A Single Recessive Gene for Resistance to the Root-Knot Nematode (Meloidogyne javanica) in Cucumis sativus var. hardwickii

S. A. Walters, T. C. Wehner, and K. R. Barker

Resistance to the root-knot nematode (Meloidogyne javanica) was identified in the Cucumis sativus var. hardwickii line LJ 90430. Parents, F₁, F₂, and BC, to both parents of a cross between Sumter (Cucumis sativus var. sativus) and LJ 90430 were evaluated in two greenhouse experiments to determine genetics of resistance to M. javanica. All F₁ progeny were susceptible, and segregation ratios in the F₂ resulted in 1 resistant:3 susceptible. Backcross progeny to the susceptible parent were susceptible, and the BC, to the resistant parent segregated 1 resistant:1 susceptible. Reciprocal crosses did not differ and therefore showed no evidence of maternal or cytoplasmic effects. Results from the crosses of several inbreds (Addis, Gy 14, Gy 57u, Poinsett 87, and Sumter) with LJ 90430 indicated that use of those five different genetic backgrounds had no influence on gene expression. The five F₂ families segregated in a 1 resistant:3 susceptible ratio. The five BC, (to LJ 90430) families segregated in a 1 resistant:1 susceptible ratio. F₂ families were developed from resistant and susceptible F₁ plants using the five inbreds. Resistant F₂ families produced progeny that were all resistant, and susceptible F₂ families fit a ratio of 1 susceptible:2 segregating. Thus, resistance to M. javanica is conferred by a single recessive gene for which we propose the symbol mj.

Root knot, caused by several species of root-knot nematodes (Meloidogyne spp.), is an important disease of cucumber (Cucumis sativus var. sativus L.) in areas of the world where it is grown (Netscher and Sikora 1990). North Carolina is a leading producer of field-grown cucumbers in the United States, ranking second in the production of picking cucumbers (USDA 1993) and fourth in the production of slicing cucumbers (Jewell 1987). Economically, root knot is the most damaging disease of cucumbers in North Carolina (St. Amand and Wehner 1991). The use of resistant cultivars would be the most economical and environmentally acceptable way to control this disease. However, no cultivars are available that have resistance to the most important root-knot nematodes in cucumber producing areas: M. incognita (Kofoid and White) Chitwood and M. arenaria (Neal) Chitwood in subtropical areas, and M. javanica (Treub) Chitwood in tropical areas. Walters et al. (1993) evaluated the U.S. cucumber germplasm collection and found only the Cucumis sativus var. hardwickii (R.) Alef. line LJ 90430 to be highly resistant to M. javanica.

An understanding of the inheritance of resistance to M. javanica in LJ 90430 is essential for the development of resistant cultivars. The mode of inheritance of resistance in cucumber to any species of root-knot nematode is not known. Thus, the objective of this study was to determine the genetics of resistance to M. javanica in LJ 90430.

Material and Methods

Germplasm

Cucumis sativus var. hardwickii line LJ 90430 was used as the resistant parent in crosses with susceptible Cucumis sativus var. sativus Sumter. Sumter, an inbred developed at Clemson University (Clemson, South Carolina), was a commonly used pickling cucumber in the previous two decades in the United States. LJ 90430 is difficult to work with because seeds often germinate slowly and at a low percentage. However, two treatments were used to overcome seed coat dormancy and improve germination: soaking the seeds overnight in acetone (Amritphale et al. 1993), or soaking the seeds in water overnight, peeling off and discarding the seed coats, and planting the seeds (Weston et al. 1992).

Resistance to M. javanica in LJ 90430 was reported in a previous study (Walters et al. 1993). Reciprocal F₁, F₂, and BC, (to the susceptible and resistant parents) crosses between Sumter and LJ 90430 were made in the greenhouse using standard pollination techniques for cucumber (Whitaker and Davis 1962). Crosses between LJ 90430 and five cucumber inbreds (Addis, Sumter, Poinsett 87, Gy 57u, and Gy 14) were made in the greenhouse to produce seeds of the F₁, and BC, (to LJ 90430) generations.

