Infection of *Taenia asiatica* in a Bai Person in Dali, China

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**Abstract:** We report here a human case of *Taenia asiatica* infection which was confirmed by genetic analyses in Dali, China. A patient was found to have symptoms of taeniasis with discharge of tapeworm proglottids. By sequencing of the mitochondrial cytochrome c oxidase subunit 1 (cox1) gene, we observed nucleotide sequence identity of 99% with *T. asiatica* and 96% with *T. saginata*. Using the cytochrome b (cytb) gene, 99% identity with *T. asiatica* and 96% identity with *T. saginata* were found. Our findings suggest that taeniasis of people in Dali, China may be mainly caused by *T. asiatica*.

**Key words:** *Taenia asiatica*, case report, cox1 gene, cytb gene

**INTRODUCTION**

Human taeniasis is caused by 3 species of taeniid tapeworms, *Taenia solium*, *Taenia saginata*, and *Taenia asiatica*. Among these 3 species, *T. asiatica* was recorded as a distinct one from *T. saginata* in 1993 both of which are morphologically similar to each other [1-3]. *T. asiatica* is more restrictedly distributed in Asian countries, i.e., Korea, China, Taiwan, Thailand, Indonesia, Vietnam, Japan, and the Philippines [1].

Because of the morphological similarity, *T. asiatica* had previously been considered as *T. saginata* [2,3]. Thus, molecular methods became an efficient tool which can provide a clearer phylogenetic resolution. The methods of PCR-RFLP, single-strand conformation polymorphism (SSCP), a loop-mediated isothermal amplification (LAMP), multiplex PCR, and co-proDNA test have been reported [4-9]. These methods have their own advantages accordingly. Their mitochondrial cytochrome c oxidase 1 (cox1) and cytochrome b (cytb) gene sequences have been determined completely, and they have been widely used to study the population structure and genetic differentiation of several tapeworm species [10-12].

A previous study indicated that short sequences of the cox1 gene can give a bias to analysis, and rather a complete sequence data would provide more reliable results [13,14]. Phylogenetic trees can show the relationships among different taxa. In the present study, we report a human case of *T. asiatica* infection by genetic analyses based on cox1 and cytb genes in Dali, China.

**CASE RECORD**

The patient (Bai nationality, Dali, China) is a healthy 30-year-old man who visited Dali People’s Hospital after finding a whitish yellow tapeworm segment in his feces on 26 May 2014. He had not experienced any abdominal discomfort or pain, and had not visited any foreign countries recently. He had a history of eating raw pork and raw pig liver mixed with sour sauce and salted garlic. His blood test results were normal.

The man was treated with traditional Chinese medicine (the combination of pumpkin seeds and areca nut extract) and 30% hydrated magnesium sulfate (MgSO₄·7H₂O) solution. An almost complete cestode (about 1.8 m long) without a scolex was expelled after about 3-6 hr of treatment. This tapeworm specimen was kept in a 50 ml centrifuge tube filled with 0.9% normal saline and forwarded to National Key Laboratory of Veterinary Etiological Biology (Lanzhou, China) for examinations.

Genomic DNA (gDNA) was extracted from the proglottid of the tapeworm using an AxyPrep small genomic DNA kit (Axygen, Beijing, China). Purified gDNA was used as a template for PCR for cox1. The PCR primers were up primer (5’-ATGAGTGT-TAAATITTTGTTAAGT-3’) and down primer (5’-TCTAAATC-AAAAACCACGACC-3’). PCR was performed in a 50 µl reac-
tion mixture containing 25 µl of PrimeSTAR® HS Premix (Taka-ra, Kyoto, Japan), 1.5 µl of 10 µM of each primers, 20 µl of dis-
tilled water, and 2 µl purified gDNA from tapeworm. The PCR
reaction was carried out for 35 cycles of 94°C for 40 sec, 55°C
for 40 sec, 72°C for 60 sec. The reaction initial denaturing step
at 95°C for 5 min and terminated with a final extension step at
72°C for 10 min. The PCR amplification of cytb sequence was
performed using a primer pair of cytb up primer (5’-ATGATTA-
GATTAT TTCGACG-3’) and down primer (5’-TTAATAAATCTTA-
AAAAGAAACATAAGC-3’). PCR conditions for cytb gene were
the same as those for cox1.

