



## **ABSTRACT**

*“The genomes of the related fungal pathogens *Cladosporium fulvum* and *Dothistroma septosporum* reveal adaptation to different hosts and lifestyles”*

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We sequenced and compared the genomes of the Dothideomycete fungal plant pathogens *Cladosporium fulvum* (*Cfu*) (syn. *Passalora fulva*) and *Dothistroma septosporum* (*Dse*) that are closely related phylogenetically, but have different lifestyles and hosts. Although both fungi grow extracellularly in close contact with host mesophyll cells, *Cfu* is a biotroph infecting tomato, while *Dse* is a hemibiotroph infecting pine. The genomes of these fungi have a similar set of genes (70% of gene content in both genomes are homologs), but differ significantly in size (*Cfu* >61.1 Mb; *Dse* 31.2 Mb), which is mainly due to the difference in repeat content (47.2% in *Cfu* versus 3.2% in *Dse*). Recent adaptation to different lifestyles and hosts is suggested by diverged sets of genes. *Cfu* contains an  $\alpha$ -tomatinase gene that we predict might be required for detoxification of tomatine, whilst this gene is absent in *Dse*. Many genes encoding secreted proteins are unique to each species and the repeat-rich areas in *Cfu* are enriched for these species-specific genes. In contrast, conserved genes suggest common host ancestry. Homologs of *Cfu* effector genes, including *Ecp2* and *Avr4*, are present in *Dse* and induce a Cf-Ecp2- and Cf-4-mediated hypersensitive response, respectively. Strikingly, genes involved in production of the toxin dothistromin, a likely virulence factor for *Dse*, are conserved in *Cfu*, but their expression differs markedly with essentially no expression by *Cfu* *in planta*. Likewise, *Cfu* has a carbohydrate-degrading enzyme catalog that is more similar to that of necrotrophs or hemibiotrophs and a larger pectinolytic gene arsenal than *Dse*, but many of these genes are not expressed *in planta* or are pseudogenized. Overall, comparison of their genomes suggests that these closely related plant pathogens had a common ancestral host but since adapted to different hosts and lifestyles by a combination of differentiated gene content, pseudogenization and gene regulation.