences among the generations within cross for all evaluated traits. Six parameter model (m, d, h, i, j, l) and scaling tests revealed the presence of inter-allelic interactions (epistasis) for most of the yield and its contributing traits. Results showed that both additive and non-additive types of gene action were significant in governing the inheritance of the yield and it's contributing traits. Hence on the basis of gene action studied in case of duplicate epistasis, it is suggested that selection should be delayed until the fixation of alleles. And in case of complementary epistasis, traits can be exploited through heterosis breeding or biparental mating.

Keywords: *Generation mean analysis, Gene action, six parameter model, mustard, joint scaling test, interspecific cross.*

I. INTRODUCTION

Oilseed crops play a crucial role in India's agricultural economy, contributing 5% to the Gross National Product and 10% to the value of agricultural products. Mustard, the second-largest indigenous oilseed crop, constitutes 32% of India's total oilseed production, mainly for oil extraction. While mustard productivity is increasing, its cultivation area is decreasing, resulting in stagnant production. India, the 7th largest importer of edible oils globally, meets 57% of domestic edible oil needs through imports. Hence, plant breeders aim to develop high-yielding, early-maturing, and high-oil-content.

Despite *B. juncea*'s adaptability to dry conditions and earlier maturation [6], it is susceptible to pests and diseases, with limited genetic variation for stress resistance. In contrast, *B. carinata* A. Braun offers rare agronomic traits, yet faces limitations such as longer crop duration and poor oil content. The investigation aims to combine the strengths of both species through interspecific hybridization, addressing the challenge of potential selfing during crosses. The variability resulting from interspecific hybridization is crucial for obtaining desired plant types with economic traits, emphasizing the importance of identifying specific genes involved in trait recovery.

Knowledge of gene action helps in the selection of parents for use in the hybridization programs and also in the choice of appropriate breeding procedures for the genetic improvement of various quantitative characteristics. Gene action involved in the expression of quantitative traits plays an important role for the adaptation of breeding methods for genetic enhancement of the crop.

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The absence or presence of epistasis can be noticed by the analysis of generation means using the scaling test, which measures epistasis accurately whether it is duplicate (Additive x Dominance) and (Dominance x Dominance) at the digenic level or complementary (Additive x Additive). Researchers use generation mean analysis to determine genotypic values of the individuals and consequently mean genotypic values of families and generations, to estimate the relative importance of average effects of the genes (additive effects), dominance deviations, and effects due to non-allelic genic interactions.

Hence present investigation was undertaken with the objective of combining the useful genetic attributes of *B. carinata* with *B. juncea* and studying the genetic nature of yield and attributing traits.

II. MATERIAL AND METHODS

The experiment material consisted of three female lines *viz.*Kranti, ACN 9 and TAM 108-1 of (*Brassica juncea*L. Czern&Coss) and male line PC 6 (*Brassica carinata* A. Braun) were crossed to produce three interspecific hybrid namely Kranti x PC -6, ACN 9 x PC-6 and TAM 108-1 x PC -6 in*rabi* 2020-2021 at All India Coordinated Research Project on Linseed and Mustard, College of Agriculture, Nagpur (M. S.).

During *Rabi* 2021-22, part of the seed from each of the four parental lines (Kranti, ACN 9, TAM 108-1, and PC-6) and their three resultant F_1 hybrids were planted in the field to produce F_2, BC_1 and BC_2 generations. The F_2 generation of each cross was produced by selfing the F_1 plants while BC_1 and BC_2 generations were developed by crossing back to each F_1 hybrids with its respective male and female parents. During *rabi*2022-23 crossed seeds of F_1, F_2, BC_1 and BC_2 along with P_1 and P_2 were planted in Randomised Block Design in three replications at AICRP on Linseed and Mustard, College of Agriculture, Nagpur (M. S.). In each of replication non segregating parents P_1, P_2 and F_1's generations were represented by two rows, BC_1 and BC_2 by three rows and F_2's by four rows.

The rows were 2 m long with row spacing 45 cm and 10 cm between plants within row. The data were recorded on 5 randomly selected plants in parents and F_1's, 30 randomly selected plants in backcrosses and 50 randomly selected plants in F_2 replication wise for days to first flower, days to maturity, plant height (cm), number of branches plant^{-1}, siliqua length (cm), number of siliquae plant^{-1}, siliquae density (%), 1000 seed weight (g) and seed yield plant^{-1} (g). The data were analysed by using OPSTAT services for testing epistasis and six generation mean analysis.

