

Tomato Breeding at University of Florida: Present Status and Future Directions

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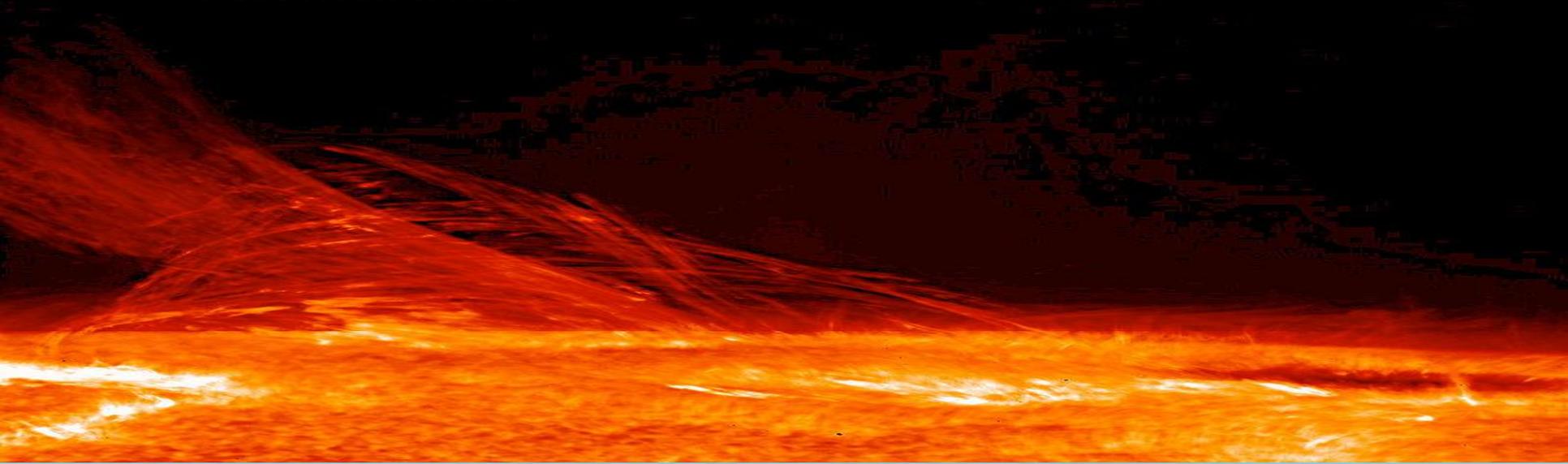
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Research Areas

Improvements are focused on:

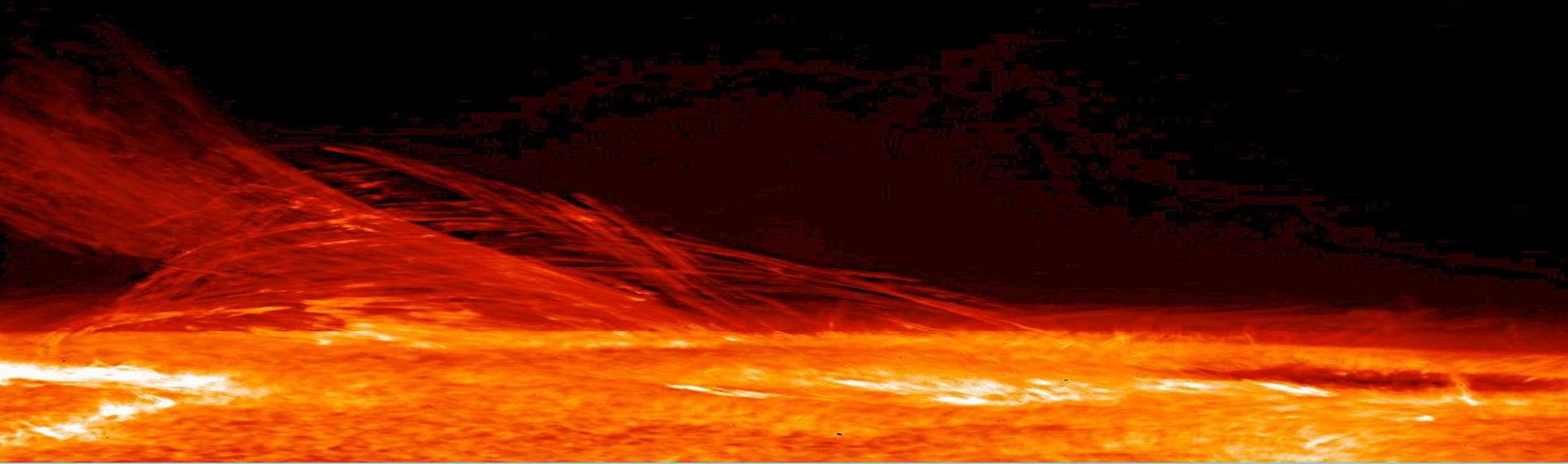
- Yield
- Fruit Quality
- Heat Tolerance
- Pest Resistance



