



Cytochrome *c* oxidase subunit I haplotype diversity of *Angiostrongylus cantonensis* (Nematoda: Angiostrongylidae)



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ARTICLE INFO

Keywords:

Angiostrongylus cantonensis

Angiostrongyliasis

Haplotype

Phylogeography

Rat lungworm

Genetic diversity

ABSTRACT

The rat lungworm *Angiostrongylus cantonensis* is a food-borne zoonotic parasite of public health importance worldwide. It is the primary etiologic agent of eosinophilic meningitis and eosinophilic meningoencephalitis in humans in many countries. It is highly endemic in Thailand especially in the northeast region. In this study, *A. cantonensis* adult worms recovered from the lungs of wild rats in different geographical regions/provinces in Thailand were used to determine their haplotype by means of the mitochondrial partial cytochrome *c* oxidase subunit I (COI) gene sequence. The results revealed three additional COI haplotypes of *A. cantonensis*. The geographical isolates of *A. cantonensis* from Thailand and other countries formed a monophyletic clade distinct from the closely related *A. malaysiensis*. In the present study, distinct haplotypes were identified in seven regions of Thailand – AC10 in Phitsanulok (northern region), AC11 in Nakhon Phanom (northeastern region), AC15 in Trat (eastern region), AC16 in Chantaburi (eastern region), AC4 in Samut Prakan (central region), AC14 in Kanchanaburi (western region), and AC13 in Ranong (southern region). Phylogenetic analysis revealed that these haplotypes formed distinct lineages. In general, the COI sequences did not differentiate the worldwide geographical isolates of *A. cantonensis*. This study has further confirmed the presence of COI haplotype diversity in various geographical isolates of *A. cantonensis*. The COI gene sequence will be a suitable marker for studying population structure, phylogeography and genetic diversity of the rat lungworm.

1. Introduction

The rat lungworm *Angiostrongylus cantonensis* is a food-borne zoonotic parasite of public health importance worldwide. It has a genome size of about 260 Mb (Yong et al., 2015a). Its life cycle involves mollusk intermediate host and rodent definitive host (Bhaibulaya, 1975). Humans act as an accidental host, acquiring the infection by consuming raw or poorly cooked snail meat which harbors the infective larvae or food contaminated with the third-stage larvae of the parasite (Cross, 1987).

A. cantonensis is the primary etiologic agent of eosinophilic meningitis and eosinophilic meningoencephalitis in humans in many countries (Wang et al., 2008, 2012; Eamsobhana, 2014). Angiostrongyliasis *cantonensis* involving the eyes and lungs have also been reported (Eamsobhana, 2014). In recent years, this neurotrophic nematode has spread from its original endemic areas of Southeast Asia and the Pacific islands to the American continent including the USA, Brazil and

Caribbean islands (Wang et al., 2008, 2012). The rapid global spread of the *Angiostrongylus* lungworms and the emerging occurrence of the disease have posed challenges in its molecular epidemiology studies.

Eosinophilic meningitis caused by rat lungworm is highly endemic in Thailand especially in the northeast region of the country where a popular uncooked snail dish “koi-hoi” is often eaten (Eamsobhana, 2014; Eamsobhana et al., 2009). The snail of *Pila* species has an important role of transmitting the infection in Thailand. Although surveys on *A. cantonensis* based on morphological features in a variety of intermediate snail host and definitive rodent host have been continuously performed and reported, there is still limited molecular data on the phylogenetic relationship of this nematode in different regions of Thailand (Vitta et al., 2016). Moreover, apart from the report of Yong et al. (2015b) on molecular phylogeography of *A. cantonensis* and genetic relationships with congeners using the cytochrome *b* gene marker, molecular data on intra-species genetic variations of this neurotrophic lungworm from the definitive rodent host has not been

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