Whole genome sequence of *Oscheius* sp. TEL-2014 entomopathogenic nematodes isolated from South Africa

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**Abstract**

We present the annotation of the draft genome sequence of *Oscheius* sp. TEL-2014 (Genbank accession number KM492926). This entomopathogenic nematode was isolated from grassland in Suikerbosrand Nature Reserve near Johannesburg in South Africa. *Oscheius* sp. Strain TEL has a genome size of 110,599,558 bp and a GC content of 42.24%. The genome sequence can be accessed at DDBJ/EMBL/GenBank under the accession number LNBV00000000.

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**Keywords:** *Oscheius* Entomopathogenic nematodes Whole-genome sequencing Genome assembly Genome annotation
distilled water under sterile conditions in a laminar flow hood. Whole genomic DNA was extracted from the sterile nematodes using a protocol adopted from Puregene® DNA Purification Kit. Centra systems 2003. 0.5% agarose gel was prepared in order to confirm the quality and integrity of the extracted DNA. A polymerase chain reaction was employed to amplify the 18S rDNA region using TW81 Forward Primer 5′-GCGGATCCTGCCATGTTGAACCTGC -3′, Tm (°C) = 71.94 and AB28 Reverse Primer 5′-GCGGATCCATATGCTTAAGTTCAGCGGGT -3′, Tm (°C) = 68.87. The same primers were used for the sequencing of this gene. The sequence obtained was subjected to NCBI BLAST under the default settings for highly similar alignments. The analysis revealed that among all the matches for the 18S rDNA gene sequences, the unknown sequence differed sufficiently from other submissions and thus the species was registered as a novel entomopathogenic nematode based on the originality of the 18S rDNA sequence. The nematode was then assigned the name Oscheius sp. TEL-2014. A phylogenetic tree was constructed using MEGA 6 to show the evolutionary relationship of Oscheius sp. TEL-2014 with selected species from genera Oscheius, Steinernema and Heterorhabditis shown in Fig. 1. Genomic DNA paired-end libraries were generated with the Nextera DNA sample preparation kit (Illumina) and indexed using the Nextera index kit (Illumina). Paired-end (2′125 bp) sequencing was performed on a Illumina Hiseq 2500 using the Illumina SBS v4 chemistry at the Agricultural Research Council Biotechnology Platform. Quality control was done using FastQC version 0.11.3 and adapter trimming was performed using Trimmomatic version 0.32. The genome was assembled using Velvet version 1.2.10, generating 53,190 contigs. The largest contig was 146,289 bp long. QUAST version 3.1 was used for the assessment of the assembly and BUSCO version 1.2.1 was used to assess the completeness of the assembly. The N50 value was 3 019 and the total genome size was 110,599,558 bp, which is on the same size range as C. elegans. Repetitive DNA sequences were masked and identified using Repeat Masker version 3.3.0. The number of bases masked was 425 3249 bp. Retroelements, long terminal repeats (LTR elements), DNA transposons, Small RNA, Satellites and Simple repeats were some of the features identified. 49 947 genes were predicted using blastx and AUGUSTUS version 2.5.5. Protein sequences of the predicted genes were subjected to SwissProt and NCBI BLASTP to identify the proteins. These gene prediction and protein identification tools have revealed the presences of protein domains, hypothetical protein and other proteins also found in nematodes. For example, the WD40 repeat domain (Fig. 2) was predicted and found on position 5208 (start) to 5385 (end). This protein was identified from Haemonchus contortus also known as Barber pole worm which also belongs to the phylum Nematoda, Chromadorea, Hinhbitida. Another protein predicted in Oscheius sp. TEL-2014 is a hypothetical protein CAEBREN_28360, also found in Caenorhabditis breneri genome. This protein may be further hypothesised to be involved in nematodes chemotaxis and behaviour. Topoisomerase II large subunit originally found in Escherichia phage PBECO 4 was predicted to be present in the Oscheius nematodes genome. Histidine kinase-like ATPases is one of the domains present in this protein. A Histidine kinase-like ATPases was predicted to be present in Oscheius nematodes. The TOPRIM superfamily also comprises of numerous ATP-binding proteins such as histidine kinase, DNA gyrase B, topoisomerases, heat shock protein HSP90, phytochrome-like ATPases and DNA mismatch repair proteins (Fig. 3). The heat shock protein HSP90 may be hypothesised to be involved in desiccation tolerance of these entomopathogenic nematodes. The genome data described in the present study offers a valuable platform for future studies of Oscheius nematodes and possesses
momentous importance in the agricultural industries and scientific research. More features of the genome will be identified and analysed using more annotation tools.

3. Nucleotide sequence accession numbers

This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession LNBV00000000.

Conflict of interest

The authors declare that there is no conflict of interest on any work published in this paper.

Acknowledgments

I, Tiisetso Elizabeth Lephoto received an Innovation Doctoral Scholarship from the NRF National Research Foundation (NRF) with the grant number [SFH1208147793] and a Wits Postgraduate Merit Award (PMA) from the University of the Witwatersrand. Thanks to Gauteng Department of Agriculture and Rural Development (GDARD) (GDARO 12TS) for funding the research project. Thanks to the Agricultural Research Council (ARC) Biotechnology platform for Illumina technology sequencing services.

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