Molecular characterization of *Clinostomum* spp. infecting cultured Snakeskin gourami (*Trichopodus pectoralis*) in Thailand



A Thesis Submitted in Partial Fulfillment of the Requirements for the Degree of Master of Science in Veterinary Science and technology FACULTY OF VETERINARY SCIENCE Chulalongkorn University Academic Year 2022 Copyright of Chulalongkorn University การระบุชนิดพยาธิ Clinostomum spp. ที่ตรวจพบในฟาร์มปลาสลิด (Trichopodus pectoralis) ด้วยวิธีทางอณูชีววิทยาในประเทศไทย



วิทยานิพนธ์นี้เป็นส่วนหนึ่งของการศึกษาตามหลักสูตรปริญญาวิทยาศาสตรมหาบัณฑิต สาขาวิชาวิทยาศาสตร์ทางการสัตวแพทย์และเทคโนโลยี ไม่สังกัดภาควิชา/เทียบเท่า คณะสัตวแพทยศาสตร์ จุฬาลงกรณ์มหาวิทยาลัย ปีการศึกษา 2565 ลิขสิทธิ์ของจุฬาลงกรณ์มหาวิทยาลัย

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เอสเค อินจามามุล อิสลาม : การระบุชนิดพยาธิ *Clinostomum* spp. ที่ตรวจพบในฟาร์มปลาสลิด (*Trichopodus pectoralis*) ด้วยวิธีทางอณูชีววิทยาในประเทศไทย. (Molecular characterization of *Clinostomum* spp. infecting cultured Snakeskin gourami (*Trichopodus pectoralis*) in Thailand) อ.ที่ปรึกษาหลัก : ปิยนันท์ ทวีลาวรสวัสดิ์, อ.ที่ปรึกษาร่วม : ชาญณรงค์ รอดคำ

