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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Original Research Article

ABSTRACT

Aims: To study of gene effects for phenological characters in chickpea crosses under different environmental conditions.
Study Design: Compact family block design (CFBD 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.,

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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 (E_1) condition and late sown (E_2) conditions which were created by different date of sowing, first- November and first-December, 2021, respectively.

Results: Pooled analysis of variance (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: Among the all crosses, the mean performance of f_1 generation of cross RSG-807 × RSG-895 was found low for days to 50 % flowering as well as maturity under both the conditions and durations of flowering and maturity were hastened under late sown conditions; therefore, early maturity varieties may be developed. However, due to presence of non-fixable gene effects selection for short durations for flowering and maturity will not effective in early segregating generations. 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.

1. 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 crops, 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 duration 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 parameters in chickpea is known to be very sensitive to changes in external environment that contributes to drastic reduction in seed yield when plants are exposed to high temperature [4,5].

"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 of the crop. 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 analyses are useful in imparting the knowledge about additive variance, dominance variance, general combining ability (GCA), specific combining ability (SCA) variances and effects, however, they do not provide the estimates of non-allelic interactions. Thus, partitioning of total genetic variance into 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 into different components in relation to individual crosses. Generation mean analysis provides estimates of main gene effects (additive and non-additive) as well as estimates of non-allelic (digenic) interactions including additive × additive [i], additive × dominance [j] and dominance × dominance [l] cross-wise" [6]. This helps in the proper understanding and selection

of potential parents or crosses for the pedigree selection or heterosis exploitation. The aim of the present study was to determine the gene effects for phonological traits in three crosses of chickpea under timely and late sown conditions through generation mean analysis.

2. MATERIALS AND METHODS

2.1 Plant Material

Five genetically diverse parental genotypes of chickpea (HC-5, Avrodhi, RSG-974, RSG-807 and RSG-895) were selected from AINP on Arid Legumes, 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 fresh F_1's, F_2's (selfing of F_1), B_1's ($F_1 \times P_1$) and B_2's ($F_1 \times P_2$) 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 (E_1) condition and late sown (E_2) 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 comprised twenty rows with two rows each allotted to P_1, P_2 and F_1; six rows to F_2 and four rows each to B_1 and B_2 generations, respectively. The row length was 3.0 m with plant to plant and row to row spacing of 15 × 30 cm, respectively.

2.2 Data Collection

1. Day to 50% flowering - days taken from sowing to flowering in 50 % of the plants in a plot were recorded as days to 50 % flowering.
2. Days to maturity-days to maturity was recorded as number of days taken from sowing to the time when 75 per cent of the plants showed physiological maturity.

2.3 Statistical Analysis

Pooled analysis of variance (ANOVA) over environments and simple ANOVA for difference

among generations within cross to each environment were done according to [7]. The generation means were used to perform individual scaling tests ('A', 'B', 'C' and 'D') to test the adequacy of additive-dominance model. The four individual scaling tests, as given by Mather (1949) and Hayman and Mather [8] were used as follows: 'A' = $2\bar{B}_1 - \bar{P}_1 - \bar{F}_1$, 'B' = $2\bar{B}_2 - \bar{P}_2 - \bar{F}_1$, 'C' = $4\bar{F}_2 - 2\bar{F}_1 - \bar{P}_1 - \bar{P}_2$ and 'D' = $2\bar{F}_2 - \bar{B}_1 - \bar{B}_2$. Non-significance of the entire individual scaling test implies the adequacy of additive-dominance model and main gene effects were computed as per three parameter model suggested by Jinks and Jones (1958). For the crosses and characters, where in any of the individual scaling test was observed significant; six parameter model as suggested by Hayman (1958) was applied to partition of gene effects into epistatic components including main/principle gene effects. However, for confirmation of adequacy of additive-dominance model and to realize presence or absence of inter-allelic/epistatic interactions, joint scaling test as suggested by Cavalli [9] was also applied. The test of significance of scaling tests and various gene effects was performed using 't' test.

3. RESULTS AND DISCUSSION

3.1 Analysis of Variance and per se Performance

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). Kumhar et al. [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 (Fig. 1).

Jumrani and Bhatia [11] also report onset of flowering and maturity were hastened progressively as the temperature increased.

