



Complete mitogenome of the invasive land flatworm *Platydemus manokwari*

Romain Gastineau, Claude Lemieux, Jean-Lou Justine, Monique Turmel

► To cite this version:

Romain Gastineau, Claude Lemieux, Jean-Lou Justine, Monique Turmel. Complete mitogenome of the invasive land flatworm *Platydemus manokwari*. Mitochondrial DNA Part B Resources, 2020, 5 (2), pp.1689-1690. 10.1080/23802359.2020.1748532 . hal-02549559

HAL Id: hal-02549559

<https://hal.science/hal-02549559>

Submitted on 21 Apr 2020

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.

MITOGENOME ANNOUNCEMENT



Complete mitogenome of the invasive land flatworm *Platydemus manokwari*

Romain Gastineau^a, Claude Lemieux^b , Monique Turmel^b and Jean-Lou Justine^c

^aInstitute of Marine and Environmental Sciences, University of Szczecin, Szczecin, Poland; ^bDépartement de biochimie, de microbiologie et de bio-informatique, Institut de Biologie Intégrative et des Systèmes, Université Laval, Québec City, Canada; ^cInstitut Systématique Évolution Biodiversité (ISYEB), Muséum National d'Histoire Naturelle, CNRS, Sorbonne Université, Paris, France

ABSTRACT

We sequenced the complete mitogenome of the invasive flatworm *Platydemus manokwari* (Tricladida order, Geoplanidae family). This 19,959-bp genome contains 36 genes and is almost colinear with the mitogenomes of the two other species previously sampled from the Geoplanidae, *Bipalium kewense* and *Obama nungara*, both of which feature an extra tRNA gene. A single *P. manokwari* gene, encoding tRNA-Cys, is rearranged compared to its orthologs in the latter flatworms. Another distinctive trait of *P. manokwari* is the unusually large *cox2* gene. In the phylogeny inferred from 12 proteins, *P. manokwari* formed a strongly supported clade with *B. kewense* and *O. nungara*.

ARTICLE HISTORY

Received 20 February 2020
Accepted 25 March 2020

KEYWORDS

Platydemus manokwari;
Invasive flatworm;
Geoplanidae; *cox2*

Platydemus manokwari de Beauchamp, 1963 (Tricladida order, Geoplanidae family) is a large flatworm originating from New Guinea. It has been introduced both accidentally and willingly in many different areas, including the neighboring Pacific Islands, Asia, America and Europe (Justine et al. 2014, 2015). It is a known predator of snails, and when it was introduced on purpose to feed on invasive Gastropoda like the Giant African snail *Lissachatina fulica*, it also had a strong impact on endemic species (Sugiura 2009; Iwai et al. 2010; Sugiura and Yamaura 2010; Gerlach 2019). We sequenced the complete mitogenome of a specimen of *P. manokwari* collected in France and registered in the Muséum National d'Histoire Naturelle as MNHN_JL081, and from which a partial COI gene sequence was previously obtained (GenBank: KR349579).

A small portion of the specimen was sent to the Beijing Genomics Institute (BGI) in Shenzhen for DNA extraction and paired-end sequencing on the DNBSEQ platform. A total of 60 million 100-bp reads were generated; after filtering, they were assembled with SPAdes 3.12.0 (Bankevich et al. 2012) using a k-mer of 85. The contig corresponding to the mitogenome was retrieved, verified using the Consed package (Gordon et al. 1998), and annotated with the help of MITOS (Bernt et al. 2013). The rest of the specimen is available in the Muséum National d'Histoire Naturelle in Paris under the registration number MNHN_JL081.