Inoculation and Rating of Resistance

The following methods were used for nematode inoculation: (1) two seeds were sown in a 15 cm diameter (1,750 cm² volume) clay pot containing a sterile, moist loamy soil (80% sand, 15% silt, and 5% clay); (2) plants were thinned to one per pot at the second true leaf stage; (3) Meloidogyne javanica inoculum was produced in the greenhouse on Rutgers tomato (Lycopersicon esculentum Mill.); (4) nematode eggs were extracted from roots for 4 min using a 1% NaOCl solution according to the method of Byrd et al. (1972); and (5) each plant was inoculated 2 weeks after planting (second true leaf stage) with 5,000 eggs that were applied to roots using a suspension of eggs in water poured onto the soil. The first two methods were different for the split-root and are explained under the materials and methods for that test.

Plants were harvested 10 weeks after inoculation (12 weeks after planting) and rated for the percentage (0–100%) of the root system galled (Barker et al. 1986). Plants were classified as resistant (<35% of root system galled) or susceptible (≥35% of root system galled) based upon the frequency of F₂ plants infected with M. javanica (Figure 1). For the split-root test, the numbers of egg masses on roots from each pot were counted using the method of Hadassegada and Sasser (1982), and plants were rated as either resistant (egg masses < 15 per root system) or susceptible (egg masses > 15 per root system). Goodness-of-fit of observed to expected segregation ratios in the F₂ and backcross progeny were determined by chi-square tests.

Inheritance

The F₁, F₂, and BC, (to the susceptible and resistant parents) of the cross Sumter × LJ 90430 (no reciprocals), as well as the parents, were evaluated in a split-root test. Seeds were initially sown in flats containing vermiculite, and at the appearance of the first true leaf, the root system of each plant was split into three separate 10 cm diameter (450 cm³ volume) plastic pots that contained a sterile, moist loamy sand soil (80% sand, 15% silt, and 5% clay). The three pots per plant as well as the single plant plots were arranged in a completely random design. Each pot containing one-third of the root system of a plant was inoculated with one of three root-knot nematodes, but only the M. javanica data will be presented here. Plants were watered and fertilized twice daily using drip irrigation with fertilizer injection.

The number of egg masses was used to confirm segregation ratios obtained from the gall index rating for the split-root greenhouse test. After rating for gall index
(percentage of roots galled), roots were placed in a solution of tap water and 0.15 g/l of Phloxine B (Sigma Chemical Company, St. Louis, Missouri) for 20 min, then rinsed with tap water to remove residual stain (Hartman and Sasser 1995). The numbers of egg masses on roots from each pot were counted using the method of Hadssoegard and Sasser (1982), and plants were rated as either resistant (egg masses ≤ 15 per root system) or susceptible (egg masses > 15 per root system). The numbers of egg masses were transformed using log_{10} (number of egg masses + 1) and correlated with the gall index rating (%). Chi-square tests were used to determine goodness-of-fit from observed to expected segregation ratios in the F₂ and BC₁ generations for gall index and number of egg masses.

### Cytoplasmic/Maternal

Parental, F₁, F₁₀, F₂, F₉, BC₁ (to each parent) and BC₁₀ (to each parent) were evaluated in a greenhouse test to determine if any paternal, maternal, or cytoplasmic effects were present for *M. javanica* resistance. Plants were grown in 15 cm diameter (1,750 cm³ volume) clay pots containing the same soil mixture as used in the previous test. Pots were arranged in a completely random design. Plants were watered twice daily and fertilized once weekly using Peter's® 2-0-20 (N-P-K) (W. R. Grace & Co., Fogelsville, Pennsylvania).

### Effect of Genetic Background

A greenhouse test was conducted to determine whether genetic background affected the expression of resistance. Forty F₂ plants from each of five families (Addis × L. 90430, Sumter × L. 90430, Poinsett 87 × L. 90430, Cy 754 × L. 90430, and Cy 14 × L. 90430) and 20 BC₁ (to L. 90430) were evaluated for resistance to *M. javanica*. Families were arranged in the greenhouse in a completely random design. Individual F₂ plants from the five families were self-pollinated to obtain seeds of the F₃ generation, which were needed to complete the next test.

Fifteen F₃ families were developed by self-pollinating 5 resistant and 10 susceptible F₂ plants in five genetic backgrounds: Addis × L. 90430, Sumter × L. 90430, Poinsett 87 × L. 90430, Cy 754 × L. 90430, and Cy 14 × L. 90430. Eight plants from each F₃ family were evaluated for *M. javanica* resistance. F₃ families from each cross were arranged in a completely random design in the greenhouse.

