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Short communication

Genetic characterization of the partial mitochondrial cytochrome oxidase c subunit I (cox 1) gene of the zoonotic parasitic nematode, *Ancylostoma ceylanicum* from humans, dogs and cats



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ABSTRACT

Ancylostoma ceylanicum is the only zoonotic hookworm species that is able to produce patent infections in humans with the majority of cases reported in South East Asia. Over the past few years, there have been an increasing number of studies investigating the prevalence of this parasitic zoonosis using molecular diagnostic tools and a single genetic locus as marker for species identification. As there can be limitations in using a single genetic locus for epidemiological studies and genetic discrimination, the complementary use of a more variable locus will provide additional evidence to support the zoonotic exchange of hookworm species between humans and animals. In the present study, the cytochrome c oxidase subunit 1 (cox 1) sequence of A. ceylanicum from positive human and animal fecal samples were determined and compared with published reference sequences. Phylogenetic analysis demonstrated that isolates of A. ceylanicum were divided into two clusters, one consisting 3 human isolates and the other comprising 19 isolates of human and animal origin from different geographical locations within Malaysia. The two groups of A. ceylanicum could be distinguished from one another through five fixed nucleotide differences at locations 891, 966, 1008, 1077 and 1083. The detection of genetically distinct groups and considerable level of genetic variation within the cox 1 sequence of A. ceylanicum might suggest potential haplotypelinked differences in zoonotic, epidemiological and pathobiological characteristics, a hypothesis that still needs further investigation.

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1. Introduction

Hookworms are blood-sucking nematodes of the Ancylostomatidae family that infect both humans and animals. *Necator americanus* and *Ancylostoma duodenale* are the two most commonly found hookworm species in humans (Chan et al., 1994). Besides anthroponotic hookworms, humans may also harbor patent infections with *Ancylostoma ceylanicum*, a zoonotic hookworm that utilize dogs and cats as their natural definitive hosts. Zoonotic ancylostomiasis caused by *A. ceylanicum* has been reported in many regions of Asia and Southeast Asia (Conlan et al., 2012; Jiraanankul et al., 2011; Ngui et al., 2012a,b; Sato et al., 2010; Traub et al., 2008).

Recently, an influx of studies has investigated the prevalence of this parasitic zoonosis using molecular tools. These advanced tools are mainly used to detect and characterize infection directly from eggs in human and animal feces particularly targeting the second internal transcribed spacer (ITS-2) of nuclear ribosomal DNA as the genetic marker for hookworm species identification (Conlan et al., 2012; Jiraanankul et al., 2011; Mahdy et al., 2012; Ngui et al., 2012a,b; Sato et al., 2010; Traub et al., 2008). This locus has a lower mutation rate and is repetitive due to less sequence variation among or between populations, which makes it suitable to be used as a species-specific marker (Hoste et al., 1995; Romstad et al., 1998; Stevenson et al., 1995).

Although the ITS region provides a highly sensitive tool for the detection and differentiation of hookworm DNA at the species level (Traub et al., 2004), it fails to provide sufficient genetic resolution at a sub-species level (Hoste et al., 1995; Romstad et al., 1998; Stevenson et al., 1995). Mitochondrial DNA genes have more

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