The *P. manokwari* mitogenome (GenBank: MT081580) is 19,959-bp long and codes for 13 proteins, 2 rRNAs, and 21 tRNAs. It is almost perfectly colinear with the mitogenomes of the two other members of the Geoplanidae family for

which complete mitogenomes are currently available, *Bipalium kewense* (Genbank: MK455837.1, Gastineau et al. 2019) and *Obama nungara* (sequence deposited in GenBank as *Obama* sp., Genbank: KP208777, Solà et al. 2015), which are invasive species too (Justine et al. 2018, 2020). The newly sequenced *P. manokwari* mitogenome displays three structural differences relative to its Geoplanidae counterparts. The gene coding for tRNA-Thr is missing and that coding for tRNA-Cys is rearranged, being located near *cox3* instead of being adjacent to *rrnS* as in *B. kewense* and *O. nungara*. Moreover, at 1350 bp, the *P. manokwari* *cox2* gene is twice as large compared to those of *B. kewense* (678 bp), *O. nungara* (780 bp) and flatworms belonging to closely related families. At the protein level, the extra nucleotides correspond to a region situated between a transmembrane domain and the copper A binding domain. As no detectable intron or intein was identified, this additional DNA sequence likely resulted from the expansion of a coding segment.

A maximum-likelihood phylogeny was inferred from 13 concatenated mitogenome-encoded proteins of eight platyhelminths from the Tricladida order using RAXML v.8.2.3 (Stamatakis 2014) and the MtArt substitution model (Abascal et al. 2007). A member of the Polycladida was used as out-group. In the best tree, *P. manokwari* clustered strongly with *B. kewense* and *Obama nungara*, while all four members of the Dugesidae family formed a highly supported sister clade (Figure 1). This result is congruent with the revised classification of Sluys et al. (2009), in which the Geoplanidae and Dugesidae constitute the superfamily Geoplanoidea.

CONTACT Romain Gastineau  gastineauromain@yahoo.fr  Institute of Marine and Environmental Sciences, University of Szczecin, Ul. Mickiewicza 16a, Szczecin 70-543, Poland

© 2020 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.

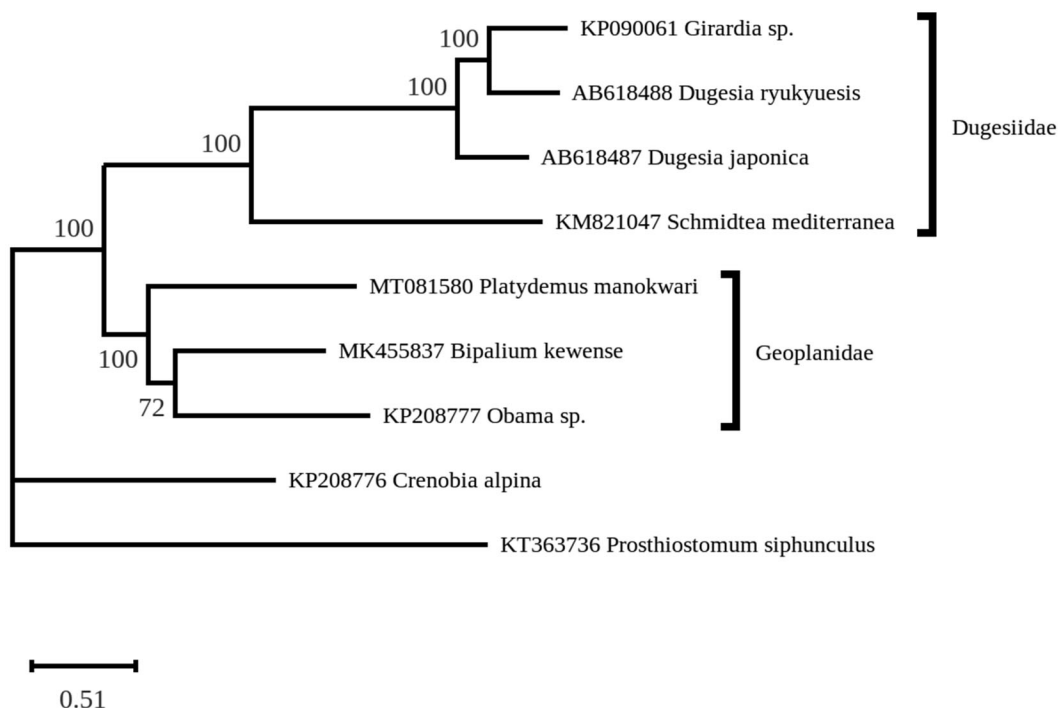


Figure 1. Maximum-likelihood tree obtained on concatenated amino-acid sequences of all mitochondrial protein-coding genes from *Platydemus manokwari* and other flatworms, using the MtArt model of evolution and after 100 bootstrap replications. The brackets represent the families..

