

ABSTRACT

A MOLECULAR LINKAGE MAP OF AVIRULENCE LOCI IN THE PLANT PATHOGENIC OOMYCETE *PHYTOPHTHORA* *CAPSICI*

Disease in plants is a highly evolved interaction between host and pathogen. Plants resist disease by detecting elicitor molecules produced by their pathogens and initiating responses to inhibit the spread of infection. The pathogen's avirulence genes, those genes that code for elicitor molecules, may recombine and create new virulence profiles to which the host plant is not resistant. AFLP molecular markers were used to generate a novel genetic linkage map of the chromosomes of *Phytophthora capsici*. Virulence assays revealed a continuous distribution of average virulence scores, which increased over time. One time-dependent and three stable QTLs for virulence were located on linkage groups 1, 3, and 4. These findings suggest that virulence in *P. capsici* is both time-sensitive and quantitative. The linkage map produced in this study may ultimately be used to characterize and predict virulence profiles and in map-based cloning for further study of factors determining virulence in *P. capsici*.

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