

34-7 - Parallel sequencing of *Heterodera schachtii* transcriptome revealed pioneer putative effectors

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Beet cyst nematode (BCN) *Heterodera schachtii* effectors are secretory proteins that are injected into the affected root cell in order to induce and maintain the syncytium (Wyss and Zunke, 1986; Grundler et.al.,1998). Many studies done to understand this interaction (Hewezi et.al.,2010) In our study, we aimed to understand more about plant-nematode interaction by identifying new nematode effectors. Comparing BCN transcriptome with available nematode ESTs resulted in the identification of 484 putative secretory proteins specific to plant-parasitic nematodes (P-PSP). We found that P-PSP datasets includes 24 sequences, which are supported by *H. schachtii* ESTs. Most of those pioneer putative effectors were not previously identified as PSP due to their partial sequences. Sequence validation of six putative effectors was done. Then the genes expression pattern study of showed that the expression of contig 45287 show no significant changes in the post-infective stages compared with the pre-infective J2s, while the other genes were up regulated in the post-infective stages in a range of 2 to 18 fold, which may indicate their role in the parasitism process (Figure1.A). Four of the upregulated contigs were localized within the esophageal gland (Figure.1B) by obtaining the in situ hybridization (de Boer, et. al. 1998). Further studies will be obtained on this PSPs to prove there importance in the parasitism prosedure, which giving a new mean of breeding programs against sugar beet cyst nematodes.

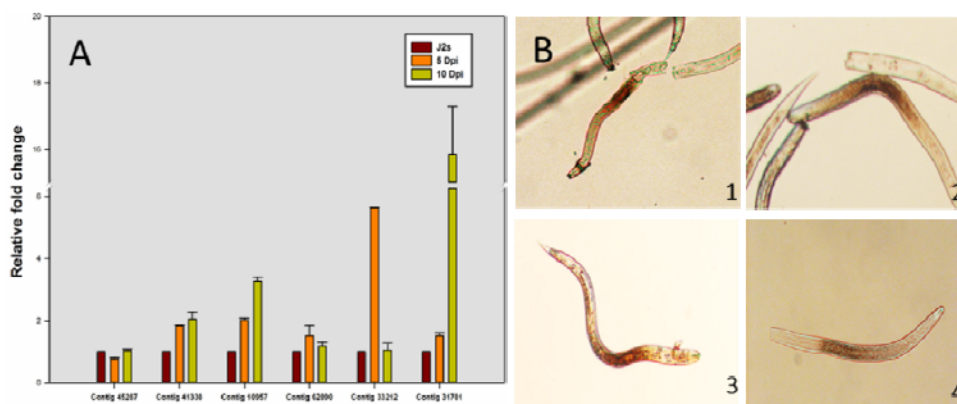


Fig. 1 A) The qPCR results testing the expression level of our genes of interest. (J2s) = second stage juveniles, 5 dpi = 5 days post inoculation, and 10 dpi = 10 days post inoculation. B) *in situ* hybridizations showing expression patterns of cDNAs encoding: (1) contig 31781, (2) contig 10957, (3) contig 62890, (4) contig 41338.

Literatur

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