

# COPRO-DIAGNOSIS OF *HAPLORCHIS TAICHUI* INFECTION USING SEDIMENTATION AND PCR-BASED METHODS

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**Abstract.** Fifty-one human fecal specimens were collected from villagers inhabiting along Mae Kuang River, Ban Sob Tha, Pa Sang District, Lamphun Province, Thailand. By the formalin-ether sedimentation technique (FEST) under a light microscope, eggs of 3 helminth species, *Haplorchis taichui*, *Ascaris lumbricoides* and unidentified hookworm species were detected with prevalences of 22, 14 and 4%, respectively. PCR amplification with *H. taichui* specific primers showed that *H. taichui* specific amplicon 260 bp was generated in all FEST-positive specimens, and also in some FEST negative specimens. This *H. taichui* specific PCR method can be used to detect this parasite in all developmental stages and in both definitive and intermediate hosts, which should be useful in prevention and control programs.

## INTRODUCTION

Helminthiasis is a public health problem in developing countries. In Thailand, opisthorchiasis and heterophyiasis are common trematode infection endemic in north-eastern and northern Thailand, respectively (Manning *et al*, 1971; Radomyos *et al*, 1998). *Haplorchis taichui* is a minute intestinal fluke in the family Heterophyidae. Several kinds of mammals including humans, rats, cats, dogs and chicken can serve as definitive hosts. (Pearson, 1964; Pearson and OW-Yang, 1982). Larval stages, miracidium, sporocyst, redia and cercaria, are found in freshwater snails, *Melanoides tuberculata*, *Stenomelania newcombi* and *Thiara granifera* (Martin, 1958; Noda, 1959), which represent first interme-

diate hosts. Metacercaria (infective stage) is found mainly in mud carp (*Henicorhynchus siamensis*) (Kumchoo *et al*, 2005), which has a high infection rate and is endemic in northern Thailand. People acquire this parasite by consuming undercooked foods prepared from fish containing metacercariae. Symptoms of *H. taichui* infection has not been clearly reported. The first clinical report revealed that *H. taichui* was found by autopsy with many embryonated eggs remaining in blood vessel of cardiac muscle (Africa *et al*, 1935). *H. taichui* can be considered as food-borne zoonotic trematode.

In northern Thailand, the prevalence of parasitic infection is still high. A previous report indicated that trematode eggs found in humans were *O. viverrini* and *H. taichui* was not detected (Chiang Mai Provincial Public Health Office, 2001). However, a subsequent report showed that *H. taichui* was found to infect villagers inhabiting Mae Ping River, Chom Thong District, Chiang Mai

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Province (Chuboon and Wongsawad, 2003). Several survey data showed that no *O. viverrini* were found in secondary intermediate hosts in northern region, whereas most of metacercariae found belong to heterophyid trematodes especially the minute intestinal fluke, *H. taichui* (Wongsawad *et al*, 2004; Kumchoo *et al*, 2005; Boonchot and Wongsawad, 2005). Hitherto, the actual trematode species endemic in this area is still not clearly determined.

DNA-based approaches are the most efficient and accurate tools used for detection and identification of organisms and for screening of genetic variations among any population. High annealing temperature-random amplified polymorphic DNA (HAT-RAPD) analysis is one of these approaches. It was developed by Anuntalabhochai *et al* (2000) and has been adapted for use in a trematode, *Stellantchasmus falcatus*, identification (Sripalwit *et al*, 2003), analysis of DNA quality and quantity of some trematodes (Wongsawad *et al*, 2006; Wongsawad and Wongsawad, 2007) and intraspecific variation analysis of three paramphistome flukes in Thailand (Sripalwit *et al*, 2007).

This study was aimed to identify the species of trematode eggs found in fecal specimens from villagers inhabiting Mae Kuang River, Lamphun Province using HAT-RAPD method and formalin-ether sedimentation technique. Since several reports have revealed that both *H. taichui* and *O. viverrini* are found in the same fish host (Wongratanacheewin *et al*, 2001). Therefore, possible mixed infection with *O. viverrini* was also determined using HAT-RAPD PCR.

## MATERIALS AND METHODS

### Formalin-ether sedimentation technique (FEST)

Fifty-one fecal specimens were collected from villagers inhabiting Mae Kuang River,

Lamphun Province, Thailand. One portion was subjected to DNA extraction and the rest was used for FEST by homogenizing with 10% formalin and filtering through two layers of gauze. The filtrate was subjected to FEST (Chai *et al*, 1998).

### Genomic DNA extraction

Genomic DNA of fecal specimens was extracted and purified using Dneasy Tissue Kit (QIAGEN) according to instructions of the manufacturer. Adult worms of *H. taichui* and *O. viverrini* were also subjected to DNA preparation. Extracted genomic DNA was diluted to a working concentration of 30 ng/μl and stored at -20°C until use.

### *H. taichui* specific PCR amplification

PCR amplification for detection of *H. taichui* was performed using *H. taichui* specific primers, Hapt-F and Hapt-R, as described previously (Wongsawad *et al*, 2008).

### HAT-RAPD PCR for detection of contamination and/or mixed infection

HAT-RAPD PCR was performed to test for contamination/mixed infection with liver fluke (*O. viverrini*) using OPP-11, random 10-mer primer (Operon technology, USA) as previously described (Wongsawad *et al*, 2008).

## RESULTS

### FEST examination of fecal specimens

FEST showed that 3 egg types of helminth parasites, namely, *H. taichui*, *Strongyloides stercoralis* and an unidentified hookworm species with prevalences of 22, 14 and 4%, respectively (Table 1).

