The mitochondrial genome of Diaphanosoma excisum Sars, 1885 (Crustacea: Branchiopoda: Cladocera) from Hainan Island, China

Jiaying Pan, Ping Liu, Franja Pajk, Henri J. Dumont, and Bo-Ping Han

ABSTRACT

Diaphanosoma excisum is the only Cladoceran in tropical freshwaters and parapatrically occurs with Diaphanosoma dubium in the transition between the tropics and subtropics. Here, we present the complete mitochondrial genome (MG) determined by next-generation sequencing and offer a phylogenetic analysis of D. excisum. The MG of D. excisum is 17,615 bp in size, including 13 protein-coding genes (PCGs), 2 ribosomal RNA, 23 tRNA, and 2 putative control regions. The MG has a biased A+T of 65.34% for base composition. Compared to D. dubium, the MG of D. excisum has one more tRNA-Met, one unknown extra putative control region and is different in the arrangement of its tRNAs. The MG sequence and tRNA order provide valuable molecular data for understanding the phylogeny and speciation of Diaphanosoma.

Diaphanosoma, the ‘tropical Daphnia’, is common and ubiquitous in the tropics and subtropics (Dumont 1994; Sarma et al. 2005; Dumont et al. 2021). Among Diaphanosoma species, Diaphanosoma excisum and Diaphanosoma dubium are two of the most common and dominant species. They are parapatrically distributed in warmer waters and rarely coexist in the transition zone between the tropics and subtropics (Korovchinsky et al. 2017; Liu et al. 2018; Pajk et al. 2018). In the tropics, D. excisum is frequently the only Cladoceran present (Kotov et al. 2013). In contrast to D. dubium, which is widespread in subtropical waters and with a dominance in China, D. excisum is restricted to the coastal islands of the southern part of the country (Chen et al. 2011). Pajk et al. (2018) measured the life history traits of clones from 16 populations of D. dubium and D. excisum under a broad temperature range from 10°C to 40°C and showed that D. excisum had a narrower thermal performance curve (TPC) and a higher optimum temperature than the subtropical D. dubium, but failed to reproduce at ≤15°C. Stable thermal niche difference is considered to play a critical role in shaping Diaphanosoma species range. To reveal the potential mechanism underlying niche divergence of the two congeners, there is a need to analyze not only ecological, but also genetic information. Here, we sequenced and annotated the mitochondrial genome (MG) of D. excisum and compared it to the published MG of D. dubium (Liu et al. 2017).

Living animals were collected from Donghu lake (110.35°E, 20.04°N) in Hainan Island, China, and mass-cultured in a controlled environment. To reveal the potential mechanism underlying niche divergence of the two congeners, there is a need to analyze not only ecological, but also genetic information. Here, we sequenced and annotated the mitochondrial genome (MG) of D. excisum and compared it to the published MG of D. dubium (Liu et al. 2017).

CONTACT Ping Liu liuping329098@163.com Department of Ecology, Jinan University, Guangzhou, PR China

© 2021 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.
number: MT356995) of another Diaphanosoma species. The arrangement of tRNA was different for the two species, but no shift of PCGs was discovered. Besides, one more putative control region was detected in D. excisum.

To explore the phylogenetic relationships of D. excisum and D. dubium and seven other species from three families in Brachiopoda which have complete MGs, a phylogenetic tree was obtained using Bayesian inference (BI) analysis based on entire PCGs sequences and two rRNA sequences. The Bayesian analysis was performed using MrBayes version 3.1.2 (Ronquist and Huelsenbeck 2003) with the GTR + G+I model of nucleotide substitution. The MGs of the two Diaphanosoma species have a similar A+T composition (65.34% for D. excisum and 65.6% for D. dubium). The phylogenetic tree shows that D. excisum was fully resolved in a clade with D. dubium in the Sididae (Figure 1). The Sididae (Ctenopda) was phylogenetically closer to the anomopod Daphniidae, but divergent from Triopsidae (order Notostraca) and Artemiidae (order Anostraca).

Disclosure statement
No potential conflict of interest was reported by the author(s).

Funding
This study was supported by the grant for National Natural Science Foundation of China (NSF) of China [No 31901098].

Data availability statement
The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at [https://www.ncbi.nlm.nih.gov] (https://www.ncbi.nlm.nih.gov) under the accession no. MW476927. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA700806, SRR13664529, and SAMN17839477, respectively.

References
Bernt M, Donath A, Juhlung 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(2):313–319.
Chen H, Lin QQ, Xu L, Han BP. 2011. Redescription of common species of Diaphanosoma (Cladocera: sididae) in China. EcoI Sci. 30:223–228.
Dumont HJ. 1994. On the diversity of the Cladocera in the tropics. Hydrobiologia. 272(1–3):27–38.
Dumont HJ, Han BP, Guo F, Chen H, Cheng D, Liu P, Xu L, Sanoamuang LO, Rietzler A, Xu S, et al. 2021. Towards a phylogeny and biogeography of Diaphanosoma (Crustacea: Cladocera). Aquat Ecol. https://doi.org/10.1007/s10452-020-09819-0.
Korovchinsky NM, Walsh EJ, Smolak R. 2017. Diaphanosoma Fischer, 1850 (Crustacea: Cladocera: Sididae) of Lake Turkana (East Africa), with the description of a new species of the genus. Zootaxa. 4250(1):77–89.
Kotov A, Korovchinsky NM, Petrussek A. 2013. World checklist of freshwater Cladocera species. http://fada.biodiversity.be/group/show/17.
Liu P, Xu S, Huang Q, Dumont HJ, Lin Q, Han BP. 2017. The mitochondrial genome of Diaphanosoma dubium with comparison with Daphnia magna. Mitochondrial DNA Part B. 2(2):926–927.
Liu P, Xu L, Xu S, Martinez A, Chen H, Cheng D, Dumont HJ, Han B-P, Fontaneto D. 2018. Species and hybrids in the genus Diaphanosoma Fischer, 1850 (Crustacea: Branchiopoda: Cladocera). Mol Phylogenet Evol. 118:369–378.
Lowe TM, Eddy SR. 1997. trRNAscan-SE: a program for improved detection of transfer RNA genes in genomic sequence. Nucleic Acids Res. 25(5):955–964.
Pajk F, Zhang JX, Han BP, Dumont HJ. 2018. Thermal reaction norms of a subtropical and a tropical species of Diaphanosoma (Cladocera) explain their distribution. Limnol Oceanogr. 63(3):1204–1220.
Ronquist F, Huelsenbeck JP. 2003. MRBAYES 3: Bayesian phylogenetic inference under mixed models. Bioinformatics. 19(12):1572–1574.
Samra SSS, Nandini S, Gulati RD. 2005. Life history strategies of cladocerans: comparisons of tropical and temperate taxa. Hydrobiologia. 542(1):315–333.
Xu SL, Guan ZY, Huang Q, Xu L, Vierstraete A, Dumont HJ, Lin QQ. 2018. The mitochondrial genome of Atrocalopteryx melli Ris, 1912 (Zaogoptera: Calopterygidae) via Ion Torrent PGM NGS sequencing. Mitochondrial DNA Part B. 3(1):115–117.