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#### ABSTRACT

The present study was conducted to study the inheritance of leaf length and leaf breadth in an eight parent diallel set of crosses (28 crosses) having six basic generations. Leaf length was measured on fourth leaf from the base of the plant as distance from the base of petiole to the apex and its maximum which was taken as leaf breadth. The inheritance was studied by generation mean analysis as outlined by Cavalli (1952) and Hayman (1958). For leaf length additive dominance model was inadequate for all the crosses. In 17 cross combinations, additive component was significant whereas dominance effects were significant in 13 crosses. Duplicate type of non-allelic interaction was shown by 16 crosses while only two crosses showed complementary type of epistasis. For leaf breadth also additive dominance model was inadequate for most of the crosses. In 14 crosses additive effects were significant whereas dominance effects in 17 crosses. Fifteen crosses showed duplicate type of interaction and only four showed complementary type. The correlation studies in parents,  $F_1$  and  $F_2$  revealed that both the characters had non significant correlation with yield in parents and F1 whereas significant and positive association was established in F2s. Long and broader leaves can be used as tool for isolating better yielding genotypes in field. Apart from this, these two characters can aid in selection procedure by a two stage staggered system and the available resources can be more effectively used.

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## INTRODUCTION

In recent years the importance of leaf characters in terms of crop yield has been increasingly recognised. Number, arrangement, inclination, shape and size of leaves determine the canopy architecture which seems to be related to light interception and photosynthetic activity and hence the production and productivity level of a genotype. These factors as far as possible should be considered in breeding varieties for higher yields and in making decisions relative to plant density for maximum production. The varieties of mustard show a great degree of variation in leaf characteristics including size and shape. Structural changes between immature and mature canopies are characteristic feature of the species. Taking in view the importance of leaf characteristics, the present study was conducted to study the inheritance of leaf length and leaf breadth in Indian mustard.

### MATERIALS AND METHODS

Eight genotypes of Indian mustard were selected on the basis of their plant types and genetic diversity for various traits. Amongst them five were improved genotypes representing different agro-climatic regions of India (RL 18, BR 40, BR 13, T 5 and KYSR) and three were stable mutants (RLM 198, RLM 240 and RLM 29/25) developed by Punjab Agricultural University, Ludhiana by irradiating RL 18 seeds. With the eight parents, six basic generations ( $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$ ,  $B_1$  and  $B_2$ ) were developed in diallel set. Eight parents, 28  $F_1$ s, 28  $F_2$ s, 28  $F_1$ s and 28  $F_2$ s were grown in randomised complete block design in three replications. Data were recorded on randomly selected plants (10 for parents, 10 for  $F_1$ s, 100 for  $F_2$ s, 50 for  $F_2$ s and 50 for  $F_2$ s) in each replication on leaf length and leaf breadth. Leaf length was measured in centimeters as distance from the plant, whereas leaf breadth was measured as maximum width of the leaf whose length was measured in centimeters.

Mean values of the six generations of all the crosses within the generations were calculated for the characters understudy. Variation of means of each generation was also worked out. These means and variations were calculated separately for each replication and then the values were pooled. A joint scaling test as supported by Cavalli (1952) was conducted. This test uses data from  $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$ ,  $B_1$  and  $B_2$  to provide estimates for mean, additive and dominance effects. These estimates are derived by the procedure of weighted least squares using as weights the inverse of the variances of generation means. This joint scaling test also evaluated the goodness of fit of the 3-parameter model (mean (m), additive (d) and dominance (h) effects). Lack of fit implies the existence of non-additive gene effects other than dominance (additive x additive (i), additive x dominance (j) and dominance x dominance (1)). Generation means were also analysed using the method of Hayman (1958) to fit six parameter model.

Significance of the various gene effects for this model were determined by computing standard errors from the variances of corresponding population means.

Phenotypic and genotypic correlations were calculated among the characters studied and yield, oil content and yield components based on components of variances and covariances, for the parents,  $F_1s$  and  $F_2s$  separately. Estimated values of phenotypic correlations only were tested for significance.

