



Mitochondrial DNA Part B

Resources

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

The mitochondrial genome of common whelk Buccinum undatum (Neogastropoda: Buccinidae)

Zophonías O. Jónsson, Snæbjörn Pálsson, Kristen Marie Westfall, Hildur Magnúsdóttir, Jake Goodall & Erla Bjork Ornolfsdottir

To cite this article: Zophonías O. Jónsson, Snæbjörn Pálsson, Kristen Marie Westfall, Hildur Magnúsdóttir, Jake Goodall & Erla Bjork Ornolfsdottir (2019) The mitochondrial genome of common whelk Buccinum undatum (Neogastropoda: Buccinidae), Mitochondrial DNA Part B, 4:1, 457-459, DOI: 10.1080/23802359.2018.1545534

To link to this article: https://doi.org/10.1080/23802359.2018.1545534

© 2018 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group.



0

Published online: 08 Jan 2019.

Submit your article to this journal 🕝





View related articles 🖸



View Crossmark data 🗹



🖨 Citing articles: 1 View citing articles 🗹

MITOGENOME ANNOUNCEMENT

OPEN ACCESS Check for updates

Taylor & Francis

Taylor & Francis Group

The mitochondrial genome of common whelk *Buccinum undatum* (Neogastropoda: Buccinidae)

Zophonías O. Jónsson^a (b), Snæbjörn Pálsson^a (b), Kristen Marie Westfall^{a,b,†}, Hildur Magnúsdóttir^a, Jake Goodall^a (b) and Erla Bjork Ornolfsdottir^c

^aDepartment of Life and Environmental Sciences, University of Iceland, Reykjavik, Iceland; ^bVör – Marine Research Centre in Breiðafjörður, Ólafsvík, Iceland; ^cDepartment of Aquaculture and Fish Biology, Hólar University College, Sauðárkrókur, Iceland

ABSTRACT

The complete mitogenome of *Buccinum undatum* obtained from transcriptome analysis is presented here. The mitogenome is 15,265 bp in length and comprises 13 protein-coding genes, 2 ribosomal subunit genes, and 22 transfer RNAs. The complete genome was used to perform a phylogenetic analysis together with other Buccinoidea representatives with mitogenome data from GenBank.

ARTICLE HISTORY

Received 10 October 2018 Accepted 20 October 2018

KEYWORDS mtDNA; genome; transcriptome; phylogeny;

marine snail

The common whelk (*Buccinum undatum* Linnaeus, 1758, (Gastropoda: Buccinidae)) is a common gastropod found in the subtidal zone mainly from 15 m down to 200 m in the North Atlantic and has been harvested for commercial fisheries. In this study, we determined the complete mitogenome sequence of *B. undatum*, contributing to further studies in population biology, species identification, evolutionary and phylogenetic analysis (e.g. Pálsson et al. 2014; Magnúsdóttir et al. 2018).

A single specimen of *B. undatum* was collected from the Bay of Breidafjördur, West Iceland (65.50°N, 23.14°W) on 25th June 2015 and stored in liquid nitrogen, RNA was extracted from mantle tissue using an Omega Biotek EZNA Mollusc RNA kit (http://omegabiotek.com/store/product/e-z-n-a-mollusc-rna-kit/), as per manufacturer's instructions. Transcriptome libraries were prepared using the Illumina TruSeq RNA library prep kit v2 and sequenced using an Illumina HiSeq2500 (DeCODE Genetics, Iceland). Sequenced transcripts were quality trimmed to an average of 132,735,808 reads, using BBDuk (http://jgi. doe.gov/data-and-tools/bb-tools).

The complete mitochondrial genome of *B. undatum* was assembled based on mapping of the transcripts to the mitochondrion genome of *Buccinum pemphigum* Dall, 1907 (Xu et al. 2016) using BBMap (Bushnell 2014). The coverage of sequences per nucleotide ranged from 60 to 434,056, with an average of 51,528. The genome was found to be circular and 15,265 bp in length with relative frequencies of A, G, C and T to be 0.295, 0.156, 0.163, 0.386, respectively. Protein-coding genes, rRNA, and tRNA genes were annotated by MITOS (Bernt et al. 2013), see Appendix 1. Gene content and order is identical to *B. pemphigum* (Xu et al. 2016), and is composed of 13



Figure 1. Phylogeny of *Buccinum undatum* based on the complete mitochondrion. The tree is reconstructed using maximum likelihood. The tree was rooted with *Rapana venosa* KM213962, (not shown). Numbers at nodes present support with the aLRT values obtained with the GTR model in seaview (Gouy et al. 2010).

protein-coding genes, two rRNA genes, and 22 tRNA genes. The potential origin of replication was located in a 50-bp non-coding region between COX3 and tRNA-Ile.

