Original Research Article

Genetic analysis for phenological characters in desi x desi crosses of chickpea (*Cicer arietinum* L.) under timely and late sown conditions

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ABSTRACT

Aims: To study of gene effects for phenological characters in chickpea crosses under different environmental conditions

Study design: Field experiment design was followed

Place and duration of study: The experiment was conducted at research farm, Rajasthan Agricultural Research Institute, Durgapura (SKNAU, Jobner, Jaipur, Rajasathan) during *rabi* 2020-2022.

Methodology: The experimental material consisted of parents (P_1, P_2), F_1's, F_2's, and back crosses with both the parents (B_1 and B_2) of three chickpea crosses. The six basic generations viz., P_1, P_2, F_1, F_2, B_1 and B_2 of the three crosses viz., RSG-807 × RSG-895, RSG-895 × HC-5 and RSG-974 × Avrodhi were raised in compact family block design (CFBD) with three replications with two environments viz., timely sown (E1) condition and late sown (E2) conditions which were created by different date of sowing, first- November and first-December, 2021, respectively.

Results: Pooled anova over environments and simple anova for difference among generations within cross in each environment were observed significant in all three crosses for both the characters. Means values of all six generations were lower in late sown condition as compare to timely sown condition in all cases. Simple additive-dominance model was found inadequate for both of the characters studied in all the crosses under both the conditions. The result of the generation mean analysis showed that non-additive gene effects were more contributed for the inheritance of traits in most of the cases, then additive gene effects.

Conclusion: The nature and magnitude of gene effects vary depending on the crosses, characters and environments studied. Hence, specific breeding strategy has to be adopted for a particular cross and environment to get improvement in different traits. The results showed that additive, dominance and epistatic genetic components were important for the expression both of the characters studied under both the conditions. In such situations, simple pedigree method of selection alone is ineffective. Instead, biparental mating followed by selection of desired recombinants from the segregating population is desirable.

Keywords: crosses, environments, gene effects, scaling tests and selection

INTRODUCTION

Pulses are the dried edible seeds of certain plants in the legume family. After cereals, pulses are the second important constituent of Indian diet. They are high in protein and fibre, and are low in fat. Among pulses, chickpea is one of the most important grain crop, grown in more than 51 countries throughout in the world in an area over 14.84 mha with an average global productivity of about 1016 Kg/ha [1]. India is the largest producer, consumer and exporter of chickpea in the world, accounting for 79.50% of world production [2].

Chickpea is an inexpensive and important source of protein for individuals who cannot afford animal protein or are mostly vegetarian. It is also a good source of minerals (calcium, phosphorus, magnesium, zinc, and iron), unsaturated fatty acids, and fibres, and it assists in maintaining soil fertility by fixing nitrogen [3].

In India, due to delay in harvest of earlier crops such as maize, sugarcane, rice and sesame the late sown chickpea gets exposed to high temperature of the summer, during flowering to maturity. Duration of flowering and maturity in chickpea is known to be very sensitive to changes in external environment and drastic reduction in seed yield was observed when plants were exposed to high temperature [4 and 5].

An understanding of the mode of gene action, knowledge of genetic variances and the importance of genetic effects may help plant breeders to enhance yield potentials. In a polygenic system underlying a quantitative character, the allelic and non-allelic interactions play a greater role in the manifestation of gene effects and inheritance pattern. Although, diallel and line × tester analysis are useful in imparting the knowledge about additive variance, dominance variance, gca, sca variances and effects but they do not provide the estimates of non-allelic interactions. However, partitioning of total genetic variance in to all its components i.e., additive, dominance and all types of epistasis with regard to individual crosses will be of immense value in formulating an effective breeding programme. Generation mean analysis using first degree statistics is an accurate technique to partition total genetic variance in to different components in relation to individual crosses. Generation mean analysis [6], besides providing estimates of main gene effects (additive and non-additive) also provide estimates of non-allelic (digenic) interactions viz., additive × additive [i], additive × dominance [j] and dominance × dominance [l] cross-wise. This helps in the proper understanding and selection of potential parents or crosses for the pedigree selection or heterosis exploitation. Keeping this in mind, the present experiment was carried out to determine the gene effects for phenological traits in three crosses of chickpea under timely and late sown conditions through generation mean analysis

