

Genetic Diversity of
Angiostrongylus
cantonensis

Praphathip Eamsobhana
Phaik Eem Lim
Hoi Sen Yong

***Angiostrongylus* spp.** **partial 66-kDa protein gene**

- AC primers successfully amplified genomic DNA of *A. cantonensis*, *A. costaricensis* and *A. malaysiensis*
- No amplification detected for DNA of *Ascaris suum*, *Ascaris lumbricoides*, *Toxocara canis*, *Anisakis simplex*, *Trichinella spiralis*, and also *Gnathostoma spinigerum*

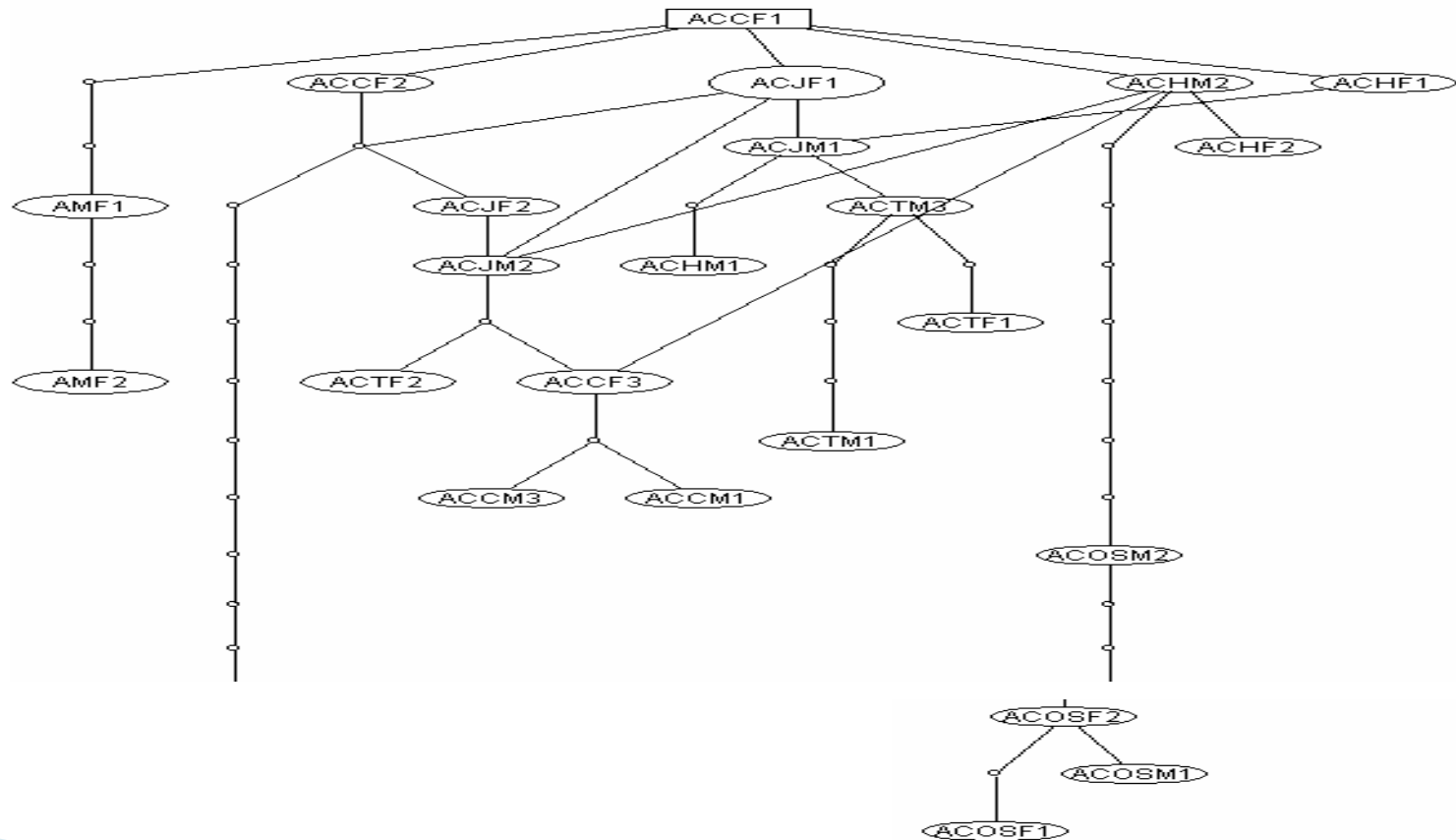
***Angiostrongylus* spp.**

partial 66-kDa protein gene

- ▶ Partial DNA sequences indicate that *A. cantonensis* is a sister group to *A. malaysiensis*
- ▶ The two species are clearly separated but are closer related than to *A. costaricensis*
- ▶ **No clear distinction between the *A. cantonensis* from 4 different geographical isolates (Thailand, China, Japan and Hawaii)**
- ▶ They are represented by a great diversity of haplotypes, indicating both inter- and intra-population variation

Angiostrongylus spp. partial 66-kDa protein gene

Haplotype diversity



Angiostrongylus 66-kDa protein gene - Genetic distance

	<i>A. malaysiensis</i>	<i>A. costaricensis</i>
<i>A. cantonensis</i>	1.70 - 4.08	3.77 - 5.77
<i>A. malaysiensis</i>		5.10

Angiostrongylus spp.

