

# A CLOSER LOOK AT FUSARIUM WILT RESISTANCE

Jessica Chitwood-Brown

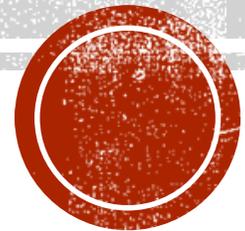
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**GCREC (1925)**

**TOMATO BREEDING**

**“1922”  
(1942)**

Race 1 resistance (*I* gene)

1940's

Race 2 resistance (*I-2*)

1969 - 'Walter'



## » Fusarium wilt race 3

- > Emerged in Australia in late 70's
- > First found in FL in 1982
- > *I-3* resistance gene from *S. pennellii*



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# I-3 ASSOCIATIONS

- I-3 cultivars available since the 1990's
  - Associated with negative traits
    - **Increased sensitivity to bacterial spot**

J. AMER. SOC. HORT. SCI. 139(3):282-289. 2014.

## Association of the Fusarium Wilt Race 3 Resistance Gene, I-3, on Chromosome 7 with Increased Susceptibility to Bacterial Spot Race T4 in Tomato

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ADDITIONAL INDEX WORDS. broad-spectrum resistance, linkage drag, pleiotropy, quantitative trait loci, *Xanthomonas*

ABSTRACT. Bacterial spot of tomato (*Solanum lycopersicum*), caused by several *Xanthomonas* species, is one of the most important diseases of the crop in humid production regions of the world. Conventional breeding approaches for resistance to bacterial spot previously identified race-specific resistances, but current efforts also seek to use quantitative trait loci (QTLs) effecting broad-spectrum resistance. Resistance QTLs and candidate QTLs have been



**Effect of a marker linked to Fusarium wilt race 3 resistance on bacterial spot race T4 foliar disease severity in tomato across four populations and two seasons. From Hutton et al. (2014) J. Amer. Soc. Hort. Sci. 139:282-289.**

<b>Population</b>	<b>Season</b>	<b>I-3 Genotype<sup>z</sup></b>	<b>Plant no.</b>	<b>Mean DSI<sup>y</sup></b>	<b>Dis. (%)<sup>x</sup></b>
<b>(Fla. 8233 x Fla. 7946)</b>	<b>Fall 2009</b>	<b>+/+</b>	<b>103</b>	<b>5.7 a</b>	<b>32</b>
		<b>+/-</b>	<b>103</b>	<b>5.4 b</b>	<b>28</b>
		<b>-/-</b>	<b>103</b>	<b>5.2 c</b>	<b>25</b>
<b>(Fla. 8517 x Fla. 7946)</b>	<b>Fall 2008</b>	<b>+/+</b>	<b>58</b>	<b>4.2 a</b>	<b>16</b>
		<b>+/-</b>	<b>111</b>	<b>3.3 b</b>	<b>9</b>
		<b>-/-</b>	<b>62</b>	<b>3.0 c</b>	<b>7</b>
<b>(Fla. 8517 x Fla. 7946)</b>	<b>Fall 2009</b>	<b>+/+</b>	<b>99</b>	<b>5.5 a</b>	<b>30</b>
		<b>+/-</b>	<b>105</b>	<b>5.7 a</b>	<b>33</b>
		<b>-/-</b>	<b>92</b>	<b>5.4 b</b>	<b>28</b>
<b>(Fla. 8326 s Fla. 7946)</b>	<b>Fall 2008</b>	<b>+/+</b>	<b>58</b>	<b>6.2 a</b>	<b>44</b>
		<b>+/-</b>	<b>100</b>	<b>5.8 b</b>	<b>35</b>
		<b>-/-</b>	<b>62</b>	<b>5.1 c</b>	<b>24</b>

<sup>z</sup> +/+ = homozygous for fusarium wilt race 3 resistance or for the resistant allele at the chromosome 11 quantitative trait loci; +/- = heterozygous; -/- = homozygous-susceptible.

<sup>y</sup> Disease severity index rated on the Horsfall-Barratt (Horsfall and Barratt, 1945) scale, where higher numbers indicated more disease. Different superscript letters represent statistically significant differences among genotypes in a population and year at P<0.05 based on Duncan's multiple range test.