Disclosure statement

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

Funding

The present work was financially supported by Ministerstwo Nauki i Szkolnictwa Wyzszego

ORCID

Claude Lemieux  <http://orcid.org/0000-0001-9580-8042>

References

- Abascal F, Posada D, Zardoya R. 2007. MtArt: a new model of amino acid replacement for Arthropoda. *Mol Biol Evol.* 24(1):1–5.
- Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Pribelski AD, et al. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. *J Comput Biol.* 19(5):455–477.
- Bernt M, Donath A, Jühling F, Externbrink F, Florentz C, Fritsch G, Pütz J, Middendorf M, Stadler PF. 2013. MITOS: improved de novo metazoan mitochondrial genome annotation. *Mol Phylogenet Evol.* 69(2): 313–319.
- Gastineau R, Jean-Lou Justine J-L, Lemieux C, Monique Turmel M, Witkowski A. 2019. Complete mitogenome of the giant invasive hammerhead flatworm *Bipalium kewense*. *Mitochondrial DNA Part B.* 4(1): 1343–1344.
- Gerlach J. 2019. Predation by invasive *Platydemus manokwari* flatworms: a laboratory study. *Biol Lett.* 54(1):47–60.
- Gordon D, Abajian C, Green P. 1998. Consed: a graphical tool for sequence finishing. *Genome Res.* 8(3):195–202.
- Iwai N, Sugiura S, Chiba S. 2010. Predation impacts of the invasive flatworm *Platydemus manokwari* on eggs and hatchlings of land snails. *J Molluscan Stud.* 76(3):275–278.
- Justine J-L, Winsor L, Barrière P, Fanai C, Gey D, Han AWK, La Quay-Velázquez G, Lee BPY, Lefevre J, Meyer J, et al. 2015. The invasive land planarian *Platydemus manokwari* (Platyhelminthes, Geoplanidae): records from six new localities. Including the First in the USA. *Peer J.* 3:e1037.
- Justine J-L, Winsor L, Gey D, Gros P, Thévenot J. 2014. The invasive New Guinea flatworm *Platydemus manokwari* in France, the first record for Europe: time for action is now. *Peer J.* 2:e297.
- Justine J-L, Winsor L, Gey D, Gros P, Thévenot J. 2018. Giant worms chez moi! Hammerhead flatworms (Platyhelminthes, Geoplanidae, *Bipalium* spp., *Diversibipalium* spp.) in metropolitan France and overseas French territories. *Peer J.* 6:e4672.
- Justine J-L, Winsor L, Gey D, Gros P, Thévenot J. 2020. Obama chez moi! The invasion of metropolitan France by the land planarian *Obama nungara* (Platyhelminthes, Geoplanidae). *Peer J.* 8:e8385.
- Sluys R, Kawakatsu M, Riutort M, Baguña J. 2009. A new higher classification of planarian flatworms (Platyhelminthes, Tricladida). *J Nat Hist.* 43(29–30):1763–1777.
- Solà E, Álvarez-Presas M, Frías-López C, Littlewood DT, Rozas J, Riutort M. 2015. Evolutionary analysis of mitogenomes from parasitic and free-living flatworms. *PLoS One.* 2010(3):e0120081.
- Stamatakis A. 2014. RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. *Bioinformatics.* 30(9): 1312–1313.
- Sugiura S. 2009. Seasonal fluctuation of invasive flatworm predation pressure on land snails: Implications for the range expansion and impacts of invasive species. *Biol Conserv.* 142:3013–3019.
- Sugiura S, Yamaura Y. 2010. Potential impacts of the invasive flatworm *Platydemus manokwari* on arboreal snails. In: Kawakami K, Okochi I, editors. *Restoring the Oceanic Island ecosystem*. Tokyo (Japan): Springer.