



HAL
open science

Complete mitogenome of *Cerithidea obtusa* , the red chut-chut snail from the C n Gi  Mangrove in Vietnam

Duc Hung Nguyen, Claude Lemieux, Monique Turmel, V n Duy Nguyen, Jean-Luc Mouget, Andrzej Witkowski, R jean Tremblay, Romain Gastineau

► To cite this version:

Duc Hung Nguyen, Claude Lemieux, Monique Turmel, V n Duy Nguyen, Jean-Luc Mouget, et al.. Complete mitogenome of *Cerithidea obtusa* , the red chut-chut snail from the C n Gi  Mangrove in Vietnam. Mitochondrial DNA Part B Resources, 2018, 3 (2), pp.1267 - 1269. 10.1080/23802359.2018.1532832 . hal-01915128

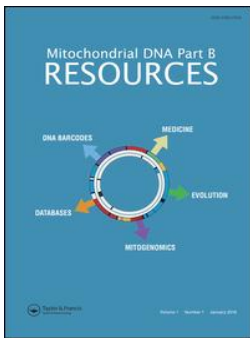
HAL Id: hal-01915128

<https://hal.science/hal-01915128>

Submitted on 7 Nov 2018

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destin e au d p t et   la diffusion de documents scientifiques de niveau recherche, publi s ou non,  manant des  tablissements d'enseignement et de recherche fran ais ou  trangers, des laboratoires publics ou priv s.



Mitochondrial DNA Part B Resources

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

Complete mitogenome of *Cerithidea obtusa*, the red chut-chut snail from the Cần Giờ Mangrove in Vietnam

Duc Hung Nguyen, Claude Lemieux, Monique Turmel, Van Duy Nguyen, Jean-Luc Mouget, Andrzej Witkowski, Réjean Tremblay & Romain Gastineau

To cite this article: Duc Hung Nguyen, Claude Lemieux, Monique Turmel, Van Duy Nguyen, Jean-Luc Mouget, Andrzej Witkowski, Réjean Tremblay & Romain Gastineau (2018) Complete mitogenome of *Cerithidea obtusa*, the red chut-chut snail from the Cần Giờ Mangrove in Vietnam, Mitochondrial DNA Part B, 3:2, 1267-1269

To link to this article: <https://doi.org/10.1080/23802359.2018.1532832>



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



Published online: 26 Oct 2018.



Submit your article to this journal [↗](#)



View Crossmark data [↗](#)

Complete mitogenome of *Cerithidea obtusa*, the red chut-chut snail from the Càn Giở Mangrove in Vietnam

Duc Hung Nguyen^a, Claude Lemieux^b, Monique Turmel^b, Van Duy Nguyen^a, Jean-Luc Mouget^c, Andrzej Witkowski^d, Réjean Tremblay^e and Romain Gastineau^d

^aFaculty of Natural Sciences Pedagogy, Saigon University, Hồ Chí Minh City, Vietnam; ^bDépartement de biochimie, de microbiologie et de bio-informatique, Institut de Biologie Intégrative et des Systèmes, Université Laval, Québec, Canada; ^cMer, Molécules, Santé (MMS), Le Mans Université, Le Mans, France; ^dFaculty of Geosciences, Natural Sciences Research and Educational Center and Palaeoceanology Unit, University of Szczecin, Szczecin, Poland; ^eISMER, Université du Québec à Rimouski, Québec, Canada

ABSTRACT

We sequenced the complete mitogenome of the red chut-chut snail *Cerithidea obtusa*, from the Càn Giở mangrove in Vietnam. The mitogenome is 15,708 bp long. It is colinear with the mitogenomes of other members of the superfamily Cerithioidea, and the maximum-likelihood phylogeny obtained with the *cox1*, *cox2* and *cox3* genes of several Caenogastropoda associated all Cerithioidea together inside a strongly supported clade.

