The complete mitochondrial genome of *Aporrectodea rosea* (Annelida: Lumbricidae)

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Despite the huge ecological importance of the Lumbricidae family (Hendrix et al. 2008), only one lumbricid mitochondrial genome was published for *Lumbricus terrestris* (Boore and Brown 1995). Mitochondrial genomes of representatives of other earthworm families from subtropical regions were also sequenced (Zhang et al. 2015; Wang et al. 2015; Zhang, Jiang, et al. 2016a, 2016b; Zhang, Sechi, et al. 2016).

*Aporrectodea rosea* is a widespread cosmopolitan earthworm found both in natural and agricultural habitats throughout the temperate zone (Vsevolodova-Perel 1997). This species is known for its high genetic diversity; the species is divided into Mediterranean and Eurosiberian lineages, each of which contains multiple genetic lineages that differ by 10–15% nucleotide substitutions in mtDNA (King et al. 2008; Fernández et al. 2016).

*Aporrectodea rosea* individuals were collected near the Vodnik station, to the north of Omsk, Russia (approximately N55.05 E73.40). Several ethanol-fixed individuals were identified morphologically. Total RNA was extracted from a typical specimen by Trizol; DNA was extracted in parallel, and by sequencing the coi barcode we confirmed that it belonged to an *A. rosea* L4 individual. Genomic DNA of the studied specimen (R41_Arosea) and ethanol-fixed specimens from the same population are stored in the collection of ICiG SB RAS in Novosibirsk. TruSeq Stranded mRNA kit (Illumina) was used to isolate and reverse transcribe poly-A mRNA. Single-end 150 bp reads were obtained on Illumina NextSeq 500 machine using a NextSeq 500 Mid Output Kit (Illumina). RNA reads were assembled using Trinity v.2.4.0 (Grabherr et al. 2011). Search for mitochondrial sequences was performed using the blastn, blastp, and blastx algorithms (Boratyn et al. 2013) with *L. terrestris* genome as a reference, which allowed us to recover *A. rosea* mtDNA sequence except for the control region. The latter could not be assembled from the RNAseq data due to repeats and was thus obtained by PCR using Herculase (Agilent Technologies). Phylogenetic analysis was performed using MrBayes v3.2.6 (Ronquist and Huelsenbeck 2003) based on the complete protein dataset of earthworm mitochondrial genomes (Figure 1).

The complete mtDNA sequence was annotated and deposited in GenBank under the MK573632 accession number. The complete mitochondrial genome of *A. rosea* L4 is 15,086 bp long and contains the typical gene complement of 13 protein-coding genes, 22 tRNAs, and 2 rRNAs. AT-content is 65.5%, and the coding strand is significantly enriched for both A (32%) and T (31%).

All genes are encoded by a single DNA strand and are thus probably transcribed as a single transcript. Compared to the *L. terrestris* mtDNA, the genome of *A. rosea* has a 56 bp deletion in the region between the cytb and tRNA-Trp genes. The control region located between the Arg- and His-tRNA genes is 512 bp long, which is about 130 bp longer than in *L. terrestris*, and contained a 130-bp long stretch of TA-microsatellite and a 22 bp long polyA tract. The nd4l and nd4 genes overlap by seven bp. All protein-coding genes start with ATG. Stop-codons are represented by TAA (for coi, nd6, nd5, and nd4l), or by TA or T (the rest of the genes), believed to be expanded to TAA by polyadenylation.

Phylogenetic analysis based on the 13 protein-coding genes (Figure 1) revealed that *A. rosea* groups together...
with *L. terrestris* is another representative of the Lumbricidae family.

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No potential conflict of interest was reported by the authors.

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