<sup>x</sup> Percentage diseased tissue as converted from Horsfall-Barratt ratings.



# *I-3* ASSOCIATIONS

- *I-3* cultivars available since the 1990's
  - Associated with negative traits
    - Increased sensitivity to bacterial spot
    - **Reduced fruit size**

*Proc. Fla. State Hort. Soc.* 112:305-307. 1999.

## **TOMATO PLANTS HETEROZYGOUS FOR FUSARIUM WILT RACE 3 RESISTANCE DEVELOP LARGER FRUIT THAN HOMOZYGOUS RESISTANT PLANTS**

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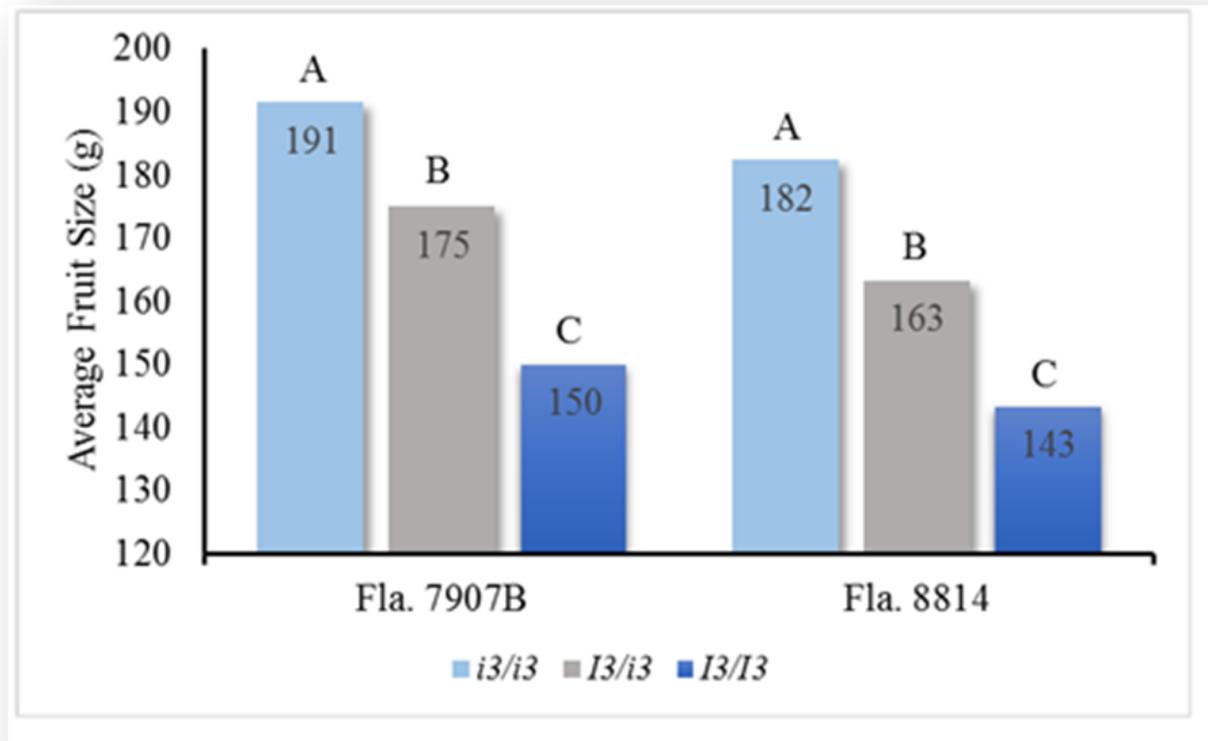
*Additional index words.* *Fusarium oxysporum* f. sp. *lycopersici*, hybrid, *Lycopersicon esculentum*, yield.

