

## Inheritance of Rust Resistance in Inbred Lines of *Vicia faba*

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### ABSTRACT

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Crosses between seven inbred faba bean (*Vicia faba*) lines, selected for uniform reaction against either isolate SP3 and/or SP51 of rust *Uromyces viciae-fabae*, revealed the presence of three different genes for resistance. Gene *Fr1* found in lines Ack-11 and 2N12-2 provides resistance only to isolate SP3. A second gene, *Fr2*, for resistance to rust isolate SP3 was

detected in lines Erf-1-4 and MB-1-2. An additional homozygous gene *Fr3* in MB-1-2 conditioned resistance only to isolate SP51. Certain heterozygous resistance genes present in Erf-1-4 and MB-1-2 had their segregation masked by the homozygous resistance genes.

Faba bean rust, which is caused by *Uromyces viciae-fabae* (Pers.) Schroet., is present in almost every area of the world where faba beans (*Vicia faba* L.) are grown (4). Since the introduction of this crop to western Canada in 1970, rust has been reported in both Manitoba and Saskatchewan (1,8). This disease has been shown to reduce yield substantially if infection occurs early and is severe (15).

Previous attempts to identify sources of rust resistance in faba beans have failed, either because of an absence of resistance (5) or a lack of cultivar uniformity (6,7). More recently, it has been demonstrated that the cultivars presently grown in Manitoba do not react uniformly to specific rust isolates (2). Cultivar heterogeneity is largely due to the partially outcrossing nature of this crop (9,13).

The genetics of rust resistance in faba beans has never been previously studied. However, similar studies have been conducted with outcrossing crops such as rye (*Secale cereale* L.) against *Puccinia graminis* f. sp. *tritici* Eriks. and E. Henn. and *P. graminis* f. sp. *secalis* Eriks. and E. Henn. (11,12), and in corn (*Zea mays* L.) to *Puccinia sorghi* Schw. (14). In these studies, crosses were made between inbred lines selected for uniform reaction to specific rust isolates.

The study reported here was undertaken to estimate the number of resistance genes acting against two distinct rust isolates in seven inbred faba bean lines. The identity of the resistance gene(s) in each of these lines was also determined.

### MATERIALS AND METHODS

Plants were grown in a mixture of clay loam, sand, and peat (2:1:1, v/v) in 15-cm-diameter clay pots in a rust-free greenhouse at 16-20 C under a 16-hr photoperiod.

Two single-pustule isolates of *U. viciae-fabae* (isolates SP3 and SP51) with very distinct virulence patterns were used in this study. Rust isolates were increased on plants of the rust susceptible line PI222128, with standard procedures to prevent contamination (3). Plants of PI222128 were grown under a plastic cap connected to a source of filtered air to prevent cross-contamination of isolates.

Plants from within faba bean lines and cultivars from various sources (Table 1) were selected and inbred for two or three generations until they appeared to react uniformly to one or both

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TABLE 1. Identity and source of inbred faba bean lines investigated for the inheritance of resistance to isolates of *Uromyces viciae-fabae*

Inbred line number <sup>a</sup>	Cultivar name or PI number <sup>b</sup>	Source
(2N12)-2	222129	Afghanistan
(2N40)-3-5	222128	Afghanistan
(2N62)-6	...	U.S.S.R.
(2N447)-7	...	Sudan
Ack-11	Ackerperle	Germany
Erf-1-4	Erfordia	Germany
MB-1-2	Maris Bead	England

<sup>a</sup>Number within brackets is the University of Manitoba accession number.

<sup>b</sup>PI = Plant Introduction.

TABLE 2. Rusting reaction of inbred faba bean lines to *Uromyces viciae-fabae* isolates SP3 and SP51

Inbred line	Rust isolate <sup>a</sup>	
	SP3	SP51
2N40-3-5	+	+
2N62-6	+	+
2N447-7	+	+
2N12-2	-	+
Ack-11	-	±
Erf-1-4	-	±
MB-1-2	-	-

<sup>a</sup>Symbols: + = susceptible; - = resistant; and ± = line did not react uniformly.