# RESULTS AND DISCUSSION

For leaf length the components of generation means based on three parameter model were inadequate, because the chisquare was significant. So, the values based on six parameter model are presented in Table 1. In 17 cross combination additive component was significant. All the crosses, where RL 18 was one of the parents showed highly significant negative value of (d) with positive and highly significant value of (i) with higher magnitude, except in RL 18 x RLM 240 where (d) value was negative and non-significant and (i) was positive and highly significant and in RL 18 x RLM 29/25 both were positive and significant. The other crosses showing positive (d) and (i) components were RLM 198 x RLM 29/25, RLM 198 x BR 40, RLM 198 x T 5, RLM 240 x BR 13, RLM 29/25 x BR 40, RLM 29/25 x T 5, BR 40 x KYSR and T 5 x KYSR. It showed trend for fixable component. In 13 crosses the dominance effects were positive and highly significant. Only in three crosses (RL 18 x BR 13, RL 18  $\times$ T  $\tilde{5}$  and RLM 240 x BR 40) the values of (h) + (l) estimates were greater than the value of (d) + (i) estimates. 16 cross combinations showed duplicate type of non-allelic interaction while only two crosses (RLM 198 x RL 18 and RL 18 x BR 13) showed complementary type of epistasis. Only in these crosses, hybrid vigour for leaf length can be exploited. In general, the magnitude of additive  $\boldsymbol{x}$ dominance type of non-allelic interaction was low though significant as compared to (i) and (l) components.

For leaf breadth, additive dominance model was adequate in three crosses only (RL 18 x RL 13, RLM 29/25 x BR 13 x BR 40 x T 5). Among the 25 crosses showing epistasis, highly significant and significant additive effects were present in 14 and 2 crosses respectively (Table 2). The sum total of additive and additive x additive effects were positive in most of the cross combinations. Dominance effects were positive and significant in 17 crosses, whereas in two crosses, the effects were negative and significant. In most of the crosses, summation of dominance and dominance x dominance effects resulted into negative values. Out of 19 crosses where (h) and (l) were significant, 15 showed duplicate type of epistasis and only four showed complementary type of epistasis.

For both the characters supermacy of additive and additive x additive effects was present, which was further confirmed by the presence of duplicate type of non-allelic interactions. Chauhan and Singh (1973) had also reported that leaf length was controlled by additive gene effects. High significant additive gene effects were found for both the traits by Singh and Singh (1971).

As expected leaf length and leaf breadth were having very close association in all the generations studied i.e., parents  $F_1s$  and  $F_2s$  (0.93\*\*, 0.83\*\* and 0.88\*\*). Leaf length showed close association with plant height, number of primary branches and

pods on main shoot and leaf breadth exhibited positive and significant association with plant height and number of primary branches in all the generations. It was interesting to note that both the traits did not show any significant association with pod length, seeds per siliqua and seed yield per plant in parents and F1s but significant and positive association was developed in segregating population (0.42\* and 0.49\* with pod length 0.57\*\* and 0.59\*\* with seeds per siliqua and 0.43\* and 0.42\* with seed yield). So broad and long leaves could be used as selection criteria for yield in segregating population. Thurling (1974) had also advocated the selection on the basis of leaf characters for improving the seed yield in rapeseed. Apart from this, both the characters can aid in selection procedure by a two stage staggered system. Thus, the available resources can be used more effectively.

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<sup>\*</sup> and \*\* represents significant at 5 per cent and 1 per cent, respectively.

Table 2: Gene effects for leaf breadth using 3 or 6 parameter model on means of 6 basic generations in crosses.

Cross	m	(d)	(h)	(i)	(j)	(†)
RLM 198 x RL 18	10.1**	-2.7**	4.5**	5.6**	-2.4**	-15.3**
RLM 198 x RLM 240	10.6**	0.3	2.5**	2.2**	1.0**	<b>-5.5**</b>
RLM 198 x RLM 29/25	10.3**	-0.9**	0.8	1.5*	1.6**	-6.7**
RLM 198 x BR 40	10.0**	2.5**	3.5	2.9**	2.9**	-5.2**
RLM 198 x BR 13	9.5**	-1.1**	-2.1*	-2.1*	-0.8*	4.9**
RLM 198 x T 5	8.6**	1.3**	9.2**	8.5**	1.9**	-10.0*1
RLM 198 x KYSR	7.6**	0.8**	11.1**	9.2**	-1.5**	-16.7*1
RL 18 x RLM 240	9.7**	-0.8**	5.2**	5.3**	-0.3	<b>-7.7*</b>
RL 18 x RLM 29/25	9.9**	1.3**	4.4**	3.7**	1.3**	-5.9 <b>*</b>
RL 18 x BR 40	8.9**	-2.2**	7.7**	7.0**	-2.1**	-7.7 <b>*</b> ·
RL 18 x BR 13	9.2**	-0.2	-1.3**			
RL 18 x T 5	9.6**	-0.4	3.0**	-0.1	-0.0	9.6*
RL 18 x KYSR	7.1**	-2.9**	12.4**	11.5**	-5.5**	-20.5*
RLM 240 x RLM 29/25	9.9**	-0.2	3.0**	4.6**	-0.6	-10.2*
RLM 240 x BR 40	10.3**	0.1*	2.4*	1.5	-0.2	-0.2
RLM 240 x BR 13	9.4**	2.9**	8.4**	3.8**	2.4**	5.8*
RLM 240 x T 5	10.6**	-1.5**	-0.3	-0.3	-1.6**	1.63
RLM 240 x KYSR	7.3**	-0.6	9.1**	7.8**	-3.8**	-11.2*
RLM 29/25 x BR 40	10.0**	0.5	4.7**	1.1	0.7	5.6*
RLM 29/25 x BR 13	10.0**	0.2	0.6			
RLM 29/25 x T 5	12.2**	1.4**	6.0**	2.7*	1.7**	_9. <b>1*</b>
RLM 29/25 x KYSR	9.7**	1.9**	-0.9	-1.3	-0.8*	-6.6*
BR 40 x BR 13	11.5**	0.1	-2.4	-1.7	-0.0	-3.9
BR 40 x T 5	10.3**	0.1	1.1*		1 1 2	
BR 40 x KYSR	8.3**	2.2**	6.1**	6.2**	-0.6	-16.1*
BR 13 x T 5	9.3**	-0.4	-2.6*	-1.6	0.8	4.9*
BR 13 x KYSR	9.5**	0.2	2.8*	-2.3*	-2.5**	6.1*
T 5 x KYSR	8.1**	1,1**	6.1**	4.7**	-2.0**	-8.2 <b>*</b>