1. MATERIALS AND METHODS

Plant material: Five genetically diverse parental genotypes of chickpea (HC-5, Avrodhi, RSG-974, RSG-807 and RSG-895) were selected from All India Coordinated Chickpea Improvement Project, Rajasthan Agricultural Research Institute, Durgapura. The parental genotypes were crossed in definite fashion during *rabi* 2019-20 to get F_1's. The parental genotypes and their F_1's were sown in *rabi* 2020-21 to get F_1's, F_2's, B_1's and B_2's generations.

The six basic generations viz., P_1, P_2, F_1, F_2, B_1 and B_2 of the three crosses viz., RSG-807 × RSG-895, RSG-895 × HC-5 and RSG-974 × Avrodhi were raised in compact family block design (CFBD) with three replications during *rabi* 2021-22 at, Research Farm, Rajasthan Agricultural Research Institute, Durgapura with two environments viz., timely sown (E1) condition and late sown (E2) conditions which were created by different date of sowing, first- November and first-December, 2021, respectively. Each replication was divided into seven compact blocks, each consists of single cross and blocks were consisted of six plots of six basic generations of each cross. Each block was comprised of twenty rows consisting two row each of P_1, P_2 and F_1; six rows of F_2 and four rows each of B_1 and B_2 generations. The row length was 3.0 m with plant to plant and row to row spacing of 15 x 30 cm, respectively.

Statistical Analysis:

Pooled ANOVA over environments and simple ANOVA for difference among generations within cross to each environment were done according to [7]. The individual scaling tests [8] and Joint scaling [9] were applied to test the presence or absence of non-allelic interaction. Significant χ2- value of joint scaling test suggested then inadequacy of additive-dominance model and it was considered appropriate to use six-parameter model of for the estimation of gene effects under both the conditions.

3. RESULTS AND DISCUSSION

Analysis of variance and per se performance

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The pooled analysis of variance over environments (timely and late sown conditions) revealed significant difference between environments in all three crosses for both of the characters revealed influence of environment on the expression of these characters. The significant values of generation × environment interaction were also observed in all the crosses for both of the characters indicating a non-linear response of generations to the change in the environment (Table 1). The analysis of variance among generations within each cross was found significant in all three crosses for both of the characters under both the conditions which indicated considerable variation in all generations in all the crosses (Table 2). [10] also support this finding in chickpea. The comparison of per se performance of both the characters indicated that the mean values of all six generations of all three crosses were lower under late sown condition as compare to timely sown condition which indicated that flowering and maturity duration is reduced due to high temperature, however different generation showed different percentage reduction (Figure 1). [11] also report onset of flowering and maturity were hastened progressively as the temperature increased.

Scaling tests and Gene effects

The scaling tests revealed the presence of epitasis or non-allelic gene interactions for both of the traits in all the crosses under both the conditions (Table 3 and 4). Moreover, chi-square (χ2) values for the simple additive-dominance model showed significant differences for the traits in all crosses, confirming the presence of non-allelic gene interactions. This led to fitting the data to the six parameters model to accommodate epitasis for these traits under both the conditions. Estimates of genetic effects from generation mean analysis according to a six parameter model for all studied traits were presented in Table 3 and 4. The estimates of mean (m) were significant for all the traits studied in all crosses under both the conditions, showing that the six generations significantly differed from each other.

The additive (a) gene effects were found to be significant and positive for days to 50 % flowering (cross 1 under E1), days to maturity (cross 1 under E1 and cross 3 under E2) suggesting the potential for obtaining further improvement of these traits by using pedigree breeding. [12] reported additive effect for days to flowering, days to maturity in different crosses of chickpea. On the other hand, highly significant negative additive effects were observed for days to 50 % flowering (cross 2 under E2 and cross 3 under E1) and days to maturity (cross1 under E2, cross 2 under E2 and cross3 under E1) indicating the additive effects were less important in the inheritance of these traits in these crosses.