TABLE 3. Rusting infection types caused on faba bean by *Uromyces viciae-fabae*

Infection type	Cultivar reaction	Reaction class
0	No sign of infection	Immune
;	Fleck	Hypersensitive
1	Uredia minute and barely sporulating	Very resistant
2	Uredia small (about 0.5 mm in diameter)	Resistant
3	Uredia large (about 1.0 mm in diameter)	Susceptible
4	Uredia very large (>1.0 mm in diameter)	Very susceptible

TABLE 4. Segregation of rusting reactions caused by *Uromyces viciae-fabae* isolate SP3 in F<sub>2</sub> and backcross populations derived from crosses of inbred faba bean lines

Parentage	Parent reaction	Population	R:S		Chi-square prob.
			Observed	Expected	
2N62-6 × 2N447-7	S × S	F <sub>2</sub>	0:104	0:1	...
2N62-6 × 2N40-3-5	S × S	F <sub>2</sub>	0:100	0:1	...
Ack-11 × 2N447-7	R × S	F <sub>2</sub>	93:26	3:1	0.50–0.25
Ack-11 × 2N62-6	R × S	F <sub>2</sub>	142:42	3:1	0.50
2N62-6 × (Ack-11 × 2N62-6)	S × (R×S)	BC	37:14	1:1	<0.001
Ack-11 × (Ack-11 × 2N62-6)	R × (R×S)	BC	27:0	1:0	...
2N12-2 × 2N40-3-5	R × S	F <sub>2</sub>	75:27	3:1	0.75–0.50
2N12-2 × 2N62-6	R × S	F <sub>2</sub>	132:31	3:1	0.10
2N62-6 × (2N12-2 × 2N62-6)	S × (R×S)	BC	23:23	1:1	...
2N12-2 × (2N12-2 × 2N62-6)	R × (R×S)	BC	29:0	1:0	...
Ack-11 × 2N12-2	R × R	F <sub>2</sub>	230:0	1:0	...
Erf-1-4 × 2N40-3-5	R × S	F <sub>2</sub>	179:23	27:5	0.10
2N40-3-5 × (Erf-1-4 × 2N40-3-5)	S × (R×S)	BC	44:16	5:3	0.10–0.05
Erf-1-4 × (Erf-1-4 × 2N40-3-5)	R × (R×S)	BC	52:0	1:0	...
Erf-1-4 × 2N62-6	R × S	F <sub>2</sub>	166:29	27:5	0.90–0.75
2N62-6 × (Erf-1-4 × 2N62-6)	S × (R×S)	BC	32:14	5:3	0.50–0.25
Erf-1-4 × (Erf-1-4 × 2N62-6)	R × (R×S)	BC	44:0	1:0	...
MB-1-2 × 2N62-6	R × S	F <sub>2</sub>	178:21	27:5	0.05
2N40-3-5 × (MB-1-2 × 2N40-3-5)	S × (R×S)	BC	21:16	5:3	0.50–0.25
MB-1-2 × (MB-1-2 × 2N40-3-5)	R × (R×S)	BC	58:0	1:0	...
MB-1-2 × 2N62-6	R × S	F <sub>2</sub>	170:25	27:5	0.50–0.25
2N62-6 × (MB-1-2 × 2N62-6)	S × (R×S)	BC	26:19	5:3	0.75–0.50
MB-1-2 × (MB-1-2 × 2N62-6)	R × (R×S)	BC	27:0	1:0	...
Erf-1-4 × 2N12-2	R × R	F <sub>2</sub>	68:7	15:1	0.50–0.25
MB-1-2 × 2N12-2	R × R	F <sub>2</sub>	175:1	63:1	0.50–0.25
MB-1-2 × Erf-1-4	R × R	F <sub>2</sub>	315:0	1:0	...

