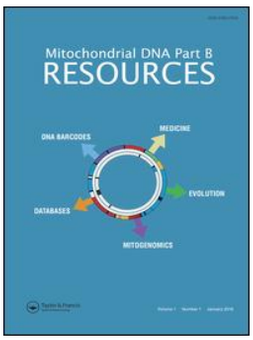

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ISSN: (Print) 2380-2359 (Online) Journal homepage: https://www.tandfonline.com/loi/tmdn20

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To cite this article: Nina V. Voronova, Derek Warner, Raman Shulinski, Sofiya Levykina, Yury Bandarenka & Dmitrii Zhorov (2019) The largest aphid mitochondrial genome found in invasive species *Therioaphis tenera* (Aizenberg, 1956), Mitochondrial DNA Part B, 4:1, 730-731, DOI: 10.1080/23802359.2018.1561217

To link to this article: https://doi.org/10.1080/23802359.2018.1561217

Published online: 08 Feb 2019.

MITOCHONDRIAL DNA PART B
2019, VOL. 4, NO. 1, 730–731
https://doi.org/10.1080/23802359.2018.1561217

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MITOGENOME ANNOUNCEMENT

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The largest aphid mitochondrial genome found in invasive species *Therioaphis tenera* (Aizenberg, 1956)

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ABSTRACT

The complete mitochondrial genome of *Therioaphis tenera* (Aizenberg) was sequenced using Ion Torrent sequencing technology. The genome is 19,200 bp in length, which is the largest mitochondrial genome of aphids that has been sequenced so far. *Therioaphis tenera* mtDNA contains the D-loop, 36 coding genes instead of typical 37 due to the absence of Phe-tRNA, and a repeat region which is extremely long (3013 bp). Among all aphids with sequenced mitochondrial genomes, only *T. tenera* has a smaller number of genes in the mtDNA.

ARTICLE HISTORY
Received 19 October 2018
Accepted 5 December 2018

KEYWORDS
Therioaphis tenera; Aphididae; Hemiptera; mitochondrial genome

Therioaphis tenera (Aizenberg, 1956) is a specialist on different species of *Caragana* Fabr. and an invader in Belarus and other European countries (Zhorov et al. 2014). The territory of origin of *T. tenera* is Middle Asia where *Caragana* are native. *Therioaphis tenera* has been introduced to Europe together with its host-plants and is now widely distributed (Ripka 2004; Ratajczak et al. 2011; Sautkin and Buga 2012). Before the current work, no whole mitochondrial genomes of Calaphidinea have been published, which makes the *T. tenera* mtDNA especially interesting to study.