III. RESULTS AND DISCUSSION

The analysis of variance for generation mean analysis carried out for days to first flower, days to maturity, plant height (cm), number of branches plant^{-1}, siliqua length (cm), number of siliquae plant^{-1}, siliquae density (%), 1000 seed weight (g), and seed yield plant^{-1}(g) revealed that mean sum of square for treatments in all crosses showed significant differences for all the characters. This indicates the existence of sufficient variation for effective selection for the characters in the material under studied. Further estimation of components of gene action was undertaken. The results are accordance with [9,7,10] who reported wide variability among the progenies (generation) within family (cross) for seed yield and yield contributing characters.

Estimates of gene effects for digenic epistasis interaction model or additive-dominance model and simple scaling test (A, B, C, D) for the evaluated traits of Kranti x PC-6, ACN-9 x PC-6 and TAM 108-1 x PC-6 presented in the Table 1.Significant estimation of one or all A, B, C and D simple scaling test in all the crosses for yield and it's contributing characters under studied indicated the presence of all three types of non-allelic interactions. The significant values of chi-square of joint scaling tests for the additive-dominance model indicated the presence of epistasis in all the crosses for yield and it's contributing characters. The existence of inadequacy of additive- dominance model and possibility of the existence of interallelic interaction in most of the yield-contributing traits were reported by [9] in generations of four crosses of Indian mustard and by [10] in generations of three crosses of yellow sarson. Therefore, six parameter models were used to explain the nature of gene action and types of epistasis for the expression of characters in Table 2.

The prevalence of dominance (h) gene effect was observed in TAM 108-1 x PC-6 cross for governing the inheritance of days to first flower, while the negative sign of (h) gene effect indicated the dominance of decreasing alleles in this cross. In crosses Kranti x PC-6 and ACN-9 x PC-6 prevalence of additive (d) gene effect was observed. In Kranti x PC-6, ACN-9 x PC-6 and TAM 108-1 x PC-6 dominance x dominance (l) gene effects was of primary importance among the digenic non-allelic interactions for controlling the inheritance of days to first flower.Similar to those observed in the data presented by [1] where dominance x dominance gene action was the most important affecting this parameter.The opposite sign of dominance (h) and dominance x dominance (l) showed the presence of duplicate epistasis for days to first flower in all the crosses.The dominance gene effect was observed in cross TAM 108-1 x PC-6 for governing the inheritance for days to maturity. Among the epistasis additive x additive (i) gene interaction was of primary importance among the digenic non-allelic interactions for controlling the inheritance of this trait in this particular cross. While additive gene effect was observed in crosses Kranti x PC-6 and ACN-9 x PC-6.

Among all three interactions, the dominance x dominance (l) gene effect was higher in Kranti x PC-6 and additive x dominance (j) was higher in ACN-9 x PC-6. Similar, results had been reported by [3], where for days to maturity, only additive (d) gene effect was found significant suggesting that improvement could be achieved through simple progeny selection. Also [7] reported significance of additive gene effect for days to maturity. The results were in agreement with [9,12]. Duplicate epistasis was observed for days to maturity in crosses ACN-9 x PC-6 and TAM 108-1 x PC-6 and complementary epistasis in Kranti x PC-6. In Kranti x PC-6 additive gene effect was highly significant, and additive gene effects were important in the inheritance of plant height although the relative proportion of dominance x dominance (l) gene effect was prominent in Kranti x PC-6 and TAM 108-1 x PC-6. Similar results found by [5]. The relative magnitude of the additive estimate was smaller compared to dominance effect, which suggested that additive gene effect made only a minor contribution to the inheritance of plant height in ACN-9 x PC-6 and TAM 108-1 x PC-6.These findings were similar to those encountered by [3,7,11]. The presence of complementary epistasis was observed for this trait among all the crosses.Number of branches plant^{-1} was controlled predominantly by dominance (h) gene action in ACN-9 x PC-6 and TAM 108-1 x PC-6, although additive (d) gene action was observed in Kranti x PC-6. Dominance x dominance components also might contribute to some extent. Considering the magnitude and direction, the dominance gene effect along with dominance × dominance (l) interaction was important for the number of branches plant^{-1} significant negative value of dominance (h) gene effect in ACN-9 x PC-6 and TAM 108-1 x PC-6. Also [5] reported significant negative estimates of the dominant gene effect for this trait. The result was supported by the findings of [10]. Some contrasting effects were also been reported by [4].The presence of duplicate epistasis was observed for a number of branches plant^{-1} in all the crosses. It is in agreement with the results obtained by [10].

