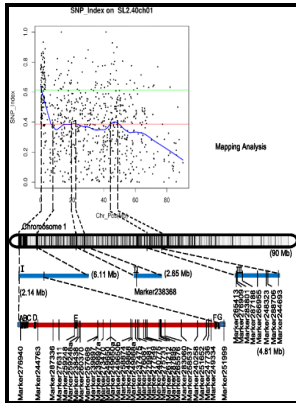


Genetic analysis of two tomato genes for resistance to Cladosporium fulvum.

University of East Anglia - RFLP linkage analysis of the Cf



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Genetic and molecular analysis of tomato Cf genes for resistance to Cladosporium fulvum

The tomato genome sequence provides insights into fleshy fruit evolution. Inoculation and assessment of disease severity ratings were performed as described by Wang et al. The qRT-PCR reaction was performed using an iQ5 system Bio-Rad, USA.

Mapping and candidate gene screening of tomato Cladosporium fulvum

At the four-five leaf stage, the abaxial surface of the Cf-12-tomato seedlings was inoculated with a suspension of 1×10^7 sporangia per ml.

RFLP linkage analysis of the Cf

In many interactions between plants and their pathogens, resistance to infection is specified by plant resistance R genes and corresponding pathogen avirulence Avr genes.

Characterization of the Tomato Cf

Significantly enriched DEG pathways were identified using the KOBAS 2. The area of necrosis was gradually enlarged at 12—15 dpi Figures. Philosophical Transactions of the Royal Society of London.

Genetic and molecular analysis of tomato Cf genes for resistance to Cladosporium fulvum

The reaction mixture contained 10 μ L of 2 \times TransStart Top Green qPCR SuperMix TransGen, China, 10 pM of each primer, 2 μ L of cDNA templates 1:10 dilution, and sterile distilled water to make up a total volume of 20 μ L. Genome resequencing can provide more details about genome sequences than SLAF-seq, and this information is useful to improve the precision of gene mapping. The Cf-12 gene was identified through the large screening of C.

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