INHERITANCE OF RESISTANCE TO ASCOCHYTA BLIGHT IN LENTIL

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ABSTRACT

Inheritance of foliar resistance to Ascochyta blight in lentil was studied using four resistant and one susceptible cultivars. Two dominant genes, one for resistance and one for moderate resistance are present in cv. ILL 5588. One dominant gene, which is allelic to the one for resistance in cv. ILL 5588 confers the resistance in cv. ILL 5684. One recessive gene is responsible for the resistance in cv. Laird. The resistance in cv. Indian head is under control of two recessive genes with additive effects.
Keywords: Ascochyta blight, *Ascochyta lentis*, inheritance model, *Lens culinaris*, resistance.

INTRODUCTION

Ascochyta blight, caused by *Ascochyta lentis*, is the major disease in many lentil (*Lens culinaris*) production areas (Muchlbauer et al. 1995). The disease has considerable effect on both seed quality and yield (Morrall & Sheppard 1981; Gossen & Morrall 1983). Although effective chemical control methods have been established, they are not economic. Breeding for improved host resistance is expected to be the most effective, efficient and environmentally friendly method of control (Erskine et al. 1994; Ye et al. 2000a).

Resistance sources were identified in both cultivated and wild lentil species (Ye et al. 2000a). The genetics of Ascochyta blight resistance in lentil has been studied using F_2 populations of different crosses, and was summarized by Ye et al. (2000a). In most of the studies, the sample sizes used were small, and only one segregating population of each cross was used to infer the inheritance model. These proposed models are inconclusive, and need to be confirmed. The purpose of this study is to investigate the inheritance of foliar resistance to Ascochyta blight in four resistant cultivars.

MATERIALS AND METHODS

Plant materials

Four resistant lentil cultivars (Indian head, Laird, ILL 5588 and ILL 5684), were crossed with one susceptible cultivar (Titore). To test the allelic relationships between resistance genes, the crosses Indian head × Laird, and ILL 5684 × ILL 5588 were also made. The F_1s were selfed to produce F_2 populations, and backcrossed to both susceptible and resistant parents to obtain BC1 and BC2, respectively.

Inoculum preparation and pathogenicity test

A pathogenic isolate of A. *lentis* was obtained from infected seeds of cv. Invincible (isolate Rakaia) following the procedure described by Ye et al. (2000b). Inoculum was prepared from 15 day old cultures using the method of Ye et al (2000b). The concentration of the spore suspension was measured using a haemocytometer and adjusted to 7.5×10^4 conidia/ml by dilution. Seedlings with four or five expanded leaves (15 days after sowing) growing in pots in a glasshouse were inoculated with the suspension (1 ml/seedling) using an atomizer. After inoculation, pots were kept in a controlled environment cabinet (18°C and high humidity) for 24 h, and then moved to a glasshouse bench for disease development to occur.

Data collection and analysis

Disease scores were recorded 7, 15 and 21 days after inoculation recorded according to a standard scoring procedure on a 1-9 scale developed by the International Centre for Agricultural Research in the Dry Areas. Based on the observed resistance levels of parental cultivars, individual plants were categorized into three categories: resistant (R) with ratings 1 and 3, moderately resistant (MR) with rating 5, and susceptible (S) with ratings 7 and 9. χ^2-statistic was used to test the goodness of fit of the observed ratio to expected ratios under various genetic models.

RESULTS

Ascochyta blight reactions of parental cultivars

Table 1 shows the blight reactions for each of the parental lines/cultivars in the order of their observed level of resistance. All plants of Indian head, ILL 5588 and ILL 5684 were scored 1 or 3, and are resistant. All plants of Laird were scored 5, and were moderately resistant. All plants of Titore were scored 7 or 9, and were susceptible. Thus potential bias caused by the presence of susceptible plants in resistant parent lines or the presence of resistant plants in the susceptible lines was avoided.

TABLE 1: Number of plants out of a total of 20 plants in each Ascochyta blight disease categories of the five parental cultivars (lines).

	Disease rating				
Cultivars/lines	1	3	5	7	9
Indian head	10	10			
ILL 5588	5	15			
ILL 5684		20			
Laird			20		
Titore				16	4

Inheritance model

In the F_2 progenies of Indian head × Titore, seven plants were resistant, 40 were moderately resistant, and 55 were susceptible. The simplest model was that two recessive genes conferred moderate resistance, and the accumulated effect of these two genes made plants resistant. The observed F_2 segregation ratio was close to the expected segregation ratio under this model. The segregation in the backcrosses also fitted this model well (Table 2). At this stage, these two recessive genes were designated Abr1 and Abr2, respectively.

In the cross Titore × ILL 5588, the segregation ratio of the F_2 gave a good fit of a model with one dominant gene for resistance and one dominant gene for moderate resistance (Table 2). Therefore, apart from the gene for resistance, there was another gene conferring moderate resistance. The backcross data supports this model (Table 2). The gene for resistance was designated AbR3 and that for moderate resistance was designated as AbR4.

