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Understanding the *Heterorhabditis* nematode factors involved in modulating symbiosis with *Photorhabdus* bacteria

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Introduction

Animal and microbe symbiosis is ubiquitous in nature. The mono-specific association of *Heterorhabditis* nematodes and *Photorhabdus* bacteria offers a powerful model to study animal-microbe symbiosis.

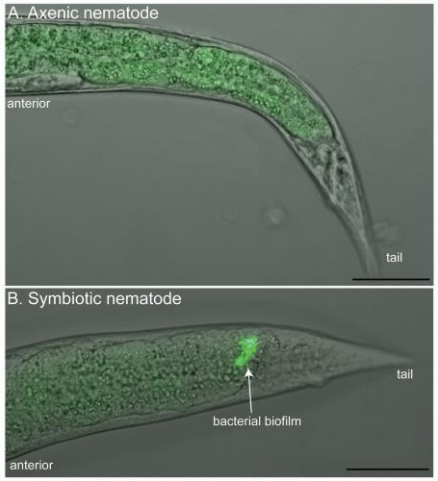

Figure 1. Early adult stage of symbiotic and axenic Heterorhabditis bacteriophora used for RNA-sequencing. A: Axenic early adult devoid of bacterial biofilm B. Bacterial biofilm in the posterior intestine of early adult stage of symbiotic nematode.

Method

RNA-sequencing was used to investigate nematode factors involved in symbiosis at the early-adult stage of *H. bacteriophora*.

Results

A total of 754 differentially expressed transcripts were identified in symbiotic nematodes.

Additionally, 12,151 transcripts expressed uniquely in symbiotic nematodes.

Endocytosis, cAMP signalling and focal adhesion were the top three enriched pathways in symbiotic nematodes, and a large number of transcripts involved in nematode immune/defence responses against bacteria were identified.

Conclusions

Our findings suggest that *Heterorhabditis* immune system plays a pivotal role in maintenance of symbiosis with *Photorhabdus* symbiont.

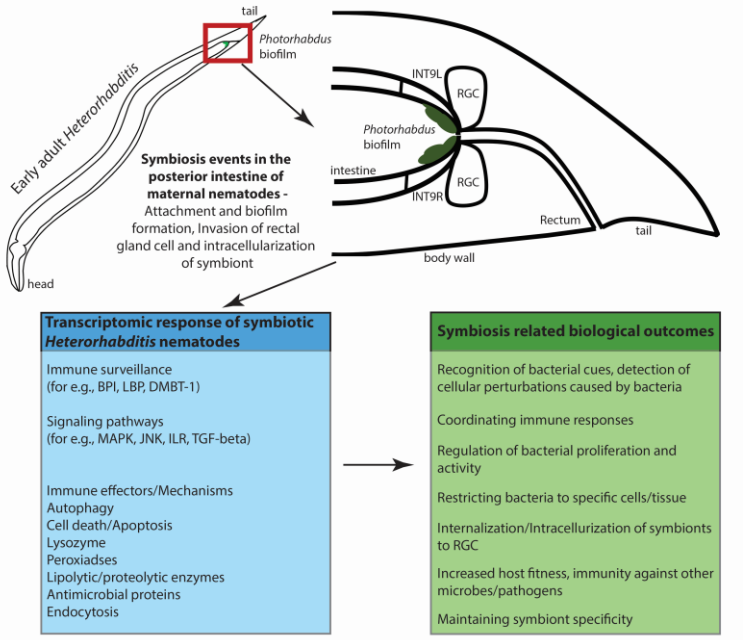

Figure 2. A model presenting symbiotic events and the transcriptomic responses in early adult stage of maternal nematodes, and their interpretation in relevance to symbiosis with *Photorhabdus* bacteria. Colonization processes involve two-way crosstalk between host and symbiont. From the nematode host side, based on gene expression profiling, expression of immune system components which are involved in the recognition of bacteria, bacteria-derived molecules and detection of any cellular perturbations caused by bacteria are observed. It leads to activation of signalling pathways and results in an array of host immune and defence responses such as autophagy, apoptosis and production of antimicrobial proteins. These effectors and mechanisms regulate symbiont bacterial numbers and help achieve successful symbiosis. INT9L/INT9R — posterior nematode intestinal cells; RGC- rectal gland cells.

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