TABLE 5. Segregation of rusting reactions to *Uromyces viciae-fabae* isolate SP51 in F<sub>2</sub> and backcross populations derived from crosses of inbred faba bean lines

Parentage	Parent reaction	R:S		Chi-square prob.
		Observed	Expected	
MB-1-2 × 2N40-3-5	R × S	177:22	27:5	0.10–0.05
2N40-3-5 × (MB-1-2 × 2N40-3-5)	S × (R×S)	27:7 <sup>a</sup>	5:3	0.05–0.025
MB-1-2 × (MB-1-2 × 2N40-3-5)	R × (R×S)	58:0	1:0	...
MB-1-2 × 2N62-6	R × S	168:27	27:5	0.50–0.25
2N62-6 × (MB-1-2 × 2N62-6)	S × (R×S)	22:23	5:3	0.10–0.05
MB-1-2 × (MB-1-2 × 2N62-6)	R × (R×S)	27:0	1:0	...
MB-1-2 × 2N12-2	R × R	146:30	27:5	0.75–0.50
MB-1-2 × Erf-1-4	R × R	289:26	27:5	<0.001

<sup>a</sup>Some plants damaged.

isolates. Of 17 lines initially tested, seven inbred lines were obtained that reacted uniformly to at least one isolate (Table 2). All resistant host-isolate combinations conditioned an immune response, except the MB-1-2 against SP3 combination, which produced a type 1 infection (Table 3). Reciprocal crosses were made for all combinations of these lines except Ack-11 and 2N447-7, which were not included in all crosses because of poor seed production. In addition, backcrosses were made for crosses between resistant and susceptible parents. Three weeks after emergence, F<sub>2</sub> and backcross populations were inoculated with the less virulent isolate, SP3. Uredospores suspended in a light oil (Soltrol 170, Philips Petroleum Co., Special Products Div., Borger, TX 79007) were applied to the two youngest sets of fully expanded leaves with a fine nylon brush. After the leaves had dried, the plants were maintained

for 24 hr in a chamber at 100% relative humidity and were then transferred to a growth room with a 16-hr photoperiod and a 16–20 C diurnal temperature cycle. Eleven days after inoculation, plants were examined for infection type (Table 3) and infected leaves were removed. Progeny from crosses involving parents with uniform resistance to rust isolate SP51 were then inoculated with SP51 and handled as described for SP3. Parental lines were included in all tests to ensure that rust isolates were free of contaminants.

Results from F<sub>2</sub> families of the same crosses were pooled only after chi-square tests for homogeneity had shown them to behave the same (10). Chi-square tests for goodness of fit were used to analyze all F<sub>2</sub> and backcross data.

## RESULTS

The F<sub>2</sub> populations from crosses of the susceptible parent 2N62-6 to each of 2N447-7 and 2N40-3-5 were uniformly susceptible to isolate SP3 (Table 4). The results from crosses of Ack-11 or 2N12-2 with the susceptible lines 2N62-6 and 2N40-3-5 segregated in a ratio of 3 resistant:1 susceptible to isolate SP3. Backcrosses involving 2N12-2 to 2N62-6 produced a good fit of a ratio of 1 resistant:1 susceptible but the similar backcross involving Ack-11 to 2N62-6 produced a poor fit of a 1:1 ratio. Overall, the results suggest that Ack-11 and 2N12-2 carry a single homozygous gene for resistance to isolate SP3. Crosses between Ack-11 and 2N12-2 produced only resistant F<sub>2</sub> plants, indicating that they carry the same gene for resistance against SP3.

