

Minerva Access is the Institutional Repository of The University of Melbourne

Author/s:

Watt, A;Haites, R;Young, N;Billman-Jacobe, H

Title:

The mitochondrial genome of *Tetrahymena rostrata*

Date:

2020-01-02

Citation:

Watt, A., Haites, R., Young, N. & Billman-Jacobe, H. (2020). The mitochondrial genome of *Tetrahymena rostrata*. *Mitochondrial DNA Part B Resources*, 5 (1), pp.53-54. <https://doi.org/10.1080/23802359.2019.1693919>.

Persistent Link:

<https://hdl.handle.net/11343/254146>

License:

CC BY

MITOGENOME ANNOUNCEMENT



The mitochondrial genome of *Tetrahymena rostrata*

A. Watt, R. Haites, N. Young and H. Billman-Jacobe 

Faculty of Veterinary and Agricultural Sciences, Melbourne Veterinary School, University of Melbourne, Parkville, Australia

ABSTRACT

Tetrahymena rostrata is a ciliated protist which can parasitize the gray field slug, *Deroceras reticulatum*. Here, we report the sequence of the mitochondrial genome (mt genome) of a strain of *T. rostrata* that was isolated from the egg of *D. reticulatum*. Whole cell genomic DNA was sequenced using Illumina[®] MiSeq and the mitochondrial DNA sequence reads were extracted and assembled. The resulting 47,235 bp assembly contained rRNAs, tRNAs, and 45 protein coding DNA sequences of which 21 encoded proteins of unknown function. Phylogenetic analysis showed *T. rostrata* clustered with *Tetrahymena thermophila*, *Tetrahymena pigmentosa*, *Tetrahymena pyriformis*, *Tetrahymena paravorax*, and *Tetrahymena malaccensis*.

ARTICLE HISTORY

Received 18 October 2019
Accepted 9 November 2019

KEYWORDS

Deroceras reticulatum;
Ciliophora; *Tetrahymena rostrata*; mitogenomics

Tetrahymena rostrata (Kahl, 1927) is a ciliate which lives in soil litter or as a parasite of some terrestrial mollusks (Brooks 1968). It is able to kill *Deroceras reticulatum* slugs and has been considered as a biological control agent for pest mollusks. There is limited sequence information for *Tetrahymena* species. The mitochondrial DNA sequence of *T. rostrata* was determined in order to make phylogenetic comparisons with other members of this genus.

Tetrahymena rostrata strain TRAUS was isolated from an egg laid by a laboratory-reared *D. reticulatum* (Melbourne,

Australia, 37°47'45.9"S; 144°57'30.7"E) and has been deposited in the American Type Culture Collection, Virginia, USA (PTA-126056). *Tetrahymena rostrata* was grown in axenic culture and genomic DNA was extracted from whole cells. A sequencing library, prepared using the Illumina[®] TruSeq kit, was enriched using KAPA Taq DNA polymerase (Kapa Biosystems) and sequenced using Illumina[®] MiSeq (Illumina, San Diego, CA). The raw data were filtered using the mitochondrial genome (mt genome) of *Tetrahymena pigmentosa* (Moradian et al. 2007) as a reference and the reads were de

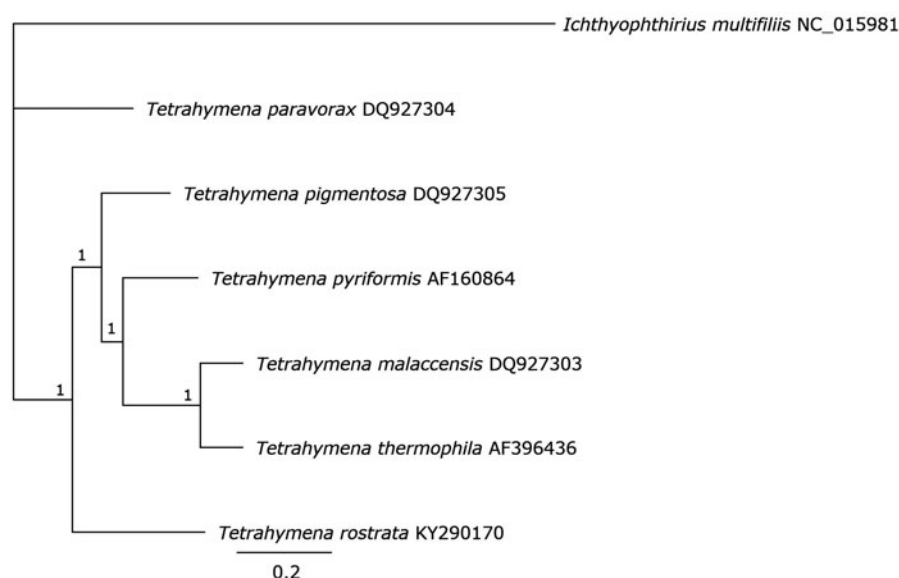


Figure 1. MrBayes tree of the translated, concatenated amino acid coding regions of the mt genomes of *T. rostrata* TRAUS, and other Hymenostomatida available in GenBank.

