34-8 - Investigation of *H. schachtii* transcriptome identifying putative novel effectors and host partner proteins

Elashry Abdelnaser, Samer Habash, Nahal Ahmadinejad[2], Heiko Schoof[2], Florian M. W. Grundler[2]

INRES Molecular Phytomedicine, University Bonn, Karlrobert-Kreiten-Str.13, 53115 Bonn, Germany
[2]INRES Crop Bioinformatics, University Bonn, Katzenburgweg2, 53115 Bonn, Germany
Friedrich-Wilhelms-Universität Bonn, INRES Crop Bioinformatics

Beet cyst nematode *Heterodera schachtii* (BCN) is one of the biotrophic sedentary endoparasite nematodes, which depends on a specific, multinucleate, syncytial feeding structure. The nematode secretes effector proteins into the affected root cell in order to induce and maintain the syncytium. We analyzed BCN transcriptome aiming to identify its secretome and functionally annotate them based on their structure by having signal peptide and lacking a transmembrane domain. We identified nearly 500 sequences as putative secretory proteins specific to plant-parasitic nematodes (P-PSP). Among P-PSPs, We identified 24 PSPs supported by previously known *H. schachtii*. However, those ESTs were not identified, in many cases, as PSP due to their truncated sequence. On the other hand, we used the Biana Interlog Prediction server (BIPs) to identify putative interacting partners of *A. thaliana* (At_Partners) with our PSP (Garcia-Garcia *et al.*, 2012). We identified 40 proteins that are predicted to have a putative interacting protein partner(s) within *A. thaliana* (Figure 1). Confirming the nature of our genes of interest to be considered as PSPs, we analyzed their level of expression and localization by qPCR and in situ hybridization, respectively.
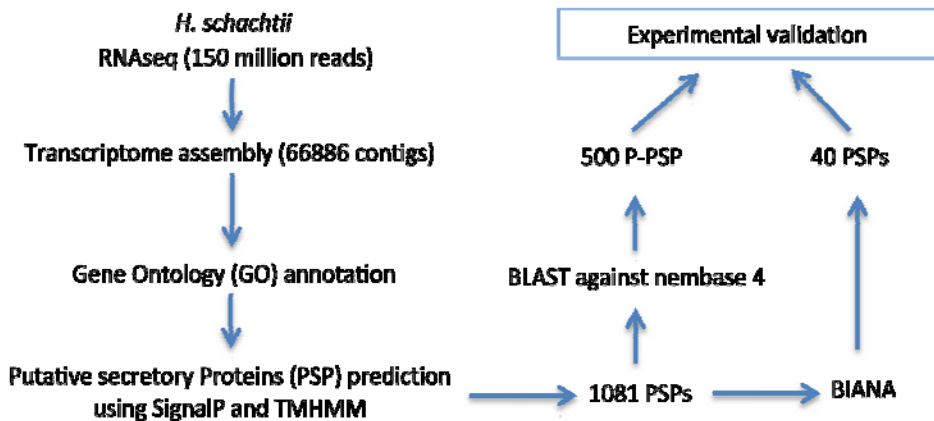

Figure 1. The scheme of the study showing the resulted portions of sequences identified as PSP, P-PSP, and predicted interacting proteins. PSP=Putative Secretory Proteins, P-PSP=Phytonematodes-specific PSP.

Literatur
Garcia-Garcia, J., Schleker, S., Klein-Seetharaman, J., & Oliva, B. (2012). BIPS: BIANA Interlog Prediction Server. A tool for protein-protein interaction inference. *Nucleic Acids Research*, *40*(Web Server issue), W147–51. doi:10.1093/nar/gks553