If a single recessive gene is responsible for the resistance, all progeny from a self-pollinated, resistant F₁ plant (F₂ resistant family) should be entirely resistant. Progeny from a self-pollinated susceptible F₁ plant (F₂ susceptible family) should be either entirely susceptible or segregating (1 resistant:3 susceptible). F₃ families developed from susceptible F₂ plants should be present in a 1 susceptible:2 segregating ratio.

### Results and Discussion

#### Inheritance

The susceptible parent Sumter had a gall index rating (percentage of roots galled) that averaged 58. The resistant parent, L. 90430, had a mean gall index rating of 5. The cross of resistant L. 90430 with susceptible Sumter produced F₁ progeny that were susceptible to *M. javanica* (Table 1), indicating that all F₁ plants had more than 35% of their roots galled. The segregation observed in the F₂ generation indicated simple inheritance with 1 resistant:3 susceptible, with resistance determined by a single recessive gene. To verify the F₂ ratios, F₁ plants were backcrossed to Sumter or L. 90430. The BC₁ progeny to Sumter were all susceptible (all had more than 35% of their roots galled) and BC₁ to L. 90430 progeny segregated 1 resistant:1

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**Table 1. Segregation for resistance (utilizing both gall indices and numbers of egg masses) to *Meloidogyne javanica* in progenies from crosses (no reciprocals) between susceptible *Cucumis sativus* var. *seitum* Sumter and resistant *Cucumis sativus* var. *hardwickii* line L. 90430**

<table>
<thead>
<tr>
<th>Generation</th>
<th>No. observed (R5)</th>
<th>No. expected (R5)</th>
<th>Fitted ratio (R5)</th>
<th>χ²</th>
<th>P</th>
</tr>
</thead>
<tbody>
<tr>
<td>Gall index</td>
<td>Su</td>
<td>0.0</td>
<td>0.10</td>
<td>All S</td>
<td>—</td>
</tr>
<tr>
<td></td>
<td>L. 90430 (P₁)</td>
<td>0.0</td>
<td>0.10</td>
<td>All R</td>
<td>—</td>
</tr>
<tr>
<td></td>
<td>F₁</td>
<td>0.0</td>
<td>0.10</td>
<td>All S</td>
<td>—</td>
</tr>
<tr>
<td></td>
<td>F₂</td>
<td>23</td>
<td>24</td>
<td>1:1</td>
<td>0.06</td>
</tr>
<tr>
<td></td>
<td>BC₁ × F₂</td>
<td>0.19</td>
<td>0.19</td>
<td>All S</td>
<td>—</td>
</tr>
<tr>
<td></td>
<td>BC₁ × F₂</td>
<td>0.2</td>
<td>0.2</td>
<td>1:1</td>
<td>0.22</td>
</tr>
<tr>
<td>Egg mass number</td>
<td>Su</td>
<td>0.0</td>
<td>0.10</td>
<td>All S</td>
<td>—</td>
</tr>
<tr>
<td></td>
<td>L. 90430 (P₁)</td>
<td>0.0</td>
<td>0.10</td>
<td>All R</td>
<td>—</td>
</tr>
<tr>
<td></td>
<td>F₁</td>
<td>0.0</td>
<td>0.10</td>
<td>All S</td>
<td>—</td>
</tr>
<tr>
<td></td>
<td>F₂</td>
<td>23</td>
<td>24</td>
<td>1:1</td>
<td>0.06</td>
</tr>
<tr>
<td></td>
<td>BC₁ × F₂</td>
<td>0.19</td>
<td>0.19</td>
<td>All S</td>
<td>—</td>
</tr>
<tr>
<td></td>
<td>BC₁ × F₂</td>
<td>0.2</td>
<td>0.2</td>
<td>1:1</td>
<td>0.22</td>
</tr>
</tbody>
</table>

* Gall index: resistant <35% of roots galled, susceptible >35% of roots galled. Egg mass number: resistant ≤15 egg masses/root system, susceptible >15 egg masses/root system. F₁ = susceptible parent and F₂ = resistant parent.

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Table 2. Segregation in progenies from crosses between susceptible *C. sativus* var. *sativus* Sumter and resistant *C. sativus* var. *hardwickii* line LJ 90430 and their reciprocal crosses after inoculation with *Melogeton* *javanica*.