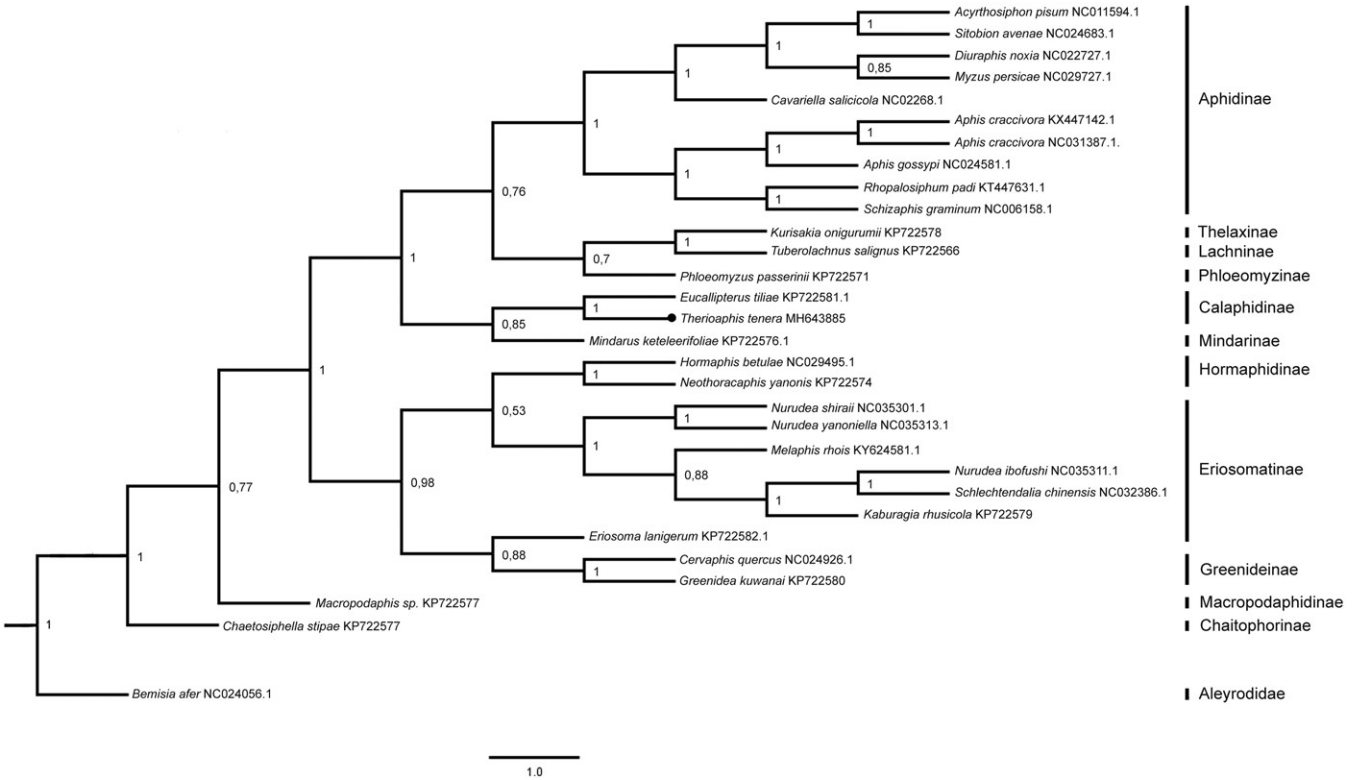

Figure 1. The phylogenetic tree of Aphididae using all mitochondrial protein-coding genes and Aleyrodidae as an outgroup. Numbers indicate the posterior probabilities of the topology. GenBank accession numbers and subfamily affiliations were indicated to the right of the terminals.

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Imagines of *T. tenera* were collected 24.06.2015 in Belarus (N 53.932154; E 27.559755) from *C. arborescens*. Spacemen vouchers and morphological slides were included into the entomological collection of the Belarusian State University's zoological museum.

The mitochondrial genome of *T. tenera* is 19,200 bp in length which is the largest known aphid mitogenome. It contains 13 protein-coding genes, two genes of ribosomal RNA and 21 tRNA genes. To date 18 aphid mitochondrial genomes were published, 15 of them concluded 37 genes, which is typical for animals, 1 did 38 and 1–39 genes due to the duplication of tRNAs (Ren et al. 2016). The Phe-tRNA is only a gene which is absent in the *T. tenera* mtDNA.

The *T. tenera* mitochondrial genome has a high A + T content of 79.1% that is slightly lower than in most of aphid mitogenomes, which usually is more than 80% (Wang et al. 2013). In protein-coding genes sequences, the A + T content is still 81.4%. Excluding the fact of one tRNA gene absence, the gene order is the same as in most of aphids, which is highly conservative. All protein-coding genes are initiated by the standard ATN codon and terminated with TAA, except the gene NAD4 with stop-codon TTT.

Aphid mitochondrial genomes have a regulatory region that is highly variable in length (Jager et al. 2014; Wang et al. 2014; Zhang et al. 2016) and usually is of 400–800 bp length but can vary from extremely short one in *Hormaphis betulae* (94 bp) (Li et al. 2017) to the largest in *M. persicae* (2531 bp). In the *T. tenera* mitochondrial genome, the regulatory region is 1451 bp long.

The repeat region was also found in *T. tenera*. Its repeat region is the largest of all known aphid repeat regions and contains two identical sequences of 161 bp each separated with a 132 bp region and with a 2553 bp non-coding region lying downstream. This type of repeat region is unusual in aphids because of both an extreme large size and a low proportion of A + T content (Ren and Wen 2017).

We used Bayesian analysis and MCMC method to estimate the phylogeny of aphids using the PCG of all 17 whole and 12 partial aphid mitogenomes available currently. In this phylogeny, all aphids were divided into two big groups (Figure 1). *Therioaphis tenera* and another member of Calaphidinae together with Aphidinae, Thelaxinae, Lachninae, Ploeomyzinae, and Mindarinae separated from other aphids.

Nucleotide sequence accession number

The complete mitogenome sequence of *T. tenera* has been assigned GenBank accession number MH643885.

Disclosure statement

No potential conflict of interest was reported by the authors.

Funding

This work is supported by Belarusian Republican Foundation for Fundamental Research.

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