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THE EPIPHYTIC TRANSCRIPTOME OF *PODOSPHAERA FUSCA* AND ITS PREDICTED SECRETOME

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The cucurbit powdery mildew fungus *Podosphaera fusca*, is a major limiting factor for cucurbit production worldwide. Despite its agronomic and economic importance, very little is known about fundamental aspects of *P. fusca* biology such as obligate biotrophy and pathogenesis. In order to design novel and more durable control strategies, genomic information of *P. fusca* is needed. In this work we aimed to analyse the epiphytic transcriptome of *P. fusca* as starting point. Total RNA was isolated from mycelia and conidia, and the corresponding cDNA library was sequenced using a 454 GS FLX platform. Annotation data was acquired for 62.6% of the assembled sequences, identifying 9,713 putative genes with different orthologues. In the transcript data set, the most represented protein functions were those involved in gene expression, protein metabolism, regulation of biological process and organelle organization. Our analysis also confirmed the existence of "missing ascomycete core genes" (MACGs) found in other powdery mildew species. After analysis of the pool of fungal secreted proteins, 118 putative secreted proteins were identified, including 35 "candidate secreted effector proteins" (CSEPs) specific for *P. fusca*. In order to validate the *in silico* assembly, the expression profile of some CSEPs was analysed, which was consequent with a canonical effector expression pattern, with a maximum of expression at the beginning of the infection process 24-48 h after inoculation. Our data open the genomics era of this very important cucurbit pathogen.