



GENETIC RESISTANCE TO PEPPER ANTHRACNOSE: LESSONS FROM TOMATO

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INTRODUCTION

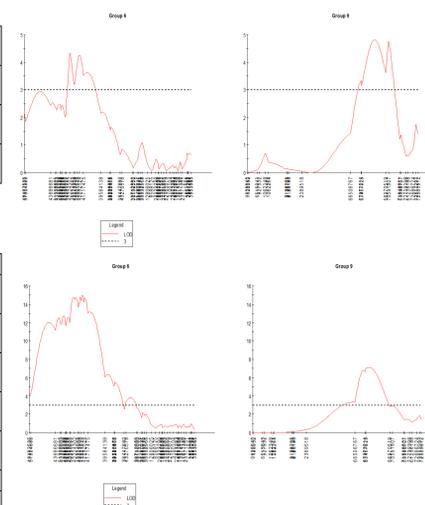
- Anthracnose caused by *Colletotrichum* species is a serious disease of Solanaceous crops grown in North America., endemic in production regions of the Eastern and Midwestern United States & south-central Canada.
- In pepper, variable modes of inheritance for anthracnose resistance have been reported & variation in *Colletotrichum* pathotypes complicates breeding for durable host resistance. Crossing barriers within *Capsicum* & segregation distortion hinder introgression of useful levels of resistance into *C. annuum*.
- We have selected an unadapted small-fruited tomato line, designated 95L368, that exhibits a high level of resistance to a broad range of *Colletotrichum* species that cause anthracnose on tomato as well as pepper. This resistant genotype is also resistant to *Colletotrichum* isolates responsible for rot of immature pepper.
- Resistance in 95L368 was primarily additive with two to three genetic factors estimated to be segregating for resistance.

Table 1. MQM analysis 2000 season

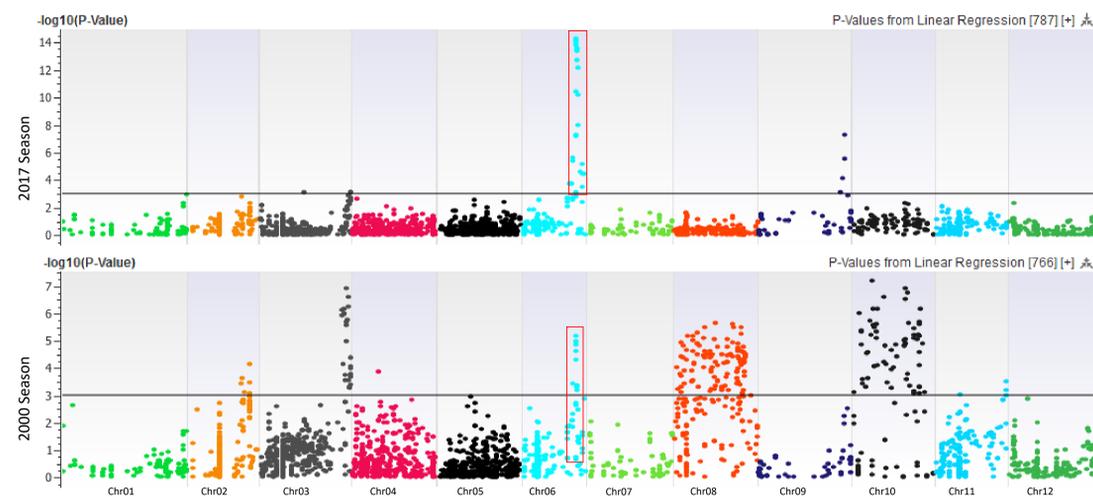
Chr	Locus	LOD	# Iter.	mu_A	mu_H	mu_B	Variance	% Expl.	Additive
9	70591807	4.77	3	7.00996	8.07661	9.14326	9.15636	6.2	-1.06665
6	42224302	4.34	4	7.00726	8.01406	9.02086	9.22583	5.7	-1.0068
6	42092524	4.27	3	7.01991	8.01306	9.0062	9.23992	5.6	-0.99315

Table 2. MQM analysis 2017 season

Chr	Locus	LOD	# Iter.	mu_A	mu_H	mu_B	Variance	% Expl.	Additive
6	42224302	14.48	4	5.89085	7.89232	9.89379	9.9203	21.6	-2.00147
6	42001528	14.38	4	6.01315	7.91905	9.82495	9.93261	21.5	-1.9059
6	42092524	14.25	4	5.91252	7.88976	9.86701	9.9614	21.3	-1.97724
6	42012308	14.11	3	5.99529	7.92749	9.85968	9.99284	21.1	-1.93219
6	49324064	13.68	3	5.99105	7.89605	9.80106	10.0688	20.5	-1.905
9	53457523	7.01	3	6.54711	8.00447	9.46183	11.4315	11.2	-1.45736
9	67973214	6.61	3	6.57276	8.00129	9.42982	11.5199	10.6	-1.42853



Composite interval mapping for 2000 & 2017 field seasons. QTLs with high LOD support were identified on chromosomes 6 & 9.



Results of association mapping (Manhattan plot) delineating clear signals on chromosomes 6 & 9 for loci associated with anthracnose resistance (2017 field season).

RESULTS

- Utilizing a recombinant inbred line population developed from a cross with the anthracnose resistant line 95L368, GBS was used to identify & map genomic regions associated with lesion development. 15300 polymorphic SNPs were identified of which 1692 SNPs were mapped, spanning a length of 2519cM.
- Utilizing MAP-QTL & MULTI-QTL, a genetic map was constructed with a marker density of 1.48 SNP per cM. Across years, oci on chromosomes 6 & 9 that were associated with anthracnose resistance were identified. Additional loci on chromosomes 2, 3, 8 & 10 exhibited strong QTL x year interaction, with significance in only one of two years of testing.
- Utilizing an additional 4500 previously unmapped SNPs, association mapping (Golden Helix) confirmed association of loci on chromosomes 6 & 9 with anthracnose resistance.