ITS-2 (internal transcribed spacer-2) ,
SSU rRNA (small subunit ribosomal RNA)

- ▶ The distinction of *A. cantonensis*, *A. malaysiensis* and *A. costaricensis* is reflected in the DNA sequences of ITS-2 and SSU rRNA sequences
- ▶ No clear distinction between the *A. cantonensis* from different geographical isolates

Angiostrongylus cantonensis

COI (cytochrome *c* oxidase subunit I)

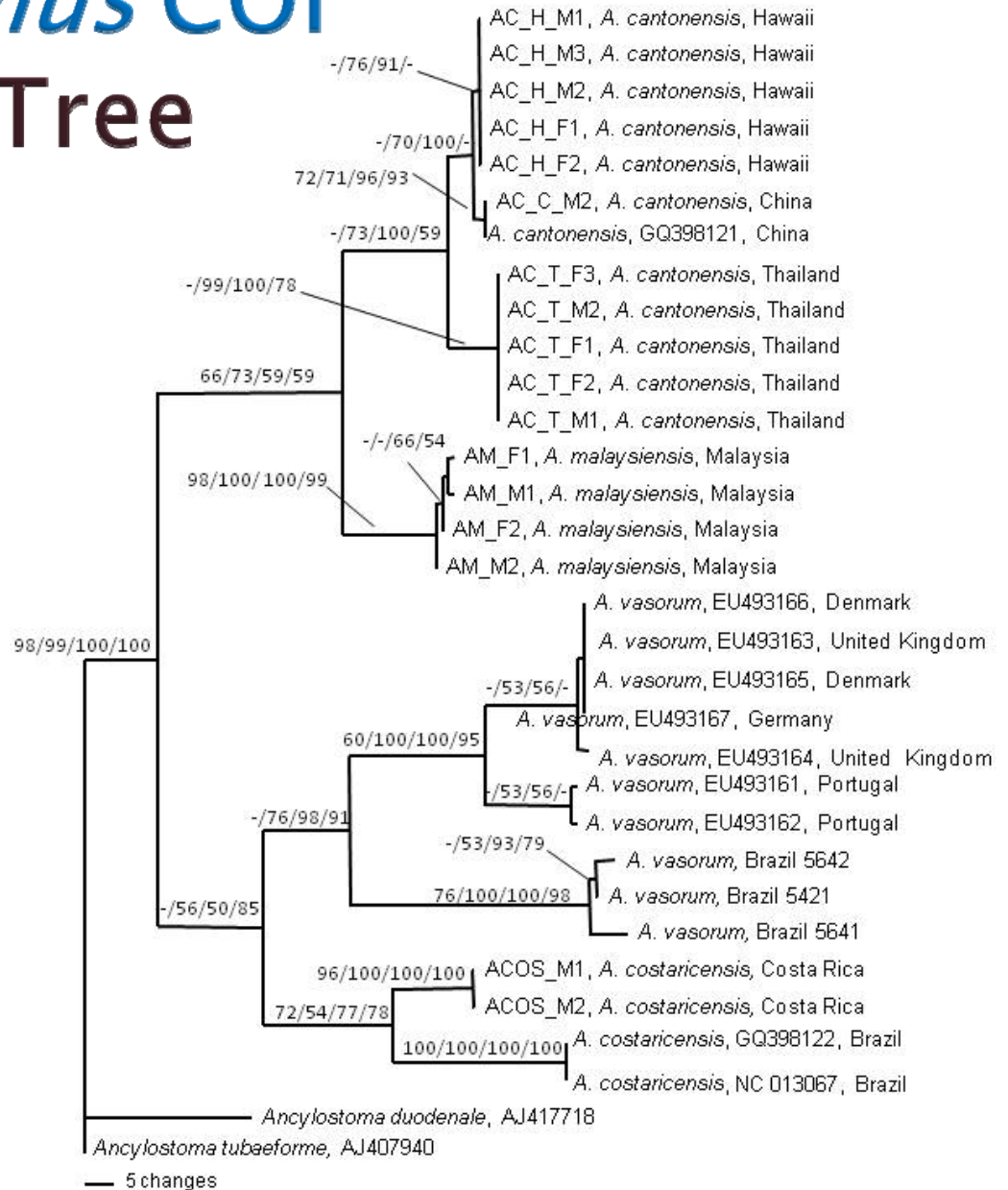
- ▶ Clear distinction of *A. cantonensis*, *A. malaysiensis* and *A. costaricensis* (as well as *A. vasorum*) is reflected in the DNA sequences of COI
- ▶ *A. cantonensis* samples from different geographical localities form distinct clusters in the maximum likelihood (ML), maximum parsimony (MP), neighbor-joining (NJ) and Bayesian inference (BI) trees

