

INHERITANCE OF SEEDLING BLACKLEG RESISTANCE IN CANOLA

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INTRODUCTION

There is little information on the inheritance of resistance to blackleg, caused by Leptosphaeria maculans (Desm.) Ces. and de Not. (Lm), in canola, Brassica napus L. ssp. oleifera. Earlier reports indicated that seedling resistance was either under polygenic (Cargeeg and Thurling, 1980) or monogenic control (Delwiche, 1980), where two linked dominant genes, Lm1 and Lm2, control resistance to different groups of Lm isolates. Resistance in cotyledons or adult plants of B. juncea (L.) Czern. is controlled by two genes interacting in dominant-recessive epistatic action (Keri, et al., 1990). Resistance in B. insularis Moris plants is controlled by two independent dominant genes (Mithen and Lewis, 1988).

As part of a long-term study of the inheritance of blackleg resistance in canola, data on the inheritance of seedling resistance, in B. napus cvs. Topas and Cyclone, and in B. juncea cv. Domo, to two Canadian Lm isolates, is presented here.

MATERIALS AND METHODS

Parental populations were selected for reaction to either Lm isolate 1190 or Lm isolate 1192, two Canadian canola isolates obtained from the Crucifer Genetics Co-operative. The isolates behave as Pathogenicity Group 2 (PG2) isolates based on their pathogenicity on cotyledons of B. napus cvs. Westar, Glacier and Quinta (Mengistu, et al., 1989).

Two true-breeding Lm1190 susceptible (S) lines (65, 66), derived from cv. Bingo, and two true-breeding Lm1190 resistant (R) lines (67, 68), derived from cv. Topas, were selected. Resistance on Topas cotyledons typically has an intermediate expression. The four lines were crossed in all 12 possible combinations, including reciprocals. The parental lines, ten F₁ and nine F₂ populations were challenged with Lm1190.

Two true-breeding Lm1192 S lines (98, 99), derived from cv. Westar, and two true-breeding Lm1192 R (44, 52) lines, derived from cv. Cyclone, were selected. Resistance on Cyclone cotyledons typically has an intermediate expression. Line 44 was reciprocally crossed with line 98 and line 52 was reciprocally crossed with line 99. The four F₁ and four F₂ populations, along with the parental lines, were challenged with Lm1192. Line 52 was also crossed with a rapid-cycling B. rapa population (CrGC1) and the F₂ population was challenged with Lm1192.

Two lines selected from B. juncea cv. Domo, a true-breeding Lm1192 R line and a true-breeding Lm1192 S line, were crossed. The F₁ and F₂ populations, along with the parental lines, were challenged with Lm1192. Resistance on cv. Domo cotyledons is strongly hypersensitive in expression.

Ten seedlings of each of the parental and F₁ populations, and 80 plants of each of the F₂ populations were grown with S control plants (cv. Westar) in peat-lite in 96-pot plastic multi-pots. Tests were conducted in a growth room at 20 °C and under continuous light (300 μmoles/sec/m² PAR). Plants were flooded daily with a fertilizer injection system that provided 75 ppm of a 15-16-17 water soluble fertilizer. Six-day-old cotyledons were wounded and inoculated using the Wisconsin method (Williams, 1985; Hill and Williams, 1988). Glucose (0.1%, w/v) and yeast extract (0.1%, w/v) were added to the inoculum to maximize pycnidiospore infectivity. Each cotyledon on each plant was inoculated once.

Seedling reactions were evaluated 10 days after inoculation. Plants showing strong, hypersensitive necrosis with limited lesion development (interaction phenotypes 1-4 - see Williams, 1985), were classified as R. Plants showing little or no hypersensitive necrosis (interaction phenotypes 5-9 - see Williams, 1985), were classified as S.

RESULTS

Bingo x Topas F₁ and F₂ data indicated that a single recessive resistance gene that interacts with Lm1190 was present in the Topas R lines. All F₁ plants were S, except for one plant (Table 1), indicating that resistance to Lm1190 was recessive. All of the F₂ populations, except one, segregated in a 1 R:3 S ratio (Table 2). The segregation of two of the F₂ populations also did not deviate significantly from a 3 R:13 S ratio. The pooled data fit a 1 R:3 S ratio, indicating the presence of a single recessive resistance gene. Heterogeneity among the F₂ populations for a 1:3 ratio was non-significant.

Topas x Topas F₁ and F₂ data indicated that two complementary dominant resistance genes that interact with Lm1190 were present in the Topas R lines. All F₁ plants were R (Table 1). Segregation in the F₂ populations fit a 9 R:7 S ratio (Table 3).

Cyclone x Westar F₁ and F₂ data indicated that Cyclone plants had one or two recessive resistance genes that interact with Lm1192. All F₁ plants were S (Table 4), indicating that resistance was recessive. The F₂ populations, derived from crosses between Cyclone line 44 and Westar line 98, segregated in a 1 R:3 S ratio (Table 5), indicating the presence of a single recessive resistance gene in line 44. The F₂ populations, derived from crosses between Cyclone line 52 and Westar line 99, segregated in a 7 R:9 S ratio (Table 6), indicating the presence of two recessive resistance genes in line 52. Line 52 x B. rapa F₂ plants segregated 22 R:57 S and fit a 1 R:3 S ratio (P=0.5-0.9). That suggests

that one of the resistant loci in line 52 may be present on the A genome while the other locus may be on the C genome.

B. juncea cv. Domo F₁ and F₂ segregation data indicated the presence of two dominant genes for resistance to Lm1192 in the resistant Domo line (Table 7).

