Identification of parasitism-related genes in the specialized esophageal gland cells from the plant-parasitic nematode, *Bursaphelenchus xylophilus*

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The pinewood nematode (PWN), *Bursaphelenchus xylophilus*, is a migratory plant-parasitic nematode responsible for the pine wilt disease (PWD), causing economic and ecological losses in the forestry industry. Current climate change predictions emphasize an increase of PWD on conifers worldwide. The absence of effective measures to control PWN and the present restrictions on the use of chemical pesticides require the discovery of sustainable control solutions. Therefore, to develop novel control strategies is essential to comprehend the molecular mechanisms by which the PWN parasitize the host. The interactions between the nematode and the host are mediated by parasitism proteins most of which are produced in the esophageal gland cells (GC), considered specialized cells crucial in parasitism. A GC transcriptomic library was generated and provided a new set of candidate genes specific to PWN, which can be useful to explore for nematode target resistance. Therefore, this work aimed to identify putative candidates of parasitism-related genes by *in silico* analysis and to validate the spatial expression of the transcripts in the nematode tissues, using *in situ* hybridization. In the top 212 most abundant transcripts in the GCs, a set of 74 candidates were tested. Out of 74, 30 transcripts were specifically localized in the nematode GC and, from those, one third are novel genes with no sequence similarity to other genes and unknown protein domain (pioneer genes). Interestingly, most of these 30 transcripts are species and genus specific, which includes aspartic and cysteine peptidases, and saposin B-type domains. Characterizing the PWN parasitism proteins could offer new potential targets regarding the control of this quarantine pathogen.

This work is funded by National Funds through FCT - Foundation for Science and Technology under the Project NemaWAARS - 10.54499/PTDC/ASP-PLA/1108/2021 and individual funding for M. Mendonça (2024.00901.BD), M. Espada (10.54499/CEECIND/00066/2018/CP1560/CT0003) and C.S.L. Vicente (10.54499/CEECIND/00040/ 2018/CP1560/CT0001).