

Functional Analysis of *Cladosporium fulvum* Effector Catalog

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In their natural environment, plants are continuously exposed to a wide range of abiotic and biotic stresses. Virus, bacteria, fungi, oomycetes, nematodes and insects are the most important biotic agents that can cause serious yield losses in plants.

Cladosporium fulvum (syn. *Passalora fulva*) is a non-obligate fungal pathogen that mainly infects tomato (*Solanum lycopersicum*) and other wild *Solanaceous* species, causing the disease known as leaf mould. During infection, *C. fulvum* secretes various small (<21 kDa), cysteine rich proteins into the tomato leaf apoplast that were known as effectors. The *C. fulvum*-tomato pathosystem is a good model in order to study plant-microbe interaction. Recently, the genome sequencing of *C. fulvum* has been done by using the 454 technology. The main objectives on this study are the identification and characterization of novel effectors, which likely contribute the fungal virulence by manipulating the host metabolism to support fungal growth and reproduction, and as well as confirmation of the gene models for *C. fulvum* genome via bioinformatics, transcriptomics and proteomics approaches. By using gene models prediction software programs, 1,275 putative secreted proteins have been identified out of the approximately 1,4000 gene models for *C. fulvum*. So far,