The race 2 resistance gene has been mapped to chromosome 11 by morphological (Laterrot, 1976) and DNA markers (Sarfatti et al., 1989). In 1982 Fusarium wilt race 3 was reported in Florida (Jones et al., 1982) and Australia (Grattidge and O'Brien, 1982). A single dominant resistance gene (*I-3*) was reported in *L. pennellii* (Corr.) D'Arcy accessions PI 494773 by McGrath et al. (1987) and in LA 716 by Scott and Jones (1989). The gene from LA 716 conferring race 2 resistance



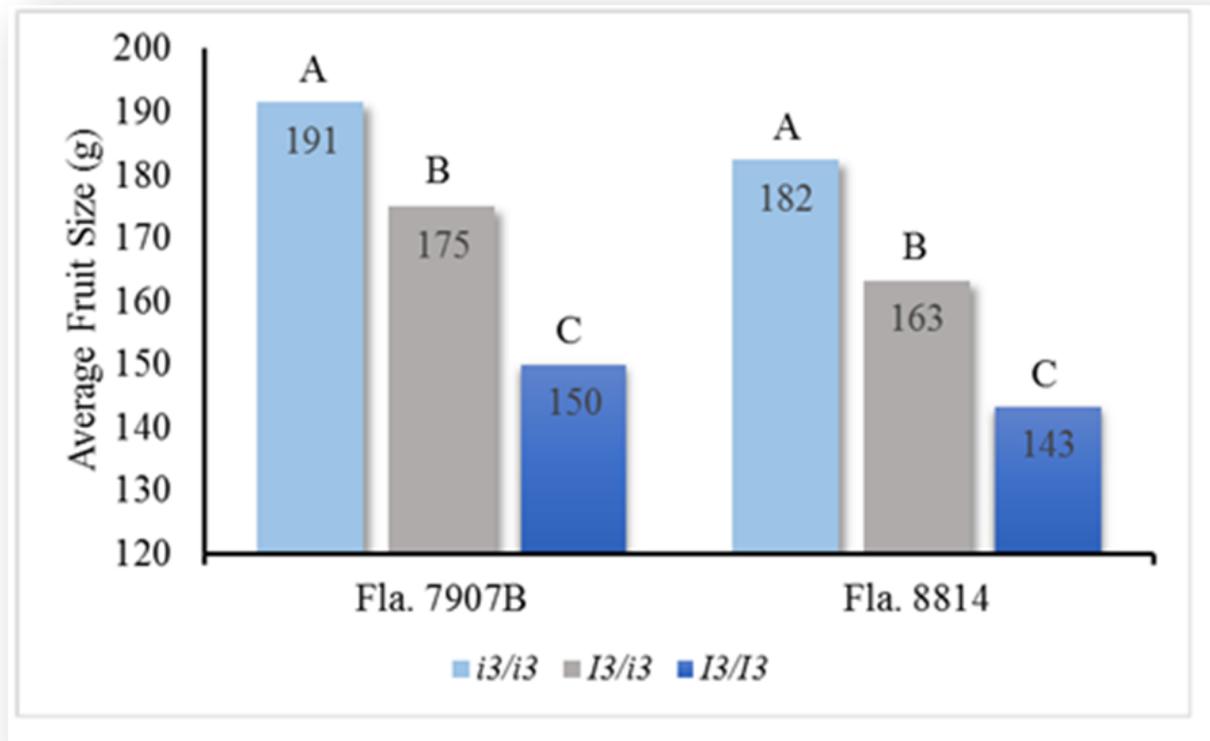
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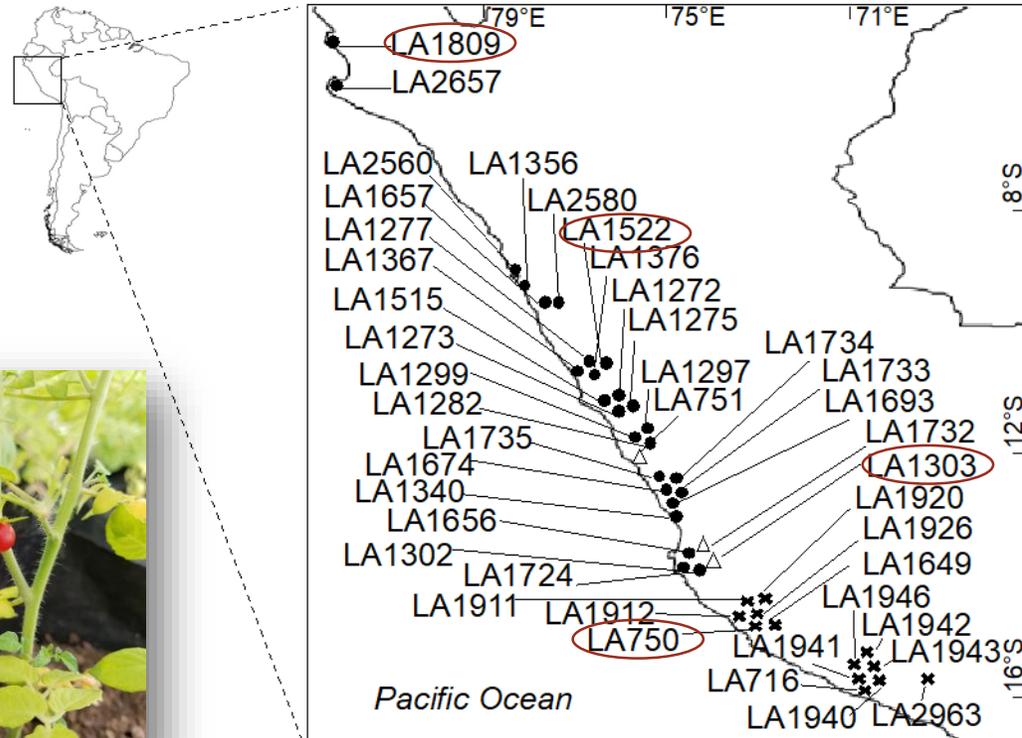
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- *I-3* cultivars available since the 1990's
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    - Increased sensitivity to bacterial spot
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  - **Linkage drag or pleiotropy?**
    - Identify new sources of resistance
    - Eliminate L.D.