The prevalence of the dominance (h) gene effect was observed in all three crosses for governing the inheritance of siliqua length, while negative sign of the dominance (h) gene effect indicated the dominance of decreasing alleles in TAM 108-1 x PC-6. In ACN-9 x PC-6 and TAM 108-1 x PC-6 dominance x dominance (l) gene effects were of primary importance among the digenic non-allelic interactions for controlling the inheritance of siliqua length. While in Kranti x PC-6 additive x additive (i) gene interaction had more importance. In regard to the inheritance of siliqua length, additive (d) gene effect as well as dominance × dominance (l) non-allelic interaction was important. Similar results were found by [7]. The opposite sign of dominance (h) and dominance x dominance (l) showed the presence of duplicate epistasis in all three crosses for siliqua length. The magnitude of additive (d) and dominance (h) gene effect were significant and additive x additive (i) gene interaction was highly significant for the number of siliquae plant^{-1}in crossKranti x PC-6 and ACN-9 x PC-6. In TAM 108-1 x PC-6, both additive (d) and dominance (h) gene effect were found to be significant with a predominance of dominance effect. The dominance gene effect was observed in all three crosses for governing the inheritance for a number of siliquae plant^{-1}. The findings that the dominance effects seemed to be the most substantial in the inheritance of a number of siliquae plant^{-1} concurred with the conclusions of [10] in mustard. However, contrasting results were reported by [9] which state that only additive gene action is important in number of siliquae plant^{-1}.

Duplicate epistasis was present in TAM 108-1 x PC-6 and complementary epistasis in Kranti x PC-6 and ACN-9 x PC-6.

The prevalence of the dominance (h) gene effect was observed in all three crosses for governing the inheritance of siliquae density on the main branch. In all three crosses additive x additive (i) gene effects was of primary importance among the digenic non-allelic interactions for controlling the inheritance of siliquae density on the main branch. These findings are similar to those encountered by [5]. The presence of duplicate epistasis was observed in Kranti x PC-6 and ACN-9 x PC-6. The findings are in agreement with [5]. The similar sign of dominance (h) and dominance x dominance (l) showed the presence of complementary epistasis for siliquae density in TAM 108-1 x PC-6. In the crosses Kranti x PC-6, ACN-9 x PC-6, and TAM 108-1 x PC-6significant dominance gene was observed along with dominance x dominance (l) gene interaction had more importance.Similarly, the importance of dominance × dominance interaction was also observed by [10]. The opposite sign of dominance (h) and dominance x dominance (l) showed the presence of duplicate epistasis in TAM 108-1 x PC-6, while similar signs of dominance (h) and dominance x dominance (l) showed the presence of complementary epistasis in Kranti x PC-6 and ACN-9 x PC-6.

The dominance (h) gene effect with the highest magnitude proved to be of major importance for this trait in all three crosses. Among non-allelic interactions highest value was observed for additive x additive (i) for Kranti x PC-6 while the dominance x dominance (l) gene effect was observed in ACN-9 x PC-6 and TAM 108-1 x PC-6. For the extraction of superior mustard hybrids, seed yield plant^{-1} could be considered as one of the important parameters in selection criteria. The preponderance of dominance (h) genetic effects and epistasis of additive x additive (i) and dominance x dominance (l) effects could be attributed uniformly and greater diversity among parent similar results found by [5]. While [8,9] concluded the significance of both additive and non-additive gene effects for seed yield plant^{-1}.