พยาธิใบไม้ชนิด Clinostom um spp. เป็นปรสิตที่สำคัญในการนำโรคในปลาน้ำจืดทั่วไป ซึ่งมีพยาธินี้ความเฉพาะเจาะจงต่อโฮสต์ต่ำและพบว่ามีกระจายทางภูมิศาสตร์อย่างกว้างขวาง การวิเคราะห์ข้อมูลทางสัณฐานวิทยาและในระดับอณูชีวโมเลกุลของพยาธิ Clinostomum พบว่ามีความหลากหลายในพยาธิชนิดนี้ ้อย่างไรก็ตามการรายงานในระดับโมเลกุลของพยาธิ Clinostomum spp. ในการเพาะเลี้ยงสัตว์น้ำในประเทศไทยยังไม่ค่อยมีรายงานมากนัก ปลาสลิด (Trichopodus pectoralis) เป็นปลาน้ำจืดที่เพาะเลี้ยงในประเทศไทย และมีความสำคัญอย่างมากในทางเศรษฐกิจ สำหรับการศึกษาครั้งนี้ มุ่งเน้นไปที่การอธิบายการพบพยาธิไปไม้ *Clinostomum* ในช่องท้องของปลาสลิด และรายงานความชุกของปรสิต ชนิดนี้จากเขตภาคกลางของประเทศไทย ปลาสลิดในช่วงอายุ 4 ถึง 8 เดือน จำนวน 260 ตัว ได้มาจากจังหวัด สมุทรสาคร สมุทรสงคราม สมุทรปราการ และกาญจนบุรีในภาคกลางของประเทศไทย ทำการวัดความยาวโดยรวมและ น้ำหนักตัวของปลาสลิด ตรวจดุภายในตัวปลาสลิด และพบระยะเมตร้าเซอร์คาร์เรียของพยาธิใบไม้ชนิด C. piscidium ภายในในช่องท้องของปลาสลิดที่ติดเชื้อ พยาธิถูกตรวจพบไม่ว่าจะอยู่เป็นอิสระหรือที่เกาะติดกับเนื้อเยื่อไขมันและ เยื่อหุ้มชั้นนอกของอวัยวะภายใน พบว่ามีความชุกรวมอยู่ที่ 13.35 % และพบสัดส่วนของการพบพยาธิใบไม้ชนิดนี้ ในปลาสลิดตัวเมียที่นำมาศึกษาจากฟาร์มสูงกว่าในปลาสลิดตัวผู้อย่างมีนัยสำคัญทางสถิติ (P<0.05) และเมื่อ เปรียบเทียบกับปลาที่ไม่เป็นโรค ปลาที่ติดเชื้อจะมีน้ำหนักตัวน้อยกว่าปลาปกติมาก ทำให้เห็นลักษณะปลาที่ติดพยาธิ ผอมกว่าอย่างเห็นได้ชัด (P<0.05) การตรวจทางจุลพยาธิวิทยาพบรูปแบบการร่องรอยของการเคลื่อนที่สีขาว บนเซลล์ตับและม้าม และเมื่อตรวจสอบร่องรอยของการเคลื่อนที่ในเนื้อเยื่อส่วนของเนื้อตับเป็นลักษณะเป็นเนื้อตาย เกิดขึ้นที่บริเวณ hepatocentralell และมีลักษณะของเลือดออกที่ล้อมรอบด้วยชั้นของมาโครฟาจและเซลล์เยื่อบุผิว ร่วมด้วย การติดเมตาเซอร์คาเรียนี้ทำให้ เนื้อเยื่อตับของโฮสต์เสียหาย ส่งผลให้เมแทบอลิซึมของตับถูกทำลาย เป็นผลให้ปลามีอัตราการเจริญเติบโตที่ช้าลงและน้ำหนักตัวลดลงนอกจากนี้การจำแนกลักษณะทางสัณฐานวิทยาและทางอณูชีวโมเลกุลของพยา ธินี้ได้ดำเนินการโดยใช้ข้อมูลในส่วนของ 185 rDNA และ internal-transcribed spacer (ITS1 และ ITS2) โดยนำผลที่ได้มาเทียบเคียงในส่วนของ 185 rDNA ในโปรแกรม BLAST แสดงให้เห็นว่าพยาธิชนิดนี้ มีความคล้ายคลึงกันกับ C. piscidium (FJ970655) 100% ที่พบในปลาสลิด (Colisa fasciata) จากอินเดีย และมีความคล้ายคลึงกันกับพยาธิกลุ่ม Clinostomum อื่นๆ ในประเทศออสเตรเลีย สหรัฐอเมริกา จีน อิสราเอล และอิตาลี ที่ 90–98% เป็นต้น นอกจากนี้ข้อมูลลำดับนิวคลีโอไทด์ของ ITSยังเผยให้เห็นความคล้ายคลึงกันของลำดับ 100% กับ *C. pisicidium* ที่แยกได้จากปลาสลิดจากอินเดียเช่นเดียวกัน และจากการวิเคราะห์แผนภูมิวิวัฒนาการใน การศึกษานี้จึงเป็นการรายงานการจำแนกในระดับอณูชีวโมเลกุลของพยาธิใบไม้ชนิด C. piscidium เป็นครั้งแรก ที่มีการเพาะเลี้ยงปลาสลิดในประเทศไทย

Chulalongkorn University

สาขาวิชา ปีการศึกษา วิทยาศาสตร์ทางการสัตวแพทย์และเทคโนโลยี 2565 ลายมือชื่อนิสิต ลายมือชื่อ อ.ที่ปรึกษาหลัก ลายมือชื่อ อ.ที่ปรึกษาร่วม

