

## How parasitism genes are regulated: a *motif* to search for genes regulators in the plant parasitic nematode *Bursaphelenchus xylophilus*

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Plant-parasitic nematodes threaten global agricultural and forestry systems. The search for new control strategies in line with the EU's sustainability goals highlight significant knowledge gaps. Like all other plant pathogens, plant-parasitic nematodes deliver several parasitism proteins (effectors) into the host plant to cause disease. NemaWAARS project focuses on mechanism(s) of regulation and gene control expression of parasitism genes in pinewood nematode, *Bursaphelenchus xylophilus*. From the previous transcriptomic data derived from the pharyngeal gland cells (considered a specialized tissue potentially related to parasitism) we have identified a non-coding DNA motif - STATAWAARS - associated in the promotor region of highly abundant and secreted expressed genes. Given that this non-coding genetic signature unifies many sequences of unrelated parasitism genes, it implies the existence of a potential major regulator(s), that binds to this sequence to control the expression of downstream genes. We hypothesize that by disrupting this regulator(s), it would be possible to simultaneously disrupt the expression of many associated parasitism-related genes. To test the hypothesis the project aims to identify proteins (or complex of proteins) that bind in the promoter regions of parasitism-related genes (*in vivo*) or identify other regulatory candidates for master regulators of parasitism-related genes expression that are enriched in the pharyngeal gland cell tissues. For the best candidate regulatory proteins, an RNAi approach will target the selected gene candidates and evaluate the regulatory role in effector genes expression and in interaction with the host (*in planta*). Under an ongoing national and international collaborative network, the strategy in NemaWAARS will include innovative approaches to explore the regulators that govern effector gene expression applied in *B. xylophilus* research.

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