Table 1 : Gene effects for leaf length using six parameter model on means of 6 basic generations in crosses in diallel.

Crosses in dialier.		T	T	T	1	1
Cross	m	(d)	(h)	(i)	(j)	(1)
RLM 198 x RL 18	23.0**	-5.7**	-19.2**	15.5**	-4.8**	-29.7**
RLM 198 x RLM 240	24.1**	-1.1	7.2**	5.0**	1.4	-9.4**
RLM 198 x RLM 29/25	23.3**	-4.5**	8.5**	7.7**	-3.9**	-22.7**
RLM 198 x BR 40	22.9**	3.1**	14.3**	8.9**	3.8**	13.6**
RLM 198 x BR 13	21.7**	-1.1*	-1.8	-3.0	0.4	10.0**
RLM 198 x T 5	20.2**	1.8**	29.2**	24.9**	2.8**	-35.8**
RLM 198 x KYSR	18.0**	0.7	22.0**	16.8**	-3.7**	-30.1**
RL 18 x RLM 240	22.1**	-1.2	8.6**	8.9**	0.5	-10.5*
RL 18 x RLM 29/25	28.6**	4.1**	8.0**	5.9**	3.8**	-9.5*
RL 18 x BR 40	20.0**	-6.6**	23.3**	18.6**	6.8**	-19.5**
RL 18 x BR 13	21.0**	-3.4**	5.2**	7.1**	-2.8**	10.0**
RL 18 x T 5	21.6**	-3.8**	12.9**	8.5**	-3.7**	-4.7
RL 18 x KYSR	17.2**	-3.5**	19.9**	19.4**	-8.8**	-38.2**
RLM 240 x RLM 29/25	22.0**	-1.0	10.9**	13.3**	3.0**	-34.2**
RLM 240 x BR 40	23.6**	1.0	11.6**	6.5*	-0.8	-2.7
RLM 240 x BR 13	20.7**	6.6**	26.7**	15.9**	5.5**	5.6
RLM 240 x T 5	25.5**	-5.7**	0.4	-2.3	7.2**	5.0
RLM 240 x KYSR	18.2**	-0.8	17.1**	14.9**	-7.7**	-23.1**
RLM 29/25 x BR 40	22.1**	1.7**	7.5**	4.9*	1.8**	-5.8
RLM 29/25 x T 5	29.8**	2.6**	16.2**	12.5**	3.0**	-48.4**
RLM 29/25 x KYSR	21.0**	0.7	-0.7	-0.7	-4.2**	15.1**
BR 40 x BR 13	26.4**	-1.1	-0.8	1.5	-0.3	-22.2**
BR 40 x T 5	26.4**	-0.1	4.8	0.7	0.1	-9.5*
BR 40 x KYSR	20.1**	6.2**	15.5**	14.5**	1.1	-40.2**
BR 13 x T 5	21.8**	0.4	-7.6**	-5.2**	-0.1	10.9**
BR 13 x KYSR	23.7**	4.1**	-9.1**	-16.6**	-1.7*	24.2**
T 5 x KYSR	17.9**	3.9**	18.3**	15.0**	-1.5	-26.4**
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