

ABSTRACT

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Title: THE SEQUENCE, GENOME ASSEMBLY, ANNOTATION AND BIOINFORMATICS ANALYSIS OF *MICROBACTERIUM NEMATOPHILUM*

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The bacterium *Microbacterium nematophilum* is a common pathogen of the nematode *Caenorhabditis elegans*. As *C. elegans* is a model organism, the mechanisms of infection by this *Microbacterium* of great interest. The purpose of this thesis study was to learn more about the bacterium and its mechanisms of infection by purifying the genomic DNA, and then sequencing, assembling, and annotating the genome. In doing so, the relationship between *M. nematophilum* and other *Microbacterium* species will be better understood as well. I also investigate the sequence of the putative plasmid (pMNI) located in *M. nematophilum*, and the DNA elements that facilitate the plasmid's replication, maintenance, and segregation during cell division. Regarding *C. elegans*, I examined if the genome contains genes that have facilitated its adaptation to being a *C. elegans* pathogen and the function of those genes.

The major advancements taking place in the field of genomics today are made possible by the recent evolution in DNA sequencing technology that is made available to researchers. The method that will be used to sequence the genome in this study is using a sequencing device called the MinION from Oxford Nanopore, UK. This device has broken down many barriers in the field of genomics. Emerging equipment like the MinION, as well as rising bioinformatics software, allow researchers to sequence, assemble, and annotate genomes from virtually anywhere and have lead to a drastic upsurge in the amount of genome announcements being published.