EVALUATING QUANTITATIVE TRAIT LOCI (QTL) SOURCES OF RESISTANCE IN TOMATO TO MULTIPLE *XANTHOMONAS SPP.*

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Introduction:

Bacterial Spot of tomato is a worldwide disease caused by four species of *Xanthomonas*. The disease produces scab-like lesions on the fruit and necrotic spots on the leaves, which affect the marketability and yield of tomato. To reduce the severity of the disease, genetic sources of resistance from wild tomato germplasm can be introgressed into cultivated tomato. Three independent sources of resistance, H7998 (S. lycopersicum; QTL-11a), PI 114490 (*S. l. var cerasiforme*; QTL-11b) and LA2533 (*S. pimpinellifolium*; QTL-11c), were identified with quantitative trait loci (QTL) mapping to the same genetic region on chromosome 11. Genome resequencing and genetic analysis suggests that these loci are not alleles. To determine which QTL source provides the greatest resistance to multiple species, we developed near isogenic lines (NILs) using marker-assisted backcrossing. In this study, the NILs will be comparatively evaluated in three fields inoculated with *Xanthomonas* species.

Objectives:

- Develop PCR based markers to select individuals for the resistant allele on chromosome 11.

- Use high-throughput genotyping technology to select individuals with a greater percentage of the recurrent parent genome, OH88119.

- Use the Horsfall-Barratt scale to evaluate selected individuals in three fields trials, each inoculated with a different species *(X. perforans, X. euvesicatoria and X. vesicatoria)*.

Methods:

Marker Assisted-Backcross Strategy

Fig 1. Schematic illustrates breeding strategy to obtain near isogenic lines. Three independent sources of resistance were introgressed into a uniform background. (1) 192 individuals from each BC_1 family were screened using flanking indel markers to identify the heterozygous allele on chromosome 11. (2) Individuals were selected from each backcross family to undergo background genome selection using Kompetitive Allele specific PCR (KASP) assay. Selected BC_1 plants were self-pollinated and homozygous resistant and susceptible plants were organized for field evaluation.

Fig 2. Plants were inoculated in the greenhouse with either *X. perforans*, *X. euvesicatoria*, or *X. gardneri* and subsequently transplanted in three fields.

Results:

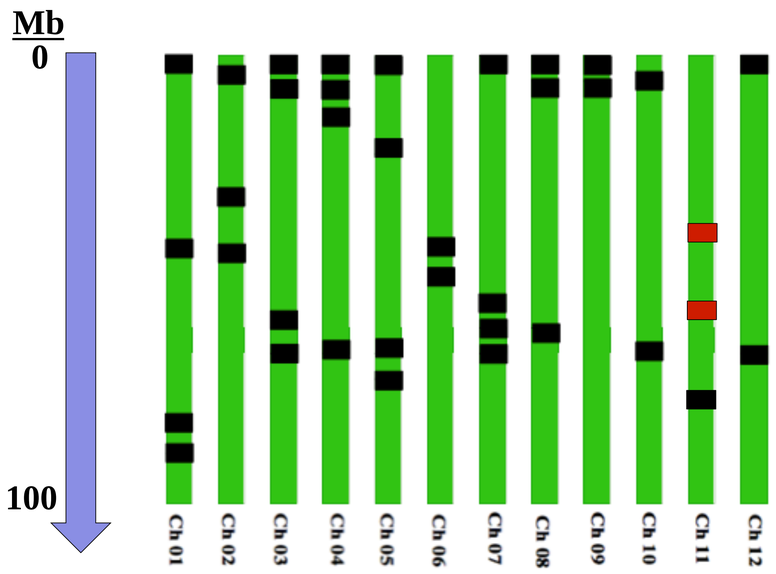


Fig 2. 34 Single Nucleotide Polymorphism (SNP) markers distinguish sources of resistance and OH88119. Selection for resistance (red bars) was followed by background genome selection using KASP assays (black bars).

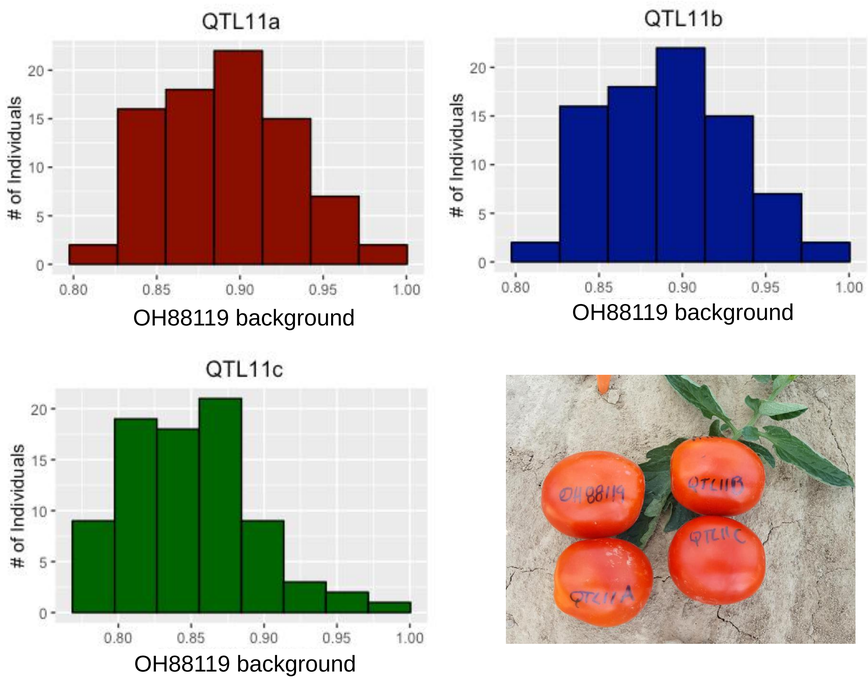


Fig 3. Histograms illustrate the proportion of recurrent parent background in each backcross population. Using background genome selection we identified individuals with 95% of the recurrent parent genome. (Bottom Right) Selected tomatoes appear similar in size to the recurrent parent, but with resistance from different sources.

