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**Interação nemátode-planta: abordagem transcriptómica revela novos genes de parasitismo no nemátode da madeira do pinheiro, *Bursaphelenchus xylophilus.***

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Plant parasitic nematodes represent a serious problem in agriculture and forestry ecosystems worldwide. The migratory endoparastic nematode, Bursaphelenchus xylophilus (Pinewood nematode) has the unique feature of being a phytophagous and a mycetophagous, feeding on host trees cells (conifers trees) and leading to its death, causing Pine wilt disease. The main goal of this work was to identify and characterise the nematode proteins related to parasitism - specifically the secreted proteins named effectors – and understand the mechanism of parasitism by using next generation sequencing tools. Genome and transcriptome analysis revealed as a neutral tool towards the search for effectors and the results showed new insights into parasitism-related proteins, putative regulatory elements of gene expression and putative function in parasitism. In this study we were able to identify and predict new efectors that are upregulated in infection of the host, expressed in the parasitism specialized-tissue – pharyngeal gland cells – by using different, neutral approaches – based on transcriptomics and bioinformatics. This study report a new DNA sequence motif that is associated to the nematode gland cells expression and can be used to predict new parasitism genes.