The estimates of dominance (d) effects were significant and positive for days to 50 % flowering (cross 1 under E2, cross 2 under E1 and cross 3 under E2) and days to maturity (cross 1 under E2) indicating the importance of dominance gene effects for the inheritance of these traits under respective conditions. [13] supported this finding in chickpea. The dominance gene effect (d) was significant and greater in magnitude than the additive effect in most of the cases demonstrating a predominant role of dominance gene action in controlling these traits in sesame. [14] also reported similar finding in different crosses. Positive dominance gene effects suggest its enhancing effects on the performance of different traits.

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However, for days to flowering (cross 2 under E2) and for days to maturity (cross 1 under E1 and cross under E1) dominance gene effects possessed negative sign, indicating that dominance is in direction of early maturity, which is desirable in chickpea breeding.

Both additive and dominance gene actions were found to be present for days to 50 % flowering (cross 2 under E2 and cross 3 under E2) and days to maturity (cross 1 under E1 and E2, cross 3 under E1). The simultaneous occurrence of the additive and dominance gene action makes it necessary for resorting to special techniques like inter-mating the segregation generations or recurrent selection to exploit the different kinds of gene effects. The additive x additive gene action was the only fixable component of genetic interaction observed for days to flowering (cross 1 under both E1 and E2, cross 2 under E1 and cross 3 under E2) and days to maturity (cross 1 under both E1 and E2, cross 2 under E1 and cross 3 under E1). In such cases, the pedigree method will be rewarding to improve the traits in a particular cross. The positive and significant additive x dominance for days to 50 % flowering (cross 1 under both E1 and E2) and days to maturity (cross1 under E1 and cross 3 under E1) revealed that selection through self-pollination is not effective for improvement of these traits. Dominance x dominance type of interaction also showed greater effects in the present study. It was found to be significant and positive for days to 50 % flowering (cross 2 under E2) and days to maturity (cross 1 under E1, cross 2 under E1 and cross 3 under E1). On the other hand, highly significant negative dominance x dominance observed for days to 50 % flowering (cross 1 under E2 and cross 3 under E2) and days to maturity (cross 1 under E2, cross 2 under E2 and cross 3 under E2). [14] also observed all three types of gene interactions ('i', 'j' and 'l') in different crosses in chickpea.

The dominance x dominance interaction was larger than the additive x additive in most of the cases. Which indicated for the inheritance of characters dominance interaction effects played greater role than additive interaction. This finding was supported by [15] for days to flowering and days to maturity in chickpea.

The opposite and significant signs of 'h' and 'l' components indicated the importance of duplicate epitasis for days to 50 % flowering (cross 1 under E2, cross 2 under E2 and cross 3 under E2) and days to maturity (cross 1 under both E1 and E2 and cross 3 under E1). Hence, there is a hindrance in selection as well as the complex nature of inheritance for improvement of these traits. In duplicate type of epitasis, the internal cancellation of 'h' and 'l' could reduce the heterosis effect. In such situation, reciprocal recurrent selection is likely to be useful for effective utilization of both types of additive and non-additive gene effects simultaneously. The findings were in accordance with the reports of [16] as they reported duplicate epistasis for most of the phonological characters in chickpea.

From the present study the inadequacy of scaling and joint scaling test for almost all traits indicated the presence of non-allelic interactions and involvement of all three kinds of gene effects viz., additive, dominance and epistasis and their interactions and suggested the application of higher order interaction model. The next possibility is to include the effect of epistasis which can be estimated as additive x additive, dominance x dominance and additive

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x dominance gene effects in the inheritance of the characters. Hence, further study will be envisaged to involve higher order interaction model to estimate the gene and their interaction effect in superior cross combinations. In such situations, simple pedigree method of selection alone is ineffective. Instead, biparental mating followed by selection of desired recombinants from the segregating population is more applicable to break the undesirable linkage and allow the accumulation of favorable alleles for the improvement of the traits