Research Areas

Improvements are focused on:

- Yield
- **Fruit Quality**
- Heat Tolerance
- Pest Resistance





Fla. 8735

**Early and total season marketable yield, fruit size and culls
for tomato hybrids grown at Pine Island Farms, Dade
county, Florida, Winter 2011.**

Hybrid	Marketable yield (25 lb box/A)		Fruit size (g)		Culls (% by wt)
	Early	Total	Early	Total	
Fla. 8806	1095 a^z	2560 ab	196 bd	176 a-c	14 b
Fla. 8757	1041 a	2762 a	188 cd	170 bc	21 a
Fla. 8759	823 ab	2622 ab	178 d	174 bc	18 ab
Fla. 8314	777 ab	2315 ab	170 d	157 c	14 b
Fla. 8709	759 ab	2507 ab	207 a-c	190 ab	14 b
Sanibel	669 b	2653 ab	218 ab	187 ab	18 ab
Florida 47	624 b	2202 b	223 a	203 a	16 ab

^zMean separation in columns by DMRT at P≤0.05.

Pest Resistance

Tomato Yellow Leaf Curl Virus (TYLCV) Resistance

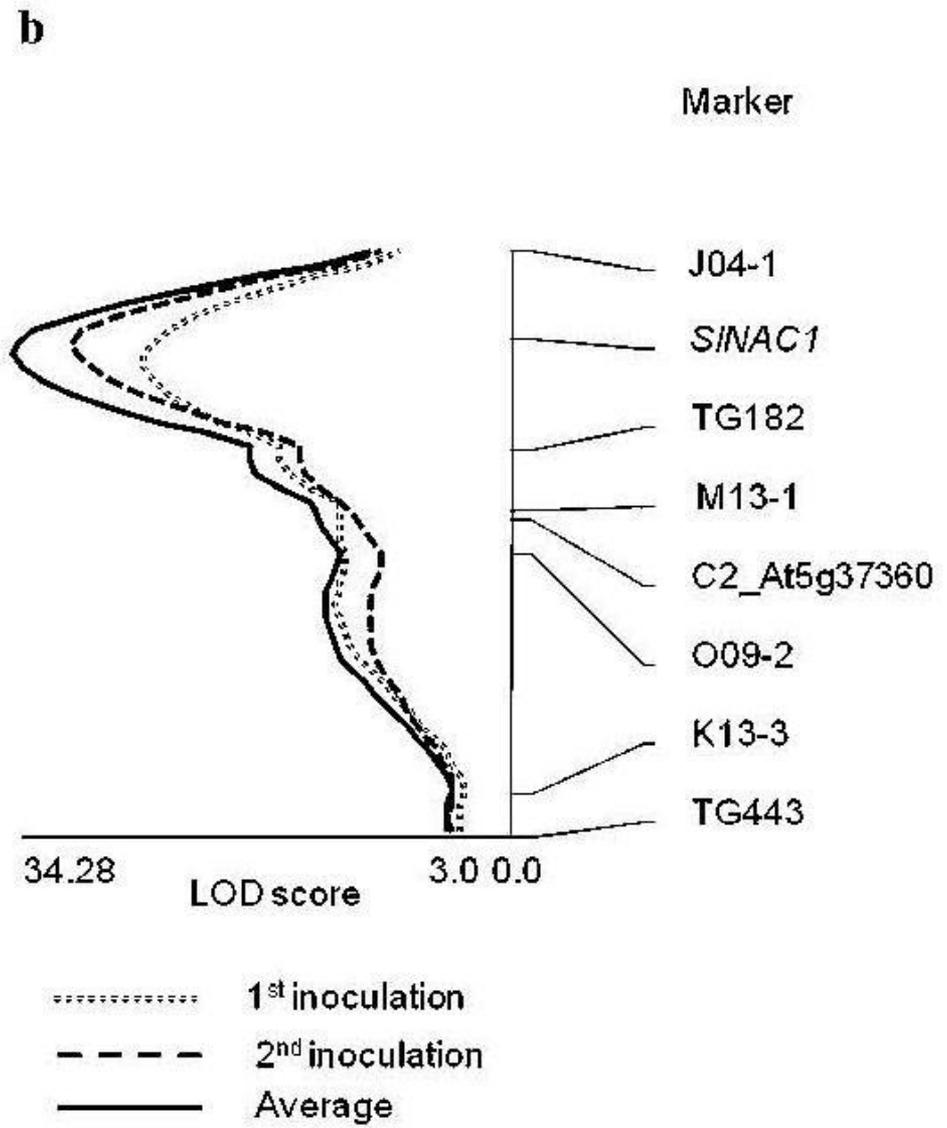
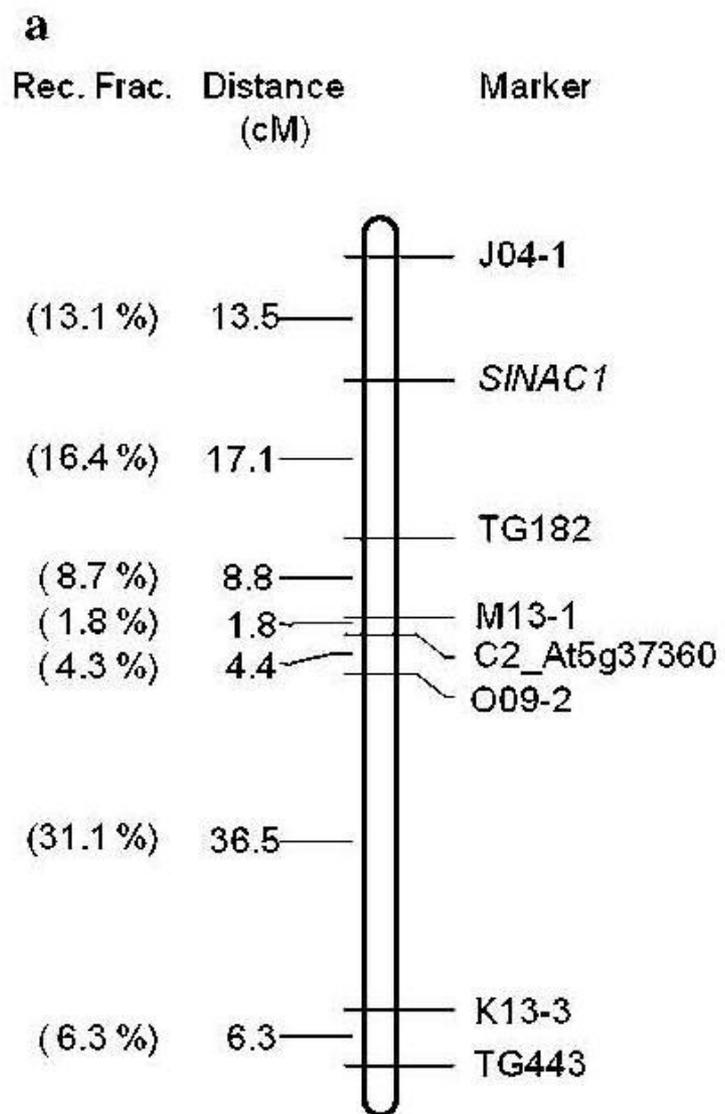
- Major emphasis since 1990
- Resistance in the program derived from *Solanum chilense* and from the cv. Tyking
- *Ty-3* and *Ty-4* identified by UF
- Utilizing multiple resistance genes in marker assisted selection (MAS) breeding approaches

