Angiostrongylus mackerrasae and A. cantonensis (Nematoda: Metastrongyloidea) belong to same genetic lineage: evidence from mitochondrial protein-coding genes

S.-L. Song¹*, H.-S. Yong² and P. Eamsobhana³*

¹Institute of Ocean and Earth Sciences, University of Malaya, 50603 Kuala Lumpur, Malaysia: ²Institute of Biological Sciences, University of Malaya, 50603 Kuala Lumpur, Malaysia: ³Department of Parasitology, Faculty of Medicine Siriraj Hospital, Mahidol University, Bangkok 10700, Thailand

(Received 26 April 2017; Accepted 9 June 2017; First published online 11 July 2017)

Abstract

Angiostrongylus mackerrasae is a parasitic nematode of rats found in Australia. When first reported, it was referred to as A. cantonensis. Recent molecular studies, including the mitochondrial genome, indicate that it is highly similar to A. cantonensis. These studies did not include A. malaysiensis, another member of the A. cantonensis species complex, for comparison. The present study examined the genetic distance and phylogenetic relationship between the component taxa (A. cantonensis, A. mackerrasae and A. malaysiensis) of the A. cantonensis species complex, based on the 12 protein-coding genes (PCGs) of their mitochondrial genome. Both the nucleotide and amino acid sequences were analysed. Angiostrongylus mackerrasae and A. cantonensis are members of the same genetic lineage and both are genetically distinct from A. malaysiensis. The genetic distance based on concatenated nucleotide sequences of 12 mt-PCGs between A. mackerrasae and A. cantonensis from Thailand is p = 1.73%, while that between the Thai and Chinese taxa of A. cantonensis is p = 3.52%; the genetic distance between A. mackerrasae and A. cantonensis from China is p = 3.70%. The results indicate that A. mackerrasae and A. cantonensis belong to the same genetic lineage, and that A. mackerrasae may be conspecific with A. cantonensis. It remains to be resolved whether A. mackerrasae is conspecific with A. cantonensis or undergoing incipient speciation.

Introduction

The genus *Angiostrongylus* is represented by 21 valid named species and an unnamed species (Spratt, 2015). Rodents serve as the definitive host for 15 species of this genus of nematode parasites (Eamsobhana, 2014). Two species, *A. cantonensis* (Chen, 1935) and *A. costaricensis* (Morera & Céspedes, 1971) are zoonotic parasites of public health importance (Cross & Chen 2007; Eamsobhana, 2014; Spratt, 2015). Two other species of the *A. cantonensis* species complex, *A. mackerrasae* (Bhaibulaya, 1968) and *A. malaysiensis* (Bhaibulaya & Cross, 1971), have not been unequivocally shown to be involved in human infections, but their potential needs to be investigated as they share a similar life cycle with *A. cantonensis*.

When first documented in Malaysia, *A. malaysiensis* was referred to as *A. cantonensis* (Schacher & Cheong, 1960; Lim *et al.*, 1965). Both mitochondrial and nuclear genes

Downloaded from https://www.cambridge.org/core. Mahidol University, on 11 Jun 2018 at 09:39:12, subject to the Cambridge Core terms of use, available at https://www.cambridge.org/core/terms. https://doi.org/10.1017/S0022149X1700061X

^{*}E-mails: szelooi@um.edu.my; praphathip.eam@mahidol.ac.th