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The digeanean Clinostomum spp. is a significant parasitic pathogen of freshwater fish. It has low host specificity and a wide distribution geographically. Morphological and molecular data analyses have been performed on Clinostomum to assess its diversity. However, the molecular occurrence of Clinostomum spp. in aquaculture in Thailand has yet to be reported. Snakeskin gourami (Trichopodus pectoralis), a freshwater fish cultured in Thailand, has significant economic importance. Herein, the study focuses on describing a digenean Clinostomum in the abdominal cavity of T. pectoralis and reports the prevalence of this parasite from central Thailand. Two hundred and sixty-two 4 to 8- month-old *T. pectoralis* were obtained from Samut Sakorn, Samut Songkhram, Samut Prakarn, and Kanchanaburi provinces of central Thailand. We measured their overall length as well as their body weight. The body cavity of *T. pectoralis* was examined, and metacercariae of *C.* piscidium were discovered inside. In the abdominal cavity of infected fish, the parasites were discovered either free or adhered to adipose tissue and the outer membrane of the visceral organs. It was found that the total prevalence was 13.35 %, and the parasite intensities were found to be higher in the females taken from the farms than in the males (P<0.05). Pathological examination showed a few white migratory patterns on liver and spleen cells. The track presented histologically as the main central hepatic necrosis and hemorrhage surrounded by layers of macrophages and epithelioid cells. This metacercaria infection caused damage to the fish hosts' hepatic tissue, which disrupted their hepatic metabolism. As a result, the fish hosts experienced a slowdown in their rate of development and a reduction in their total body mass. In addition, morphological and molecular characterization of species was conducted using 18S rDNA and inter-transcribed spacer (ITS1 and ITS2) sequence data. A BLAST search of 18S rDNA sequence revealed 100% sequence similarity with C. piscidium (FJ970655) infecting banded gourami (Colisa fasciata) from India and 90-98% sequence similarity with other clinostomid in Australia, USA, China, Israel, and Italy. ITS sequence data also revealed 100% sequence homology with the C. pisicidium isolated from C. fasciata from India. Based on phylogenetic analysis, this study reports the first molecular identification of C. piscidium species in cultured T. pectoralis in Thailand.

Field of Study: Academic Year: Veterinary Science and technology 2022

nology Student's Signature Advisor's Signature Co-advisor's Signature

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Sk Injamamul Islam

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LIST of ABBREVIATIONS

AFA	Alcohol Formalin Acetic Acid
ANOVA	Analysis of variance
BLAST	Basic Local Alignment Search Tool
CI	Confidence Level
DoF	Department of Fisheries
DNA	Deoxyribonucleic Acid
FAO	Food Aid Organization
ITS	Internal Transcribed Spacer
MCL	Maximum Composite Likelihood
MEGA	Molecular Evolutionary Genetics Analysis
PCR	Polymerase Chain Reaction
PH	Potential for Hydrogen
SEM	Scanning Electron Microscope
SE	Standard Error

Chapter 1: Introduction

1.1. Importance and rationale

The snakeskin gourami (Trichopodus pectoralis, Regan 1910; Anabantoidei: Osphronemidae) is among the most widespread species of air-breathing fish from freshwater in the Indo-China Peninsula (Eegan, 2009; Morioka et al., 2013). It is native to the river systems of Cambodia, Indonesia, Laos, Vietnam, and Thailand. According to the observations of a researcher, this fish is an excellent species for aquaculture (Phong, 2014). This fish produces a lot of meat and is a popular dried fish in Southeast Asian countries. It is among the most important freshwater fish species because of its excellent flavor, taste and high export demand (Ahmadi, 2021). Most snakeskin gourami production in Thailand previously came from large, converted rice fields, with the greatest concentration in central Thailand. The Thai Department of Fisheries (DoF) extended Trichopodus sp. culture as a type of rice-fish farming in the 1950s. The capacity to increase production quickly became evident. The farmers extended the growing season of the fish, resulting in the modern aquaculture production of the species in Central Thailand (Yoonpundh & Little, 1997). The provinces of Samutprakarn, Suphanburi, Ubon Ratchathani, and Samutsakorn, the primary sources of supplies to the market, are abundant with snakeskin gourami fish farms. It is a highly economic species and has become one of the five most important freshwater species in the aquaculture of Thailand (Table 1) (DoF Thailand, 2018; FAO, 2019). The production of snakeskin gourami in Thailand ranked fourth among freshwater resources in 2016 (with a total of 26,077 metric tons) and accounted for 5.7% of the total annual production of freshwater in the nation (FAO, 2019). However, in the last decade, production has been on the decrease. The Mekong River basin and Chao Phraya basins of Thailand are home to this species (Kottelat et al., 1993) and later recorded in the Mekong and Southeast Thailand river systems.

