

PhD Defence Dao Thi Ha Thanh

Epidemiology of *Opisthorchis* spp. in Central Vietnam

23 nov 2017 17:00

Ghent University - Merelbeke

Reservatie aangeraden



Dit is de omschrijving

Supervisors

- Prof. Dr. Pierre Dorny (ITM/Ghent University)
- Prof. Dr. Sarah Gabriël (Ghent University)
- Dr. Thanh Thi Giang Nguyen (Ministry of Health, Vietnam)

Summary

The Southeast Asian liver fluke *Opisthorchis viverrini* causes serious morbidity and mortality in the greater Mekong region. People infected with *O. viverrini* are at risk of developing cholangiocarcinoma. While *O. viverrini* is endemic in Central and South Vietnam, the epidemiology and the burden of disease that it causes have received little attention. Recently, our research group found a *O. viverrini*-like species in domestic ducks in a *O. viverrini* endemic area in Binh Dinh Province, Central Vietnam. This thesis aimed to study the occurrence and the life cycle of *O. viverrini* and the *O. viverrini*-like fluke in Central Vietnam. In the **first chapter** a general review of the literature of the *Opisthorchis* genus and opisthorchiasis is given, focusing on the morphology and the molecular biology, and on the epidemiology and the diagnosis of opisthorchiasis in SE Asia, including Vietnam. The chapter also gives a description on the finding of an *Opisthorchis* sp. in domestic ducks in Central Vietnam (further referred to as *Opisthorchis* sp. BD2013). Following this chapter, the **rationale** and **objectives** of the thesis are given. The **second chapter** describes the current status of opisthorchiasis in a Central Vietnamese community. The apparent prevalence of *O. viverrini* in the population determined by stool examination was 11.4%. The mean number of worms recovered after treatment was 14.5. Male gender and the consumption of raw freshwater fish were found to be significant risk factors associated with opisthorchiasis in the area. In the **third chapter**, morphological and molecular identification was performed of an *Opisthorchis* sp. found in the bile ducts of domestic ducks in Binh Dinh Province. Morphological characteristics of the bird flukes were compatible with *O. viverrini*, although some characteristics differed from those described in specimens collected from mammal hosts. Computation of the phylogenetic trees on the partial sequences of ITS2 of the ribosomal (rb) DNA and COI markers of the mitochondrial (mt) DNA showed close similarity of *Opisthorchis* sp. BD2013 with *O. viverrini*. We speculated that these bird flukes were *O. viverrini* that showed intra-species morphological and molecular variability compared to isolates from mammals. In the **fourth chapter**, we provide new sequence data from the mitochondrial genome and the nuclear ribosomal transcription unit of *Opisthorchis* sp. BD2013. A phylogenetic analysis was conducted to clarify the basal taxonomic position of this species from ducks within the genus *Opisthorchis*. From four developmental life stages, the complete cytochrome b (cob), nicotinamide dehydrogenase subunit 1 (nad1) and cytochrome oxidase subunit 1 (cox1) genes; and near-complete 18S and partial 28S rb DNA sequences were obtained by PCR-coupled sequencing. Phylogenetic trees were inferred from concatenated (cob+nad1+cox1) nucleotide sequences and from combined 18S+28SrDNA nucleotide sequences of five *Opisthorchis* sp. BD2013 samples and additional reference taxa. Both trees demonstrated the anticipated clustering of taxa within the Opisthorchioidea, the paraphyly of the genus *Opisthorchis* and the sister-species relationship of *Opisthorchis* sp. BD2013 with *O. viverrini*. In the **fifth chapter**, we determined the infection rate and intensity of infection with *Opisthorchis* sp. BD2013 in ducks in 4 districts of Binh Dinh province. An infection rate of 34.3% was found; the intensity of infection was 13.8 worms per infected duck. The **sixth chapter** describes a study on the occurrence of *O. viverrini* and *Opisthorchis* sp. BD2013 in snails and fish intermediate hosts in the endemic area. A total of 12,000 snails belonging to six families, as well as 754 fish representing 12 species were examined. Shedding of *O. viverrini* cercariae was observed only in *Bithynia s. goniomphalos* and *B. funiculata*, at infection rates of 0.86% and 0.14%, respectively. *O. viverrini* metacercariae were found in 10 fish species. *Carassius auratus*, a fish species commonly eaten raw, had the highest prevalence of 74.0%. Sharing of the same snail and fish intermediate host species was found for *O. viverrini* and *Opisthorchis* sp. BD2013. In the **seventh chapter**, the life cycle of *Opisthorchis* sp. BD2013 was

developed. In the **eighth chapter**, we discuss the findings of our research on *Opisthorchis* sp. BD2013 in the context of its co-existence with *O. viverrini* in Central Vietnam and of the sharing of snail and fish intermediate hosts. There is a need to perform studies to define the host range of *Opisthorchis* sp. BD2013. Meanwhile, a One Health control program should be built for prevention and control of the neglected *O. viverrini* in the region.