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Complete mitogenome of the invasive land flatworm *Platydemus manokwari*

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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*.

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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.

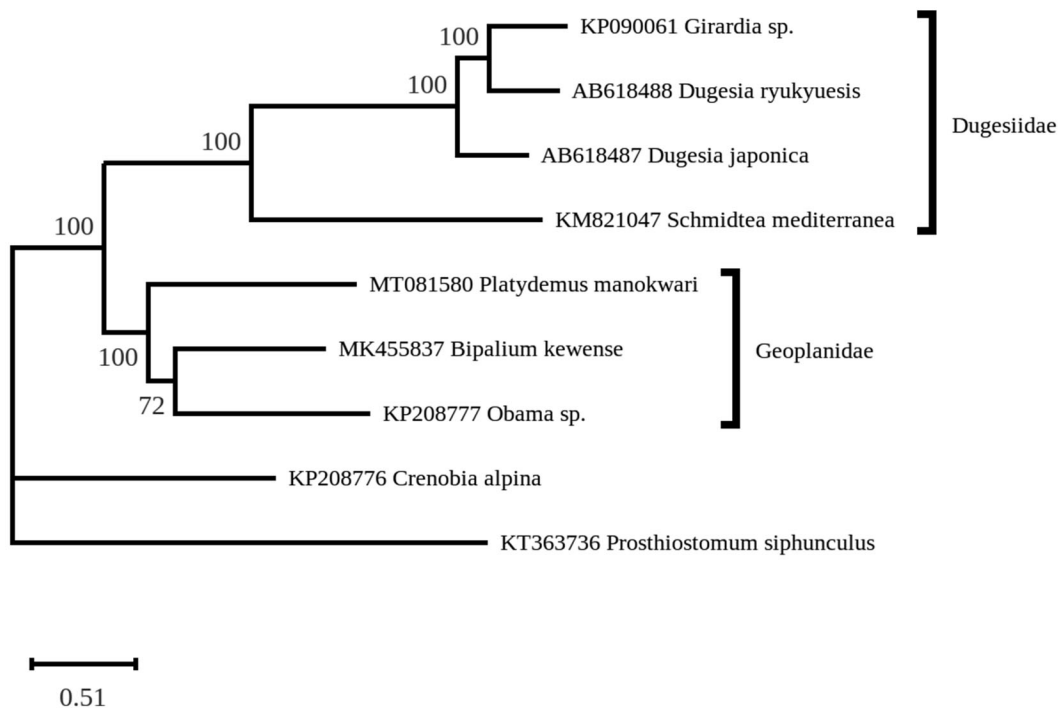


Figure 1. Maximum-likelihood tree obtained on concatenated amino-acid sequences of all mitochondrial protein-coding genes from *Platydemus manokwari* and other flatworms, using the MtArt model of evolution and after 100 bootstrap replications. The brackets represent the families.

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