Sympatric Occurrence of Taenia solium, T. saginata, and T. asiatica, Thailand

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We confirmed sympatric occurrence of Taenia solium, T. saginata, and T. asiatica in western Thailand. DNA analysis of morphologically identified T. saginata, in a dual infection with T. solium, indicated it was T. asiatica. To our knowledge, this report is the first of T. asiatica and a dual Taenia infection from Thailand.

Taeniid tapeworm infections in the human intestine are caused by Taenia solium, T. saginata, and T. asiatica in Asia and the Pacific (1–3). Taeniasis caused by T. solium is a serious public health problem worldwide because eggs and proglottids expelled in the stool can infect humans through contamination of the environment and cause fatal neurocysticercosis. Neurocysticercosis cases caused by T. solium have increased in non–taeniasis-endemic areas (3–5).

A related taeniid tapeworm, Asian Taenia (= T. asiatica), has been described in Taiwan and the Republic of Korea (1–3,6–8). Although T. asiatica is phylogenetically closely related and is considered to be a sister species of T. saginata (1–3,6,7), the important intermediate host for T. asiatica is the domestic pig and the metacestodes mainly develop in the pigs’ liver (6). The morphologic characteristics of adult T. asiatica are very similar to those of T. saginata. Morphologic differentiation by either scolex or gravid proglottid of these 2 species is practically impossible (1,3). On the basis of molecular analysis of taeniid isolates from Asia and the Pacific, T. asiatica is distributed in Taiwan, the Republic of Korea, Malaysia, People’s Republic of China, Philippines, Indonesia, and Vietnam (1–3,6–11). However, there has been no evidence of the distribution of T. asiatica in Thailand (8,12).

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29 scolices were con-
Conclusions

We documented sympatric distribution of *T. solium*, *T. saginata*, and *T. asiatica* in western Thailand on the basis of mitochondrial DNA analysis. Our study indicated that 53.3% (8/15) of taeniid specimens expected to be *T. solium* were used: F3 (5’-TATTTAGCTGAAATTTATTTCTCT-3’, corresponding to nucleotide (nt) positions 629–651) and R7 (5’-ATTAACACATAACCTCGGGA-3’, nt positions 740–720) for Cox1 of *T. solium*, F1 (5’-GTCAAAAGATTCTTTTTTACTTGGT-3’, nt positions 180–205) and R2 (5’-CCCTTTTTCTATAACTTGAATAAAT-3’, nt positions 305–281) for cob for *T. solium*. DNA sequencing of the products amplified by multiplex PCR was performed for confirmation. DNA samples for sequencing were prepared with a BigDye Terminator v3.1 Cycle Sequencing Kit (Applied Biosystems, Foster City, CA, USA). DNA sequencing was performed on an ABI PRISM 310 Genetic Analyzer (Applied Biosystems), and the nucleotide sequence data were analyzed by using DNASTAR version 3.75 (DNASTAR Inc., Madison, WI, USA).

Multiplex PCR applied on 19 proglottids from 17 patients with *cox1* (10) showed that 5, 7, and 7 proglottids were *T. solium* (Asian genotype) (10,13), *T. saginata*, and *T. asiatica*, respectively (data not shown). These results were supported by DNA sequencing of the amplicons (data not shown). By contrast, small sizes of 112-bp *cox1* products were successfully amplified from samples taken from patients 3–6. These samples had been preserved in 10% formalin for years and BESS T-base analysis indicated that they were *T. solium* (Asian genotype) (Figure 2A) (14). BESS T-base analysis showed that scolices with and without hooklets from a dual infection (patient 7) were *T. solium* (Asian genotype) and *T. asiatica*, respectively (Figure 2B and C). To our knowledge, this is the first report demonstrating a dual infection with *T. solium* and *T. asiatica* in which 3 human taeniid cestodes are sympatrically distributed (1).

Conclusions

We documented sympatric distribution of *T. solium*, *T. saginata*, and *T. asiatica* in western Thailand on the basis of mitochondrial DNA analysis. Our study indicated that 53.3% (8/15) of taeniid specimens expected to be *T. saginata* were *T. asiatica* and that both *T. asiatica* and *T. saginata* are codistributed in Kanchanaburi Province. Although *T. solium* taeniasis has seldom been reported in the literature in Thailand (15), our study has shown infection with *T. solium* (Asian genotype) in 11 (45.8%) of 24 *Taenia*-infected patients. The number of *T. solium* organisms expelled from taeniasis patients varied from 1 to 6, and ≥2 tapeworms were found in 36.4% (4/11) of *T. solium* taeniasis patients. In addition, we confirmed a dual infection with *T. solium* and *T. asiatica* (in patient 7). This experience indicates that molecular analysis is preferable and necessary for precise re-identification of so-called *T. saginata* in Asia and the Pacific (1).

Although *T. solium* cysticercosis in humans has not been reported in this study area, these populations appear to pose a risk for environmental contamination and person-to-person spread of *T. solium* leading to cysticercosis in humans and swine. Raw or inadequately cooked beef, pork, or pig viscera, and fresh blood are commonly consumed by local people in the study areas, and consequently they are at high risk of acquiring taeniasis. Therefore, to improve sanitation and quality of life, sustainable health education should be introduced and stressed to the population in the community.

Acknowledgments

We thank Vajiralongkorn Dam for accommodations during our field work and Peter M. Schantz for his comments and suggestions for improving this article.

The field survey in Thailand from 2002 until 2005 was funded by Mahidol University research grant 02011285-0002 to J.W. The molecular work was supported by a grant-in-aid for Scientific Research from the Japan Society for Promotion of Science (JSPS) to A.I. (14256001, 17256002) and to M.O. (18406008) and by a JSPS-Asia/Africa Sciences Platform Fund (2006–2008) to A.I.
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References


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