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Mitochondrial genome of *Dinophilus gyrociliatus* (Annelida: Dinophilidae)

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ABSTRACT

Here we report the 14,678 bp mitochondrial genome of the annelid *Dinophilus gyrociliatus*, the first mitochondrial genome from Dinophilidae. We recovered 13 protein-coding genes, two rRNA, and 21 tRNA, the order of which is different from other annelid species. Interestingly, trnS1 was not recovered. The GC% across the genome was 34.20%.

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Mitochondrial genome; annelid; gene-order

Dinophilus gyrociliatus is a small interstitial polychaete worm which inhabits littoral zones worldwide (Prevedelli and Vandini 1999; Prevedelli and Simonini 2000). They undergo dimorphic programmatic sex determination; males are ~50μm long whereas females may reach 1.2 mm (Windoffer and Westheide 1988). Males possess no organs save those required for reproduction and die shortly after fertilizing their sisters (Åkesson and Costlow 1991). These features make *D. gyrociliatus* a popular candidate for studying sex ratio and determination (Åkesson and Costlow 1991; Prevedelli and Vandini 1999; Prevedelli and Simonini 2000; Simonini and Prevedelli 2003). Relatively easy to culture, *D. gyrociliatus* also make a good model for neurological studies (Müller and Westheide 2002; Fofanova and Voronezhskaya 2012). Although Dinophilidae were once placed close to dorvilleid annelids, their phylogenetic affinities are uncertain (Figure 1) (Struck et al. 2015).

Animals were originally collected from fouling material on dock pilings near the Duke Marine Laboratory, Beaufort, NC (34°43′04″N 76°40'14″W). Cultures were obtained from the late Bertil Åkesson in 2000 and grown on a spinach diet. Multiple individuals were harvested and frozen at −80 °C until their DNA was extracted in 2012 using a Qiagen DNEasy blood and tissue extraction kit (Qiagen Inc., Valencia, CA) according to the protocol from the manufacturer. Total genomic DNA was prepared with Illunina's Nextera DNA sample preparation kit (Illumina, San Diego, CA) and run on an Illumina MiSeq sequencer using a 2 × 250 paired-end protocol in the Molette Laboratory, Department of Biological Sciences, Auburn University. Mitochondrial genomes were assembled de novo using Ray 2.2.0 (Boisvert et al. 2010) after digital normalization. To identify putative mitochondrial contigs, BLASTn (Altschul et al. 1997) was employed with the *Riftia pachyptila* mitochondrial genome (GenBank Accession AY741662; Jennings and Halanych 2004) as a bait. One contig was recovered which was long enough to represent the entire mtDNA genome. This contig was annotated using MITOS 2 (Bernt et al. 2013) and gene boundaries were compared manually with published annelid mitochondrial genomes.

The mitochondrial genome of *Dinophilus gyrociliatus* (GenBank Accession MG428625) is 14,678 bp long, making them the eighth shortest (12th percentile) of the 70 annelid mitochondrial genomes currently listed on Genbank. The overall nucleotide composition is as follows: A = 33.9% (4978 bp), C = 11.8% (1738 bp), G = 22.3% (3283 bp), and T = 31.8% (4679 bp). A GC content of 34.20% puts the *D. gyrociliatus* mitochondrial genome in the 47th percentile among annelids.

Thirteen protein-coding genes were found, consistent with other animal mitochondrial genomes. The ribosomal RNA rrnL was not initially recovered by MITOS (Bernt et al. 2013) but it was subsequently identified via a Blastn search of positions 4369–5457. Surprisingly trnS1, a transfer RNA prevalent throughout animal mitochondrial genomes, was absent from searches in both MITOS and ARWEN v1.2 server (Laslett and Canbäck 2007).

Mitochondrial gene order is expected to be conserved in Pleistoannelida, of which *Dinophilus* is a member (Struck et al. 2015). However, the ATP6 to NAD5 block was found switched with the adjacent COX3-NAD6-CYTB block in *D. gyrociliatus* compared with the hypothesized ground state of mtDNA for Pleistoannelida (Weigert et al. 2016). As anticipated, tRNA gene order is less conserved, no two tRNAs remain consistently adjacent across seven Pleistoannelids (including *Marphysa sanguinea* – KF733802.1, *Nephtys* sp – EU293739.1, *Platynereis dumerilii* – AF178678.1, *Typosyllis*

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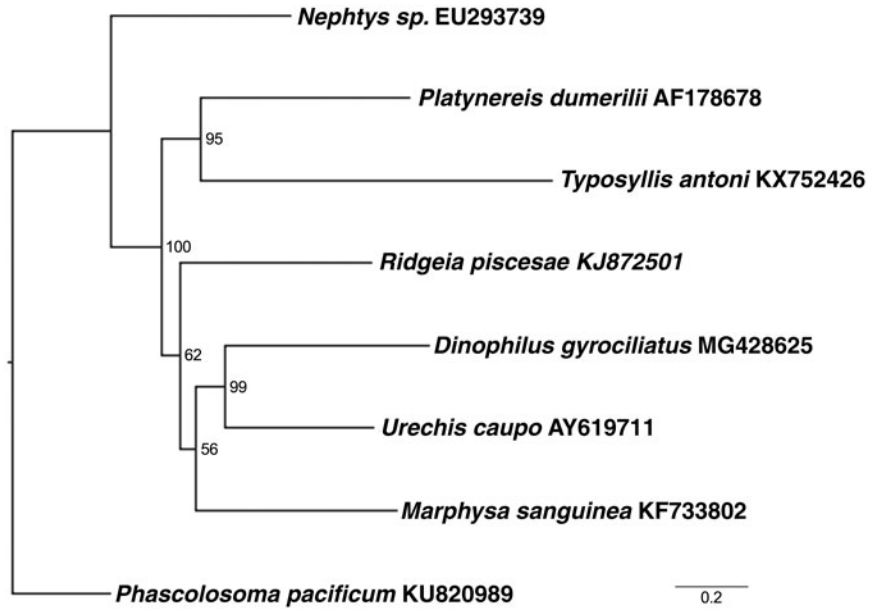

Figure 1. Maximum-likelihood tree with boostrap support (1000 iterations) of concatenated nucleotide sequenes for thirteen mitochondrial protein-coding genes in seven Pleistoannelid species (see text). The GTRGAMMA model was employed using RAxML (Stamatakis 2014). *Phascolosoma pacificum* – KU820989.1 was used as the outgroup.

antoni – KX752426.1, *Ridgeia piscesae* – KJ872501.1, and *Urechis caupo* – AY619711.1).

Disclosure statement

The authors report no conflicts of interest.

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