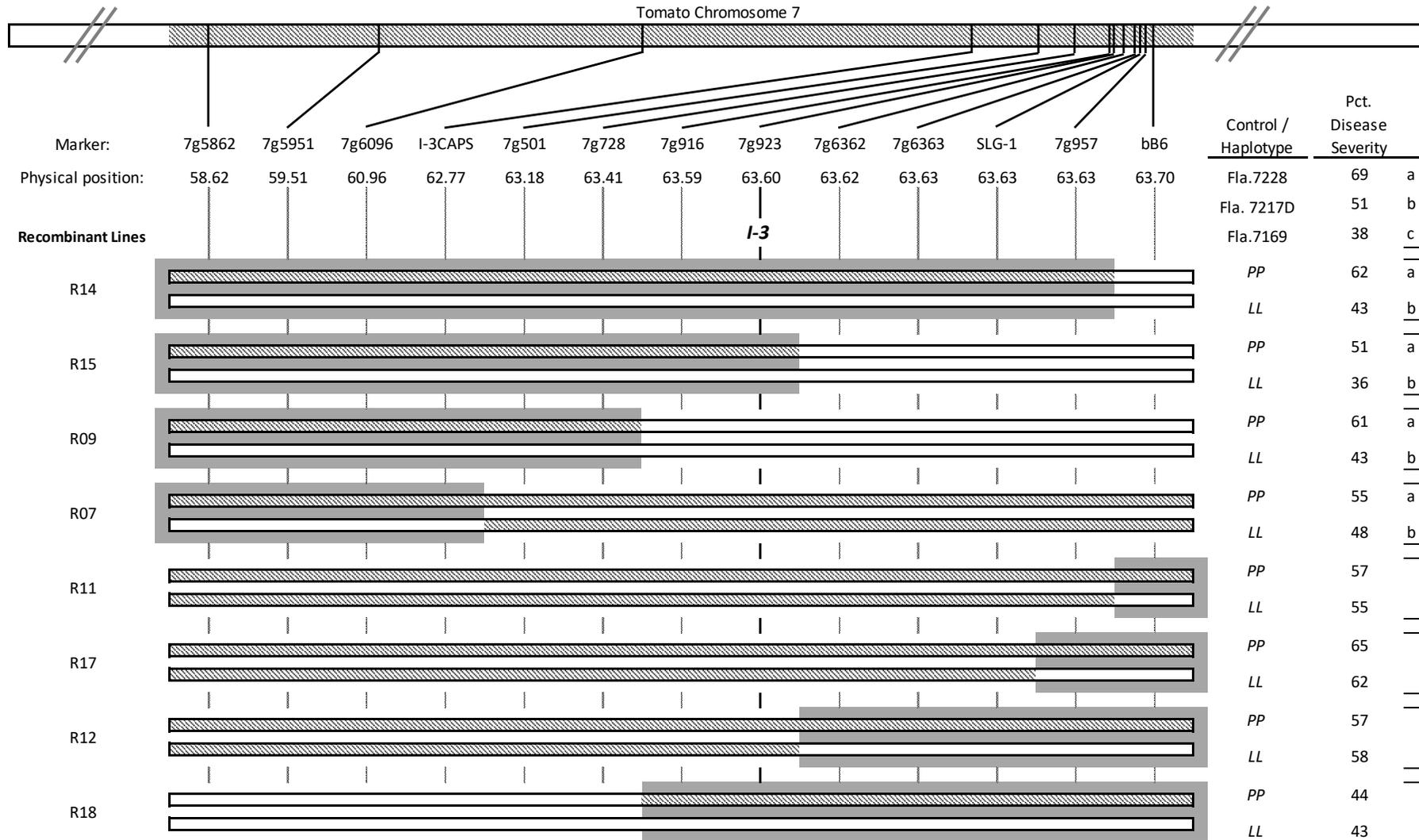
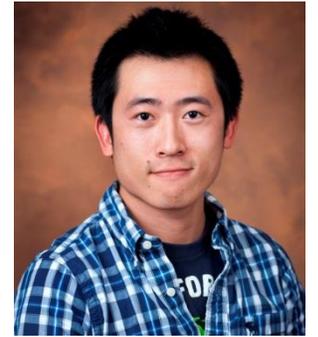
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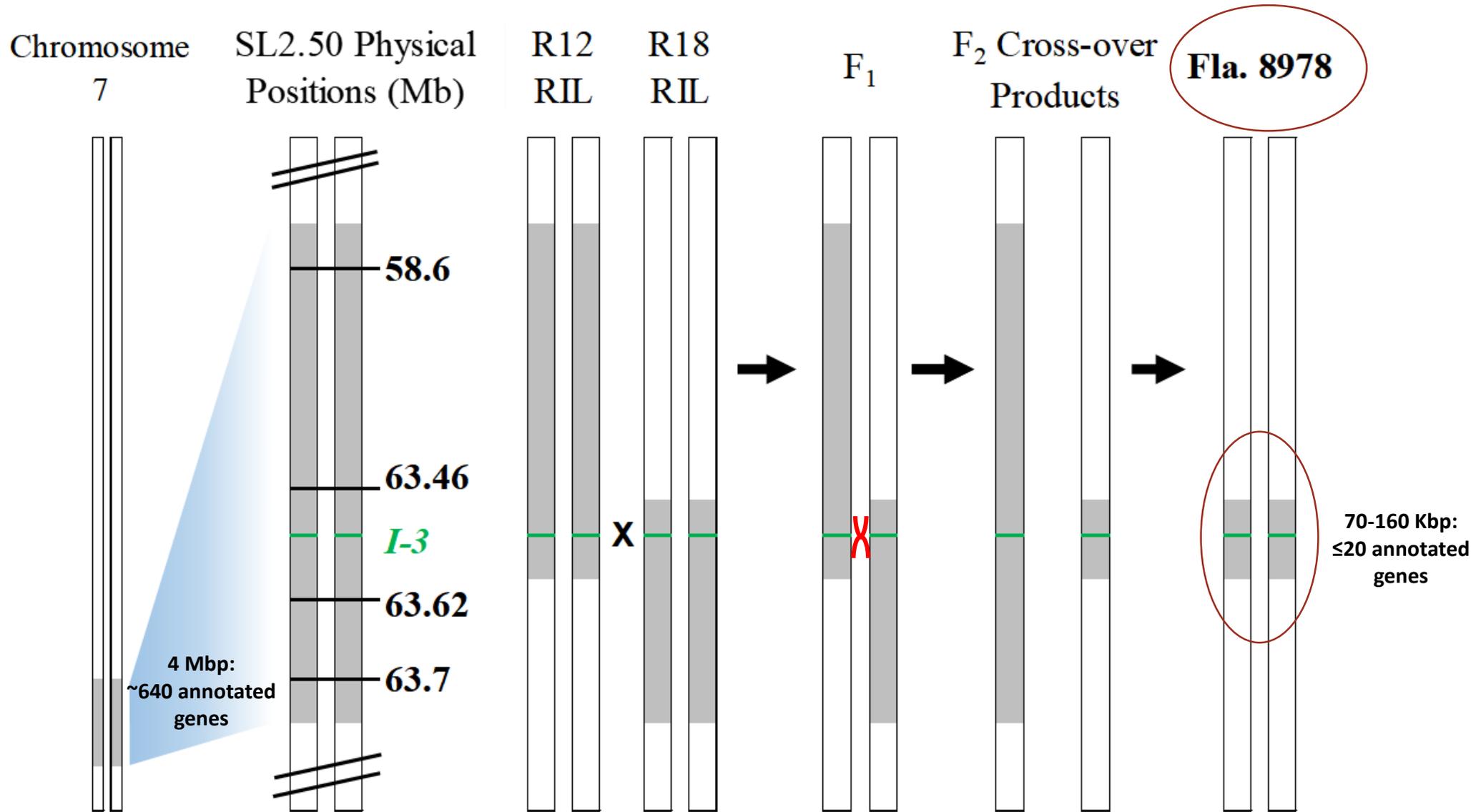
- Linkage drag or pleiotropy?
  - **Identify new sources of resistance**
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- Linkage drag or pleiotropy?
  - Identify new sources of resistance
  - **Eliminate Linkage Drag**

