

331 DE NOVO ANALYSIS OF THE HAUSTORIAL TRANSCRIPTOME OF THE CUCURBIT POWDERY MILDEW FUNGUS PODOSPHAERA XANTHII REVEALS NEW CANDIDATE SECRETED EFFECTOR PROTEINS

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Backgrounds

Cucurbit crops are affected, among other pathogens, by the obligate biotrophic fungus *Podosphaera xanthii*, the main causal agent of powdery mildew in cucurbits. This fungus develops a specialized structure of parasitism termed haustorium. Haustoria are developed into epidermal cells and are responsible for nutrients uptake and effectors delivery.

Objectives

The aim of this study was to obtain the haustorial transcriptome of *P. xanthii* to complete the panel of effector candidates of this fungal pathogen.

Methods

To obtain the haustorial transcriptome, we have developed an effective method for isolation of haustoria without contaminants by flow cytometry. The cDNA library was built using a combination of dT primers and random primers followed by a depletion of ribosomal sequences. Sequencing was carried out by Illumina NextSeq550.

Conclusions

After bioinformatic analysis, we were able to identify 25 new effector candidates secreted by the classic pathway (with signal peptide) and 269 new candidates secreted by the non-classic pathway (without signal peptide). Most proteins had no functional annotation. By protein modelling and ligand predictions, we are now being able to assign putative functions to some of these candidates to select those with potential roles in pathogenesis for subsequent functional *in vivo* analysis by HIGS (host-induced gene silencing). By these approaches, we are starting to shed some light into the molecular mechanisms of pathogenesis in this very important pathogen of cucurbits.

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