The complete mitochondrial DNA of the tropical oyster *Crassostrea belcheri* from the Cần Giờ’ mangrove in Vietnam

Romain Gastineau, Đức-Hùng Nguyễn, Claude Lemieux, Monique Turmel, Réjean Tremblay, Văn Duy Nguyễn, Ita Widowati, Andrzej Witkowski, Jean-Luc Mouget

To cite this version:

Romain Gastineau, Đức-Hùng Nguyễn, Claude Lemieux, Monique Turmel, Réjean Tremblay, et al.. The complete mitochondrial DNA of the tropical oyster *Crassostrea belcheri* from the Cần Giờ’ mangrove in Vietnam. Mitochondrial DNA Part B Resources, Taylor & Francis Online, 2018, 3 (1), pp.462-463. 10.1080/23802359.2018.1462126 . hal-02101149

HAL Id: hal-02101149
https://hal.archives-ouvertes.fr/hal-02101149
Submitted on 9 May 2019

**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 destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d’enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.
The complete mitochondrial DNA of the tropical oyster *Crassostrea belcheri* from the Cần Giò' mangrove in Vietnam

Romain Gastineau, Đŭc-Hùng Nguyễn, Claude Lemieux, Monique Turmel, Réjean Tremblay, Văn Duy Nguyễn, Ita Widowati, Andrzej Witkowski & Jean-Luc Mouget

To cite this article: Romain Gastineau, Đŭc-Hùng Nguyễn, Claude Lemieux, Monique Turmel, Réjean Tremblay, Văn Duy Nguyễn, Ita Widowati, Andrzej Witkowski & Jean-Luc Mouget (2018) The complete mitochondrial DNA of the tropical oyster *Crassostrea belcheri* from the Cần Giò' mangrove in Vietnam, Mitochondrial DNA Part B, 3:1, 462-463, DOI: 10.1080/23802359.2018.1462126

To link to this article: https://doi.org/10.1080/23802359.2018.1462126
The complete mitochondrial DNA of the tropical oyster *Crassostrea belcheri* from the Cân Gio’ mangrove in Vietnam

Romain Gastineau, Duc-Hung Nguyen, Claude Lemieux, Monique Turmel, Rejean Tremblay, Van Duy Nguyen, Ita Widowati, Andrzej Witkowski and Jean-Luc Mouget

**ABSTRACT**

The complete mitochondrial genome of the oyster *Crassostrea belcheri* from the Cân Gio’ mangrove in Vietnam has been sequenced. It consists of a circular DNA molecule of 21020 base pairs (bp), coding for 12 proteins, 20 transfer RNAs, and two ribosomal RNAs. Like the mitogenomes of *Crassostrea iredalei* and *Crassostrea* sp. DB1, it contains a non-coding region and two ORFs. The *C. belcheri* mitogenome provides information that could improve the molecular phylogeny of Asian oysters and be useful to the development of oyster aquaculture in South East Asia.

The tropical oyster *Crassostrea belcheri* is cultured commercially in South-East Asia (Tan and Wong 1996; Klinbuga et al. 2000, 2003, 2005) and Indonesian archipelago (Yoo and Ryu 1984). Its commercialization is an important activity in the Cân Gio’ mangrove, located near Hồ Chí Minh City in Vietnam, where it is sold under the vernacular name of Hậu Đèp. In this study, we present the complete mitogenome of *C. belcheri*. The specimen was collected in the mangrove in

**CONTACT**

Romain Gastineau
gastineuromain@yahoo.fr
Natural Sciences Research and Educational Center and Palaeoceanology Unit, Faculty of Geosciences, University of Szczecin, Szczecin, Poland