The F<sub>2</sub> data from crosses of Erf-1-4 to either 2N40-3-5 or 2N62-6 consistently fit a ratio of 27 resistant:5 susceptible to isolate SP3 (ie, half of the F<sub>1</sub> plants were *Fr2fr2Rr* and half were *Fr2fr2rr*). This indicates that resistance is controlled by two dominant genes, only one of which is homozygous. The fairly good fit of a ratio of 5 resistant:3 susceptible for data from backcrosses to the susceptible parent confirms this. F<sub>2</sub> populations from crosses of Erf-1-4 to

TABLE 6. Relation of rust resistance in faba bean to isolates SP3 and SP51 of *Uromyces viciae-fabae* in F<sub>2</sub> populations derived from MB-1-2 × susceptible crosses

Parentage	No. of plants:				Expected ratio	Chi-square prob.
	not infected	infected				
		by SP3	by SP51	by both isolates		
MB-1-2 × 2N40-3-5	158	20	18	3	93:15:15:5	0.25-0.10
MB-1-2 × 2N62-6	150	20	20	7	93:15:15:5	0.75

TABLE 7. Proposed genotypes of inbred faba bean lines based on responses to isolates SP3 and SP51 of *Uromyces viciae-fabae*

Host	Proposed genotypes <sup>a</sup>
2N447-7	<i>fr1fr1, fr2fr2, fr3fr3, rr</i>
2N40-3-5	<i>fr1fr1, fr2fr2, fr3fr3, rr</i>
2N62-6	<i>fr1fr1, fr2fr2, fr3fr3, rr</i>
2N12-2	<i>Fr1Fr1, fr2fr2, fr3fr3, rr</i>
Ack-11	<i>Fr1Fr1, fr2fr2, fr3fr3, Rr</i>
Erf-1-4	<i>fr1fr1, Fr2Fr2, fr3fr3, Rr</i>
MB-1-2	<i>fr1fr1, Fr2Fr2, Fr3Fr3, Rr</i>

<sup>a</sup> *Fr1 Fr2* provides resistance against isolate SP3; *Fr3* provides resistance against isolate SP51 only; and *Rr* and *rr* represents unidentified resistance genes.

2N12-2 segregated in a ratio of 15 resistant:1 susceptible, indicating that the homozygous genes for resistance to SP3 in these lines are different. The good fit of a 15:1 ratio for crosses of Erf-1-4 to 2N12-2 indicated that the recessive allele of the heterozygous gene in Erf-1-4 might be homozygous in certain plants. The homozygous genes for resistance to SP3 in Erf-1-4 and MB-1-2 appear to be the same because crosses between these two lines produced only resistant F<sub>2</sub> progeny.

Certain F<sub>2</sub> and backcross progeny from crosses involving Ack-11, 2N12-2, and Erf-1-4 to susceptible lines were found to be resistant to SP51. This resistance might be due to the presence of heterozygous genes for resistance in some of these lines. The lack of uniformity for the reactions of Ack-11 and Erf-1-4 to SP51 (Table 2) and the heterogeneity found between F<sub>2</sub> families of certain crosses (Table 5) seem to support this. It could also be that some of these plants escaped infection.

Data from crosses of MB-1-2 to either 2N40-3-5 or 2N62-6 best fit a ratio of 27 resistant:5 susceptible for both isolates. The combined data against both isolates produced a good fit of a 93:15:15:5 ratio (ie, half of the F<sub>1</sub> plants were *Fr2fr2, Fr3fr3, Rr* and half were *Fr2fr2, Fr3fr3, rr*) (Table 6). This suggests that MB-1-2 carries one homozygous gene for resistance only to SP3 and also a homozygous gene for resistance only to SP51 and a third heterozygous gene for resistance to both isolates.

## DISCUSSION

Crosses between different resistant lines allowed three different homozygous genes for resistance to be identified (Table 7). The lines 2N12-2 and Ack-11 carry the same dominant gene for resistance to isolate SP3, which has been designated *Fr1*. A second gene for resistance to SP3, found in Erf-1-4 and MB-1-2, has been designated *Fr2*. MB-1-2 carries an additional homozygous dominant gene, *Fr3*, which provides resistance only to isolate SP51.

In addition to these homozygous genes, other heterozygous resistance genes are present in some of these lines. Heterozygous genes in Erf-1-4 for resistance to SP3 and in MB-1-2 for resistance to both rust isolates were masked by the homozygous resistance genes in these lines.

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