Spring 2011 Survey of TYLCV-R Inbreds

- 53 advanced breeding lines
- CRBD with 2 replications; 4 plant-plots
- Seedlings inoculated with TYLCV prior to planting
- Lines were:
 - Rated for viral disease severity
 - Genotyped at resistance loci
 - Rated for non-viral foliar disease severity

Spring 2011 Survey Results

- 53 advanced breeding lines:
 - 21 inbreds carry *Ty-3*
 - 2 inbreds carry *Ty-4*
- 'Tyking' in the pedigree of many lines lacking *Ty-3* and *Ty-4*.



Disease severity and *SINAC1* genotype for parents and F₂ generation, Fall 2009.

Line	Plant No.	Genotype at the <i>SINAC1</i> locus	Mean DSI
Fla. 7547 (7547)	18	-/- (S parent)	4.0 a ^z ± 0.0
994344-SBK	18	+/+ (R parent)	1.1 d ± 0.1
	34 ^y	+/+	1.8 c ± 0.1
(7547 x 994344-SBK)	39	+/-	3.4 b ± 0.1
	28	-/-	3.3 b ± 0.1

^z Mean separation in columns by DMRT at $P \leq 0.05$.

^y F₂ segregation fits 1:2:1 and 3:1 (+/-, -/-:+/+) ratios at $P = .9 - .5$ with χ^2 values of 0.669 (2dF) and 0.223 (1dF), respectively.

Spring 2011 Survey Results

- 53 advanced breeding lines:
 - 21 inbreds carry *Ty-3*
 - 2 inbreds carry *Ty-4*
 - 16 inbreds carry *Ty-5*
 - 15⁺ inbreds carry unidentified R gene, “*Ty-6*”

Fla. 8383

F₁

Fla. 7776



Mean non-viral foliar disease severity of advanced TYLCV-resistant breeding lines as affected by genotype at three resistance loci.

