

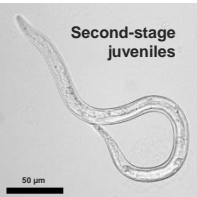
# Transcriptional changes of *Meloidogyne luci* second-stage juveniles after exposure to 1,4-naphthoquinone

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*Meloidogyne luci*, added to the EPPO Alert list in 2017, represents a threat to several important crops. The phasing out of nematicides from the market has intensified the search for phytochemicals with bionematicidal properties. The 1,4-naphthoquinone (1,4-NTQ) displayed strong nematicidal activity against *M. luci*. However, knowledge on potential mode(s) of action of 1,4-NTQ is still scarce. In this study, **transcriptome profile of *M. luci* second-stage juveniles (J2) after exposure to 1,4-NTQ was obtained achieved** to identify genes and pathways that might be involved on its mode of action.

## Methodology



- Water (H, control sample)
- Tween® 80, (T, 1,4-NTQ solvent)
- 1,4-NTQ 20 ppm (N) (3 biological replicates)



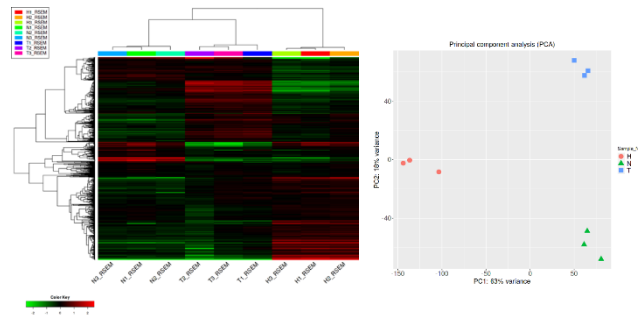
- RNA extraction
- Libraries generation
- Transcriptome sequencing
- Data processing/*de novo* transcriptome assembly
- Transcripts abundance and differential expressed genes (DEGs) identification and annotation



## *M. luci* transcriptome

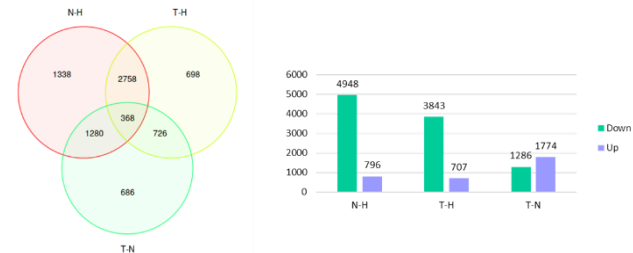
- *De novo* assembly of *M. luci* J2 transcriptome with 58,042 transcripts
- Gene abundance matrix with a total of 47,435 expected counted genes

## Heatmap and PCA analyses in IDEP.95



- Clear differences between the H, N and T treatments
- Minimal variations among biological replicates

## DEGs in response to treatments



- 7,854 DEGs among the 3 conditions
- Higher number of DEGs between N-H than between T-H or T-N treatments
- Higher number of down-regulated genes in both N-H and T-H comparisons, than up-regulated genes
- Closer number of up or down regulated genes between T-N comparison
- Perceptible antagonist effect of 1,4-NTQ on *M. luci*

On going: gene annotation of DEGs to identify nematode gene networks and metabolic pathways affected by 1,4-NTQ