Generation mean analysis by using a parameters model and scaling test suggested the presence of duplicate or complementary epistasis that indicates the inadequacy of the additive-dominance model in all crosses for all the traits studied. The estimates of joint scaling test showed significant chi-square values for all the evaluated traits in three crosses. It further confirmed the inadequacy of the additive-dominance model. In the present study, yield and its contributing characters were governed by additive, dominance and epistasis gene effect. In general, when quantitative traits are governed by dominance or epistasis gene action, hybrid breeding programs may easily be resorted using male sterility [7,9,10]. The application of methods like biparental mating and diallel selective mating system may be recommended for exploitation of dominance and epistatic effects for purpose of isolating transgressive segregants in advanced generations or inter-mating among the selected segregants followed by at least one selfing, could be suggested to knockdown the undesirable linkage and allow the accumulation of favorable alleles for the improvement of desired traits[9,10]. Results showed that both additive and non-additive types of gene action were significant in governing the inheritance of the yield and it's contributing traits, population improvement through biparental mating and reciprocal recurrent selection or diallel selective mating. The significance of additive gene effects for the evaluated traits in three crosses indicated that substantial improvement in yield could be achieved by following conventional breeding methods like pedigree breeding method [7,9].

IV. CONCLUSION

On the basis of gene action studied duplicate epistasis was observed for days to first flower, number of branches plant^{-1}, siliqua length and seed yield plant^{-1} in all three crosses, days to maturity in ACN-9 x PC-6 and TAM 108-1 x PC-6, number of siliquae plant^{-1} in TAM 108-1 x PC-6, siliqua density on main branch in Kranti x PC-6 and ACN-9 x PC-6 and 1000 seed weight in TAM 108-1 x PC-6. It is suggested that selection should be delayed until the fixation of alleles for these traits. Complementary epistasis was observed for plant height in all three crosses, days to maturity in Kranti x PC-6, number of siliquae plant^{-1} in Kranti x PC-6 and ACN-9 x PC-6, siliqua density on main branch in TAM 108-1 x PC-6, 1000 seed weight in Kranti x PC-6 and ACN-9 x PC-6, thus these traits can be exploited through heterosis breeding or biparental mating and diallel selective mating system may be recommended for isolating transgressive segregants in advanced generations or inter-mating among the selected segregants followed by at least one selfing, could be suggested to knockdown the undesirable linkage and allow the accumulation of favorable alleles for the improvement of desired traits. Future Scope of study of Generation mean analysis concludes; Genomic Selection, Multi-Environment Trials, Quantitative Trait Locus (QTL) Mapping, Marker-Assisted Selection, Stress Tolerance that is use GMA to identify genotypes with improved tolerance to abiotic stresses (e.g., drought, salinity, heat) and biotic stresses (e.g., pests, diseases).

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Table 1.Scaling and joint scaling test for three crosses for various characters in mustard

