Pentastomida are an intriguing group of highly adapted worm-like hematophagous parasitic crustaceans (Riley 1986). The pentastomid genus Linguatula usually infests the nasal sinuses of carnivorous mammals belonging to the families Canidae, Hyaenidae and Felidae while using other mammals, particularly ruminants (Rezaei et al. 2011), as intermediate hosts. In fact, a wide range of mammals have been recorded as intermediates (Christoffersen & De Assis 2013) and humans as definitive hosts. In other words, L. arctica, parasites the upper respiratory (nasal) passages and maxillary sinuses of reindeer and caribou and is sometimes referred informally to as the ‘reindeer sinus worm’. For an overview of its morphology and biology, see Nikander and Saari (2006) and Riley et al. (1987). An interesting aspect is thus the fact that, unlike the other four Linguatula species, it appears to have a direct life cycle (Haugerud and Nilssen 1990). In other words, L. arctica does not require an intermediate host and, unusually, has an unglute – as opposed to a carnivore – as its definitive host.

DNA for the present study was obtained from an adult female L. arctica specimen that had been collected from the nasal passages of a domesticated reindeer in the municipality of Tromsø (69°39′50″N, 18°58′02″E), northern Norway (Gjerde 2013). The complete mitogenome was obtained from next-generation shotgun sequencing. Paired-end Illumina sequencing libraries were generated from tissue sample and sequenced on an Illumina NextSeq 500 platform, using Illumina NextSeq® 500/500 High Output Kit V2. Sequencing yielded over 2 million 150 bp paired end reads. A complete mitochondrial genome was obtained with NOVOplasty 2.4 (Dierckxsens et al. 2017) using kmer 51, and the mitogenome of Linguatula serrata (MG951756) as bait reference.

Annotations were carried out with MITOchondrial genome annotation Server (MITOS) (Bernt et al. 2013), and manual validation of the coding regions using the NCBI ORF Finder (http://www.ncbi.nlm.nih.gov/gorf/gorf.html) in combination with NCBI’s Conserved Domain Database (CDD) (Marchler-Bauer et al. 2017). The annotated sequence file was submitted to NCBI (accession MN792849), and a voucher of the specimen is deposited in the Museum für Naturkunde Berlin under the accession code ZMB_Arach 49469. The phylogenetic position of the new sequence of L. arctica according to the gene Cytochrome B is shown in Figure 1.

The complete mitochondrial transcript of L. arctica was 14,789 bp in length and contained 13 protein-coding genes (PCGs), 2 ribosomal RNA genes and 22 transfer RNA genes. As described for other related pentastomid mitogenomes (Grau et al. 2017; Naude et al. 2018), the mitochondrial genome of L. arctica contained an A + T bias with an overall base composition of 32.6% A, 27.5% T, 32.8% C, and 7.1% G, and a GC content of 39.9%. The gene arrangement is identical to that of previously described pentastomid mitogenomes.
The mitochondrial genome of *Linguatula serrata* was sequenced, with a focus on accurately determining the control region length. Mitogenomes, while difficult to establish precisely, are expected to aid in classification. The mitochondrial genome of *Linguatula arctica* was also sequenced, with gene length measurements of *ND1, ND2, ND3, ND5, ND6, COX1, COX2, COX3*, and *COX4*. A total of nine PCGs were identified as having ATG as their initiation codon. Incomplete termination codons were found for three PCGs (ND4L, COX2, and ND4). The mitochondrial genome of *Linguatula serrata* was compared to the *Linguatula arctica* gene sequence, illustrating phylogenetic position. The authors acknowledge financial support and funding from Innovationsfond of Museum für Naturkunde Berlin.

**Data availability statement**

The data supporting the findings of this study are available in GenBank (accession numbers MT200757–MT200777). Seven PCGs were found to be useful for phylogenetic analysis, including ND2, COX1, ATP8, ATP6, ND3, ND5, and ND4L. Incomplete termination codons were found for three PCGs, and additional 3'-A residues were present. Nine PCGs (ND2, COX1, ATP8, ATP6, ND3, ND4, ND6, CYTB, and ND1) used a TAA termination codon, while ND4L used a TAG termination codon. The 12S and 16S rRNA genes and the mitochondrial cytochrome c oxidase subunit I gene were also sequenced.

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