Field Experimental Design:

Model: Y= μ+ QTL allele + block+ error	
Three Fields	Three replications per field
One *Xanthomonas* species per field	Randomized complete block design

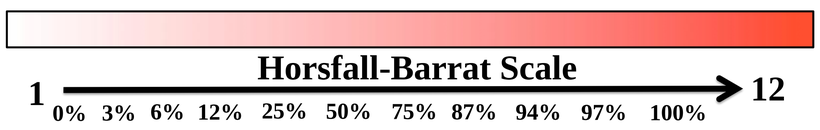
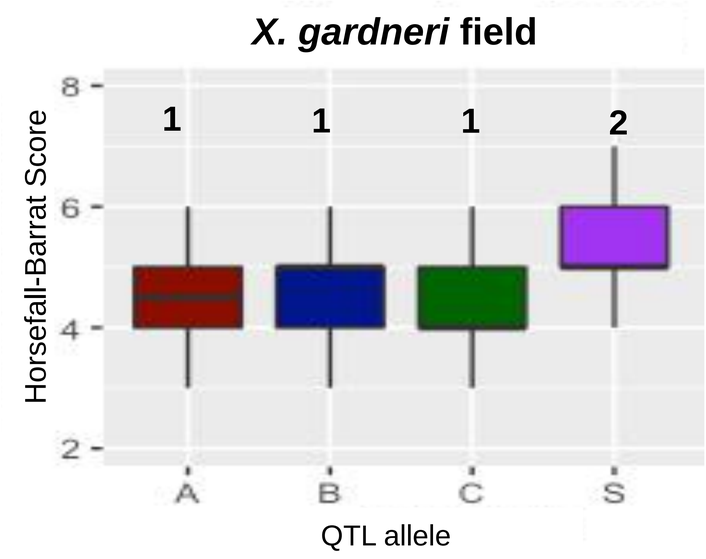
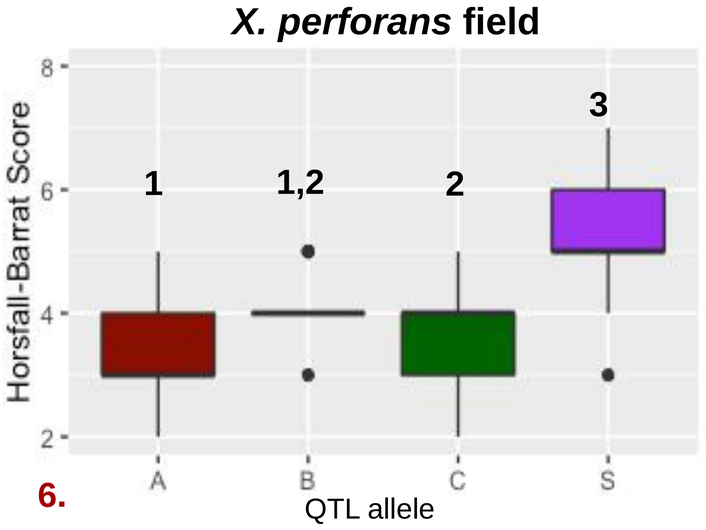


Fig 4. Field ratings were conducted using the Horsfall-Barrat scale. Each plot is assigned a numerical value based off the percentage of disease present.





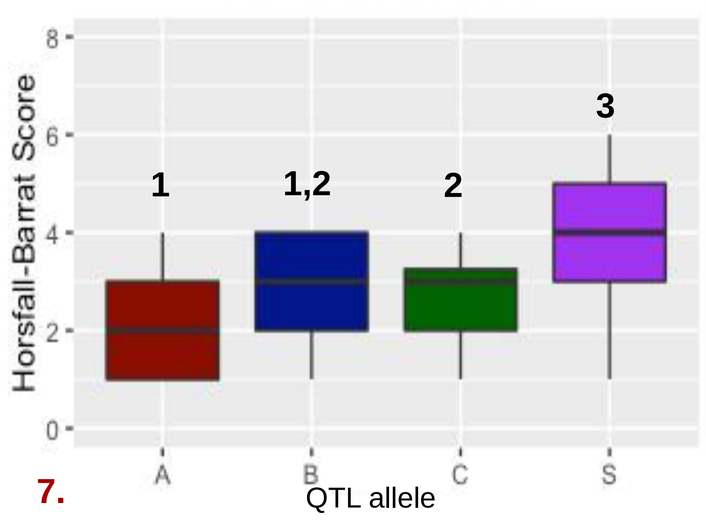


Fig 5,6,7. Boxplots illustrate evaluation of three independent QTL for resistance and the susceptible allele in the three fields, each containing a different *Xanthomonas* species. The numerical value above each boxplot represents the Fishers's Least Significance test (alpha= .05) performed following ANOVA (protected LSD).

Conclusions

1) QTL11a provides the best resistance in both the *X. perforans* and *X. euvesicatoria* inoculated fields.

2) Additional field ratings will be conducted when plants reach 80% maturity. Disease symptoms are expected to be more severe, with better separation of resistant and susceptible controls.

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USDA NIFA United States Department of Agriculture National Institute of Food and Agriculture

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