Genotype ¹	Mean Foliar DSI ²		
	<i>Ty-3</i>	<i>Ty-4</i>	<i>Ty-5</i>
+/+	6.1 a (<i>n</i> = 130)	4.6 b (<i>n</i> = 16)	5.4 a (<i>n</i> = 174)
+/-	5.7 b (<i>n</i> = 46)	6.0 a (<i>n</i> = 5)	4.4 b (<i>n</i> = 15)
-/-	5.3 c (<i>n</i> = 346)	5.6 a (<i>n</i> = 501)	5.7 a (<i>n</i> = 333)

¹ +/+ homozygous resistant; +/- heterozygous; -/- homozygous susceptible

² DSI disease severity index of non-viral infections (primarily bacterial spot and early blight) based on the Horsfall-Barratt scale, lower number means less disease; *n* number of plants in each group; means in column with same letter are not significantly different at $P \leq 0.05$ based on Duncan's multiple range test



Ty-5-based resistance

Ty-3-based resistance

Chr. 6

LA2779-AL-F2

LA1

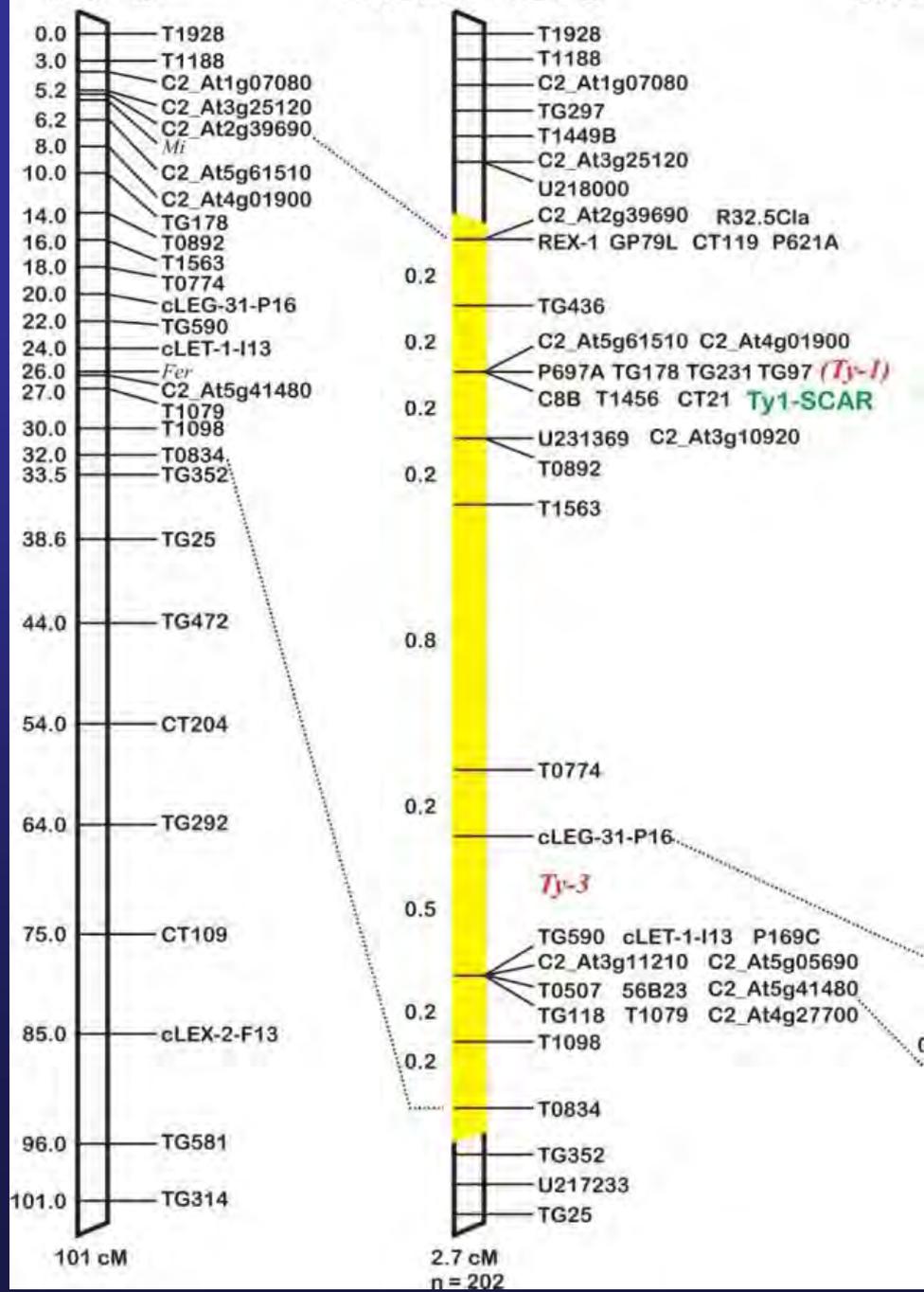


Table 1. Recombinant inbred lines (RILs) and their genotypes for the Ty-3 region of chromosome 6.

