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Nikola Palevich

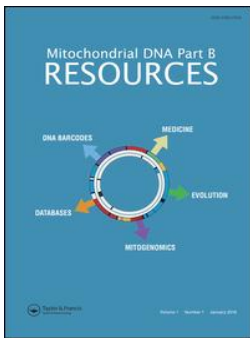
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The complete mitochondrial genome of the New Zealand parasitic roundworm *Teladorsagia circumcincta* (Trichostrongyloidea: Haemonchidae) field strain NZ_Teci_NP

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ABSTRACT

The complete mitochondrial genome of the New Zealand parasitic nematode *Teladorsagia circumcincta* field strain NZ_Teci_NP was sequenced and annotated. The 14,083 bp-long mitogenome contains 12 protein-coding genes (atp8 gene missing), two ribosomal RNAs (rRNAs), and 22 transfer RNAs (tRNAs). Phylogenetic analysis showed that *T. circumcincta* NZ_Teci_NP forms a monophyletic cluster with the remaining Haemonchidae species and further reinforces the high levels of diversity and gene flow observed among Trichostrongylidae.

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The large and highly variable mitochondrial (mt) genomes of helminths (worms), including parasitic nematodes (roundworms), are ideal sources of molecular markers suitable for studying population genetic structures and evolution. *Teladorsagia circumcincta* NZ_Teci_NP was selected for genome sequencing as a representative of an anthelmintic-susceptible NZ field strain of *T. circumcincta*. The specimen was collected from the Palmerston North area (40°21.3'S, 175°36.7'E) and is stored (accession number: NPX120886) and available upon request from AgResearch Ltd., Grasslands Research Centre. High molecular weight genomic DNA was isolated from multiple *T. circumcincta* adult males using a modified phenol:chloroform protocol (Palevich et al. 2017; Palevich, Kelly, et al. 2019). The Illumina MiSeq (Macrogen, Korea) platform was used to amplify the entire mitochondrial genome sequence (GenBank accession number: MN013406).

The mitogenome of NZ_Teci_NP (14,083 bp) is standard in size and comparable to the *T. circumcincta* (GQ888720) strain (Jex et al. 2010; Choi et al. 2017; Palevich, Maclean, et al. 2019). For example, all genes are transcribed in the same direction, there is a lack of the Atp8 gene, it contains 12 protein-coding genes (PCGs), two rRNAs, and 22 tRNAs. All 12 PCGs use standard ATN/TAN start/stop codons, respectively. The studied

genome has a high T content (46.1%) and a low C content (7.2%), resulting in a very strong A+T bias (77.3%). Gene order, sizes, and all common organization features are relatively conserved among the 43 nematode mitogenomes (usually 13.6–14.3 kb) (Jex et al. 2009; Palevich et al. 2018; Palevich, Maclean, Baten et al. 2019; Palevich, Maclean, et al. 2019).

The phylogenetic position of *T. circumcincta* was estimated using maximum-likelihood, implemented in RAxML version 8.2.11 (1000 bootstrap replications) (Stamatakis 2014), and the Bayesian inference (BI), implemented in MrBayes version 3.2.6 (default settings, four MCMC chains, 6.34–106 generations) (Huelsenbeck and Ronquist 2001) approaches. Mitogenome sequences of all 36 available nematode species were retrieved from GenBank. Analyses were performed both on the entire nucleotide sequences of the complete mitogenomes and using only the concatenated mitochondrial PCGs and rRNA genes, producing identical dendrogram topologies (Figure 1). *Teladorsagia circumcincta* formed a monophyletic cluster with the remaining Trichostrongylidae species, which then formed a sister clade with the Strongylidae family. Overall, the dendrogram topology is highly congruent with recent results (Palevich, Maclean, et al. 2019). In the pursuit of improving the phylogenetic resolution within the phylum Nematoda, future efforts should focus on the availability of