<table>
<thead>
<tr>
<th>Generation</th>
<th>No. observed (RS)</th>
<th>No. expected (RS)</th>
<th>Fitted ratio (RS)</th>
<th>$\chi^2$</th>
<th>$P$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sumter (P$_s$)</td>
<td>0:50</td>
<td>0:50</td>
<td>All S</td>
<td>—</td>
<td>—</td>
</tr>
<tr>
<td>LJ 90430 (P$_r$)</td>
<td>50:8</td>
<td>56:0</td>
<td>All R</td>
<td>—</td>
<td>—</td>
</tr>
<tr>
<td>F$_1$ (P$_s$ × P$_r$)</td>
<td>6:75</td>
<td>6:75</td>
<td>All S</td>
<td>—</td>
<td>—</td>
</tr>
<tr>
<td>F$_1$ (P$_s$ × P$_r$)</td>
<td>6:75</td>
<td>6:75</td>
<td>All S</td>
<td>—</td>
<td>—</td>
</tr>
<tr>
<td>F$_1$ (P$_s$ × P$_r$)</td>
<td>66:73</td>
<td>58:175</td>
<td>1:3</td>
<td>0.09</td>
<td>0.77</td>
</tr>
<tr>
<td>F$_1$ (P$_s$ × P$_r$)</td>
<td>51:151</td>
<td>51:151</td>
<td>1:3</td>
<td>0.10</td>
<td>0.75</td>
</tr>
<tr>
<td>F$_2$ (P$_s$ × P$_r$)</td>
<td>113:324</td>
<td>109:328</td>
<td>1:3</td>
<td>0.20</td>
<td>0.68</td>
</tr>
<tr>
<td>BC$_1$ (P$_s$ × P$_r$) × P$_s$</td>
<td>0:32</td>
<td>6:62</td>
<td>All S</td>
<td>—</td>
<td>—</td>
</tr>
<tr>
<td>BC$_1$ (P$_s$ × P$_r$) × P$_s$</td>
<td>0:73</td>
<td>6:73</td>
<td>All S</td>
<td>—</td>
<td>—</td>
</tr>
<tr>
<td>BC$_1$ (P$_s$ × P$_r$) × P$_r$</td>
<td>36:32</td>
<td>34:34</td>
<td>1:1</td>
<td>0.24</td>
<td>0.55</td>
</tr>
<tr>
<td>BC$_1$ (P$_s$ × P$_r$) × P$_r$</td>
<td>35:17</td>
<td>36:36</td>
<td>1:1</td>
<td>0.06</td>
<td>0.82</td>
</tr>
<tr>
<td>BC$_1$ to P$_r$ (pooled)</td>
<td>71:99</td>
<td>70:70</td>
<td>1:1</td>
<td>0.03</td>
<td>0.86</td>
</tr>
</tbody>
</table>

* $\chi^2$ value for 1 degree of freedom.

— Gall index: resistant ≤35% of roots galled, susceptible >35% of roots galled. P$_s$ = susceptible parent and P$_r$ = resistant parent.

Susceptible (with similar numbers of plants found in the <20% and >35% range, and none found in the 21–35% range). The two BC$_1$ families reacted as expected if resistance were determined by a single recessive gene. Figure 1 shows the distribution of progeny infected with *M. javanica* from the F$_2$ and BC$_1$ to LJ 90430 generations. For F$_2$ plants, two distinct classes were formed with plants segregating in a 1 resistant:3 susceptible ratio. Observing plants of the BC$_1$ to LJ 90430 generation, two classes were formed with equal numbers of plants in each class.

Plants of parental, F$_1$, F$_2$, and BC$_1$ generations of Sumter × LJ 90430 were classified similarly using egg masses as they were using the gall index rating (Table 1). For numbers of egg masses, Sumter ranged from 75 to 175 with an average of 104. The resistant parent, LJ 90430, ranged from 0 to 6 with a mean of 2. All F$_1$ plants had egg mass numbers greater than 25. F$_2$ plants segregated in a 1 resistant:3 susceptible ratio using 15 egg masses as the cutoff point between the two classes. The backcross to Sumter produced plants that had egg masses ranging from 18 to 925. The plants from the backcross to LJ 90430 all had low numbers of egg masses, ranging from 0 to 10.