The complete mitogenome sequence of *B. undatum* has been deposited to GenBank database with the accession number MK035573.

The sequence was aligned with complete mitogenome sequences of nine species from two families of true

CONTACT Snæbjörn Pálsson 🖾 snaebj@hi.is 🗊 Department of Life and Environmental Sciences, University of Iceland, Reykjavik, Iceland [†]Present address: Fisheries and Oceans Canada, Pacific Biological Station, Nanaimo, Canada

© 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.

whelks (Buccinidae) and dog whelks (Nassariidae) of the superfamily Buccinoidea as well as *Rapana venosa* (Gastropoda: Muricidae), using Muscle version 3.8.31 (Edgar 2004). A phylogenetic tree of the whole genome was reconstructed based on maximum-likelihood analyses applying phyml (Guindon et al. 2010) in seaview (Gouy et al. 2010), with *R. venosa* KM213962.1 as an outgroup. The tree was redrawn using the R-package ape (Paradis et al. 2004). The tree was well resolved with highly supported nodes (Figure 1).

Disclosure statement

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the article.

Funding

Icelandic Research CouncilThis work is supported by the Icelandic Research Council, under grant number 141302051.

ORCID

Zophonías O. Jónsson (b) http://orcid.org/0000-0001-5798-9647 Snæbjörn Pálsson (b) http://orcid.org/0000-0002-4297-3500 Jake Goodall (b) http://orcid.org/0000-0003-0960-4241

References

- Bernt M, Donath A, Jühling F, Externbrink F, Florentz C, Fritzsch G, Pütz J, Middendorf M, Stadler PF. 2013. MITOS: improved de novo metazoan mitochondrial genome annotation. Mol Phylogenet Evol. 69: 313–319.
- Bushnell B. (2014). BBMap: a fast, accurate, splice-aware aligner. Report Number: LBNL-7065E
- Edgar RC. 2004. MUSCLE: multiple sequence alignment with high accuracy and high throughput. Nucleic Acids Res. 32:1792–1797.
- Guindon S, Dufayard JF, Lefort V, Anisimova M, Hordijk W, Gascuel O. 2010. New algorithms and methods to estimate maximum-likelihood phylogenies: assessing the performance of PhyML 3.0. Syst Biol. 59: 307–321.
- Gouy M, Guindon S, Gascuel O. 2010. SeaView version 4: a multiplatform graphical user interface for sequence alignment and phylogenetic tree building. Mol Biol Evol. 27:221–224.
- Magnúsdóttir H, Pálsson S, Westfall KM, Jónsson ZO, Örnólfsdóttir EB. 2018. Shell morphology and color of the subtidal whelk Buccinum undatum exhibit fine-scaled spatial patterns. Ecol Evol. 8: 4552–4563.
- Pálsson S, Magnúsdóttir H, Reynisdóttir S, Jónsson ZO, Örnólfsdóttir EB. 2014. Divergence and molecular variation in common whelk *Buccinum undatum* (Buccinidae) in Iceland – a trans-Atlantic comparison. Biol J Linnean Soc. 111:145–159.
- Paradis E, Claude J, Strimmer K. 2004. APE: analyses of phylogenetics and evolution in R language. Bioinformatics. 20:289–290.
- Xu Y, Bao X, Gao L, He C, Liu W, Chai X. 2016. The complete mitochondrial genome of *Buccinum pemphigum* (Neogastropoda: Buccinidae). Mitochondrial DNA Part B. 1:98–99.

Appendix



Appendix 1. Visual representation of the complete mitochondrial genome of the common whelk *Buccinum undatum* (Gastropoda: Buccinidae), obtained with MITOS (Bernt et al.2013)