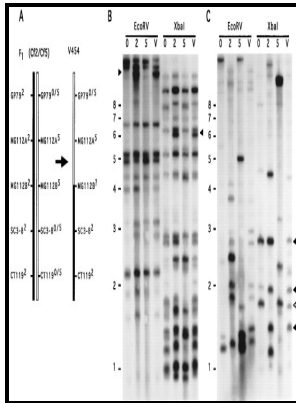


Genetic analysis of two tomato genes for resistance to Cladosporium fulvum.

University of East Anglia - Characterization of the tomato Cf



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Characterization of the Tomato Cf

Amino acid differences distinguishing Cf-4 and Cf-9 are confined to their N termini, delimiting a region that determines the recognitional specificity of ligand binding.

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

The effector proteins are secreted into the apoplastic space during infection , and induce either a compatible or incompatible interaction between the fungus and infected plant. RNA-Seq correlation analysis between samples. The top 10 enrichment terms of the biological process, cellular component and molecular function were selected, respectively, as the main nodes of the directed acyclic graph.

Characterization of the Tomato Cf

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

RNA Extraction, Library Preparation, and Sequencing Total RNA from Cf-12-tomato leaves was extracted and analyzed, as previously described. Development of molecular markers linked to Cladosporium fulvum resistant gene Cf-6 in tomato by RAPD and SSR methods.

Frontiers

The identified DEGs were further verified by qRT-PCR and analyzed using gene ontology GO and Kyoto Encyclopedia of Genes and Genomes KEGG. Here, we describe the cloning and characterization of Cf-4, which also encodes a membrane-anchored extracellular glycoprotein.

Characterization of the tomato Cf

Validation of DEGs by Quantitative Real-Time PCR Eighteen DEGs involved in plant disease resistance pathways were validated using quantitative real-time PCR qRT-PCR. Sequence alignment showed that the DNA sequences of both loci contained mutations between CGN18423 and Moneymaker. RFLP linkage analysis of the Cf-4 and Cf-9 genes for resistance to *Cladosporium fulvum* in tomato.

Characterization of the tomato Cf

The DNA sequences we obtained were submitted to the NCBI database and analyzed using the Blast and Open Reading Frame Finder ORF Finder tools of NCBI.

RFLP linkage analysis of the Cf

Three association regions are shown as I, II and III based on the F 2 SLAF-seq analysis. From the 119,504 SLAF tags, 4108 Diff-markers were obtained. Leaf samples were harvested at 0—15 days of post-infection dpi for microscopic analysis.

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