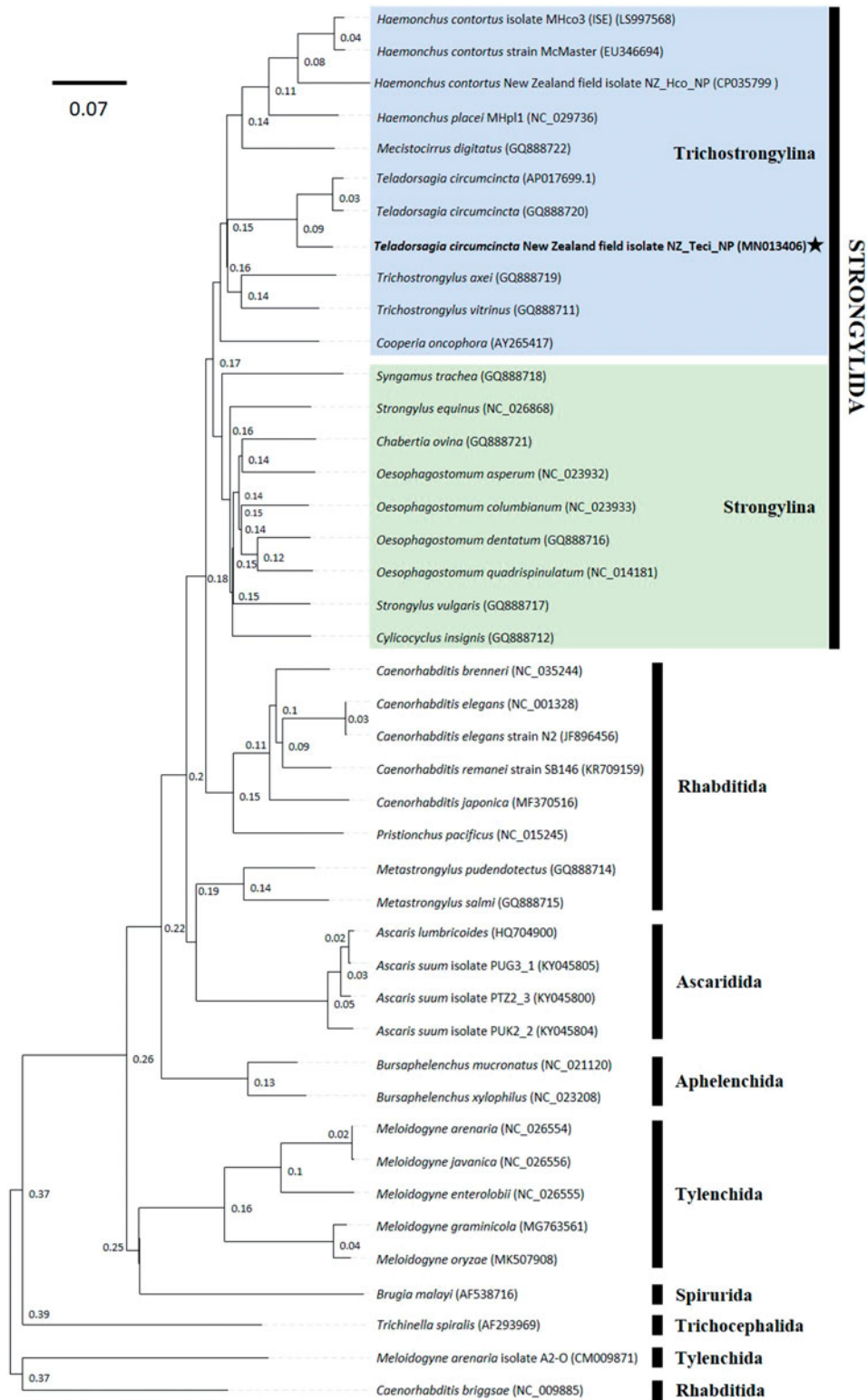


Figure 1. Phylogenetic analysis of the complete mt genomes for all 43 nematode species or isolates available in GenBank. The evolutionary relationships between the *T. circumcincta* field strain NZ_Teci_NP (highlighted by a black star) and the two major suborders of the Strongylida are represented by coloured boxes (Trichostrongylina (blue) and Strongylinina (green)). Species representing the Rhabditida, Ascaridida, Aphelenchida, Spirurida, and Trichocephalida have been included as outgroups. Phylogenetic analysis was conducted using maximum-likelihood and Bayesian inference (MrBayes). The numbers above the midpoint of each tree branch represent the statistical support for each node (based on posterior probability score). The phylogram provided is presented to scale (scale bar = 0.07 estimated number of substitutions per site) and GenBank accession numbers are provided (in parentheses) for all reference sequences. An identical topology was found with maximum-likelihood; all nodes were supported by >99% bootstrap re-sampling ($n = 1000$).

more complete mitogenomes across all nematode species, and especially for different strains/isolates.

Disclosure statement

No potential conflict of interest was reported by the authors.

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