F ₂ Plant	Chromosome 6 Introgressed Segment												Category ^z	Mean RIL Ratings	
	C2_At2g39590 5.3	Mi 1.2 5.5	TG436 10	TG178 10	T0892 14	T1563 16	T0774 18	cLEG-31-P16 20	P6-25 ~25	T1079 27	T1098 30	T0834 32		Fall 2007	Spring 2008
683	[Blue bar]												S		3.4 ab
343	[Blue bar]												TS ^y	1.8 f-i	2.5 c-e
463	[Blue bar]												S		3.3 ab
11	[Blue bar]												S	3.0 b	3.7 a
359	[Blue bar]												S	3.2 ab	3.9 a
503	[Blue bar]												RS ^y	1.2 k-n	3.0 bc
506	[Blue bar]												TS ^y	2.4 cd	3.0 bc
724	[Blue bar]												TS ^y	2.3 de	2.7 c-e
186	[Blue bar]												S	3.0 b	3.7 a
403	[Blue bar]												T	2.0 d-g	2.1 e-h
554	[Blue bar]												RT	2.1 d-f	0.9 o-r
78	[Blue bar]												R	1.3 j-m	1.0 m-r
705	[Blue bar]												RT ^y	1.1 k-n	2.1 e-h
432	[Blue bar]												R	0.8 n-p	1.6 h-n
362	[Blue bar]												RT ^y	0.6 o-q	1.6 h-m
116	[Blue bar]												R	0.6 o-r	0.9 o-r
718	[Blue bar]												RT ^y	1.3 j-l	1.9 f-j
688	[Blue bar]												R	1.1 l-m	0.9 o-r
552	[Blue bar]												RT ^y	1.2 k-n	2.0 f-i
71	[Blue bar]												R		1.5 h-o
719	[Blue bar]												R	1.0 l-o	1.1 l-r
157	[Blue bar]												T	1.8 f-i	2.4 d-g
553	[Blue bar]												R	0.9 m-o	1.5 h-o
367	[Blue bar]												RT ^y	0.9 m-o	2.0 f-h
18	[Blue bar]												RT ^y	1.0 l-o	1.6 h-m
6	[Blue bar]														
616	[Blue bar]												S	3.1 b	3.7 a
517	[Blue bar]												S	2.8 bc	
390	[Blue bar]												S	3.5 a	2.9 b-d
405	[Blue bar]												TS ^y	1.9 e-h	2.7 c-e
Horizon	[Blue bar]												S	2.8 bc	2.9 b-d
Fla. 8602	[Blue bar]												T	1.7 g-j	
Tygress	[Orange bar]												T		1.9 g-k
HA3074	[Orange bar]												R	0.4 p-s	
Security	[Orange bar]												T		1.5 h-o

^z Resistant (R), tolerant (T), susceptible (S)

^y Conflicting data between seasons

Ty-3 Fine Mapping

- Spring 2009: Screened ~10,500 F₂ plants for recombination
 - ~300 total recombinants
 - ~100 informative recombinants