Chromosome	Position	Gene Name	Reference	Alternates	P-Value	Minor Allele	Major Allele	Minor Allele D Frequency	Major Allele d Frequency	Mutation type
Chr06	42092524	Solyc06g066790.3	G	C	8.13E-15	C	G	0.454183267	0.545816733	Non Synonymous (Lys ---> Gln)
Chr09	67973214	Solyc09g075920.1	C	T	5.80E-08	C	T	0.494023904	0.505976096	Synonymous (Ile ---> Ile)

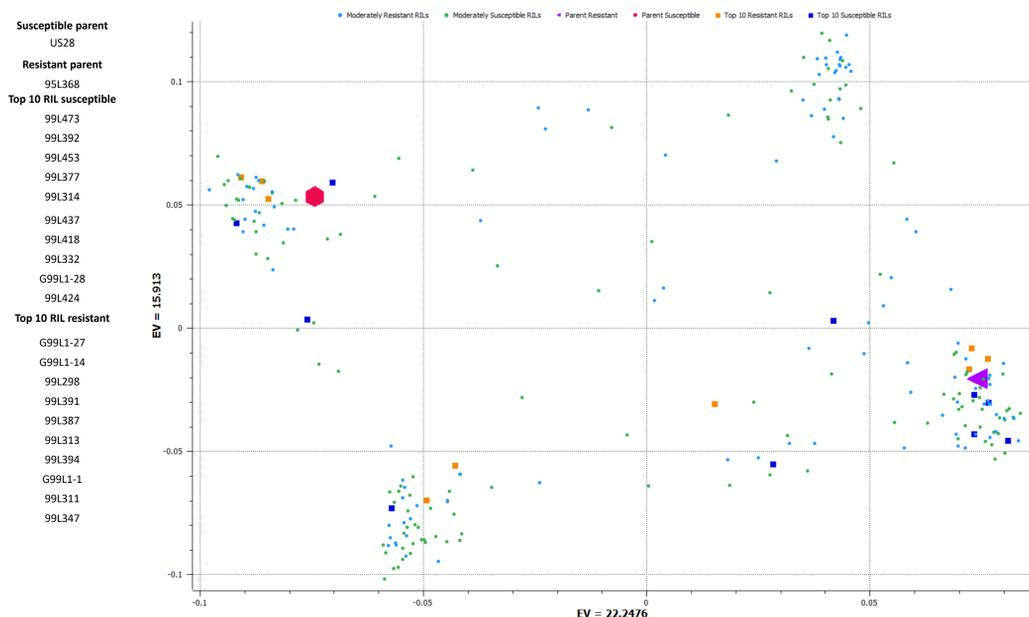
Gene Name

Solyc06g066790.3
Solyc09g075920.1

Annotation

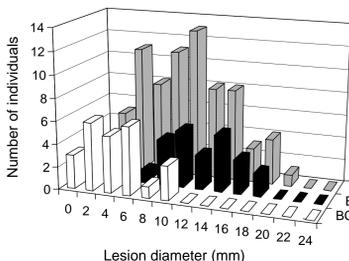
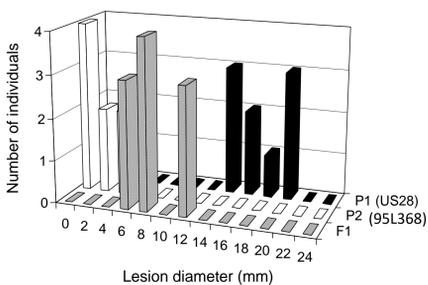
N-alpha-acetyltransferase 16, NatA auxiliary subunit (AHRD V3.3 *** AOA0B2P106_GLYSO)
Serine/threonine-protein kinase (AHRD V3.3 *** K4CVG9_SOLLIC);Dbxref=InterPro:IPR024171;Ontology_term=GO:0004674

PCA based on SNP data 2000 & 2017 seasons



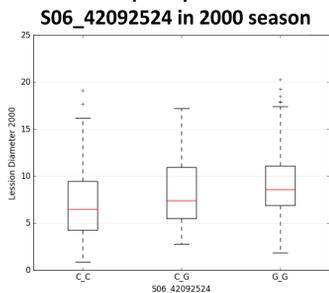
FUTURE DIRECTIONS

- Mapping of additional SNP markers is in progress to facilitate fine mapping.
- Detailed syntenic relationships between the tomato & pepper genomes, together with reference genomes for the respective crops facilitate comparative mapping between tomato & pepper for anthracnose resistance homologues.

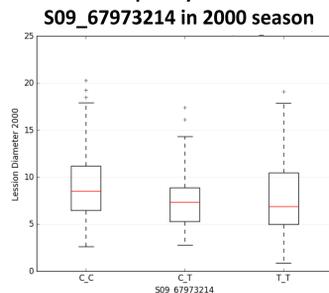


Population distributions from a cross of the anthracnose resistant tomato parent 95L368 and the susceptible line US28 utilized for RIL development.

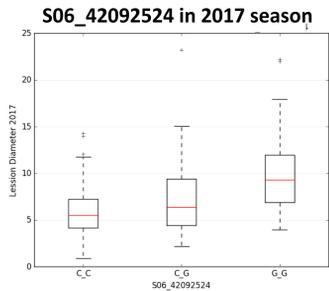
Allele Frequency of S06_42092524 in 2000 season



Allele Frequency of S09_67973214 in 2000 season



Allele Frequency of S06_42092524 in 2017 season



Allele Frequency of S09_67973214 in 2017 season