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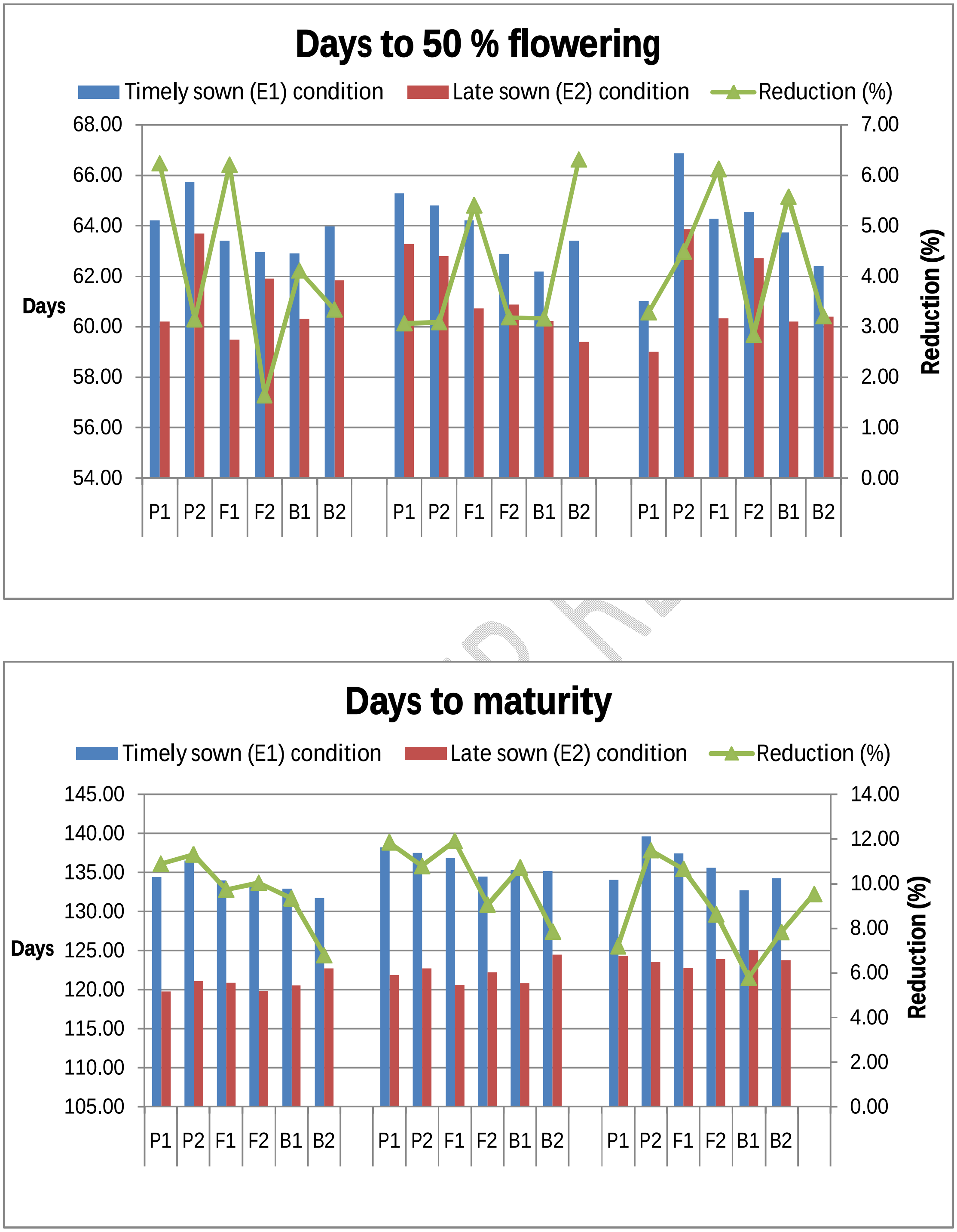