Ty-3 Fine Mapping

- Spring 2009:
Mapped within ~2.5 cM
between M1 and M8

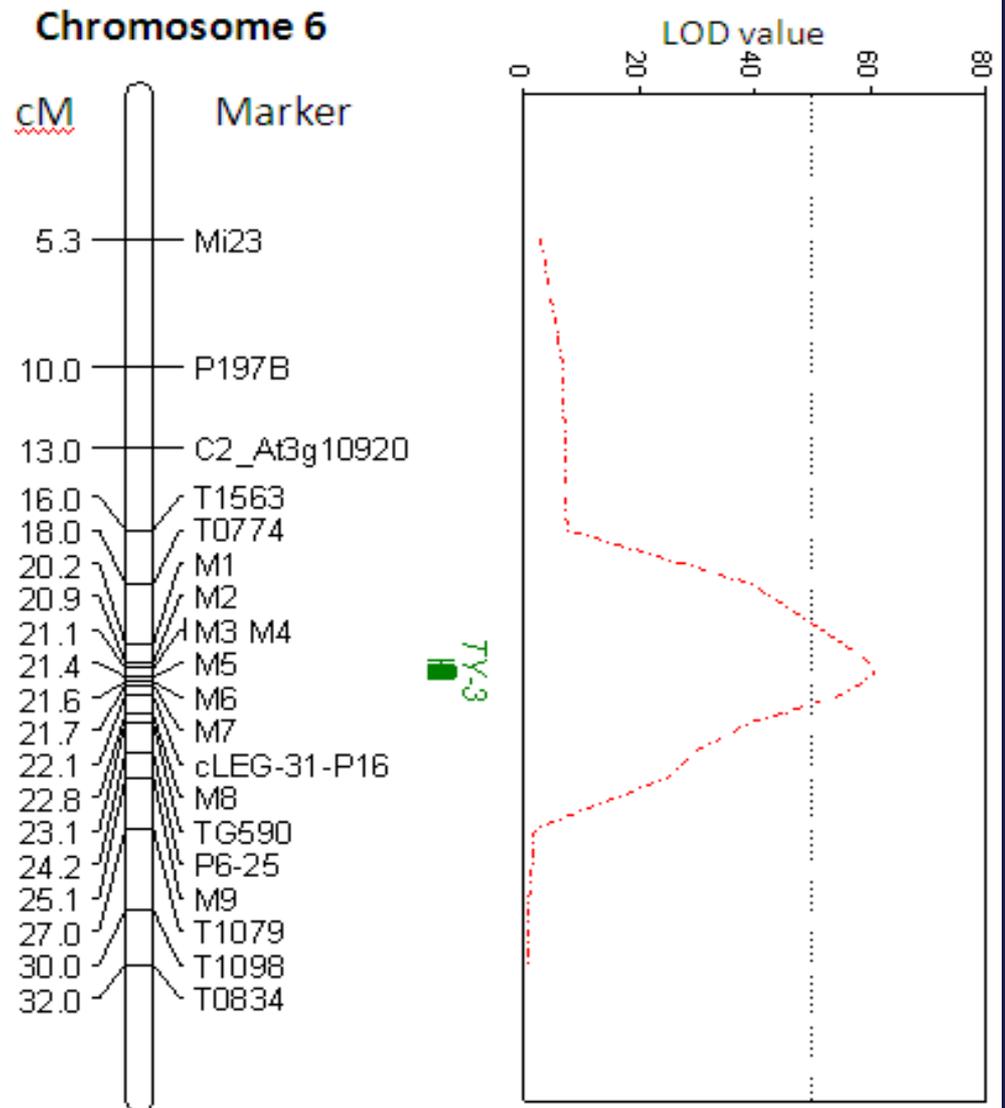


Figure 2. Mapping and interval analysis of *Ty-3* (map distance in cM) among the markers analyzed on chromosome 6; Interval analysis displaying LOD scores along Chromosome 6 for disease severity of approximately 300 recombinant plants. Mappings between 18 and 26 cM are based on recombination data from the present population.