Crosses	A	B	C	D	x^2 value
Days to first flower					
Kranti x PC-6	9.13** ± 1.59	10.00** ± 1.28	15.21** ± 2.26	1.96* ± 0.76	**
ACN-9 x PC-6	3.00 ± 1.55	3.20* ± 1.46	-2.25 ± 2.47	4.23** ± 0.93	**
TAM 108-1 x PC-6	-1.93 ± 2.74	17.47** ± 2.62	-1.85 ± 5.20	8.69** ± 0.69	**
Days to maturity					
Kranti x PC-6	9.13** ± 1.96	26.53** ± 2.20	37.03** ± 3.45	-0.68 ± 1.41	**
ACN-9 x PC-6	-0.49 ± 1.93	16.13** ± 1.95	19.87** ± 3.07	-2.11 ± 1.22	**
TAM 108-1 x PC-6	-3.13 ± 2.10	5.73** ± 1.90	37.72** ± 3.75	-17.56** ± 1.53	**
Plant height (cm)					
Kranti x PC-6	31.93** ± 9.31	25.12** ± 8.94	21.31 ± 15.14	17.87** ± 4.16	**
ACN-9 x PC-6	39.76** ± 5.41	8.93 ± 7.00	73.51** ± 11.99	-12.41 ± 4.48	**
TAM 108-1 x PC-6	16.20 ± 11.78	46.98** ± 9.57	-73.40** ± 18.20	68.29** ± 5.71	**
Number of branches plant^{-1}					
Kranti x PC-6	0.8 ± 0.54	2.07** ± 0.58	4.01** ± 0.94	-0.57* ± 0.24	**
ACN-9 x PC-6	0.16 ± 0.43	3.73** ± 0.47	2.16** ± 0.79	0.86** ± 0.24	**
TAM 108-1 x PC-6	0.60 ± 0.43	3.04** ± 0.50	3.40** ± 0.80	0.12 ± 0.23	**
Siliqua length (cm)					
Kranti x PC-6	0.20 ± 0.24	0.62** ± 0.23	2.71** ± 0.40	-0.95* ± 0.11	**
ACN-9 x PC-6	-0.80 ± 0.24	0.53* ± 0.21	1.43** ± 0.39	-0.85 ± 0.16	**
TAM 108-1 x PC-6	1.80** ± 0.27	2.27** ± 0.23	2.30** ± 0.38	0.88** ± 0.16	**
Number of siliquae plant^{-1}					
Kranti x PC-6	126.69** ± 34.71	90.18* ± 36.48	357.64** ± 67.46	-70.39* ± 9.46	**
ACN-9 x PC-6	55.84** ± 17.72	171.69** ± 16.33	8.45 ± 35.42	117.99** ± 17.42	**
TAM 108-1 x PC-6	30.04 ± 19.36	83.04** ± 20.46	284.35** ± 33.67	-85.63** ± 10.94	**
Siliquae density on main branch (%)					
Kranti x PC-6	0.17** ± 0.05	0.09* ± 0.04	0.09** ± 0.04	-0.20* ± 0.02	**
ACN-9 x PC-6	0.15** ± 0.05	0.01 ± 0.05	0.01** ± 0.05	-0.19 ± 0.04	**
TAM 108-1 x PC-6	0.08* ± 0.04	0.12** ± 0.04	0.12** ± 0.04	-0.06 ± 0.03	**
1000 seed weight (g)					
Kranti x PC-6	2.74** ± 0.23	1.76** ± 0.20	5.38** ± 0.36	-0.44* ± 0.18	**
ACN-9 x PC-6	2.19** ± 0.27	2.18** ± 0.22	5.63** ± 0.36	-0.63 ± 0.22	**
TAM 108-1 x PC-6	2.20** ± 0.23	0.84** ± 0.19	0.89** ± 0.30	1.07** ± 0.17	**
Seed yield plant^{-1}					
Kranti x PC-6	1.45 ± 1.06	1.40 ± 0.92	14.32** ± 1.33	-7.14* ± 0.61	**
ACN-9 x PC-6	3.19** ± 0.81	4.73** ± 0.81	2.29 ± 1.17	5.11** ± 0.64	**
TAM 108-1 x PC-6	8.47** ± 0.74	4.26** ± 0.97	7.25** ± 1.48	2.74** ± 0.69	**

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

Table 2. Estimation of gene effect in three crosses for various characters in mustard

Estimation of gene effects in three crosses for various characters in mustard							
Crosses	**m**	**d**	**h**	**i**	**j**	**l**	**Type of epistasis**
Days to first flower							
Kranti x PC-6	45.68** ± 0.21	-4.46** ± 0.63	-4.087* ± 1.83	-3.92* ± 1.51	0.867 ± 1.55	23.053** ± 3.38	DH
ACN-9 x PC-6	48.51** ± 0.31	-7.47** ± 0.69	-6.35** ± 2.14	-8.45** ± 1.85	0.20 ± 1.61	14.65** ± 3.70	DH
TAM 108-1 x PC-6	49.61** ± 0.24	4.53** ± 0.49	-17.69** ± 2.90	-17.39** ± 1.38	19.40** ± 1.31	32.92** ± 5.55	DH
Days to maturity							
Kranti x PC-6	112.69** ± 0.51	-4.06** ± 0.95	3.86 ± 3.12	1.36 ± 2.81	17.4** ± 2.46	34.30** ± 5.14	CH
ACN-9 x PC-6	111.07** ± 0.43	-6.69** ± 0.87	-0.64 ± 2.75	4.22 ± 2.44	16.62** ± 2.34	11.42* ± 4.64	DH
TAM 108-1 x PC-6	114.55** ± 0.64	-6.53** ± 0.85	38.09** ± 3.36	35.12** ± 3.06	8.87** ± 2.35	-32.52** ± 5.07	DH
Plant height (cm)							
Kranti x PC-6	168.92** ± 1.31	9.96** ± 3.22	6.15 ± 10.93	-35.74** ± 8.31	-6.81 ± 9.49	92.8** ± 19.89	CH
ACN-9 x PC-6	142.77** ± 1.97	-9.91** ± 2.12	56.25** ± 10.03	24.82** ± 8.95	-30.82** ± 7.54	23.87 ± 14.69	CH