3.2 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 (Tables 3 and 4). Moreover, chi-square ($\chi 2$) 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 Tables 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 E_1), days to maturity (cross 1 under E_1 and cross 3 under E_2) suggesting the potential for obtaining further improvement of these traits by using pedigree breeding. Nehra et al. [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 E_2 and cross 3 under E_1) and days to maturity (cross 1 under E_2, cross 2 under E_2 and cross3 under E_1) 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 E_2, cross 2 under E_1 and cross 3 under E_2) and days to maturity (cross 1 under E_2) indicating the importance of dominance gene effects for the inheritance of these traits under respective conditions. Samad et al. [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. Deshmukh and Gawande [14] also reported similar finding in different crosses. Positive dominance gene effects suggest its enhancing effects on the performance of different traits. However, for days to flowering (cross 2 under E_2) and for days to maturity (cross 1 under E_1 and cross under E_1) 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 E_2 and cross 3 under E_2) and days to maturity (cross 1 under E_1 and E_2, cross 3 under E_1). 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 E_1 and E_2, cross 2 under E_1 and cross 3 under E_2) and days to maturity (cross 1 under both E_1 and E_2, cross 2 under E_1 and cross 3 under E_1). 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 E_1 and E_2) and days to maturity (cross1 under E_1 and cross 3 under E_1) 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 E_2) and days to maturity (cross 1 under E_1, cross 2 under E_1 and cross 3 under E_1). On the other hand, highly significant negative dominance x dominance observed for days to 50 % flowering (cross 1 under E_2 and cross 3 under E_2) and days to maturity (cross 1 under E_2, cross 2 under E_2 and cross 3 under E_2). Deshmukh and Gawande [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 Najan and Kadam [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 E_2, cross 2 under E_2 and cross 3

under E_2) and days to maturity (cross 1 under both E_1 and E_2 and cross 3 under E_1). 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 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.

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)	Gen. (5)	Gen × 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

*, ** *Significant at 5 per cent and 1 per cent, respectivelEnv.- Environment, R.-Replication, Gen.- Generation*

Table 2. Analysis of variance (mean squares) among generations within cross for days to 50 % flowering and days to maturity under timely (E_1) and late sown (E_2) conditions

Crosses	Environments	Source of variations/d.f.		
		Replication (2)	Treatment (5)	Error (10)
Days to 50 % flowering				
RSG-807 × RSG-895 (C1)	E_1	0.509	3.376**	0.479
	E_2	0.587	7.052**	0.453
RSG-895 × HC-5 (C2)	E_1	0.223	4.172**	0.379
	E_2	0.168	6.819**	0.407
RSG-974 × Avrodhi (C3)	E_1	0.194	11.978**	0.329
	E_2	0.487	9.924**	0.501
Days to maturity				
RSG-807 × RSG-895 (C1)	E_1	0.452	8.127**	1.237
	E_2	1.846	3.538*	0.858
RSG-895 × HC-5 (C2)	E_1	1.33	6.74**	0.549
	E_2	1.356	6.158**	0.601
RSG-974 × Avrodhi (C3)	E_1	1.285	19.140**	1.333
	E_2	0.622	1.744*	0.385

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

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

	Crosses					
	RSG-807 × RSG-895 (C1)		RSG-895 × HC-5 (C2)		RSG-974 × Avrodhi (C3)	
	Environments (Timely sown condition (E_1) and late sown condition (E_2))					
	E_1	E_2	E_1	E_2	E_1	E_2
Individual scaling tests (A, B, C and D) and chi-square ($\chi2$) 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
$\chi2$	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

m- generation mean, d- additive gene effect, h- dominance gene effect, i- additive × additive gene effect, j- additive × dominance gene effect and l- dominance × dominance gene effect

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 (E_1) and late sown (E_2) conditions

