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Role of inter genic interactions in inheritance of *Alternaria* leaf blight resistance in inter and intraspecific crosses of *Brassica carinata* and *Brassica juncea*

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Abstract

The present study was carried out to study the genetics of inheritance of Alternaria blight resistance in rapeseed-mustard. Three crosses involving susceptible × moderately resistant genotypes *viz.,* Jayanti × P(4)2b, Jayanti × EC-399300 and RCC-4 × EC-399300 were developed and evaluated. However, no concrete ratio could be fitted in F_2 population as disease reaction varied from moderate to high susceptibility and the available donor sources do not have high level of resistance. Therefore, six-parameter model was used to find out the gene effects for inheritance to Alternaria blight resistance using per cent disease index (PDI) with square root transformation. Significance of A, C and D tests confirmed the presence of epistasis. The study confirmed that at least more than one gene controls the inheritance of Alternaria blight resistance. Six-parameter model showed significant estimates of additive [d], and non-additive [h] effects as well as all the three types of epistasis *viz.,* additive × additive [i], additive × dominance [j] and dominance × dominance [l]. The opposite signs of [h] and [l] indicated the presence of duplicate epistasis for the inheritance of Alternaria blight resistance.

Key words: *Alternaria blight, epistasis, generation mean, rapeseed-mustard*

Introduction

Rapeseed-mustard is an important oilseed crop which is grown over an area of 36.62 million hectares worldwide with total production of 72.41 million tons. Canada is the leading country in terms of area and production of rapeseed-mustard followed by china and India. In India, it is cultivated over 7.20 million hectares area with the production of 8.0 million tons (Anonymous, 2020). In India, rapeseed-mustard is the second most important oilseed crop, next to groundnut, contributing nearly 25-30 per cent of the total oilseeds production (Anonymous, 2018).

The various factors such as lack of suitable cultivars for different ecosystems, fluctuations in weather conditions, cultivation in marginal and sub marginal lands and prevalence of various biotic and abiotic stresses are the major reasons for low productivity of this crop. Among the biotic stresses, Alternaria blight (AB) disease caused by *Alternaria brassicae* (Berk.) Sacc. is the utmost constraint in production in rapeseed-mustard. Alternaria blight is characterized by formation of dark brown coloured spots on leaves, stem and siliquae. Lower leaves show the symptoms first, with the appearance of black points which later on enlarge into prominent concentric rings or lesions of various sizes. Alternaria blight has been reported from all the continents of the world and is one among the important diseases of rapeseed-mustard causing yield losses up to 35-45 per cent with no proven source of transferable resistance in any of the hosts (Kolte, 1985). Hence, the most suitable alternate way to increase productivity is by adoption of high yielding and input responsive genotypes having resistance against various biotic and abiotic stresses with high stability index. In order to initiate systematic breeding programme for the development of resistant varieties against AB, it is essential to understand the inheritance pattern. Therefore, concerted efforts are needed to incorporate resistance/tolerance for AB through conventional and non-conventional breeding to overcome the productivity constrains in improved cultivars. Keeping this in view, the present study was aimed to assess the information on genetic control of inheritance of AB resistance.

Materials and Methods

The experimental material comprised of different generations of two crosses of rapeseed-mustard. Four parents comprising two susceptible varieties; Jayanti (*Brassica carinata*) and RCC-4 (*B. juncea*) and two moderately resistant lines; P(4)2b (*B. carinata* line developed through mutation breeding) and EC-399300 were used to develop three cross combinations i.e.

Jayanti× P(4)2b, Jayanti × EC-399300 and RCC-4×EC-399300 (Table 1). The genotype EC-399300 (Indian mustard), moderately resistant line to AB was procured from ICAR-DRMR Bharatpur, Rajasthan, during the year 2016.

Two parents; Jayanti and P(4)2b were sown during *rabi* 2015-16 at the experimental farm of Department of Genetics & Plant Breeding, CSK HPKV Palampur (H.P.) and crosses were attempted among the parents to develop F_1s. The off-season nursery facilities at CSK HPKV-HAREC, Kukumseri (Lahaul & Sipiti) were used to advance F_1 population to F_2 during *kharif* 2016. Similarly during *rabi* 2016-17, RCC-4 and EC-399300 were crossed and their F_1s were advanced to F_2 and simultaneously BC_1 and BC_2 populations were produced. The different generations of the two cross combinations were sown in screening nursery during *rabi* 2016-17 and 2017-18 at CSK HPKV-SAREC, Kangra. One row of each parent, two rows of F_1s, BC_1 and BC_2 and ten rows of F_2 were sown. Each genotype was raised in a 2.5 m long row with row to row and plant to plant spacings of 30×15 cm, respectively. The check varieties Jayanti and RCC-4 were planted as an indicator-cum infector rows after every 5 rows of test material. The recommended package and practices were followed to raise the crop. All the parents and crosses were exposed to natural epiphytotic field conditions at CSK HPKV-SAREC, Kangra, which is a hot spot for AB screening. The individual plants were scored for disease reaction on 0-9 scale (Plate 1). The assessment of the disease per plant was obtained by observing the intensity of lesions present on the leaves. For assessment of disease reaction of parents and different generations, ten leaves per selected plant were randomly taken from each generation to calculate Per cent Disease Index (PDI) by using the formula of McKinney (1923).

$$PDI = \frac{\text{Total sum of all numerical ratings}}{\text{Number of observations taken} \times \text{maximum disease score}} \times 100$$

The observations on Per cent Disease Index (PDI) with square root transformation were subjected to statistical analysis by following simple scaling tests (Mather, 1949) and Joint scaling test (Cavalli, 1952). The values of A, B, C and D scaling tests were used for testing of presence or absence of epistasis. In order to detect digenic interactions, six-parameter model was fitted by following generation mean analysis (Jinks and Jones, 1958 and Hayman, 1958).