Freshwater fish species	Production (%)
Nile Tilapia	45.8
Catfish	29.8
Silver barb	11.2
Snakeskin gourami	5.7
Striped Catfish	4.6

Table 1 Lists of economically important fish species of Thailand (DoF, Thailand,2018).

One of the most significant barriers to snakeskin gourami cultivation is the increased occurrence of parasitic infections (Kanchan et al., 2020). Parasite-infected fish developed ascites, with exudate fluids in the body cavity (Kanchan et al., 2020). Infection by Clinostomum spp. had previously been identified as the most serious problem with snakeskin gourami in aquaculture, leading to weight loss and decreased development of the fish (Paperna, 1991; Tansatit et al., 2014). The parasites can be found in the abdominal cavity of infected fish, either free or adhered to adipose tissue and the surface of visceral organs. It is well known that encysted and nonencysted forms of metacercariae of clinostomids may be found inside the host's tissue. These two forms of metacercariae can be distinguished by the presence or absence of an encysted form (Tansatit et al., 2014). As the non-cysted metacercaria of the species may migrate freely across the internal organs of their host, they have the potential to damage infected fish to a greater extent (Echi et al., 2012). Fish in the aquaculture environment may have growth retardation as a result of a severe Clinostomum spp. infestation. Thus, the objective of the present study was to investigate *Clinostomum* spp. by molecular techniques following statistical analysis to know the level of *Clinostomum* spp. prevalence in farmed snakeskin gourami in Thailand.

1.2 Statement of the problem

Fishes serve as hosts for parasites in the vast majority of aquatic habitats; sometimes, the biology and health of fish may be negatively impacted by these parasites (Lafferty, 2008). Fish serve as intermediate hosts for a variety of parasites, which may result in some of the most spectacular instances. One of the challenges that the fishing community is now experiencing in the aquatic population is the prevalence of parasites and diseases among fish. In the event that parasitic diseases are not kept under control, they may lead to widespread death tolls, decrease fish productivity, and, in certain instances, serve as a vector for the transmission of infections to people and other animals that consume diseased fish. An increase in fish parasites may be because of many events, including heavy stocking density, environmental changes, and external animals, such as birds, who are the definitive host for *Clinostomum* spp. *Clinostomum* spp. has the potential to transmit zoonotic diseases to humans as well as function as a source of secondary infections in fish species. Previously, there has been no research carried out in Thailand to determine the genetic identity of the Clinostomum spp. species found in snakeskin gourami. This study therefore investigated the molecular identification of *Clinostomum* parasites in snakeskin gourami culturing central part of Thailand, and by analyzing the level of prevalence of the parasite infestation, this research emphasis the information of overall scenario of parasites burden in the farmed snakeskin gourami.

1.3 Justification of the study MGKORN UNIVERSITY

Since almost every population in the world consumes fish as a major source of protein, research is necessary to guarantee the production of healthy fish (FAO, 2009). It is imperative that research be conducted on fish parasites since it has been shown that parasites decrease fish productivity, negatively impact fish health, make fish more susceptible to other diseases, and even lead to the death of fish. Fish parasites cause a decrease in economic return and a reduction in the quantity of fish that may be consumed as sources of protein-rich foods (Barber, 2005). In order to use a strategy that is either successful in management or prevention, proper identification of parasites down to the level of the genus and species is required. This

is because the etiology of parasitic diseases, which in turn determines the choice of potential control. Furthermore, the prevalence and incidence of disease are two of the most basic indicators in epidemiology. Prevalence quantifies the prevalence of a disease in a population in a certain area and period by counting the number of affected individuals (Ward, 2013). Thai aquaculture relies significantly on the snakeskin gourami, thus the study of parasites is crucial to the aquaculture sector's sustainable future. Previously, *Clinostomum* spp. have been reported to cause both farmed Snakeskin gourami and human in Thailand (Tansatit et al., 2014; Tiewchaloern et al., 1999; Yooyen et al., 2006). Despite the relevance of farmed snakeskin gourami, the molecular identification of *Clinostomum* spp., as well as parasite prevalence studies, had not been addressed, prompting the present study.

