

Preliminary analysis of microRNAs and their pathway genes in the genome of *Globodera pallida*.

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The *Globodera pallida* or potato cyst nematode (PCN) is one of the more specialized species of plant-parasitic nematode. *G. pallida* is a serious pest of potatoes around the world and causes loss of approximately 50% of European production. One of the most representative small noncoding RNA class is the microRNAs (miRNAs). They're responsible for gene expression control posttranscriptionally involved in multiples biological processes. This control is performed by transcriptional gene silencing, inhibition of translation or RNA-target cleavage. The miRNA processing pathway has several proteins including the key proteins of the pathway Argonaute, Dicer and Drosha. Recently, the genome of *G. pallida* was sequenced and deposited in WormBase – ParaSite. The aim of this work was to identify and characterize the miRNAs and miRNA pathway genes in the genome of *G. pallida* using bioinformatics approaches. Proteins from *Drosophila melanogaster* and *Caenorhabditis elegans* species were used as queries to search and predict the putative *G. pallida* miRNA pathway proteins. We also characterized the distribution of the conserved domains and also conserved amino acids in the active sites. The putative Argonaute and Dicer proteins predicted in *G. pallida* displayed highly conserved domains and amino acid in active sites when compared to their orthologue proteins. Besides phylogenetic analysis confirmed the conservation of the *G. pallida* proteins with their respective orthologues. Using a robust algorithm, we also found 51 mature miRNAs and 68 precursor miRNAs in the genome of *G. pallida*. We analyzed the thermodynamic and structural features of the precursor miRNAs and the conservation of the secondary and primary structure of the miRNAs identified. We found that several *G. pallida* miRNAs were much conserved compared to miRNAs from different species. The miRNAs glo-miR-87 and glo-miR-124 were 100% conserved when compared to miRNAs from nematode species displaying high conservation at mature miRNA level. The GC content and MFE (minimal free energy) values of *G. pallida* miRNA precursors displayed high conservation compared to ortholog miRNA values. The finding of this work provided better knowledge about miRNAs and miRNA pathway genes in nematode species collaborating with the understanding of the essential biological processes in *G. pallida*. The data obtained are unprecedented and could help to elucidate new methods to control this pest in potato species.

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