In the F_2 generation of the cross Titore × ILL 5684, 98 individuals were resistant, and 30 were susceptible, which fitted the 3 resistant: 1 susceptible ratio. In the backcross with the resistant parent all plants were resistant, whereas in the backcross with the susceptible parent a segregation ratio close to 1:1 was observed. These ratios suggest that ILL 5684 has one dominant resistance gene. Because no plants scored 5 in both F_2 and the backcross with the susceptible parent, there was no gene conferring moderate resistance. The gene in 'ILL 5684' was designated AbR5 though it could be allelic to AbR3.

In the F_2 progenies of Titore × Laird, 25 plants were moderately resistant and 70 were

TABLE 2: Observed segregation patterns of reactions to *Ascochyta lentis* of lentil crosses, and χ^2 test for the goodness of fit of various inheritance models.

Cross (Inheritance model)	G[1]	R	MR	S	Expected ratio	P
Titore × Indian head	F_2	7	40	55	1:6:9	0.887
(Two additive recessive genes)	BC_1	-	-	59	-	-
	BC_2	16	30	13	1:2:1	0.851
'Titore' × 'ILL 5588'	F_2	73	20	7	12:3:1	0.893
(One dominant R, one dominant	BC_1	28	17	15	2:1:1	0.819
MR[2])	BC_2	55	-	-	-	-
Titore × ILL 5684	F_2	98		30	3:1	0.683
(One dominant R)	BC_1	35		30	1:1	0.535
	BC_2	60	-	-	-	
Titore × Laird	F_2	-	25	70	1:3	0.767
(One recessive MR)	BC_1	-	-	60	-	-
	BC_2	-	28	42	1:1	0.146

[1]G=Generation, [2]R=resistant, MR=moderately resistant, S=susceptible.

susceptible. This could be fitted to the 1 MR: 3 S ratio. The backcross with the resistant parent showed a 1 resistant: 1 susceptible ratio, while in the backcross with the susceptible parent all plants were susceptible. These segregation patterns suggested the presence of one recessive resistance gene in Laird, and it is designated Abr6 though it could be Abr1 or Abr2.

Six resistance genes were postulated in the four resistant cultivars but this assumes the genes are all different. However, it is possible that Abr6 is allelic to Abr1 or Abr2, while AbR5 may be allelic to AbR3.

In the F_2 progenies of ILL 5588 × ILL 5684, no plants were moderately resistant or susceptible. Therefore, the dominant gene in ILL 5684 (AbR5) is allelic to the dominant gene conferring resistance in ILL 5588 (AbR 3) (Table 3). The F_2 population of the cross of Laird × Indian head showed a 4 R: 33 MR: 27 S ratio (Table 3). Therefore, the recessive gene in Laird (Abr6) was not allelic to the recessive genes in Indian head (Abr 1 and Abr 2).

TABLE 3: Observed segregation patterns of Ascochyta blight reactions of lentil crosses made to test allelic relationships.

Cross	R[1]	MR	S	Expected ratio	P
Indian head × Laird	7	68	50	4:33:27	0.810
ILL 5684 × ILL 5588	100	0	0	-	-

[1]R = resistant, MR = moderately resistant, S = susceptible.

DISCUSSION

The results showed that ILL 5588 had two dominant genes, one for resistance and one for moderate resistance. Ford et al. (1999) proposed a one dominant gene model for the foliar resistance in ILL 5588. However, their data would support our model if they regarded plants scored 5 as moderately resistance. It is likely that the gene identified by Ford et al. (1999) was the one for resistance (data not shown). This highlights an important issue in inferring inheritance model for disease resistance using segregation analysis. To make

segregation analysis feasible it is necessary to set threshold values to group plants in segregating populations. Using different thresholds may lead to different inheritance models. A simple way to set thresholds is to use the resistance levels of the parents as a reference. All plants with resistance scores being in the resistance range of resistant parent are regarded as resistant and vice visa. The plants with scores that do not fall in the resistance ranges of either parent need to be classified carefully. In lentil breeding practice, plants scored 5 are regarded as moderately resistant. Therefore, we grouped plants with score 5 as moderately resistant. We are not aware of reported studies of the inheritance of foliar resistance to Ascochta blight of the other three resistant cultivars.

Most previous studies of the inheritance of lentil Ascochyta blight have used seed infection rate to develop the inheritance model. The lack of an established relationship between seed resistance and foliar resistance makes it difficult to compare our results with the reported results. Although all the four resistant cultivars used in the present study were resistant when seed infection rate was used to measure resistance, the inheritance models established for foliar resistance were different from those proposed for seed resistance. For instance, Tay (1989) suggested that two dominant complementary genes for resistance and one recessive gene for moderate resistance were responsible for seed resistance in ILL 5588. Two dominant complementary genes were proposed for seed resistance in ILL 5684 (Tay 1989), compared with one dominant gene for foliar resistance in our study. Similarly, two recessive genes with additive effect were responsible for foliar resistance in Indian head in this study, while two duplicated recessive genes were proposed for seed resistance (Andrahennadi 1997). Only for cultivar Laird, was the model for foliar resistance (one recessive gene) the same as that proposed for seed resistance (Andrahennadi 1997).

The dominant gene for resistance in ILL 5684 was found to be allelic to the dominant gene conferring resistance in ILL 5588. However, it should be pointed out that the resistance level of ILL 5684 was lower than that of ILL 5588.

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