ARTICLE HISTORY

Received 30 July 2018
Accepted 31 August 2018

KEYWORDS

Cerithioidea; mangrove;
Vietnam; mitogenome;
Cerithidea

Cerithidea obtusa (Caenogastropoda, Cerithioidea, Potamididae) (Lamarck, 1822) is an aquatic gastropod commonly found in South-East Asia, with a broad distribution ranging from Madagascar to Australia (Reid et al. 2013, 2014). This snail generally lives in mud flats and mangroves and is famous for its peculiar behavior of climbing on tree tops during tidal inundation and letting itself fall on the mud. Known as 'Ốc len' in Vietnam, *C. obtusa* has economic and gastro-nomic value. It is considered a delicatessen by inhabitants of the Càn Giở Mangrove Biosphere Reserve, near Hồ Chí Minh City, who cook it in coconut milk.

We obtained a specimen of *C. obtusa* from a local fisherman (10°25'55"N; 106°54'530"E), extracted total DNA and sent this preparation to the Beijing Genomic Institute (Shenzhen) for DNA sequencing on the BGISEQ-500 platform. A total of 50 million paired-end reads of 100 bp were assembled using SPAdes 3.12.0 (Bankevich et al. 2012) with a k-mer value of 55. The shell of the individual used for sequencing remains in the collection of the Đại học Sài Gòn – Saigon University. The remaining flesh of the individual and

the rest of the DNA extracted for sequencing are stored in the University of Szczecin (Poland) at –20 °C.

The 15,708-bp mitogenome sequence of *C. obtusa* (GenBank: MH682098) is the first complete mitogenome reported for a member of the Potamididae family. It contains 37 genes that encode two rRNAs, 22 tRNAs and 13 proteins. Coding sequences are located on both DNA strands and protein-coding genes are found in the following order: *cox1*, *cox2*, *ND4L*, *ND4*, *ND5*, *cox3*, *cob*, *ND6*, *ND1*, *ND2*, *atp8*, *atp6*, *ND3*. The *C. obtusa* mitogenome is similar in size and colinear with its homologues in the superfamily Cerithioidea (KT153076, KF736848, KJ696780, KU221394, KU878411 and LC006055); however, it differs in gene order relative to other mitogenomes of Caenogastropoda (Cunha et al. 2009; Rawlings et al. 2010). A maximum-likelihood tree was inferred using MEGA6 (Tamura et al. 2013) and three concatenated genes (first and second codon positions of *cox1*, *cox2* and *cox3*) from 45 taxa of Caenogastropoda. *Cerithidea obtusa* was found to be part of a highly supported clade containing all eight taxa sampled from the Cerithioidea (Figure 1).