Results and Discussion

All the parents and their crosses were evaluated under natural epiphytotic field conditions. In the cross Jayanti × P(4)2b, the F_1 appeared to be highly susceptible for the AB. However, when F_2 population involving 226 plants was screened, disease reaction varied from moderate to high susceptibility. Therefore, no concrete ratio could be fitted in this cross combination. In the cross Jayanti × EC-399300, only few F_1 seeds were obtained which were found to be sterile, hence, F_2 population was not available for disease screening. In the third cross *viz.,* RCC-4 × EC-399300, the six generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) were screened for AB reaction under natural epiphytotic field conditions at CSK HPKV-SAREC Kangra during *rabi* 2017-18. The disease reaction of F_2 population of this cross varied from moderate to high susceptibility as observed for Jayanti × P(4)2b cross. Therefore, no concrete ratio could be fitted in F_2 population of this cross. This indicated that AB resistance is not at least monogenic in nature.

Results of simple scaling tests showed significant estimates of all the scales except for scale B, indicating thereby the inadequacy of simple additive dominance model for the inheritance of AB. Significance of scale 'A' indicated the presence of all three types of non-allelic gene interactions *viz.,* additive × additive (i), additive × dominance (j) and dominance × dominance (l) types. The significance of scale 'C' provides a test largely of [l] and 'D' indicates (i) type of gene interaction. Significance of both 'C' and 'D' scales indicates both [i] and [l] type of gene interactions.

Perusal of the results (Table 2) indicated that a simple additive-dominance model was found to be inadequate for the variability observed in AB reaction. Therefore, six-parameter model that detects and estimates additive, dominance as well as epistatic effects was applied. Six-parameter model showed significant estimates of additive [d] and non-additive [h] effects as well as all the three types of epistasis *viz.,* additive × additive [i], additive × dominance [j] and dominance × dominance [l] types. The opposite signs of [h] and [l] indicated the persistence of duplicate type of gene interaction for the inheritance of AB resistance. Results were in conformity with the findings of Chaurasia and Bhajan (2015) who have reported significant estimates of additive [d], dominance [h] effects as well as all the three types of epistasis and duplicate type of epistasis in the inheritance of AB resistance in Indian mustard. However on the contrary, Krishnia *et al.* (2000) and Panja and De (2005) reported that resistance to this disease was mainly controlled by only additive genes. Therefore, it is evident that fixable as well as non-fixable types of gene effects are important in the genetic control of AB resistance. Presence of fixable effects in the form of [d] and [i] in all the crosses suggested

Table 1: Details of parents and their cross combinations studied for inheritance of Alternaria blight resistance

Sr. No.	Name of the parent	Name of species	Reaction to Alternaria blight
1	Jayanti	*B. carinata*	Highly susceptible
2	P(4)2b	*B. carinata*	Moderately susceptible
3	RCC-4	*B. juncea*	Highly susceptible
4	EC-399300	*B. juncea*	Moderately susceptible
		Crosses attempted	
1	Jayanti × P(4)2b	*B. carinata* × *B.carinata*	(HS) × (MR)
2	Jayanti × EC-399300	*B. carinata* × *B. juncea*	(HS) × (MR)
3	RCC-4 × EC-399300	*B. juncea* × *B. juncea*	(HS) × (MR)

Table 2: Estimates of scaling tests and genic effects for Alternaria blight resistance

Gene effects	RCC-4 × EC-399300
Scaling tests	Estimates
A	0.927* ± 0.251
B	-0.071 ± 0.278
C	-3.447* ± 0.307
D	2.151* ± 0.179

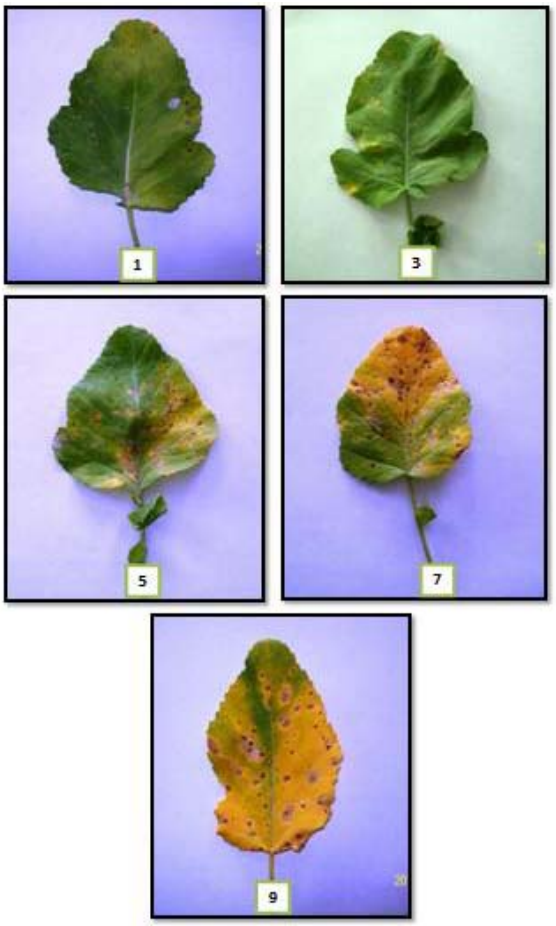

Plate 1: Alteranaria blight reaction on a scale of 0-9

the scope for enhancing the level of resistance for this disease through simple phenotypic selection.

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