1.4 Objectives of the study

- To identify and characterize *Clinostomum* spp. of snakeskin gourami cultivated in Thailand using morphological and molecular characteristics.
- To investigate the prevalence, intensity, and pathological change in snakeskin gourami because of *Clinostomum* spp. infection since this parasite critically affects production.

1.5 Research Questions

To address our hypothesis, the question needs to be answered.

- ➢ Which species of Clinostomum spp. and what level of prevalence can be found on snakeskin gourami farms in central Thailand?
- What is the relationship between fish size and sexes with parasite's burden, and what will be the pathological changes that may affect the fish species?

1.6 Significance of the study

The findings of this study will improve our ability to identify parasites, monitor their behavior, link their expansion to environmental conditions, and comprehend their contribution to disease etiology. It will also help the fisheries community, government agencies, and other interested individuals comprehend how prevalent *Clinostomum* parasites are in snakeskin gourami aquaculture. The study addresses an important element of food safety and aquaculture management since snakeskin

gourami is an important source of nutrition for Thais. Knowing about the interactions of humans, animals, and aquatic species with their surroundings and spreading diseases between them is essential for effective molecular evidence-based parasite identification, which is necessary for protecting animal health. As a result, this will help to control parasites and boost aquaculture production.



Chapter 2: Literature Review

2.1 Fish

"Fish" refers to an animal with a backbone, gills that grow throughout life, and finshaped limbs. Fish are a significant source of nourishment for people all around the globe. Various people in many nations rely on fishing for a livelihood (FAO, 2009). Most fish species prefer to inhabit saltwater, although freshwater is home to roughly 40% of all fish species. Fish may get a wide range of diseases and be infected with parasites (Yimer and Enyew, 2003).

2.1.2 Snakeskin gourami

The snakeskin gourami (*Trichopodus pectoralis*) has a high meat output and is one of Thailand's top five freshwater-farmed fishes (Panthum et al., 2021). They can live in environments with very little dissolved oxygen and high organic loads and are often found in densely vegetated rice paddies, ditches, and streams (Froese, 2006). The snakeskin gourami consumes zooplankton, crustaceans, and the larvae of insects as its primary food sources (Tacon et al., 2011). It is also one of the most well-known and beautiful kinds of fish that can be kept in aquariums, and it is a fascinating species that can be farmed for commercial purposes (Minh et al., 2019). Snakeskin gourami produces a lot of meat, and traditional dried snakeskin gourami is a popular food (Figures 1 and 2) (Froese, 2006). Dried snakeskin gourami is popular in Southeast Asia, and new advancements have resulted in higher prices for snakeskin gourami in the aquaculture market (Needham et al. 2015).



Figure 1 Picture of *Trichopodus pectoralis* (snakeskin gourami). (Source: Internet, Accessed on 22 March 2023)



Figure 2 Sun-dried snakeskin gourami fish. (Source: Internet, Accessed on 22 March, 2023)

People in Southeast Asian nations are familiar with this species under several distinct names (Berra, 2011), i.e., sepat siam in Malaysia (Ambak et al., 2010), pla salid in Thailand, *cà sac ran* in Vietnam, trey kawnthor in Myanmar, and pa salid in Laos (Boonsom, 1986). It is native to Thailand's central plain, which runs from the Chao Phraya Basin to Cambodia, Vietnam, and Laos (Boonsom, 1986); however, owing to several initial introductions, it is currently widespread across Southeast Asian nations. Numerous research has shown that it is endemic to the Chao Phraya and Mekong basins of Laos, Thailand, Cambodia, and Vietnam (Kottelat, 2001). and that it has been widely introduced to Malaysia (Boonsom, 1986), India, Bangladesh, Sri Lanka, Indonesia, and the Philippines (Boonsom, 1986). This fish is both a food source and an attractive fish. Nonetheless, because of habitat loss and degradation, notably in Thailand, its natural population has declined, although more aquaculture of this species has been developed (Vidthayanon, 2012).