DISCUSSION

One possible explanation for a 1 R:3 S segregation pattern in R x S F₂ populations with a 9 resistant:7 susceptible segregation in R x R populations derived from the same R lines, is that dominance of the resistance gene can be altered when the gene is in different genetic backgrounds, or when plants possessing the gene are exposed to high inoculum levels (Crute and Norwood, 1978; Norwood and Crute, 1984). In the Bingo x Topas background, resistance appeared to be recessive or possibly incompletely dominant, while in the Topas background, it appeared to be dominant with complementary gene interaction. Incomplete dominance of the resistance genes in heterozygotes could result in R interaction phenotypes in some genetic backgrounds and S interaction phenotypes in other backgrounds. This could produce segregations that are difficult to interpret.

In total, however, the data reported here indicate that the inheritance of intermediate resistance expression on B. napus cotyledons is simple and recessive, or possibly incompletely dominant. Strong hypersensitive cotyledon resistance in B. juncea is simple and dominant.

It is not known how the seedling reactions reported here correspond with reactions in the field. However, cvs. Cyclone and Topas are considered to be resistant-moderately blackleg resistant in Canada.

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Table 1. Reaction of Bingo and Topas lines and their F₁ populations to Lm1190.

Population	No. of Resistant Plants	No. of Susceptible Plants
65 (Bingo)	0	9
66 (Bingo)	0	10
67 (Topas)	10	0
68 (Topas)	9	0
65 x 67	0	10
65 x 68	0	10
66 x 67	1	5
66 x 68	0	3
67 x 65	0	10
67 x 66	0	10
68 x 65	0	10
68 x 66	0	10
67 x 68	10	0
68 x 67	10	0

Table 2. Reactions of Bingo x Topas F₂ populations to Lm1190.

Cross	No. of	No. of	Chi-square and significance					
	Resistant Plants	Susceptible Plants	1:3	1:3 _{adj}	P	3:13	3:13 _{adj}	P
65 x 67	26	54	2.40	2.22	>0.1	9.93	9.38	<0.005
67 x 65	21	57	0.15	0.12	>0.5	3.45	3.13	>0.05
66 x 67	23	57	0.60	0.52	>0.1	5.25	4.86	<0.05
67 x 66	21	59	0.07	0.05	>0.5	2.95	2.67	>0.1
65 x 68	29	51	5.40	5.11	<0.05	16.08	15.38	<0.001
68 x 65	13	67	3.26	3.52	>0.05	0.33	0.45	>0.5
68 x 66	26	54	2.40	2.23	>0.1	9.93	9.38	<0.005
Total (7 df)			14.28		<0.05	47.92		<0.001
Pooled (1 df)	159	399	3.63		>0.05	34.8		<0.001
Heterogeneity (6 df)			10.65		>0.05	13.12		<0.05

adj = Yate's chi-square adjusted for continuity.

P = probability of equaling or exceeding the tabular chi-square by chance.

Table 3. Reactions of Topas x Topas F₂ populations to Lm1190.

Cross	No. of	No. of	Chi-square and significance		
	Resistant Plants	Susceptible Plants	9:7	9:7 _{adj}	P
67 x 68	41	36	0.29	0.29	0.5-0.9
68 x 67	46	34	0.05	0.07	0.5-0.9
Total (2 df)			0.34		0.5-0.9
Pooled (1 df)	87	70	0.04		0.5-0.9
Heterogeneity (1 df)			0.30		0.5-0.9

adj = Yate's chi-square adjusted for continuity.

P = probability of equaling or exceeding the tabular chi-square by chance.

Table 4. Reactions of Cyclone and Westar lines and their F₁ populations to Lm1192.

Population	No. of Resistant Plants	No. of Susceptible Plants
44 (Cyclone)	10	0
52 (Cyclone)	10	0
98 (Westar)	0	10
99 (Westar)	0	10
44 x 98	0	10
98 x 44	0	10
52 x 99	0	10
99 x 52	0	10

Table 5. Reactions of Cyclone line 44 x Westar line 98 F₂ populations to Lm1192.

Cross	No. of Resistant Plants	No. of Susceptible Plants	Chi-square and significance		
			1:3	1:3 _{adj}	P
44 x 98	26	54	2.4	2.2	0.1-0.5
98 x 44	22	57	0.3	0.3	0.5-0.9
Total (2 df)			2.7		0.1-0.5
Pooled (1 df)	48	111	2.3		0.1-0.5
Heterogeneity (1 df)			0.4		0.5-0.9

adj = Yate's chi-square adjusted for continuity.

P = probability of equaling or exceeding the tabular chi-square by chance.

Table 6. Reactions of Cyclone line 52 x Westar line 99 F₂ populations to Lm1192.

Cross	No. of Resistant Plants	No. of Susceptible Plants	Chi-square and significance		
			7:9	7:9 _{adj}	P
52 x 99	38	42	0.5	0.4	0.5-0.9
99 x 52	35	45	0	0	1.0
Total (2 df)			0.5		0.5-0.9
Pooled (1 df)	73	87	0.2		0.5-0.9
Heterogeneity (1 df)			0.3		0.5-0.9

adj = Yate's chi-square adjusted for continuity.

P = probability of equaling or exceeding the tabular chi-square by chance.

Table 7. Reactions of resistant and susceptible lines, derived from B. juncea cv. Domo, and F₁ and F₂ populations, derived from crossing the two lines, to Lm1192.

Population	No. of Resistant Plants	No. of Susceptible Plants	Chi-square and significance	
			15:1 _{adj}	P
Resistant	10	0		
Susceptible	0	10		
F ₁	10	0		
F ₂	71	9	2.7	0.1-0.5

adj = Yate's chi-square adjusted for continuity.

P = probability of equaling or exceeding the tabular chi-square by chance.