

RESEARCH ARTICLE

# Mitochondrial Genome Supports Sibling Species of *Angiostrongylus costaricensis* (Nematoda: Angiostrongylidae)

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## Abstract

*Angiostrongylus costaricensis* is a zoonotic parasitic nematode that causes abdominal or intestinal angiostrongyliasis in humans. It is endemic to the Americas. Although the mitochondrial genome of the Brazil taxon has been published, there is no available mitochondrial genome data on the Costa Rica taxon. We report here the complete mitochondrial genome of the Costa Rica taxon and its genetic differentiation from the Brazil taxon. The whole mitochondrial genome was obtained from next-generation sequencing of genomic DNA. It had a total length of 13,652 bp, comprising 36 genes (12 protein-coding genes—PCGs, 2 rRNA and 22 tRNA genes) and a control region (A + T rich non-coding region). It is longer than that of the Brazil taxon (13,585 bp). The larger mitogenome size of the Costa Rica taxon is due to the size of the control region as the Brazil taxon has a shorter length (265 bp) than the Costa Rica taxon (318 bp). The size of 6 PCGs and the start codon for ATP6, CYTB and NAD5 genes are different between the Costa Rica and Brazil taxa. Additionally, the two taxa differ in the stop codon of 6 PCGs. Molecular phylogeny based on 12 PCGs was concordant with two rRNA, 22 tRNA and 36 mitochondrial genes. The two taxa have a genetic distance of  $p = 16.2\%$  based on 12 PCGs,  $p = 15.3\%$  based on 36 mitochondrial genes,  $p = 13.1\%$  based on 2 rRNA genes and  $p = 10.7\%$  based on 22 tRNA genes, indicating status of sibling species. The Costa Rica and Brazil taxa of *A. costaricensis* are proposed to be accorded specific status as members of a species complex.

## Introduction

*Angiostrongylus costaricensis* Morera and Céspedes, 1971 is a zoonotic parasitic nematode of the Angiostrongylidae family (superfamily Metastrongyloidea) [1]. It resides in the mesenteric arteries of its definitive hosts and its eggs embryonate in the intestinal wall [1]. There are some