2.1.3 Physical characteristics of snakeskin gourami

There are multiple species in the genus *Trichopodus*, but the snakeskin gourami is the most often traded species (Prianto et al., 2021). Before they combined, the snakeskin gourami was supposed to be the largest member of the Osphronemidae and Belontidae families. It is still the largest species in its genus and subfamily (Frose, 2006). When sexually mature, *Trichopodus* species are substantially bigger and have a shorter dorsal fin base. The snakeskin gourami (*T. pectoralis*) is the largest, reaching lengths of over 20 cm (Pinter, 1986). The snakeskin gourami is an elongated fish that is compressed and has a small dorsal fin.

Additionally, the fish has a tight body. It has a pelvic fin that is very long and threadlike, in addition to an anal fin that is almost as long as the body itself. The back is more of an olive tint, while the flanks are more of a greenish gray with a silvery shine to them. It is possible to make out a clear and curved black band going from the snout to the eye and then all the caudal peduncle (Frose, 2004). In addition, the fins have a color that may be described as grayish-green, and the iris of the eye can sometimes take on an amber hue when the conditions in the water are just right. In addition to being slenderer than its female counterpart, the male snakeskin gourami also has dorsal and anal fins that are longer and pointier than those of its female partner.

In contrast, the female has a considerably less vibrant coloration than the male. In specific individuals, an orange-red fringe will also grow around the outside edge of the male's pelvic fin. In juvenile snakeskin gouramis, the lines that extend from the eye to the base of the tail have a prominent zigzag pattern that is very spectacular. This pattern can be seen throughout the body.

2.2 Parasites in snakeskin gourami

Parasitic diseases of fish have consequences not only for human health but also for the economy, and these repercussions are felt equally in devloped and developing nations (Poulin, 2006). Each and every parasite consumes energy that would otherwise be available for the maintenance, expansion, establishment, and reproduction of its host, which may result in a variety of negative effects for the host (Barber, 2005) and affects the host's production (Marcogliese, 2005). In addition to inflicting harm to their hosts, parasites may occasionally cause large mortalities, which can result in considerable financial losses for commercial fisheries and aquaculture operations (Roberts, 1986). Parasites have the potential to behave as serious infections, either directly leading to the death of the fish or making it more susceptible to other pathogens. Castration or mechanical interference with spawning, weight loss, and gross bodily deformation are some of the effects of parasites in fish. Muscle degeneration, liver dysfunction, interference with nutrition, cardiac disruption, nervous system impairment, and nutritional disruption are all caused by parasites. Other severe pathological conditions include visceral inflammation and atrophy brought on by the parasites' pressing of the organs, which often also results in an accumulation of ascetic fluid tinged with blood (Poulin, 2006). In natural water bodies, parasitic infection is widespread and inhibits fish growth, development, and reproduction. A continuous reduction in fishing resources is brought on by these diseases in addition to other causes. Additionally, parasites are held responsible for the severe pathological problems in the afflicted fish that devalue them economically and nutritionally.

2.2.1 External parasites in snakeskin gourami

Among the six genera of the family Trichodinidae, Trichodina represents over 30 species and causes trichodiniasis (Valladão et al., 2016). Trichodina is saucer-shaped and uses its cilia to travel around the surface of fish skin, fins, and gills (Wellborn, 1967). It uses tooth-like structures called denticles to feed on detritus and other particles present on the surface of the fish. The parasite scrapes the debris from the surface of the fish into its mouth with these denticles. When these organisms are plentiful, their scraping and movement irritate the skin and gill surfaces, causing epithelial hyperplasia (Bruno et al., 2006). In severe cases of hyperplasia, the fish host may experience decreased gas exchange or osmoregulation. More severe infestations may arise when environmental circumstances are unfavorable or when fish tissues are manually injured. Trichodina is transmitted to fish by direct contact with them or by water organisms from a subclinically infected reservoir host. Binary fission is a method of reproduction in which daughter organisms either adhere to the original host or seek a new host in the water column (Bruno et al., 2006). Compared to other external protozoans that infest fish, Trichodina protozoa are relatively mild pathogens. When parasite counts are modest, and the fish are not stressed, the prognosis for parasitized fish is favorable (MacMillan, 1991).