	Crosses					
	RSG-807 × RSG-895 (C1)		RSG-895 × HC-5 (C2)		RSG-974 × Avrodhi (C3)	
	Environments (Timely sown condition (E_1) and late sown condition (E2)					
	E_1	E_2	E_1	E_2	E_1	E_2
Individual scaling tests (A, B, C and D) and chi-square ($\chi 2$) value						
A	-2.53** ± 0.74	0.33 ± 0.71	4.46 ± 0.81	-0.79 ± 0.82	-5.99** ± 0.7	2.93** ± 0.78
B	-7.13** ± 0.59	3.46** ± 0.76	-4.20** ± 0.82	5.73** ± 0.87	-8.40** ± 0.79	1.26 ± 0.74
C	-5.93** ± 1.02	-3.26** ± 0.99	-11.6** ± 1.29	3.46* ± 1.48	-4.46** ± 0.81	2.06 ± 1.19
D	1.86** ± 0.47	-3.53** ± 0.53	-1.46** ± 0.52	-0.73 ± 0.62	4.13** ± 0.54	-4.46** ± 0.81
$\chi 2$	91.42**	38.98**	81.68**	50.93**	-4.46** ± 0.81	13.03**
Gene effects (six parameter model) and type of epistasis						
m	133.28** ± 0.16	119.88** ± 0.16	134.53** ± 0.16	122.31** ± 0.23	135.63** ± 0.18	123.91** ± 0.21
d	1.23** ± 0.34	-2.23** ± 0.41	0.20 ± 0.40	-3.70** ± 0.41	-1.59** ± 0.4	1.23** ± 0.41
h	-5.26** ± 1.02	7.53** ± 1.12	1.93 ± 1.18	-0.23 ± 1.37	-7.66** ± 1.17	0.93 ± 1.26
i	-3.73** ± 0.94	7.06** ± 1.06	2.93** ± 1.04	1.46 ± 1.25	-8.26** ± 1.09	2.13 ± 1.18
j	2.30** ± 0.42	-1.56** ± 0.48	-0.13 ± 0.45	-3.26** ± 0.46	1.20* ± 0.46	0.83 ± 0.47
l	13.39** ± 1.71	-10.86** ± 1.93	5.73** ± 2.06	-6.40** ± 2.22	22.66** ± 1.97	-6.33** ± 2.05
	Duplicate	Duplicate	--	--	Duplicate	--

