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GENOME SEQUENCING

The Complete Genome Sequence of Splendidofilaria pectoralis (Onchocercidae, Rhabditida, Chromadorea, Nematoda)

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Biodiversity Genomes

We present the complete genome sequence of Splendidofilaria pectoralis, a nematode parasite of grouse (Aves: Galliformes: Tetraonini). Illumina paired-end reads were assembled by a de novo method followed by a finishing step. The raw and assembled data are publicly available via GenBank: Sequence Read Archive (SRR28509439) and assembled genome (JBFSWT000000000).

Introduction

The nematode *Splendidofilaria pectoralis* is a parasite of grouse and their relatives (Aves: Tetraonini). Adult nematodes are typically found in the subcutaneous tissue in the pectoral muscles of their hosts, but microfilarial larval stages can be present in other tissues (e.g., blood) (Gibson 1967). Notably, *S. pectoralis* is becoming more prevalent in birds at higher latitudes, likely as a result of climate change (Van Hemert, Pearce, and Handel 2014; Greiman et al. 2022). Despite its relevance to avian disease, no genomic resources exist for *S. pectoralis*. Here, we sequence the first genome of this species.

Methods

A single adult specimen of *S. pectoralis* collected from a wild Spruce Grouse (*Canachites canadensis*) near Wiseman, AK was used for sequencing. DNA extraction was performed using the Qiagen DNAeasy genomic extraction kit using the standard process. A paired-end sequencing library was constructed using the Illumina TruSeq kit according to the manufacturer's instructions. The library was sequenced on an Illumina Hi-Seq platform in paired-end, 2 × 150 bp format. The resulting fastq files were trimmed of adapter/primer sequences and low-quality regions with Trimmomatic v0.33 (Bolger, Lohse, and Usadel 2014). The trimmed sequence was assembled by SPAdes v2.5 (Bankevich, Nurk, Antipov, et al. 2012) followed by a finishing step using Zanfona v1.0 (Kieras 2021) to make additional contig joins based on conserved regions in related species.

Results and Data Availability

Raw and assembled data are publicly available via GenBank.

Raw reads: https://trace.ncbi.nlm.nih.gov/Traces/?view=run_browser&acc=SRR28509439

Assembled genome: https://www.ncbi.nlm.nih.gov/nuccore/JBFSWT000000000

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