### PCR detection of *H. taichui*

A 260 bp amplicon was generated in all fecal specimens in which trematode eggs were found based on FEST (Fig 1). The 260 bp amplicons were obtained in FEST negative specimens.

Table 1

Prevalence of parasitic infections among villagers inhabiting Mae Kuang River, Pa Sang district, Lamphun Province using FEST.

Parasite egg	No. infected /examined	% prevalence
<i>Haplochis taichui</i>	11/51	22
<i>Strongyloides stercoralis</i>	7/51	14
Hookworm <sup>a</sup>	2/51	4

<sup>a</sup>Species of hookworm was not determined.

### Contamination/mixed infection using HAT-RAPD PCR

No *O. viverrini* HAT-RAPD profile was observed among *H. taichui*-positive fecal specimens (Fig 2).

### DISCUSSION

This study shows that trematode infecting humans in Chiang Mai Province was identified as *H. taichui*. This is in contrast to a previous report indicating that trematode eggs found in human stool are *O. viverrini* and none of *H. taichui* (Chiang Mai provincial Public Health Office, 2001). Heterophyiasis, mostly *H. taichui*, was the common trematode infection endemic in northern Thailand (Radomyos *et al*, 1998) and a subsequent report revealed that *H. taichui* was found to infect villagers inhabiting Mae Ping River, Chom Thong District, Chiang Mai Province (Chuboon and Wongsawad, 2003). Several survey data showed that no *O. viverrini* were found to be infecting secondary intermediate hosts in northern region, whereas most of the metacercariae found were identified as heterophyid trematode with *H. taichui* showing highest prevalence and intensity (Wongsawad *et al*, 2004; Boonchot and Wongsawad, 2005; Kumchoo *et al*, 2005). Eggs of minute intestinal flukes are similar in shape

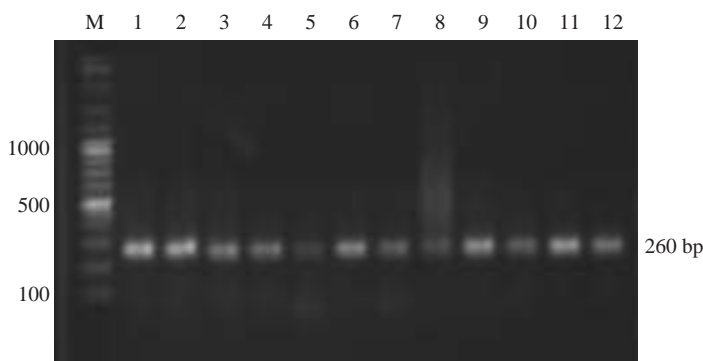


Fig 1-*H. taichui* specific PCR amplification. The 260 bp *H. taichui* specific amplicon was generated in all fecal specimens in which trematode eggs were found. (Lane M: 100 bp marker; lane 1: *H. taichui* positive control; lanes 2-12 : *H. taichui* positive specimens from fecal examination.

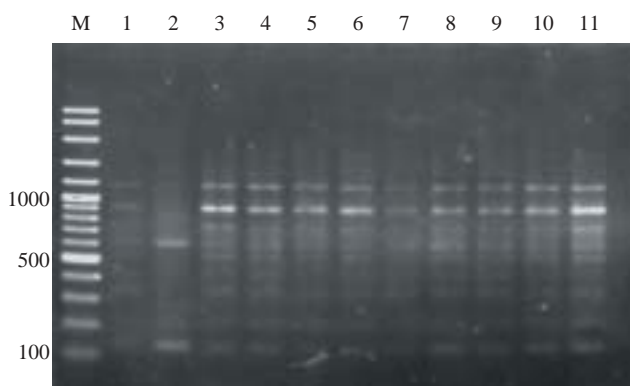


Fig 2-HAT-RAPD PCR was conducted as described in Materials and Methods, demonstrating that there was no contamination/mixed infection of *O. viverrini* among *H. taichui* positive specimens from fecal examination. Lane M: 100 bp marker; lane 1: *H. taichui* positive control; lane 2 : *O. viverrini* positive control; lanes 3-11 : *H. taichui* positive specimens.

and size to that of a liver fluke, *O. viverrini* (Tesana *et al*, 1991; Radomyos *et al*, 1998), which makes it difficult to identify the actual species by using only egg morphology.

Moreover, the 260 bp *H. taichui* specific amplicon was obtained only in *H. taichui* positive samples and there was no mixed infection with *O. viverrini* when using HAT-RAPD PCR. Interestingly, the 260 bp amplicon was also generated in negative specimens based on FEST. The advantages of copro-diagnosis using a combination of FEST and PCR methods were the significantly decrease in cost and time consumption, while it is accurate.

Two nematodes, *S. stercoralis* and hookworm, were also found in this study, as in the report of Chuboon and Wongsawad (2003). However, in this study, hookworm eggs were observed but not in the report of Chuboon and Wongsawad (2003). Different environmental conditions affecting *S. stercoralis* and hookworms, which are members of soil transmitted helminths whose infection rates are dependent on humidity, precipitation and soil composition.

In summary, our research demonstrated that PCR methods showed a high sensitivity and specificity for the detection of *H. taichui* DNA in fecal specimens. These techniques should be applied for the detection of this parasite in all larval stages in both definitive and intermediate hosts, which will be useful in prevention and epidemiological control programs.

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