(Adapted from Li et al. (2018) TAG 131:145-155)





- **Linkage drag or pleiotropy?**

- Identify new sources of resistance

- **Eliminate Linkage Drag**

- Cross/backcross minimal introgression into elite lines

- Test segregating populations to confirm no effect on bact. spot or fruit size

<b>Genotype</b>	<b>Introgression</b>
Fla. 7946	Lg/Lg
	Lg/Min
	Min/Min
Fla. 8059	-/-
	Min/-
	Min/Min



# EFFECTS OF THE LARGE AND MINIMAL INTROGRESSION ON BACTERIAL SPOT SEVERITY

		DSI for <i>I-3</i> introgression haplotypes <sup>z</sup>					
Background	Introgression	Spring 2017		Fall 2017		Spring 2018	
Fla. 7946	Lg/Lg	6.0	A	5.8	A	8.6	ns
	Lg/Min	5.7	B	5.6	AB	8.8	
	Min/Min	5.6	B	5.2	B	8.7	
Fla. 8059	-/-			4.8	ns	6.4	ns
	Min/-			4.9		6.6	
	Min/Min			4.8		6.8	

<sup>z</sup>Disease severity index (DSI). Mean separations based on ranked mean analysis and 95% confidence intervals analyzed using SAS 9.4.



# EFFECTS OF THE LARGE AND MINIMAL INTROGRESSION ON AVERAGE FRUIT SIZE

		Average fruit size (g) <sup>z</sup>					
Background	Introgression	Spring 2017		Fall 2017		Spring 2018	
Fla. 7946	Lg/Lg	162	ns	132	A	167	ns
	Lg/Min	185		149	AB	165	
	Min/Min	222		154	B	157	
Fla. 8059	-/-			111	ns	159	ns
	Min/-			110		152	
	Min/Min			115		152	

<sup>z</sup>Fruit size data was analyzed using PROC GLIMMIX of SAS 9.4 with block treated as a random effect and means compared with Tukey-Kramer mean separation.



# *I-3* ASSOCIATIONS

- **Linkage drag or pleiotropy?**
  - Li et al. (2018) → L.D. likely cause of bacterial spot
  - Minimal *I-3* introgression
    - <20 foreign genes
    - No evidence of negative assoc.
- **Alternative sources of race 3 resistance**
  - Novel genes from 30+ *S. pennellii* accessions
  - Mapping efforts currently underway



# THANKS!

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