Mitochondrial DNA

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MITOGENOME ANNOUNCEMENT

Complete mitochondrial genome of the Antarctic midge *Parochlus steinenii* (Diptera: Chironomidae)

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Abstract

Parochlus steinenii is a winged midge found in the Antarctic Peninsula and its offshore islands. We determined the complete mitochondrial genome sequence of *P. steinenii*, which is comprised of 16 803 nucleotides and contains 13 protein-coding genes (PCGs), 22 tRNA genes, and the large (rrnL) and small (rrnS) rRNA genes. Its total A + T content is 72.5%. The PCG arrangement of *P. steinenii* is identical to that of the ancestral Diptera ground pattern. This is the first report on the mitogenome sequence of an Antarctic midge, and provides insights into the evolution of dipterans in Antarctica.

Keywords

Antarctic winged midge, complete mitochondrial genome, *Parochlus steinenii*

History

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Two species of *Chironomidae* are found in the Antarctic Peninsula: the wingless midge *Belgica antarctica,* and the winged midge *Parochlus steinenii* (Edwards & Usher, 1985; Shimada et al., 1991). *Belgica antarctica* is famous for its unusual adaptations, including winglessness, freeze tolerance, and desiccation tolerance. *Parochlus steinenii*, even though it occurs naturally in the Antarctic with *B. antarctica*, is by contrast not tolerant to freezing and is winged (Shimada et al., 1991). Recently, the genome sequence of the wingless midge *B. antarctica* was announced as the first Antarctic eukaryote (Kelley et al., 2014). To understand the freeze tolerance of *B. antarctica*, *P. steinenii* could be a good species for comparative analysis.

To identify the phylogenetic relationships of the taxa, we sequenced the mitochondrial genome of *P. steinenii*. Specimens of *P. steinenii* were collected from King George Island, West Antarctica (62°14′S, 58°47′W) during the summer activity in 2015. Genomic DNA was extracted using a DNeasy Tissue Kit (Qiagen, Valencia, CA). Mitochondrial genome sequencing was performed with the MiSeq platform (Illumina, San Diego, CA). Shotgun libraries were prepared and sequenced according to the manufacturer's instructions. In order to identify reads of mitochondrial origin, reads were mapped against the mitochondrial genome sequence of *Chironomus tepperi* (NC_016167) using Bowtie 2 (Langmead & Salzberg, 2012), and read pairs where at least one read was mapped were collected. Assembly was performed with ABYSS (Simpson et al., 2009) and annotation was performed using MITOS webserver (Bernt et al., 2013).

The complete sequence of the mitochondrial genome of *P. steinenii* (GenBank accession number: KT003702) was found to be 16 803 bp in length, and it was comprised of 13 protein-coding genes (PCGs), 22 tRNA genes, and the large (rrnL) and small (rrnS) ribosomal RNA subunits genes. A + T contents of the total coding region, N-strand genes, and J-strand genes are about 70.58%, 73.05%, and 68.31%, respectively.

Phylogenetic analyses were performed to examine the relationships of *P. steinenii* and other closely related dipterans for which complete mitogenomes exist, including *Anopheles quadrimaculatus* A (NC_000875), *Trichocera bimacula* (NC_016169), *Aedes albopictus* (NC_020662), *Aedes aegypti* (NC_010241), *Chironomus tepperi* (NC_016167), *Paracladura trichoptera* (NC_016173), *Sylvicola fenestralis* (NC_016176), *Cramptonomyia spenceri* (NC_016203), *Arachnocampa flava* (NC_016204), and *Drosophila melanogaster* (NC_024511). Protein-coding gene sequences were aligned using PRANK (Ver. 130820) under a codon model (Loytynoja & Goldman, 2005), poorly aligned regions were removed using Gblock (Ver. 0.91) (Castresana, 2000), and then the remaining alignment regions were concatenated. Bayesian methods were used to reconstruct phylogenetic relationships using MrBayes 3 (Ver. 3.2.2) with third codon positions excluded (Nst = 6, Rrates = Invgamma, Ngen = 10 000 000, sampling every 10 gen, nchains = 8, nruns = 2, burnin = 0.2, outgroup = *D. melanogaster*, all other parameters set at default values) (Ronquist & Huelsenbeck, 2003) (Figure 1). The resulting phylogenetic tree showed that *P. steinenii* forms a clade with *C. tepperi* (Chironomidae).

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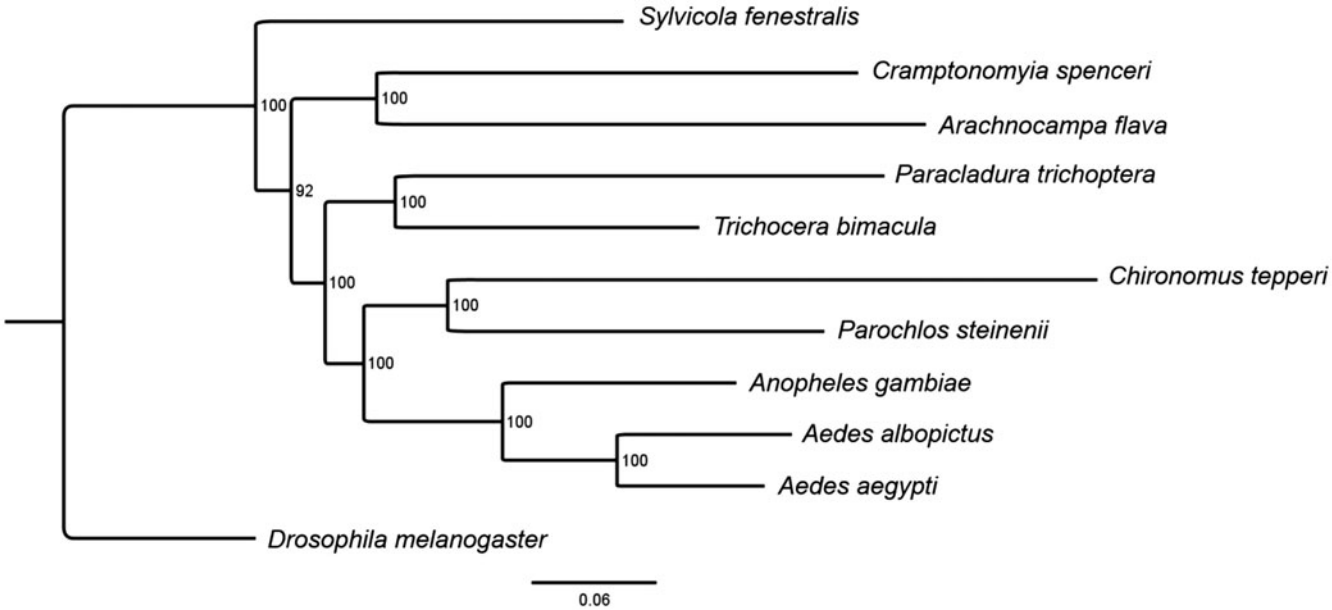

Figure 1. Bayesian phylogeny of concatenated mitochondrial genome protein sequences (excluding third position of codon) with posterior probabilities.

Declaration of interest

This study was supported by the Korea Polar Research Institute (grants PE15070 and PE15080). The authors report no conflicts of interest. The authors alone are responsible for the content and the writing of the paper.

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