Ty-3 Fine Mapping

- Spring 2010:
Confirmed within 0.2 cM between M3 and M5

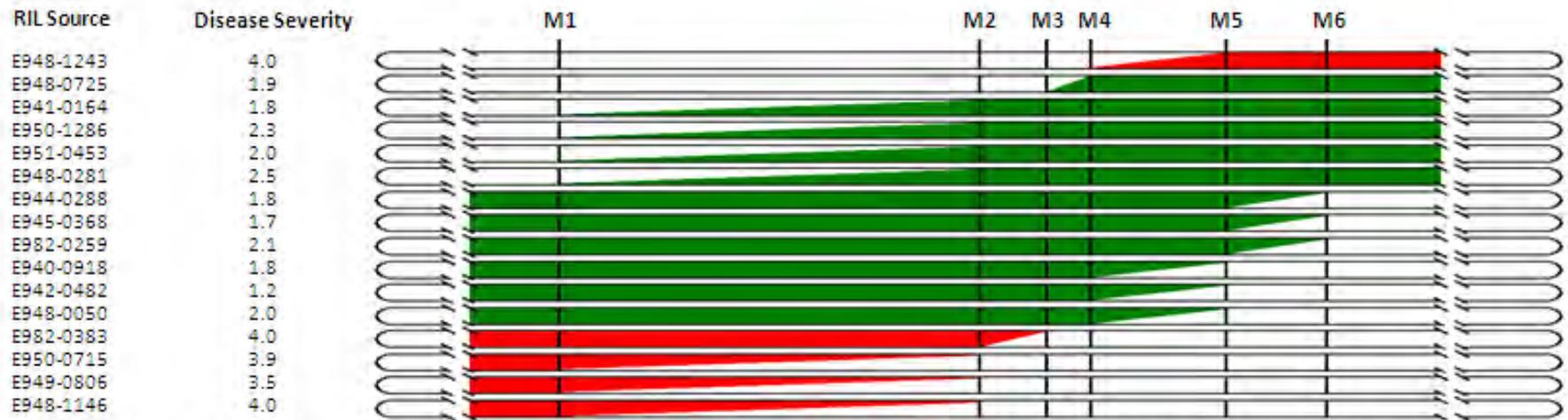
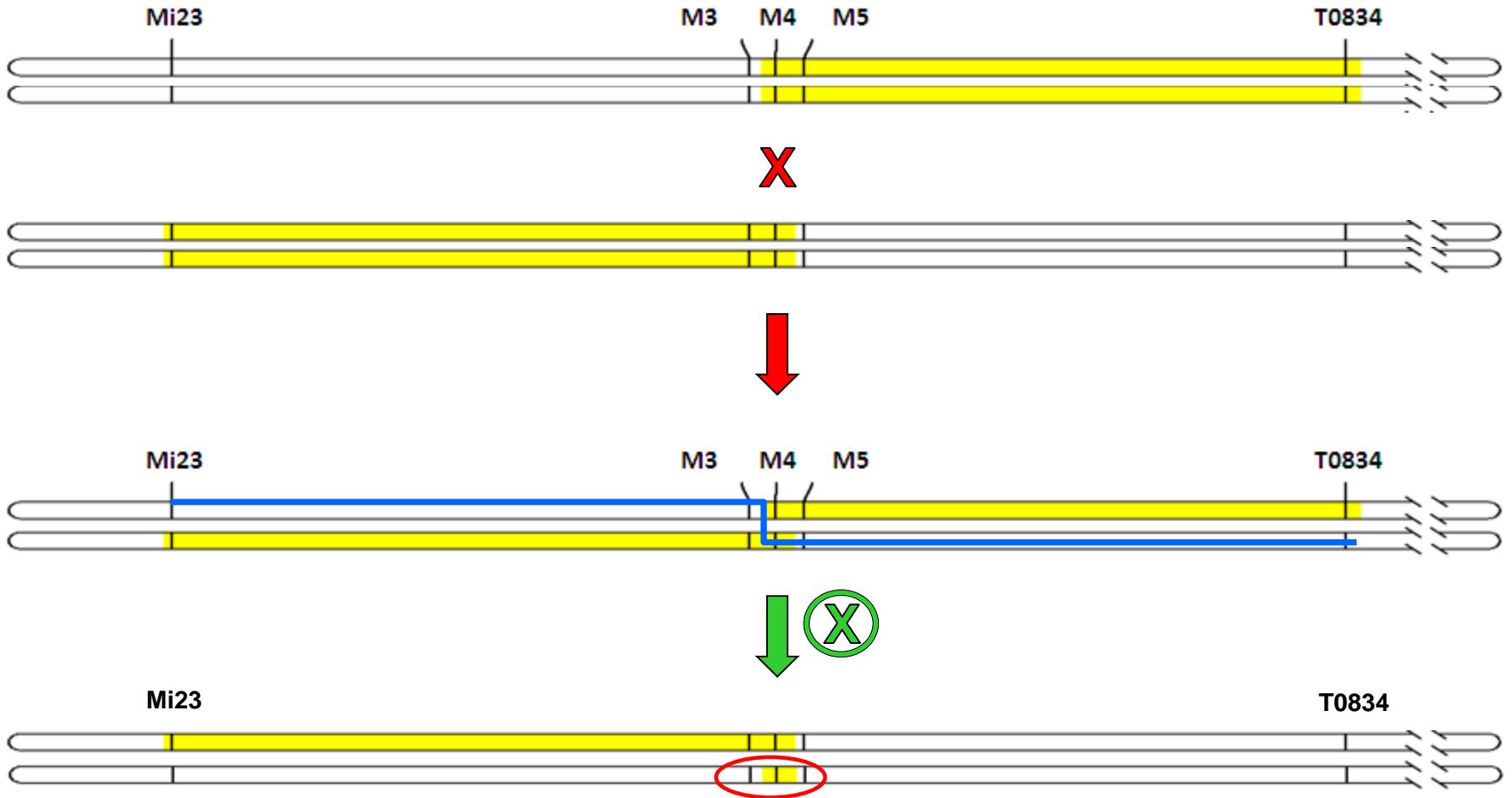


Figure 3. Evaluation of 16 RILs with recombination between markers M1 and M6. Each RIL is identified by the F_2 recombinant from which it was derived. Average disease severity for each RIL is presented. Introgression patterns are shown in green for resistant RILs and in red for susceptible RILs. Diagonally shaded intervals represent regions in which the crossover occurred.

