

Genetics of Alternaria blight resistance in linseed (*Linum usiatissimum* L.)

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SUMMARY

Genetic analysis of Alternaria blight resistance was carried out in linseed using Hayman's (1958) procedure. Estimates of variance components showed significant values of additive and non additive gene effects in the inheritance of Alternaria blight resistance with predominance of the additive component. Digenic epistatic interactions also revealed the preponderance of fixable component but with duplicate type of epistasis in all the three crosses. Average degree of dominance was less than unity over generations indicating partial dominance accompanied with high heritability in narrow sense. The present investigation suggested the bi-parental mating model III would be more effective for the development of Alternaria blight resistant varieties in linseed.

Key Words : Linseed, Genetics, Alternaria blight, Generation mean

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Linseed is an important non-edible oilseed crop grown through out the world for its oil and fibre properties. Globally India ranks second in area after Canada and fourth in production after Canada, China and USA. Uttar Pradesh is the major linseed growing state but its average yield is very low (411 kg/ha) in comparison to world's average of 1006 kg/ha (2009-2010) and the highest producing (2163 kg/ha) country in the world is Tunisia. Besides, several other constraints, susceptibility to major diseases like Alternaria blight is the most limiting factor for low yield in linseed. As of now, none of the released varieties of linseed have in-built resistance against this disease causing economic loss of about 60-70 per cent. In order to formulate sound and

efficient breeding programmes, information on nature and magnitude of gene action for the traits to be improved must be known. Hence, the present investigation was undertaken to gather information about the genetic architecture of Alternaria blight resistance in linseed.

MATERIALS AND METHODS

Experimental material comprising six basic populations (P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2) of three crosses viz., Neelum x Ayogi (S x R), Chambal x Ayogi (S x R) and Chambal x ES-44 (S x R) were grown in a Randomized Block Design with three replications during 2003-2004 at Crop Research Farm, Nawabganj, C.S. Azad University of Agriculture and Technology, Kanpur. Parents and F_1 's were sown in 3 meter single rows whereas, back crosses and F_2 populations were represented by three and six rows, respectively. Inter and intra spacing was maintained at 30 x 5 cm. Every sixth row was of the infector cultivar, Chambal. The entire plot was also surrounded by two rows of the infector cultivar to create epiphytotic condition in the material. The recommended agronomic practices were followed and frequent irrigations were applied in order to provide congenial environment for disease development. The incidence of Alternaria blight was recorded on plant basis from appearance of disease till the

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Table 1 :Nature and magnitude of gene effects studied for Alternaria blight resistance on linseed through generation mean analysis

Crosses	m	d	h	i	j	l	Type of epistasis	Heritability	Degree of dominance
Neelum x Ayogi	22.00**	24.00**	14.33**	14.67**	3.33**	-11.32**	D	47.58	0.24
Chambal x Ayogi	23.67**	31.00**	10.00**	12.67**	6.63**	-4.06**	D	56.07	0.54
Chambal x ES-44	23.67**	40.83**	24.00**	40.00** ±	4.17**	-37.67**	D	33.50	0.46
	±0.88	±6.54	±2.02	6.33	±2.74	±11.50d			

** indicate significance of value at P=0.01, respectively, m=mean, d=additive gene effect, h=dominant gene effect, i=additive x additive gene interaction, j=additive x dominance gene interaction and l=dominance x dominance gene interaction, D=duplicate epistasis

maturity at 10 days interval in 0-5 scale (0-free *i.e.*, no disease, 1-resistant *i.e.*, 0-10 per cent area of leaves/bud infection, 2-moderately resistant *i.e.*, 10.1 to 25 per cent area of leaves/bud infection, 3-moderately susceptible *i.e.*, 25.1 to 50 per cent area of leaves/bud infection, 4-susceptible *i.e.*, 50.1 to 75 per cent area of leaves/bud infection and 5-highly susceptible *i.e.*, above 75 per cent area of leaves/bud infection). Final disease score was taken at the time of complete maturity. Mather's scaling test was applied in all the three crosses to test the adequacy of additive-dominance model. The gene effects and interactions were estimated following Hayman (1958).

RESULTS AND DISCUSSION

The estimates of variance components presented in Table 1 indicated the significance of both additive and dominance genetic variation. All crosses *viz.*, Neelum x Ayogi, Chambal x Ayogi and Chambal x ES-44 were reported to have highly significant additive value for Alternaria blight incidence indicating the preponderance of additive gene action in the inheritance of this trait. The crosses Chambal x ES 44, Neelum x Ayogi and Chambal x Ayogi showed the highly significant and positive value for dominance effect which was also reported by Singh and Chauhan (1988).

Digenic epistatic interactions showed that additive x additive (i) effects was highly significant for Chambal x ES-44, Neelum x Ayogi and Chambal x Ayogi. The significant values of dominance x dominance interaction effect with negative sign revealed that the recessive genes were more frequent in the expression of this trait. Highly significant positive value of h for Alternaria blight incidence indicated that heterozygous gene combination significantly contributed to the over all dominance in positive direction. Since these effects are likely to be influenced by degree and direction of dispersion of interacting pairs of genes so that their overall estimates may not always be helpful to precisely classify the epistasis. Hence, the only safe and possible way to classify the epistasis is based on the sign of [h] and [l] components which are not influenced by gene dispersion. In the present set of crosses, duplicate type of epistasis was observed

which will in turn minimize the manifestation of heterotic disease expression and delay the selection.

The fact that the inheritance of Alternaria blight resistance in linseed crop was observed to exhibit preponderance in the form of significant and high magnitude of additive and additive x additive genetic interactions along with significant and lower estimates of dominance gene effects. The results clearly revealed that the resistance against Alternaria blight is mainly controlled by additive genes with the minor role of non-additive gene effect in the studied crosses as it also confirms the results of Bhadauria *et al.* (2003). These crosses are valuable because of the predominance of additive x additive type gene action with can further be exploited through simple selection scheme. It is, therefore, suggested that where additive x additive gene action is present, the bi-parental mating on the model of design NC III (Comstock and Robinson, 1948) may be followed in order to get transgressive segregates from crosses involving these parents. Such crosses may be effectively utilized in appropriate breeding programmes for the development of Alternaria blight resistant genotypes in linseed.

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