Angiostrongylus cantonensis

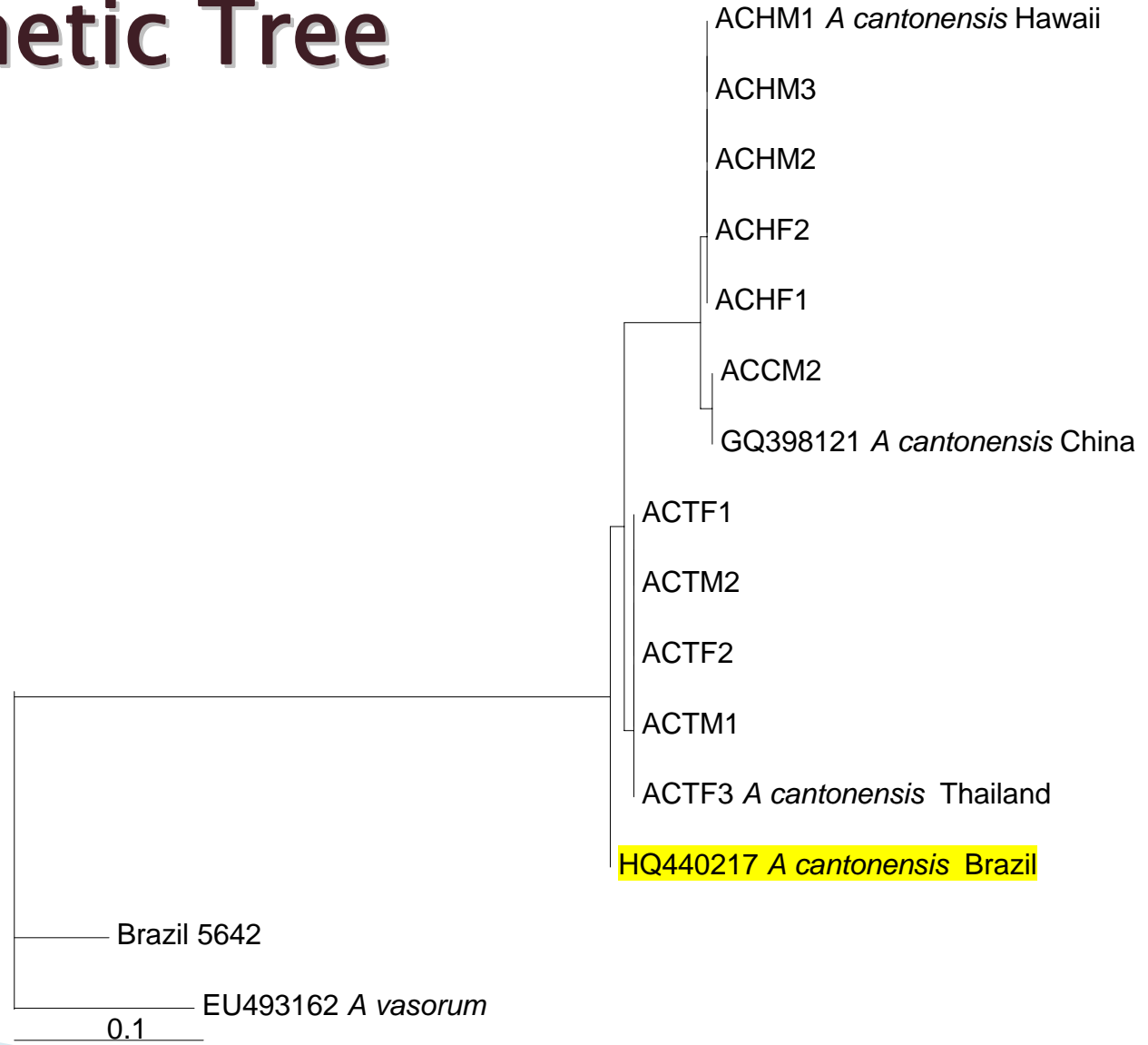
COI genetic distance

Sample	China	Hawaii
AC_C_M2, China		
AC_H_M1, Hawaii	0.83	
AC_T_F2, Thailand	3.61	3.61

Angiostrongylus COI Phylogenetic Tree



Angiostrongylus COI Phylogenetic Tree



Angiostrongylus COI gene

Useful and suitable for:

- differentiating closely related species (e.g. *A. cantonensis* and *A. malaysiensis*)
- differentiating geographical isolates of *A. cantonensis*
- determining the phylogenetic relationship of *A. cantonensis*, *A. costaricensis*, *A. malaysiensis* and *A. vasorum*

References:

1. Eamsobhana P, Lim PE, Zhang HM, Gan XX, Yong HS. Molecular differentiation and phylogenetic relationships of three *Angiostromylus* species and *A. cantonensis* geographical isolates based on a 66-kDa protein gene of *A. cantonensis* (Nematoda: Angiostromylidae). *Experimental Parasitology* 2010; 126: 564-569.
2. Eamsobhana P, Lim PE, Solano G, Zhang HM, Gan XX, Yong HS. Molecular differentiation of *Angiostromylus* taxa (Nematoda: Angiostromylidae) by cytochrome c oxidase subunit I (COI) gene sequences. *Acta Tropica* 2010; 116: 152-156.