Figure 1 Mean values of parents (P_1 and P_2), F_1's, F_2's and backcrosses (B_1's and B_2's) of three crosses of days to 50 % flowering and days to maturity under timely (E1) and late sown (E2) conditions and reduction percentage over the conditions

Table 1 Pooled analysis of variance (mean squares) for days to 50 % flowering and days to maturity in three crosses of chickpea

Crosses	Source of variations/d.f.				
	Env. (1)	R./Env (2)	Gener. (5)	Gener × Env. (5)	Error (20)
Days to 50 % flowering					
RSG-807 × RSG-895(C1)	62.000**	0.553	8.422	2.010**	0.466
RSG-895 × HC-5 (C2)	59.547**	0.197	9.735*	1.256*	0.394
RSG-974 × Avrodhi (C3)	66.559**	0.347	20.688**	1.219*	0.415
Days to maturity					
RSG-807 × RSG-895(C1)	1521.06**	1.154	3.997	7.670**	1.047
RSG-895 × HC-5 (C2)	1805.49**	1.315	4.893	7.991**	0.582
RSG-974 × Avrodhi (C3)	1237.28**	0.955	6.080	14.809**	0.859

Env.- Environment, R.-Replication, Gener.- Generation

Table 2 Analysis of variance (mean squares) among generations within cross for days to 50 % flowering and days to maturity under timely (E1) and late sown (E2) conditions.

Crosses	Environments	Source of variations/d.f.		
		Replication (2)	Treatment (5)	Error (10)
Days to 50 % flowering				
RSG-807 × RSG-895 (C1)	E1	0.509	3.376**	0.479
	E2	0.587	7.052**	0.453
RSG-895 × HC-5 (C2)	E1	0.223	4.172**	0.379
	E2	0.168	6.819**	0.407
RSG-974 × Avrodhi (C3)	E1	0.194	11.978**	0.329
	E2	0.487	9.924**	0.501
Days to maturity				
RSG-807 × RSG-895 (C1)	E1	0.452	8.127**	1.237
	E2	1.846	3.538*	0.858
RSG-895 × HC-5 (C2)	E1	1.33	6.74**	0.549
	E2	1.356	6.158**	0.601
RSG-974 × Avrodhi (C3)	E1	1.285	19.140**	1.333
	E2	0.622	1.744*	0.385

*,** Significant at 5 per cent and 1 per cent, respectively

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Table 3 Estimates of individual scaling tests, chi-square value (joint scaling test) and gene effects using six generations of three crosses for days to 50 % flowering under timely (E1) and late sown (E2) conditions

	RSG-807 × RSG-895 (C1)		RSG-895 × HC-5 (C2)		RSG-974 × Avrodhi (C3)	
	E1	E2	E1	E2	E1	E2
Individual scaling tests and chi-square ($\chi 2$) value						
A	0.33 ± 0.57	3.99** ± 0.79	-2.66** ± 0.53	-5.20** ± 0.52	-0.46 ± 0.69	1.46* ± 0.72
B	-3.26** ± 0.51	0.66 ± 0.68	-3.26** ± 0.54	-1.80** ± 0.53	-2.06* ± 0.9	1.20 ± 0.88
C	-5.13** ± 0.92	-1.53 ± 1.37	-9.73** ± 0.77	-6.66** ± 0.75	-1.46 ± 1.24	-2.79* ± 1.25
D	-1.10** ± 0.39	-3.10** ± 0.43	-1.89** ± 0.40	0.16 ± 0.40	0.53 ± 0.46	-2.73** ± 0.46
$\chi 2$	50.69**	62.62**	155.70**	125.40**	5.50	41.53**
Gene effects (six parameter model) and type of epistasis						
m	62.90** ± 0.14	60.31** ± 0.16	62.18** ± 0.13	60.21** ± 0.13	63.73** ± 0.14	60.18** ± 0.13
d	1.03** ± 0.25	-0.06 ± 0.27	0.53 ± 0.30	-1.46** ± 0.30	-2.13** ± 0.36	-2.30** ± 0.37
h	0.63 ± 0.85	3.73** ± 1.05	2.96** ± 0.86	-2.63** ± 0.85	-0.73 ± 1.08	4.36** ± 1.08
i	2.20** ± 0.78	6.20** ± 0.86	3.79** ± 0.81	-0.33 ± 0.81	-1.06 ± 0.93	5.46** ± 0.92
j	1.80** ± 0.33	1.66** ± 0.34	0.29 ± 0.34	-1.70** ± 0.34	0.79 ± 0.45	0.13 ± 0.43
l	0.73 ± 1.37	-10.86** ± 1.76	2.13 ± 1.45	7.33** ± 1.44	3.59 ± 1.92	-8.13** ± 1.95
	---	Duplicate	--	Duplicate	--	Duplicate

