



# Complete mitochondrial genome reveals genetic diversity of *Angiostrongylus cantonensis* (Nematoda: Angiostrongylidae)



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## ABSTRACT

*Angiostrongylus cantonensis* is a zoonotic parasite that causes eosinophilic meningitis in humans. Earlier work on its mitochondrial genome was based on long polymerase chain reaction method. To date, only the mitogenome of the isolates from China has been studied. We report here the complete mitogenome of the Thailand isolate based on next generation sequencing and compare the genetic diversity with other isolates. The mitogenome of the Thailand isolate (13,519 bp) is longer than those of the China isolates (13,497–13,502 bp). Five protein-coding genes (*atp6*, *cox1*, *cox2*, *cob*, *nad2*) show variations in length among the isolates. The stop codon of the Thailand isolate differs from the China and Taiwan isolates in 4 genes (*atp6*, *cob*, *nad2*, *nad6*). Additionally, the Thailand isolate has 4 incomplete T stop codon compared to 3 in the China and Taiwan isolates. The control region is longer in the Thailand isolate (258 bp) than the China (230–236 bp) and Taiwan (237 bp) isolates. The intergenic sequence between *nad4* and *cox1* genes in the Thailand isolate lacks 2 bp (indels) at the 5'-end of the sequence as well as differs at 7 other sites compared to the China and Taiwan isolates. In the Thailand isolate, 18 tRNAs lack the entire TΨC-arm, compared to 17 in the China isolate and 16 in the Taiwan isolate. Phylogenetic analyses based on 36 mt-genes, 12 PCGs, 2 rRNA genes, 22 tRNA genes and control region all indicate closer genetic affinity between the China and Taiwan isolates compared to the Thailand isolate. Based on 36 mt-genes, the inter-isolate genetic distance varies from  $p=3.2\%$  between China and Taiwan isolates to  $p=11.6\%$  between Thailand and China isolates. The mitogenome will be useful for population, phylogenetics and phylogeography studies.

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## 1. Introduction

The rat lungworm *Angiostrongylus cantonensis* is a food-borne zoonotic parasite of public health importance in the tropics and subtropics. It causes eosinophilic meningitis or meningoencephalitis (Alicata, 1962; Rosen et al., 1962; Eamsobhana, 2014). It is endemic to Asia and the Pacific Basin but has spread to other parts of the world, including Caribbean islands, North and South America, and Africa (Eamsobhana, 2014). It was first observed in Canton (now Guangzhou), China in the lungs of *Rattus norvegicus* and *Rattus rattus* (Chen, 1935). Humans are non-permissive accidental host, acquiring the infection by consuming raw or inadequately cooked food harboring the infective larvae of the parasite (Cross, 1987).

Because of public health importance, immunodiagnosis of human angiostrongyliasis has been investigated extensively (Eamsobhana and Yong, 2009). Additionally, the parasite has received much attention in clinical and laboratory studies (Graeff-Teixeira et al., 2009). Mitochondrial genes in particular have been applied for systematics, population and phylogenetic studies (Dusitsittipon et al., 2014; Eamsobhana et al., 2010; Foronda et al., 2010; Lee et al., 2014; Monte et al., 2012; Tokiwa et al., 2012; Yong et al., 2015a).

The *Angiostrongylus* genus is represented by some 22 species in the world (Spratt, 2015). To date, the complete mitochondrial genome (mitogenome) of *A. cantonensis* from China has been studied based on long PCR method (Lv et al., 2012, 2014). Five mitogenome haplotypes with 745 variable sites have been reported from three provinces in China (Lv et al., 2014). We report here the complete mitogenome of *A. cantonensis* from Thailand and Taiwan based on next-generation sequencing, and comparison of the genetic diversity in different geographical isolates.

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