© 2018 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.
The C. belcheri mitogenome is 21020 bp long (GenBank accession no. MH051332), making it the third longest mitogenome sequenced among the genus Crassostrea (Wu et al. 2010, 2012). The nucleotide composition of this mitogenome is A 28.3%, C 14.3%, G 21.4%, T 36%. It encodes 12 proteins, 20 transfer RNAs, and two ribosomal RNAs. The rrnL gene is split into two parts and the rrnS gene is duplicated, both features being commonly found among Asian oysters (Wu et al. 2010). As in other Crassostrea mitogenomes, there is a major non-coding region whose size is 797 bp in C. belcheri. Also, the C. belcheri mitogenome shares with Crassostrea iredi alei (FJ841967) and Crassostrea sp. DB1 (JQ060958) two ORFs originating from the duplication of the NAD2 gene. The latter ORFs are separated from one another by a putative suppressor tRNA gene.

A maximum-likelihood phylogenetic analysis was performed using the complete mitogenome sequences of 11 Crassostrea species and the resulting tree was rooted using the mitogenome of Ostrea edulis (Figure 1). C. belcheri was recovered between a strongly supported cluster containing C. hongkongensis, C. ariakensis, C. nippona, C. sika mea, C. angulate, and C. gigas, which all have mitogenomes very similar in size and nucleotide composition, and a second robust cluster containing C. iredi alei and Crassostrea sp. DB1, which feature the longest mitogenomes and the two conserved ORFs. The highly supported clade formed by all nine Crassostrea species was sister to that containing C. virginica and C. gasar, both from the American continent.

The C. belcheri mitogenome thus provides new information regarding the phylogeny and genome evolution of Asian Crassostrea species. It may also serve as a reliable reference sequence for accurate molecular barcoding of the different populations of C. belcheri and identification of specimens, a tool that may be helpful for the development of the aquaculture of this species in South East Asia.

Disclosure statement
The authors report no conflict of interest. The authors alone are responsible for the content and writing of this article.

Funding
This publication benefited from funding from 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]), and the International research collaboration-scientific publication (Indonesia – France) Sustainable valorization of Indonesian phytoplankton in aquaculture: new approaches to control infectious disease (SALINA, 2015-2018).

References
Boisvert S, Laviolette F, Corbeil J. 2010. Ray: simultaneous assembly of reads from a mix of high-throughput sequencing technologies. J Comput Biol. 17:1519–1533.
Klinbuga S, Ampayup P, Tassanakajon A, Yaosukh W. 2000. Development of species-specific markers of the tropical oyster (Crassostrea belcheri) in Thailand. Mar Biotechnol. 2:476–484.
Klinbuga S, Khamnantong N, Puanglarp N, Jarayabhand P, Yoosukh W. 2005. Molecular Taxonomy of Cupped Oysters (Crassostrea, Saccostrea, and Striostrea) in Thailand Based on COI, 16S, and 18S rDNA Polymorphism. Mar Biotechnol. 7:306–317.
Klinbuga S, Khamnantong N, Tassanakajon A, Yaosukh W, Menasvet P. 2006. Molecular Genetic Identification Tools for Three Commercially Cultured Oysters (Crassostrea belcheri, Crassostrea iredi alei, and Saccostrea cucullata) in Thailand. Mar Biotechnol. 5:27–36.
Tan SH, Wong TM. 1996. Effect of salinity on hatching, larval growth, survival and settling in the tropical oyster Crassostrea belcheri (Sowerby). Aquaculture. 145:129–139.
Wu X, Li X, Li L, Xu X, Xia X, Yu Z. 2012. New features of Asian Crassostrea oyster mitochondrial genomes: a novel alloacceptor tRNA gene recruitment and two novels ORFs. Gene. 507:112–118.
Wu X, Xu X, Yu Z, Wei Z, Xia J. 2010. Comparison of seven Crassostrea mitogenomes and phylogenetic analyses. Mol Phylogenet Evol. 57:448–454.
Yoo SK, Ryu HY. 1984. Comparative morphological characteristics of mangrove oysters. Bull Korean Fish Soc. 17:321–326.