*,** Significant at 5 per cent and 1 per cent, respectively

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Table 4 Estimates of individual scaling tests, chi- square value (joint scaling test) and gene effects using six generations of three crosses for days to maturity under timely (E1) and late sown (E2) conditions

	RSG-807 × RSG-895 (C1)		RSG-895 × HC-5 (C2)		RSG-974 × Avrodhi (C3)	
	E1	E2	E1	E2	E1	E2
Individual scaling tests and chi-square (χ2) value						
A	0.33 ± 0.57	3.99** ± 0.79	-2.66** ± 0.53	-5.20** ± 0.52	-0.46 ± 0.69	1.46* ± 0.72
B	-3.26** ± 0.51	0.66 ± 0.68	-3.26** ± 0.54	-1.80** ± 0.53	-2.06* ± 0.9	1.20 ± 0.88
C	-5.13** ± 0.92	-1.53 ± 1.37	-9.73** ± 0.77	-6.66** ± 0.75	-1.46 ± 1.24	-2.79* ± 1.25
D	-1.10** ± 0.39	-3.10** ± 0.43	-1.89** ± 0.40	0.16 ± 0.40	0.53 ± 0.46	-2.73** ± 0.46
χ2	50.69**	62.62**	155.70**	125.40**	5.50	41.53**
Gene effects (six parameter model) and type of epistasis						
m	62.90** ± 0.14	60.31** ± 0.16	62.18** ± 0.13	60.21** ± 0.13	63.73** ± 0.14	60.18** ± 0.13
d	1.03** ± 0.25	-0.06 ± 0.27	0.53 ± 0.30	-1.46** ± 0.30	-2.13** ± 0.36	-2.30** ± 0.37
h	0.63 ± 0.85	3.73** ± 1.05	2.96** ± 0.86	-2.63** ± 0.85	-0.73 ± 1.08	4.36** ± 1.08
i	2.20** ± 0.78	6.20** ± 0.86	3.79** ± 0.81	-0.33 ± 0.81	-1.06 ± 0.93	5.46** ± 0.92
j	1.80** ± 0.33	1.66** ± 0.34	0.29 ± 0.34	-1.70** ± 0.34	0.79 ± 0.45	0.13 ± 0.43
l	0.73 ± 1.37	-10.86** ± 1.76	2.13 ± 1.45	7.33** ± 1.44	3.59 ± 1.92	-8.13** ± 1.95
	---	Duplicate	--	Duplicate	--	Duplicate

*,** Significant at 5 per cent and 1 per cent, respectively

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4 CONCLUSIONS

The duration of flowering and maturity was hastened under late sown conditions; therefore early maturity verities may be developed. The nature and magnitude of gene effects vary depending on the crosses, characters and environments studied. Hence, specific breeding strategy has to be adopted for a particular cross and environment to get improvement in different traits. Besides, the results showed that additive, dominance and epistatic genetic components were important for the expression of most of characters studied under both the conditions. In such situations, simple pedigree method of selection alone is ineffective. Instead, biparental mating followed by selection of desired recombinants from the segregating population is desirable. Since considerable amount of dominance effect was also present for most of the traits, selection of superior segregants has to be delayed to later generations until homozygosity is achieved.

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