TAM 108-1 x PC-6	178.70** ± 2.06	25.42** ± 3.95	115.81** ± 14.01	136.58** ± 11.43	30.78** ± 11.61	199.76** ± 24.11	CH
Number of branches plant^{-1}							
Kranti x PC-6	3.71** ± 0.07	-0.26 ± 0.19	-0.15 ± 0.65	1.15* ± 0.48	1.26* ± 0.56	1.72 ± 1.21	DH
ACN-9 x PC-6	3.46** ± 0.10	0.39** ± 0.14	-3.46** ± 0.59	-1.73** ± 0.48	3.58** ± 0.51	5.62** ± 0.97	DH
TAM 108-1 x PC-6	3.93** ± 0.09	0.39* ± 0.16	-1.54** ± 0.59	-0.24 ± 0.47	2.44** ± 0.50	3.89** ± 1.02	DH
Siliqua length (cm)							
Kranti x PC-6	3.78** ± 0.04	0.19** ± 0.07	1.15** ± 0.29	1.89** ± 0.22	0.42 ± 0.25	-1.07* ± 0.49	DH
ACN-9 x PC-6	3.36** ± 0.06	0.22* ± 0.09	0.32 ± 0.35	1.69** ± 0.32	1.33** ± 0.29	-1.95** ± 0.54	DH
TAM 108-1 x PC-6	4.53** ± 0.06	0.39** ± 0.11	-1.54** ± 0.35	-1.76** ± 0.31	0.48 ± 0.33	5.83** ± 0.58	DH
Number of siliquae plant^{-1}							
Kranti x PC-6	113.84** ± 3.24	22.69** ± 6.89	179.61** ±38.13	140.77**±18.93	-36.51±22.35	76.09 ±72.87	CH
ACN-9 x PC-6	248.68** ± 7.58	64.46** ± 8.59	132.45**±36.03	235.99**±34.85	115.85**±23.01	463.52**±49.36	CH
TAM 108-1 x PC-6	116.08** ± 4.25	24.77** ± 6.89	172.52**±26.26	171.26**±21.87	53.00*±23.49	-58.17±43.51	DH
Siliquae density on main branch (%)							
Kranti x PC-6	0.48** ± 0.01	-0.02 ± 0.01	0.48** ± 0.06	0.41** ± 0.05	-0.08 ± 0.05	-0.15 ± 0.09	DH
ACN-9 x PC-6	0.50** ± 0.01	-0.05 ± 0.03	0.42** ± 0.08	0.37** ± 0.07	-0.14* ± 0.07	-0.21 ± 0.13	DH
TAM 108-1 x PC-6	0.52** ± 0.01	0.04 ± 0.02	0.08 ± 0.07	0.11 ± 0.07	0.05 ± 0.05	0.09 ± 0.11	CH
1000 seed weight (g)							
Kranti x PC-6	3.38** ± 0.07	0.28* ± 0.12	1.72** ± 0.38	0.88* ± 0.36	-0.97** ± 0.26	3.63** ± 0.6	CH
ACN-9 x PC-6	3.41** ± 0.08	0.48** ± 0.15	2.85** ± 0.44	1.27** ± 0.43	-0.01 ± 0.34	3.10** ± 0.71	CH
TAM 108-1 x PC-6	4.06** ± 0.06	0.11 ± 0.36	-2.25** ± 0.36	-2.14** ± 0.34	-1.36** ± 0.27	5.17** ± 0.59	DH
Seed yield plant^{-1} (g)							
Kranti x PC-6	5.04** ± 0.19	0.16 ± 0.48	13.96** ± 1.34	14.27** ± 1.22	-2.85* ± 1.34	-14.23** ± 2.34	DH
ACN-9 x PC-6	10.02** ± 0.22	2.76** ± 0.46	-9.44** ± 1.33	-10.21** ± 1.27	1.54 ± 1.10	18.13** ± 2.17	DH
TAM 108-1 x PC-6	8.81** ± 0.27	0.38 ± 0.43	-3.59* ± 1.47	-5.49** ± 1.39	-4.21** ± 1.12	18.22** ± 2.27	DH

**Significant at 5% level **Significant at 1% level DH-Dominance heterosis, CH-Complementary heterosis*

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