The correlation between gall index and number of egg masses was high (r = 0.73, $P = .0001$) when the numbers of egg masses were transformed using log$_e$ (number of egg masses + 1). Therefore, the number of egg masses would be an excellent measure of resistance. The criterion we used of ≤15 and >15 egg masses for designating resistant and susceptible classes, respectively, was valid since it produced results similar to the gall index data.

**Cytoplasmic/Maternial**

Progeny of reciprocal crosses reacted similarly in the F$_1$ and F$_2$ generations, so there were no maternal or paternal, or cytoplasmic effects for *M. javanica* resistance (Table 2). Data from the reciprocal crosses were pooled for the F$_2$ and BC$_1$ to LJ 90430 and are shown in Figure 2. The data indicated that resistant and susceptible F$_2$ plants were in two distinct classes, with the resistant plants in the smaller class. Also, the BC$_1$ to LJ 90430 plants form two distinct classes with similar numbers of plants in each class. This again indicated that a single recessive gene was responsible for the resistance.

**Effect of Genetic Background**

Crosses of five cucumber inbreds (Addis, Poinsett 87, Gy 14, Gy 57u, and Sumter) with LJ 90430 confirmed that the inheritance of resistance to *M. javanica* was conditioned by a single recessive gene. F$_2$ from all crosses segregated in a ratio of 1 resistant:3 susceptible, and progeny of the BC$_1$ (to LJ 90430) segregated in a ratio of 1 resistant:1 susceptible (Table 3). Genetic background had no influence on the inheritance of resistance, and thus the gene was expressed in a stable manner and was not affected by epistatic interactions.

Resistant F$_2$ plants that were self-pollinated to make F$_3$ families (F$_{3k}$ resistant families) produced progeny that were entirely resistant (Table 4), with gall indices ranging from 0 to 25%. Susceptible F$_{3k}$ families fit the expected ratio of 1 susceptible:2 segregating (Table 4). The five crosses had the same pattern (Table 4), indicating that genetic background had no influence on the expression of the gene. It was apparent from F$_2$ family data that resistance to *M. javanica* in the *C. sativus* var. *hardwickii* line LJ 90430 was consistent with the hypothesis that resistance was controlled by a single recessive gene.

**New Gene for Resistance**

The results obtained from all tests indicated that resistance to *M. javanica* in LJ 90430 was controlled by a single recessive gene. The pooled F$_2$ data from all experiments showed 183 plants resistant and 550 susceptible (conforming exactly to the expected numbers for a 3:1 ratio; $x^2 = 0.0, P = 1.0$). The pooled data for the BC$_1$ to LJ 90430 had 130 resistant and 127 suscep-
Table 3. Evaluation of the $m$ gene in five cucumber backgrounds utilizing segregation ratios in the $F_2$ and BC, to LJ 90430 generation

<table>
<thead>
<tr>
<th>Generation</th>
<th>No. observed (R:S)</th>
<th>No. expected (S:S)</th>
<th>Fitted ratio (R:S)</th>
<th>$\chi^2$</th>
<th>P</th>
</tr>
</thead>
<tbody>
<tr>
<td>$F_2$</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>(Addis $\times$ LJ 90430)</td>
<td>8:32</td>
<td>10:30</td>
<td>1:3</td>
<td>0.53</td>
<td>.48</td>
</tr>
<tr>
<td>(Sunter $\times$ LJ 90430)</td>
<td>10:30</td>
<td>10:30</td>
<td>1:3</td>
<td>0.69</td>
<td>.00</td>
</tr>
<tr>
<td>(Gy 14 $\times$ LJ 90430)</td>
<td>8:32</td>
<td>10:30</td>
<td>1:3</td>
<td>0.53</td>
<td>.48</td>
</tr>
<tr>
<td>(Poinsett 87 $\times$ LJ 90430)</td>
<td>13:27</td>
<td>10:30</td>
<td>1:3</td>
<td>1.20</td>
<td>.28</td>
</tr>
<tr>
<td>(Gy 57u $\times$ LJ 90430)</td>
<td>8:32</td>
<td>10:30</td>
<td>1:3</td>
<td>0.53</td>
<td>.48</td>
</tr>
<tr>
<td>Pooled</td>
<td>47:153</td>
<td>50:150</td>
<td>1:1</td>
<td>0.24</td>
<td>.65</td>
</tr>
<tr>
<td>BC, to recessive parent</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>(Addis $\times$ LJ 90430)</td>
<td>11:2</td>
<td>10:10</td>
<td>1:1</td>
<td>0.20</td>
<td>.68</td>
</tr>
<tr>
<td>(Sunter $\times$ LJ 90430)</td>
<td>9:11</td>
<td>10:10</td>
<td>1:1</td>
<td>0.20</td>
<td>.68</td>
</tr>
<tr>
<td>(Gy 14 $\times$ LJ 90430)</td>
<td>12:8</td>
<td>10:10</td>
<td>1:1</td>
<td>0.80</td>
<td>.40</td>
</tr>
<tr>
<td>(Poinsett 87 $\times$ LJ 90430)</td>
<td>9:11</td>
<td>10:10</td>
<td>1:1</td>
<td>0.20</td>
<td>.68</td>
</tr>
<tr>
<td>(Gy 57u $\times$ LJ 90430)</td>
<td>11:9</td>
<td>10:10</td>
<td>1:1</td>
<td>0.20</td>
<td>.68</td>
</tr>
<tr>
<td>Pooled</td>
<td>52:48</td>
<td>50:50</td>
<td>1:1</td>
<td>0.16</td>
<td>.71</td>
</tr>
</tbody>
</table>