CONTACT H. Billman-Jacobe  hbj@unimelb.edu.au  Faculty of Veterinary and Agricultural Sciences, Melbourne Veterinary School, University of Melbourne, Royal Parade, Parkville, Victoria, Australia

© 2019 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group.
This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0/>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

novo assembled with Unicycler version 0.4.7 (Wick et al. 2017) followed by gap filling. The sequence was annotated using Geneious Prime version 1.3 (Biomatters Ltd., Auckland, New Zealand) (Kearse et al. 2012) with reference to other *Tetrahymena* mt genomes (Burger et al. 2000; Brunk et al. 2003; Moradian et al. 2007) and was deposited in GenBank (accession number MN025427).

The *T. rostrata* mt genome was a 47,235 bp linear DNA and had a GC% of 21.8%. The gene organization was the same as other *Tetrahymena* mt genomes (Burger et al. 2000; Brunk et al. 2003; Moradian et al. 2007). The genome has two rRNAs (large and small subunits, each consisting of two units), seven tRNAs, and 23 genes encoding proteins of predicted function (ribosomal proteins L2, L14, L16, S3, S12, S13, S14, and S19; NADH dehydrogenase subunit proteins Nad1, Nad1a, Nad2, Nad3, Nad4, Nad4L, Nad5, Nad6, Nad7, and Nad9; ATP synthase F0 subunit 9, cytochrome oxidase 1 and 2, apocytochrome b and heme maturase). This species shared the genes of unknown function, *ymf56*, 57, 59–61, 63–78, also identified in other *Tetrahymena* (Burger et al. 2000). The small ribosomal RNA sequence was located centrally and the large ribosomal RNA subunits occurred as terminal inverted repeats which were flanked by tRNAs and telomeric repeats. The amino acid coding regions of *T. rostrata* and other Hymenostomatida mt genomes were translated and concatenated for comparison using MAFFT version 7.388 (Katoh and Standley 2013) and the Bayesian phylogenetic inference was performed using a Markov chain Monte Carlo (MCMC) analysis in MrBayes version 3.2.6 (<https://github.com/NBISweden/MrBayes>) using a 11,000,000 MCMC generation chain length with consensus trees generated using the 50% majority rule criterion and the final 90% of trees generated by Bayesian inference after a burn-in of 100,000 generations. *T. rostrata* clustered with other members of the *Tetrahymena* genus although *Tetrahymena paravorax* appears to be an out-group (Figure 1).

Disclosure statement

The authors report no conflict of interest.

Funding

This work was funded by the Grains Research and Development Corporation and University of Melbourne, Australia.

ORCID

H. Billman-Jacobe  <http://orcid.org/0000-0001-5713-4657>

References

- Brooks W. 1968. Tetrahymenid ciliates as parasites of the gray garden slug. *Hilgardia*. 39:205–276.
- Brunk CF, Lee LC, Tran AB, Li J. 2003. Complete sequence of the mitochondrial genome of *Tetrahymena thermophila* and comparative methods for identifying highly divergent genes. *Nucleic Acids Res*. 31: 1673–1682.
- Burger G, Zhu Y, Littlejohn TG, Greenwood SJ, Schnare MN, Lang BF, Gray MW. 2000. Complete sequence of the mitochondrial genome of *Tetrahymena pyriformis* and comparison with *Paramecium aurelia* mitochondrial DNA. *J Mol Biol*. 297:365–380.
- Katoh K, Standley DM. 2013. MAFFT multiple sequence alignment software version 7: improvements in performance and usability. *Mol Biol Evol*. 30:772–780.
- Kearse M, Moir R, Wilson A, Stones-Havas S, Cheung M, Sturrock S, Buxton S, Cooper A, Markowitz S, Duran C. 2012. Geneious basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. *Bioinformatics*. 28:1647–1649.
- Moradian MM, Beglaryan D, Skozylas JM, Kerikorian V. 2007. Complete mitochondrial genome sequence of three *Tetrahymena* species reveals mutation hot spots and accelerated nonsynonymous substitutions in *Ymf* genes. *PLoS One*. 2:e650.
- Wick R, Judd L, Gorrie C, Holt K. 2017. Unicycler: Resolving bacterial genome assemblies from short and long sequence reads. *PLoS Comput Biol*. 13(6):e1005595.