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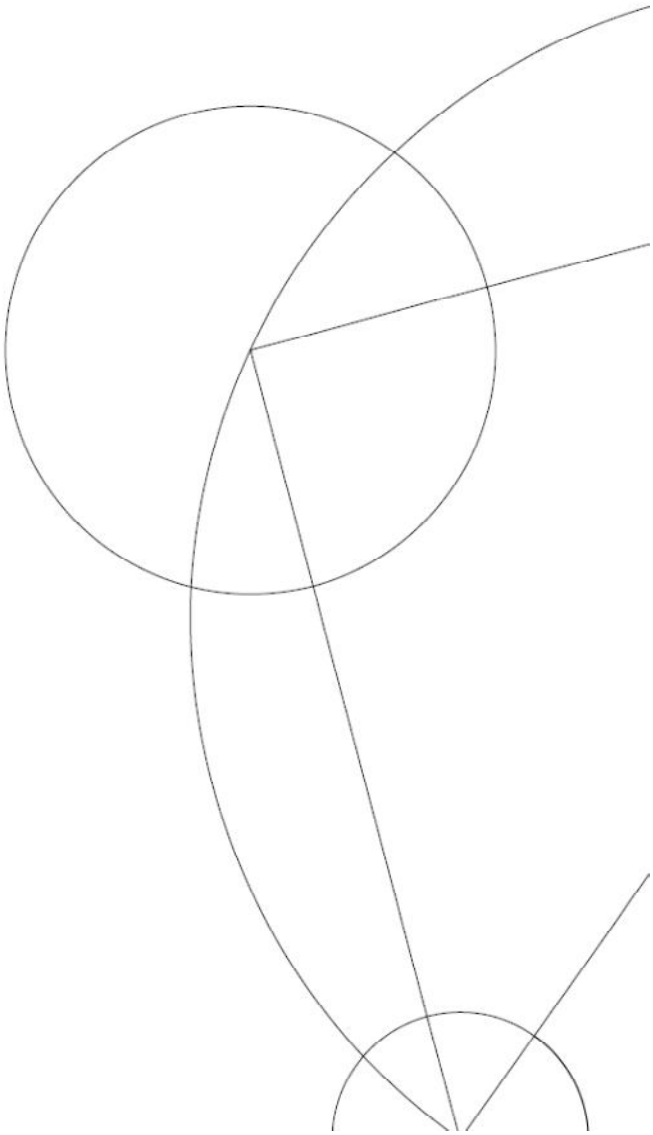

2.1. The epiphytic transcriptome of *Podosphaera fusca*, the causal agent of cucurbit powdery mildew

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Cucurbits are one of the most important crops in Spain with an annual production of 2.7 million tons and of benefits €1.2 billion. Unfortunately, diseases plague the production of cucurbits. Among then, one of the most important limiting factors for cucurbit production is powdery mildew. The disease can be caused by two species, *Podosphaera fusca* and *Golovinomyces orontii*. In Spain, however, *P. fusca* is considered to be the main causal agent of the disease, due to the climatic conditions of low moisture and high temperatures during the most of the growing season. Until now, most of the research efforts performed to study *P. fusca* have been focused on different aspects of disease control but in spite of these efforts, powdery mildew continues to impose serious limitations on cucurbit production throughout the world. Our knowledge on its basic biology and pathogenesis is very limited. In order to design novel and more durable control strategies, genomic information of *P. fusca* is needed, this is the reason why in this work we aimed to obtain and analyse the epiphytic transcriptome. Total RNA was isolated from epiphytic fungal material and sequenced using a 454 sequencing platform and the data were filtered with SeqTrimNEXT and assembled with the MIRA and Euler assemblers. Finally, the result of assembly process was merged with CAP3 to yield a total of 9565 contigs, which were then annotated. The annotation process was performed using three different annotation programmes, which increased significantly the accuracy of the process. To get insight into the relationships between the pathogen and the host plant, we focused our analysis on the pool of fungal secreted proteins, also named as the secretome. To identify the secretome, several features on putative proteins such as presence of signal peptide and absence of transmembrane domains were identified. After analysis, 117 putative secreted proteins were identified. This analysis allowed us to identify candidate effector proteins present in other powdery mildew species such as *G. orontii* and *Blumeria graminis* as well as others present exclusively in *P. fusca.* In order to validate the *in silico* assembly, a time-course transcriptional profiling of some selected genes was performed during the course of infection. We observed that the expression profile of candidate effector proteins was consequent with a canonical effector expression profile with a maximum of expression at the beginning of the infection process between 24 and 48 hours after inoculation. Functional analysis of these proteins remains to be done to confirm the effector function and to identify the target into the host plant.

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