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

m- generation mean, d- additive gene effect, h- dominance gene effect, i- additive × additive gene effect, j- additive × dominance gene effect and l- dominance × dominance gene effect
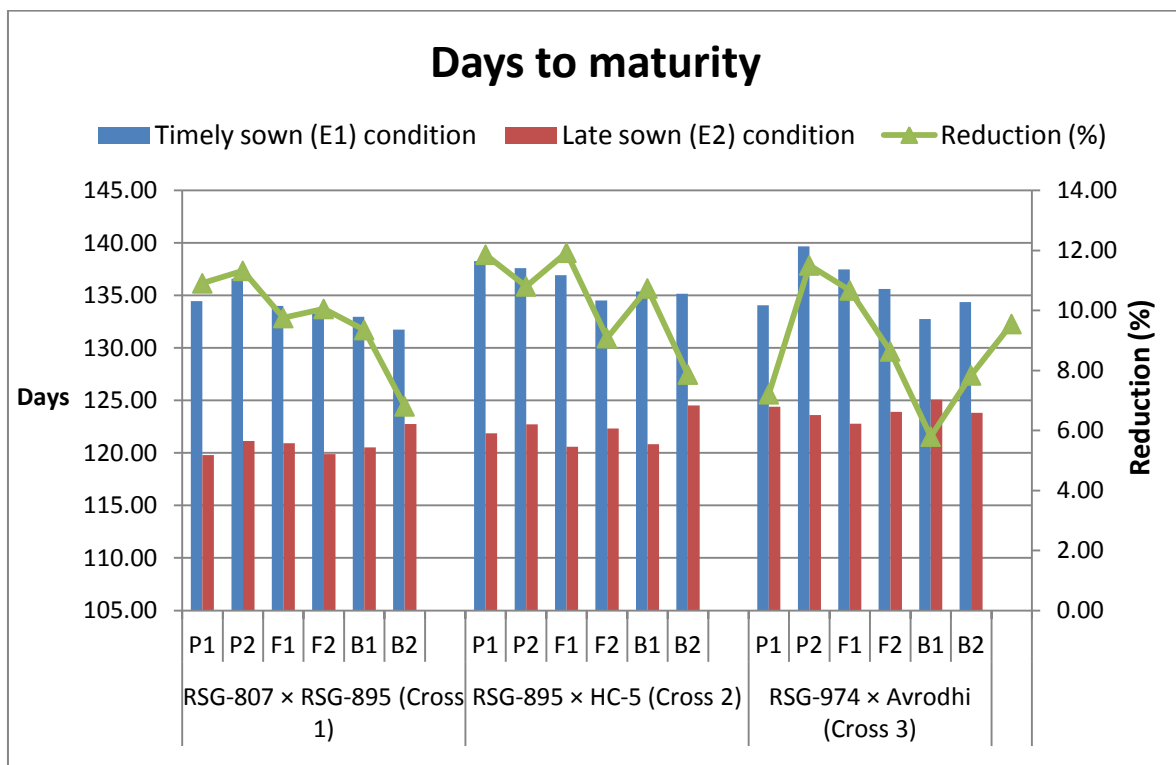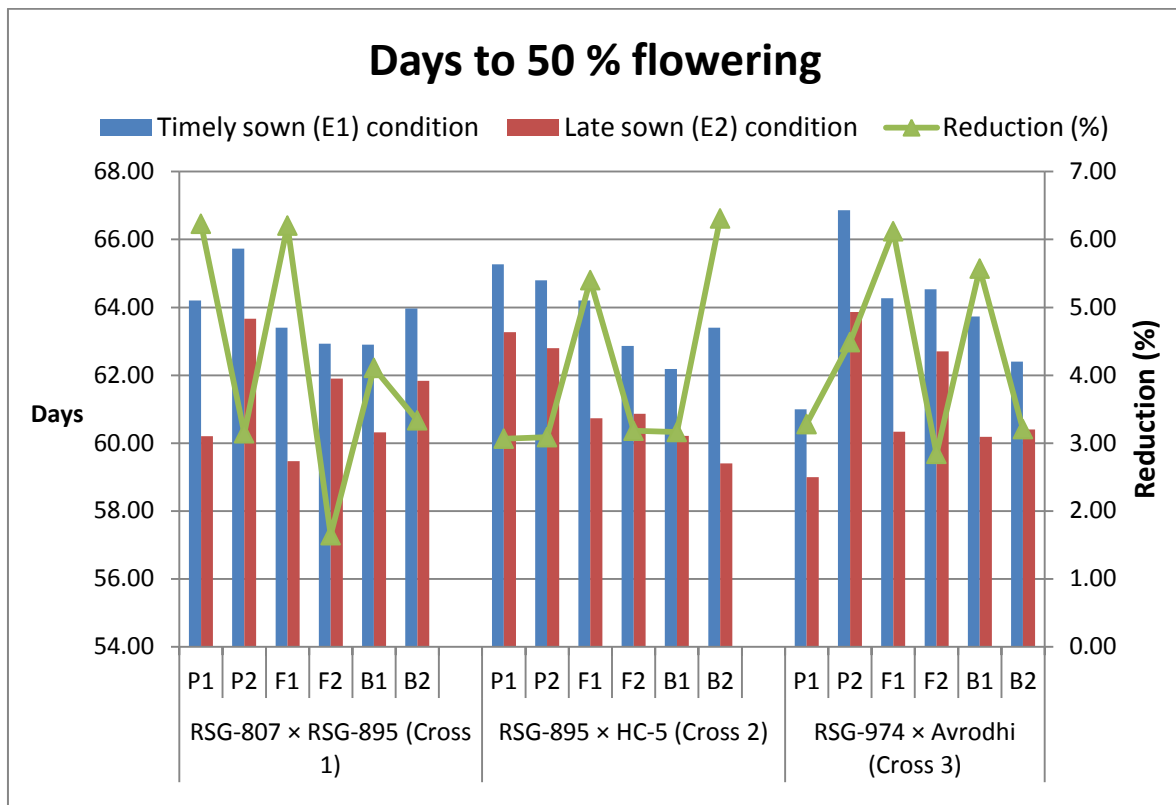
Fig. 1. Mean values of parents (P_1 and P_2), F_1's, F_2's and backcrosses (B_1's and B_2's) of three crosses of days to 50 % flowering and days to maturity under timely (E_1) and late sown (E_2) conditions and reduction percentage over the conditions

4. CONCLUSIONS

Among the all crosses, the mean performance of f_1 generation of cross RSG-807 × RSG-895 was found low for days to 50 % flowering as well as maturity under both the conditions and durations of flowering and maturity were hastened under late sown conditions; therefore, early maturity varieties may be developed. However, due to presence of non-fixable gene effects selection for short durations for flowering and maturity will not effective in early segregating generations. 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.

ACKNOWLEDGEMENT

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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The peer review history for this paper can be accessed here:
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