The complete mitogenome of the Eurasian blindsnake *Xerotyphlops vermicularis* (Reptilia, Typhlopidae)

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Snake are divided into two major infraorders, the ‘true snakes’ Alethinophidia and the ‘wormsnakes’ Scolecophidia. The latter are small to medium-sized burrowing snakes with no external eyes that, despite their worldwide distribution (except Antarctica) and their great number of species, they have been very poorly studied (Nagy et al. 2015). Their higher-level phylogenetics, systematics, and taxonomy have only recently been assessed (Adalsteinsson et al. 2009; Vidal et al. 2010; Kornilios et al. 2013; Hedges et al. 2014; Pyron and Wallach 2014; Nagy et al. 2015; Miralles et al. 2018). They include more than 400 species and about 40 genera organized in five families: Anomalepididae, Gerrhopilidae, Typhlopidae, Leptotyphlopidae and Xenotyphlopidae (Uetz et al. 2019).

The available mitochondrial genomes for Scolecophidia are very few. In fact, only five mitogenomes have been sequenced, representing five species and genera and three of the families. Here I present the complete mitochondrial genome of *Xerotyphlops vermicularis* Merrem, 1820, which is also the first sequenced mitogenome of this genus, as a new addition to the poor existing record of wormsnake mitogenomes. *Xerotyphlops vermicularis*, known as the Eurasian blindsnake, belongs to Typhlopidae and is the only extant scolecophidian representative occurring in Europe. It is most probably a species-complex (Kornilios et al. 2011, 2012; Kornilios 2017) and its type locality is ‘Greece’. An adult specimen was collected in 2009 in Makri (Thrace, Greece: 40.853932°, 25.747042°) and deposited in the Biology Department, University of Patras (sample code TV071). Total genomic DNA was extracted and used, together with other squamate samples, in a comparative analysis that utilized ultraconserved elements (UCEs) under a sequence capture protocol (Faircloth et al. 2012). The 150 bp paired-end library was prepared using the Truseq Nano DNA kit (Illumina Inc., San Diego, CA) and sequenced on a single Illumina HiSeq 4000 lane. The mitogenome was assembled de novo from the off-target sequences with NOVOPlasty 2.7.1 (Dierckxsens et al. 2017). Genes were annotated using the MITOS WebServer (Bernt et al. 2013) and checked manually. Alignment with all available scolecophidian mitogenomes was done with MAFFT (Katoh et al. 2017). This dataset, after removing the poorly aligned control region, was used to reconstruct a maximum-likelihood (ML) tree with IQ-TREE1.4.3 (Nguyen et al. 2015), using 1000 ultrafast bootstrap alignments (Minh et al. 2013).

The Eurasian blindsnake’s mitogenome (Genbank accession number MH745105) is 16,568 bp long and includes 22 transfer RNA genes (duplicate tRNA-Leu and tRNA-Ser), 2 ribosomal RNA genes, 13 protein-coding genes, and a control region, showing the typical gene-arrangement for Typhlopidae (type II in Qian et al. 2018). Eight tRNAs and ND6 are encoded on the light strand, while all others are encoded on the heavy strand. The overall composition of the heavy strand is A (33.0%), T (27.7%), C (26.2%), and G (13.1%). The ML mitogenomic phylogeny, rooted with the leptotyphlopid *Rena humilis*, is shown in Figure 1. Within the monophyletic unit of Typhlopidae, *Amerotyphlops* represents the South America group of typhlopids, while *Xerotyphlops*, *Indotyphlops*, and *Anilios* represent the Asian one, as resulted in all contemporary DNA phylogenies (e.g. Miralles et al. 2018). The presented tree does not exhibit this phylogenetic configuration, but it is the very limited available
scolecophidian mitogenomes and the overall representation gap that is responsible for this conflict.

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