



ID 9

THE COMPLETE MITOGENOME OF LIVE-BEARING FISH *Xenotoca variata* (CYPRINODONTIFORMES: GOODEIDAE)

*Corona-Santiago D.K. (1), O. Domínguez-Domínguez (2) and F. J. García-De León (3)

(1) Departamento de Biodiversidad y Biología Evolutiva, Museo Nacional de Ciencias Naturales, Madrid, España

(2) Laboratorio de Biología Acuática, Facultad de Biología, Universidad Michoacana de San Nicolás de Hidalgo, Morelia, México.

(3) Laboratorio de Genética para la Conservación, Centro de Investigaciones Biológicas del Noroeste, S.C. La Paz, México.

*Email: diushi.keri.c@gmail.com

ABSTRACT

Xenotoca variata is a live-bearing fish species representative of the endemic ichthyofauna in the central Mexico, and member of a non-monophyletic genus within the Goodeidae family. This omnivore species shows a deep sexual dimorphism and high phenotypic plasticity. *Xenotoca variata* is distributed from the Middle Lerma River (including Cuitzeo basin) to Aguanaval River, including Chapala Lake, and Verde and Pánuco rivers. The aim of this research was to describe the mitogenome of endemic goodeid species *Xenotoca variata*. Library of genomic-DNA was prepared in paired-end libraries, tagged and subjected to next generation sequencing on Illumina MiSeq2500. A total of 2,448,528 reads were obtained. Reads quality was analyzed using FastQC to assembly using SOAPdenovo2 software, and contig belonging to the mtDNA was extracted. Genome annotation was performed using MitoFish and checked manually. As most vertebrate, *X. variata* circular mitogenome consists of 37 genes in 16462pb (13 protein-coding genes, 2 rRNA genes and 22 tRNA genes) with 12 intergenic spacer sequences (of 1-37pb). The base composition of the genome was as follows: A=28.7, C=26.8, G=15.3 and T=29.3 (GC-rich=42). Comparing with *Xenotoca eiseni*, which whole mitogenome is available (38 genes in 16735pb, 13 intergenic spacer sequences and GC-rich=41.8%), an identity of 91.1% was founded. Interesting in *X. variata* mitogenome the duplication of tRNA-Met gene is absent. The size of the tRNA genes in both mitogenomes is 65-74pb. The number of nucleotide differences between both mitogenomes is 1206pb corresponding to a 7.3% of divergence. The complete mitochondrial genome of *X. variata* provides relevant information for developing research on evolution of *Xenotoca* genus and for phylogenetic, population genetics, evolutionary genomics or epigenetics analysis in the species of the Goodeidae family.