The amplification products were fractionated using 1% (w/ v) agarose gel, and then purified (Axygen). The purified prod-
ucts were then ligated into PMD-18T vector (Takara), followed
by transformation into Escherichia coli DH5α and sequencing.
The sequences for cox1 and cytb were aligned with the corre-
sponding sequences of tapeworms obtained from GenBank
database. Molecular identification of the tapeworm specimens
was based on a comparison with the nucleotide sequences of
cox1 and cytb genes of T. solium, T. Saginata, and T. asiatica. Phy-
logenetic analyses were performed using the neighbor-joining
(NJ) method by MEGA (Version 5) with the Kimura-2 param-
eter model [15]. Bootstrap analysis was performed with 1,000
replications.

The whitish yellow tapeworm from the patient was shown
in Fig. 1. Approximately, 1,620 bp nucleotide sequence from
the mitochondrial cox1 gene of the tapeworm in the present

![Fig. 1. An almost complete strobila (about 1.8 m in length), without the scolex, of Taenia asiatica recovered from our patient.](image)

![Fig. 2. Phylogenetic tree of 3 Taenia spp. using the mitochondrial cox1 gene sequences. Our tapeworm specimen showed 99% identity (1 different base) with T. asiatica (AB533175.1) and 96% identity (65 different bases) with T. saginata (AB465239.1).](image)
study was obtained, which showed an identity of 99% (1 different base) with *T. asiatica* (AB533175.1) and 96% (65 different bases) with *T. saginata* (AB465239.1), respectively. The phylogenetic analysis revealed that our tapeworm was closely related to *T. asiatica* (Fig. 2). Furthermore, approximately 1,068 bp sequence of the mitochondrial *cytb* gene had an identity of 99% (2 bp differences) with *T. asiatica* (no. AB066580.1) and 96% (43 bp different bases) with *T. saginata*, respectively. Phylogenetic analysis showed that the cestode was closely related to *T. asiatica* (Fig. 3). Sequences of all *Taenia* specimens derived from different Asian countries formed a monophyletic group.

**DISCUSSION**

To date, taeniasis still occurs in the majority of regions in Southwest China including Yunnan, Sichuan, Guizhou, Qinghai, and many other provinces where a minority of people like to eat raw pork, undercooked beef, and raw pig liver mixed with sour sauce and salted garlic, and the prevalence and incidence of human taeniasis remains unknown in southwest China [1,16-18]. Eating raw liver which contains cysticerci is the main risk factor of tapeworm infection. In the present study, since infection of the patient was a result of consumption of undercooked pig liver, it is reasonable to guess that the taeniasis is due to *T. asiatica* caused in Dali of Yunnan Province. Neither *T. saginata* nor *T. solium* were detected during the same period, so *T. asiatica* was considered to be the dominant species causing human taeniasis in Dali.

As the living standards of people improve, the incidence of taeniasis became markedly lower in Dali, but the local Bai people still have the habit of eating raw pork and raw pig liver. So, it is necessary for them to know the dangers of taeniasis and to understand the routes of tapeworm transmission through continuous public health educations. There are 2 strategies for cutting off the domestic life of *T. asiatica*. First, local people should pay attention to prevent human taeniasis avoiding intake of uncooked or undercooked pig liver. Second, the patient who is infected with the tapeworm must be treated early with anthelmintics and keep pigs without contacting human feces. We believe that the taeniasis will be eliminated someday in the future if native people take above these 2 advices in Dali.

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**CONFLICT OF INTEREST**

We have no conflict of interest related to this study.
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