*Gal index: resistant ≤35% of roots galled, susceptible ≥35% of roots galled.

Table 4. Segregation of resistance to Meloidogyne javanica in $F_2$ families developed from self-pollination of resistant and susceptible $F_1$ plants from five crosses

<table>
<thead>
<tr>
<th>Family</th>
<th>$F_1$ parent reaction</th>
<th>$F_2$ observed</th>
<th>Fitted ratio (R:S)</th>
<th>$\chi^2$</th>
<th>P</th>
</tr>
</thead>
<tbody>
<tr>
<td>Addis $\times$ LJ 90430</td>
<td>R*</td>
<td>5</td>
<td>0</td>
<td>0:2</td>
<td>.05</td>
</tr>
<tr>
<td>S*</td>
<td></td>
<td>0</td>
<td>3</td>
<td>1:0</td>
<td>.05</td>
</tr>
<tr>
<td>Sumter $\times$ LJ 90430</td>
<td>R*</td>
<td>5</td>
<td>0</td>
<td>0:2</td>
<td>.05</td>
</tr>
<tr>
<td>S*</td>
<td></td>
<td>0</td>
<td>3</td>
<td>1:0</td>
<td>.05</td>
</tr>
<tr>
<td>Gy 14 $\times$ LJ 90430</td>
<td>R*</td>
<td>5</td>
<td>0</td>
<td>0:2</td>
<td>.05</td>
</tr>
<tr>
<td>S*</td>
<td></td>
<td>0</td>
<td>3</td>
<td>1:0</td>
<td>.05</td>
</tr>
<tr>
<td>Poinsett 87 $\times$ LJ 90430</td>
<td>R*</td>
<td>5</td>
<td>0</td>
<td>0:2</td>
<td>.05</td>
</tr>
<tr>
<td>S*</td>
<td></td>
<td>0</td>
<td>3</td>
<td>1:0</td>
<td>.05</td>
</tr>
<tr>
<td>Gy 57u $\times$ LJ 90430</td>
<td>R*</td>
<td>5</td>
<td>0</td>
<td>0:2</td>
<td>.05</td>
</tr>
<tr>
<td>S*</td>
<td></td>
<td>0</td>
<td>3</td>
<td>1:0</td>
<td>.05</td>
</tr>
<tr>
<td>Pooled</td>
<td>R*</td>
<td>25</td>
<td>0</td>
<td>0:2</td>
<td>.05</td>
</tr>
<tr>
<td>S*</td>
<td></td>
<td>0</td>
<td>14</td>
<td>1:0</td>
<td>.05</td>
</tr>
</tbody>
</table>

* All plants resistant.
* Some plants resistant, some susceptible.
* All plants susceptible.

* $F_2$ families developed from resistant $F_1$ plants ($F_{1R}$). Expect 5:0:0:0 (25:0:0:0 pooled).
* $F_2$ families developed from susceptible $F_1$ plants ($F_{1S}$). Expect 0:7:0 (25:0:0:0 pooled).

References


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