Cladosporium fulvum is a biotrophic fungal pathogen that causes leaf mold of tomato. During infe
fulvum secretes a number of small proteins into the apoplast of tomato leaves, which are collective
effectors. So far, ten effector proteins have been characterized that in general show no or limited s
similarity to other proteins present in public databases. In this study we try to identify and fun
characterize additional *C. fulvum* effector proteins that are involved in fungal pathogenesis. Rece
genome of *C. fulvum* has been sequenced using the 454 technology. This genome sequence ena
identification of all secreted proteins from the fungus, collectively called the secretome. Howe
accurate mining and annotation of the effector secretome, gene calling programs need to be first o
by analyzing high quality expressed sequence tags (ESTs). Therefore, several cDNA libraries of *C*
grown under various *in vitro* and *in planta* conditions were constructed and are sequenced to
genome annotation. Initial automated annotation of the genome revealed that the fungus
approximately 13.000 genes, of which approximately 1200 encode putatively secreted
Bioinformatic analyses identified a subset of 300 putative effectors within the predicted secretom
additional proteomics analysis from apoplastic fluids of tomato leaves infected by *C. fulvum*, reve
proteins that are specifically produced in the compatible interaction. At this moment we are per
functional profiling of these novel effector proteins by examining their ability to inhibit PAMP t
Immunity and/or effector-triggered immunity in custom made assays.