Ty-3 Fine Mapping



Trait Integration

<u>Traits</u>	<u>Recurrent Parents</u>		
<i>Ty-2</i>	7770	8208	8599
<i>Ty-3</i>	7776	8249	8608
<i>Ty-4</i>	7781	8283	8611
<i>Ty-5</i>	7804	8293	8620
<i>(Ty-6)</i>	7907B	8296	8623
<i>Sw-5</i>	7946	8297	8626
<i>Sw-7</i>	7949B	8436B	8640
<i>Frl</i>	7987	8490B	8646
<i>Pto</i>	8000	8493C	8650
<i>(Graywall R)</i>	8021	8495	8653B
<i>(Non-blighting)</i>	8044	8499	8735
	8059	8589	8820
	8083	8590	8834
	8111B	8591	8835
	8124C	8592	

7946 x 8517 F₈ selections (Spring 2009):



090630

Severity Rating = 2.5





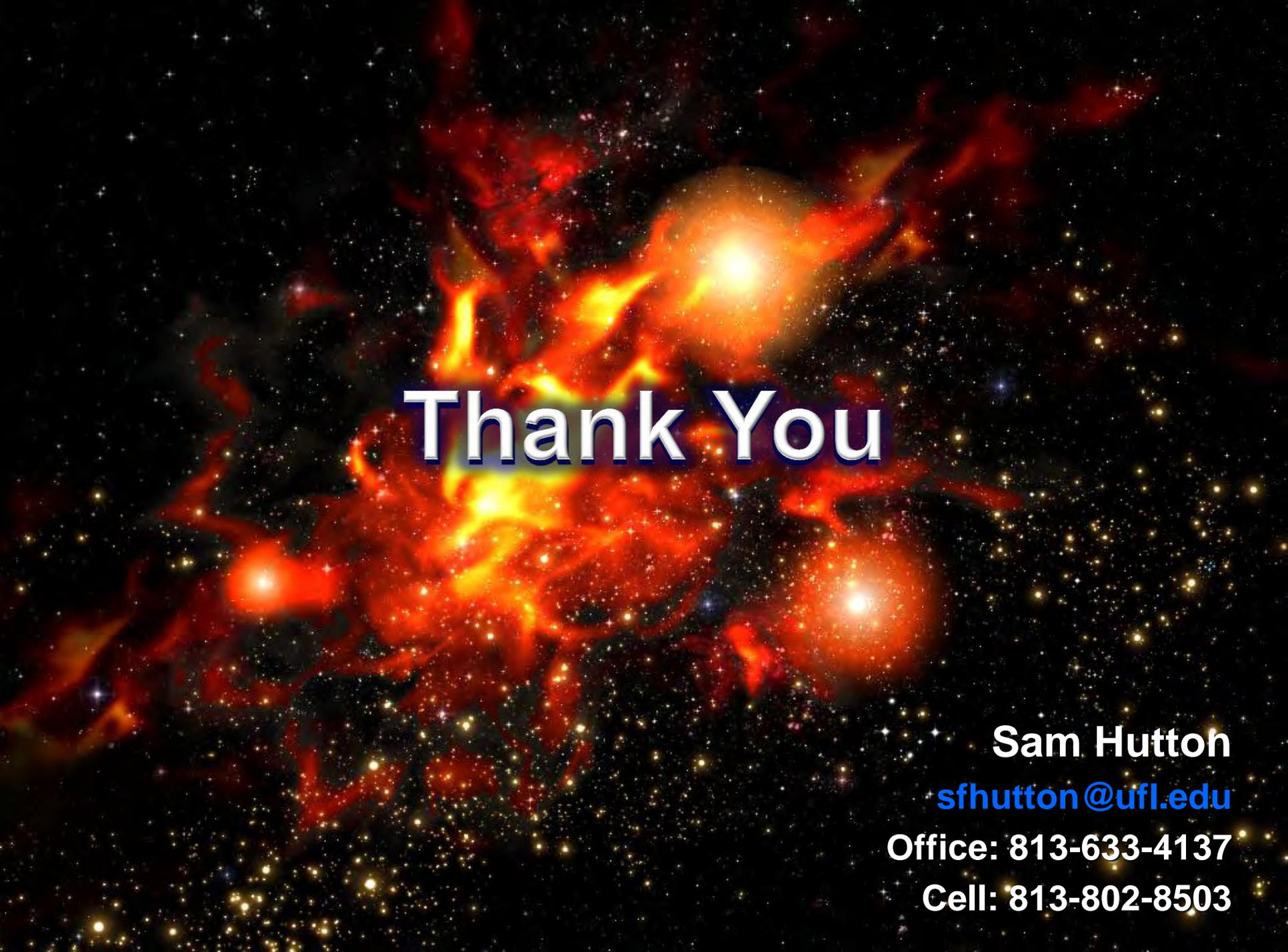
Fla. 8208 x Fla. 8626





Fla. 8208 x Fla. 8626

Brand X



Thank You

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