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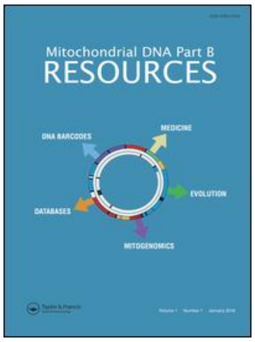

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MITOGENOME ANNOUNCEMENT

Complete mitogenome of the giant invasive hammerhead flatworm *Bipalium kewense*

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ABSTRACT

We determined the sequence of the complete mitogenome of *Bipalium kewense*, an invasive land flatworm with worldwide distribution. All 37 genes encoded on this 15,666-bp genome reside on the same DNA strand. Phylogenomic analyses of mitochondrial proteins from taxa of the order Tricladida associated *B. kewense* with another invasive species of land planarians (*Obama* sp.).

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Bipalium; flatworm; invasive; Tricladida; Geoplanidae

The platyhelminth *Bipalium kewense* (family Geoplanidae) is an invasive land flatworm originating from southeastern Asia (Winsor 1983; Justine et al. 2018). Like other Bipaliinae, it features a hammerhead but is exceptional by its giant size (up to 30 cm). Remarkably, *B. kewense* and *Bipalium adventitium* were shown to produce tetrodotoxin, making these species the first known terrestrial invertebrates to possess this neurotoxin (Stokes et al. 2014). The current worldwide distribution of *B. kewense* is believed to be the result of man-mediated transportation of plants (Winsor 1983; Justine et al. 2018). Given that this invasive species preys on earthworms in cultivated areas (Justine et al. 2018), its dispersal has potentially devastating ecological impact. Recently, analysis of *cox1* from 22 *B. kewense* specimens collected from Metropolitan France, other European countries, and overseas French territories on three continents revealed 100% sequence identity for this mitochondrial gene (Justine et al. 2018), suggesting that worldwide dispersal of a single invasive clone occurred through asexual reproduction.

We sequenced the complete mitogenome of *B. kewense*. DNA was obtained from a specimen that was previously sampled for *cox1* analysis; this specimen collected in Ustaritz (Pyrénées-Atlantiques, France) is registered as MNHN JL184A in the collections of the Muséum National d'Histoire Naturelle (Paris, France). Sequencing was performed by the Beijing Genomic Institute (Shenzhen, China) on the BGISEQ-500 platform. A total of 60 million paired-end reads were assembled using SPAdes 3.12.0 (Bankevich et al. 2012) and a single mitogenome contig was recovered. Gene identification was carried out using MITOS (Bernt et al. 2013).

The *B. kewense* mitogenome (GenBank: MK455837) is 15,666 bp long and encodes 13 proteins, two rRNAs, and 22 tRNAs. All genes are located on the same DNA strand, with the protein- and rRNA- coding genes ordered as follows: *cox1*, *ND6*, *ND5*, *cox3*, *atp6*, *ND1*, *cox2*, *ND3*, *ND2*, *rrnS*, *rrnL*, *cob*, *ND4L*, and *ND4*. We inferred a maximum likelihood tree using the mitogenome-encoded proteins of *B. kewense* and the few Tricladida taxa whose complete mitogenomes were available (Figure 1). The sequences of the proteins shared by all taxa were concatenated and analyzed with RAxML version 8.2.12 (Stamatakis 2014) using the MtArt model of sequence evolution (Abascal et al. 2007) and the Polycladida *Prosthiostomum siphunculus* (KT363736) as outgroup. *B. kewense* was found to strongly associate with the only other Geoplanidae taxon in the tree (*Obama* sp., most probably *O. nungara*), a strain from South America which is also an invasive land flatworm.

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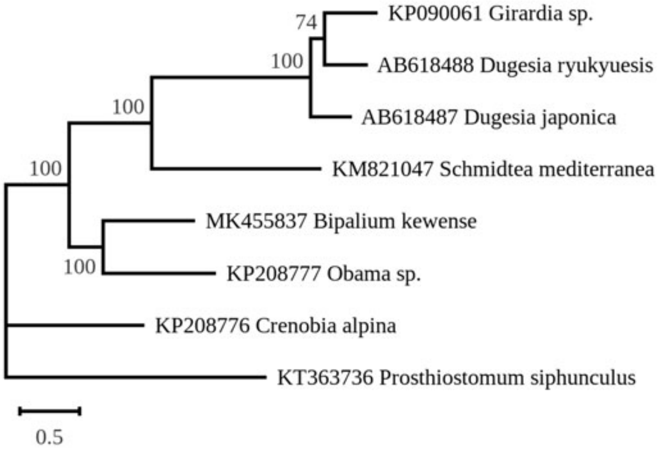

Figure 1. Maximum Likelihood tree obtained on concatenated amino-acid sequences of all mitochondrial proteincoding genes from Bipalium kewense and other flatworms, using the MtArt model of evolution and after 100 bootstrap replications.

Disclosure statement

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

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