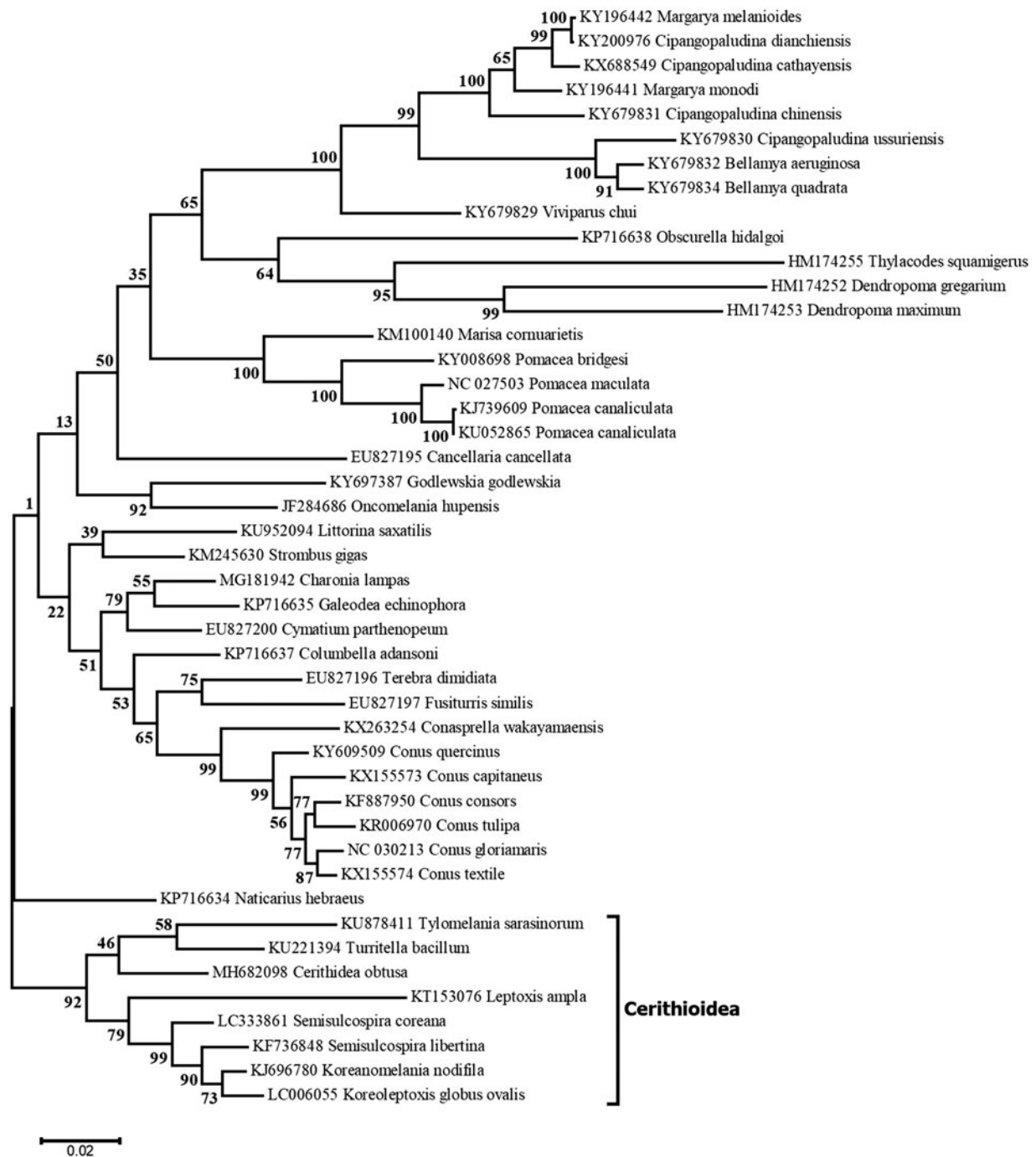


Figure 1. Maximum-likelihood tree of concatenated *cox1*, *cox2* and *cox3* genes of various Caenogastropoda. The tree with the highest likelihood is shown, with bootstrap values obtained after 1000 replications. The bracket indicates the position of the superfamily Cerithioidea.

Acknowledgements

We thank Jean Wang, Regional sales director of Central and Eastern European Countries for BGI Genomics, for all the help provided.

Disclosure statement

No potential conflict of interest was reported by the authors.

Funding

This publication has been funded by the European Commission under the Horizon 2020 Research and Innovation Programme GhaNA [The

Genus *Haslea*, New Marine Resources for blue biotechnology and Aquaculture, grant agreement no. 734708/GHANA/H2020-MSCA-RISE-2016].

References

- Bankevich A, Nurk S, Antipov D, Gurevich A, Dvorkin M, Kulikov AS, Lesin V, Nikolenko S, Pham S, Pribelski A, et al. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. *J Comput Biol.* 19:455–477.
- Cunha RL, Grande C, Zardoya R. 2009. Neogastropod phylogenetic relationships based on entire mitochondrial genomes. *BMC Evol Biol.* 9: 210.

- Rawlings TA, Maclnnis MJ, Bieler R, Boore JL, Collins TM. 2010. Sessile snails, dynamic genomes: gene rearrangements within the mitochondrial genome of a family of caenogastropod molluscs. *BMC Genomics*. 11:440.
- Reid DG. 2014. The genus *Cerithidea* Swainson, 1840 (Gastropoda: Potamididae) in the Indo-West Pacific region. *Zootaxa*. 3775:1–65.
- Reid DG, Claremont M, Smith L, Shamoto M, Glaubrecht M, Ozawa T. 2013. Mosaics in the mangroves: allopatric diversification of tree-climbing mudwhelks (Gastropoda: Potamididae: Cerithidea) in the Indo-West Pacific. *Biol J Linn Soc Lond*. 110:564–580.
- Tamura K, Stecher G, Peterson D, Filipski A, Kumar S. 2013. MEGA6: molecular evolutionary genetics analysis version 6.0. *Mol Biol Evol*. 30:2725–2729.