

# Cytochrome *c* oxidase subunit I haplotype reveals high genetic diversity of *Angiostrongylus malaysiensis* (Nematoda: Angiostrongylidae)

P. Eamsobhana<sup>1\*</sup>, H.S. Yong<sup>2</sup>, S.L. Song<sup>3</sup>, A. Prasartvit<sup>4</sup>,  
S. Boonyong<sup>1</sup> and A. Tungtrongchitr<sup>1\*</sup>

<sup>1</sup>Department of Parasitology, Faculty of Medicine Siriraj Hospital, Mahidol University, Bangkok 10700, Thailand; <sup>2</sup>Institute of Biological Sciences, University of Malaya, 50603 Kuala Lumpur, Malaysia; <sup>3</sup>Institute of Ocean and Earth Sciences, University of Malaya, 50603 Kuala Lumpur, Malaysia; <sup>4</sup>Department of Disease Control, Ministry of Public Health, Nonthaburi 11000, Thailand

(Received 16 January 2017; Accepted 20 February 2017; First published online 23 March 2017)

## Abstract

The rat lungworm *Angiostrongylus malaysiensis* is a metastrongyloid nematode parasite. It has been reported in Malaysia, Thailand, Laos, Myanmar, Indonesia and Japan. In this study, *A. malaysiensis* 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 high COI haplotype diversity of *A. malaysiensis* from Thailand. The geographical isolates of *A. malaysiensis* from Thailand and other countries formed a monophyletic clade distinct from the closely related *A. cantonensis*. In the present study, five new haplotypes were identified in addition to the four haplotypes reported in the literature. Phylogenetic analysis revealed that four of these five new haplotypes – one from Mae Hong Song (northern region), two from Tak (western region) and one from Phang Nga (southern region) – formed a distinct clade with those from Phatthalung (southern region) and Malaysia. The haplotype from Malaysia was identical to that of Phatthalung (haplotype AM1). In general, the COI sequences did not differentiate unambiguously the various geographical isolates of *A. malaysiensis*. This study has confirmed the presence of high COI genetic diversity in various geographical isolates of *A. malaysiensis*. The COI gene sequence will be suitable for studying genetic diversity, population structure and phylogeography.

## Introduction

*Angiostrongylus malaysiensis* (Bhaibulaya & Cross, 1971) is a metastrongyloid nematode parasite of the family Angiostrongylidae (Eamsobhana, 2014; Spratt, 2015).

When first documented in Malaysia it was referred to as *A. cantonensis* (Lim *et al.*, 1965; Schacher & Cheong, 1960). It was subsequently recognized as a valid species and named as *A. malaysiensis* (Bhaibulaya & Cross, 1971). Its species status was confirmed by cross-breeding experiments with *A. cantonensis* (Cross & Bhaibulaya, 1974). In addition to Malaysia, *A. malaysiensis* has been reported to occur in Thailand (Bhaibulaya & Techasoponmani, 1972), Indonesia (Carney & Stafford,

\*E-mails: [praphathip.eam@mahidol.ac.th](mailto:praphathip.eam@mahidol.ac.th);  
[anchalee.tun@mahidol.ac.th](mailto:anchalee.tun@mahidol.ac.th)