



Molecular phylogeography of *Angiostrongylus cantonensis* (Nematoda: Angiostrongylidae) and genetic relationships with congeners using cytochrome *b* gene marker

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ABSTRACT

Angiostrongylus cantonensis is an important emerging zoonotic parasite causing human eosinophilic meningitis (or meningoencephalitis) in many parts of the world. To-date there is only a single study using mitochondrial cytochrome *b* (CYTB) gene to determine its genetic structure in eight geographical localities in Thailand. The present study examined the molecular phylogeography of this rat lungworm and its phylogenetic relationship with congeners using CYTB gene marker. A total of 15 CYTB haplotypes was found in 37 sequences from 14 geographical localities (covering north, west, east, central and south regions) in Thailand. These CYTB haplotypes were distinct from those of *A. cantonensis* for China and Hawaii. In Thailand, some CYTB haplotypes appeared to be confined to specific geographical localities. The partial CYTB DNA nucleotide sequences separated unequivocally the *A. cantonensis* isolates of Thailand, China and Hawaii as well as the congeners *Angiostrongylus malaysiensis*, *A. costaricensis* and *Angiostrongylus vasorum*, with *A. malaysiensis* grouped with *A. cantonensis* and *A. costaricensis* grouped with *A. vasorum*. Likewise the congeners of *Metastrongylus* and *Onchocerca* genera could also be clearly differentiated. The present study added two new definitive hosts (*Bandicota savilei* and *Rattus losea*) and three new localities (Mae Hong Son in the north, Tak in the west, and Phang Nga in the south) for *A. malaysiensis* in Thailand, indicating its wide occurrence in the country. Three CYTB haplotypes were found in the Thailand samples of *A. malaysiensis*. In addition to differentiation of congeners, CYTB gene marker could be used for determining the genetic diversity of a given population/taxon.

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1. Introduction

Angiostrongylus cantonensis (Nematoda: Angiostrongylidae) is an important emerging pathogen causing human angiostrongyliasis with thousands of cases in many parts of the world (Kliks and Palumbo, 1992; Wang et al., 2012). Its typical endemic regions were Asia and the Pacific but has now spread to many other regions of the world, including Africa, Australia, Caribbean islands and the Americas (Eamsobhana, 2014).

Human infections with *A. cantonensis* are accidental or incidental in nature, as a result of ingestion of the third-stage larvae in

intermediate hosts, paratenic hosts or contaminated raw or undercooked vegetables (Eamsobhana, 2014). The outcome may be fatal because of cerebral hemorrhage and eosinophilic meningitis for which treatment is generally symptomatic and supportive in nature (Eamsobhana, 2014). Over the years there have been extensive laboratory and clinical studies (Graeff-Teixeira et al., 2009) and development of immunodiagnosis (Eamsobhana and Yong, 2009).

Genetic aspects of *A. cantonensis* and related taxa have been explored vis-a-vis systematics and phylogenetics. The molecular gene markers include the nuclear 66 kDa protein gene (Caldeira et al., 2003; Eamsobhana et al., 2010a), internal transcribed spacers (Jefferies et al., 2009; Foronda et al., 2010; Liu et al., 2011; Lee et al., 2014), small subunit ribosomal RNA (Fontanilla and Wade, 2008; Eamsobhana et al., 2014), and mitochondrial cytochrome *c* oxidase subunit I (Jefferies et al., 2009; Eamsobhana et al., 2010b; Foronda

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