On the other hand, some of these protozoa are dangerous diseases that cause substantial fish mortality, particularly in hatchery-cultured species. This family of parasitic protozoa can be found parasitizing freshwater and marine fish species worldwide. These parasites are more common in young fish (yearlings and younger). Trichodinosis parasitic infestations in *Trichopodus pectoralis* were first discovered in the Philippines years ago (Arthur and Lumanlan-Mayo, 1997). Researchers found infestations occur most commonly in the gills and skin of the fish species. After that, no records of *Trichodina* spp. have been reported on snakeskin fish species.

Another parasitic disease previously identified in snakeskin gourami is ichthyobodiasis or costiasis (Bassleer, 1997). However, the researcher provided little evidence regarding costiasis infection in snakeskin gourami and the presence of the parasite genus Ichthyobodo in farmed or aquarium conditions. Moreover, in 2006 Froese mentioned costiasis in *T. pectoralis* (Froese, 2006). These parasites are quite minute (5-10 um) and have free-swimming and attached stages, making them easy to miss during a physical examination. It is an obligatory parasite on fish's skin and/or gills. Ichthyobodo, which resides on the gills of juvenile fish, impairs their ability to adapt to their environment. Furthermore, this organism is transmitted from fish to fish horizontally. In the environment, subclinically parasitized fish act as reservoirs for parasites.

A novel Myxozoa parasite, *Henneguya* spp., was simultaneously found with a chlamydia-like organism in snakeskin gourami (*T. pectoralis*) in Thailand (Dinh et al., 2021). In the gill sections, typical myxospores of the species *Henneguya* with tails were found. Infection with *Henneguya* spp. caused significant gill filament damage, which most likely resulted in respiratory distress. *Henneguya* is one of the most widespread myxosporean genera in the family Myxobolidae, with more than 200 species (Eiras and Adriano, 2012). Several *Henneguya* taxa are known to be responsible for diseases that cause significant death rates, while most species are thought to have little or no harmful impact on fish health (Kent et al., 2001; Lom and Dyková, 2006). *Henneguya* spp. infection is characterized by cyst-like formations on the gill filaments and usually occurs in the gills (Kent et al., 2001; Molnár, 2002). Two equal polar caps, sporoplasm at the posterior pole, and two independent caudal processes distinguish *Henneguya* spp. from the other species of the Myxobolidae family (Eiras, 2002; Lom and Arthur, 1989; Molnár, 2002). The genus

Henneguya interacts with fish gill structures in various ways, resulting in differing degrees of damage (Dykova and Lom, 1978; Molnár and Eszterbauer, 2015). A farmer observed symptoms similar to those previously reported in fish infected with *Henneguya* species in the snakeskin gourami, including lethargy, gasping for oxygen, and loss of appetite (Dinh et al., 2021).

2.2.2 Internal parasites in snakeskin gourami

Gnathostoma spinigerum is a nematode in dogs and cat's native to Southeast Asia, Japan, China, Bangladesh, and India. Still, it has also been found in Mexico and parts of South America. Poelen et al., 2014 on the other hand, identified *G. spinigerum* as a pathogen of *T. pectoralis* (Poelen et al., 2014). *G. spinigerum* has a multi-host in the life cycle. The eggs hatch in freshwater, and water fleas of the genus Cyclops eat the larvae. Small fish eat the water fleas, the second intermediate host. Eventually, the larvae end up in the stomachs of carnivores, usually cats and dogs. Humans are accidental hosts; the only *G. spinigerum* forms discovered in humans are larvae or immature adults that never achieve reproductive maturity. Ingestion of intermediate hosts containing parasite larvae, such as raw or undercooked freshwater fish, chickens, snails, or frogs, causes infection. It has also been described that those larval forms penetrate the skin, and prenatal transmission occurs. Non-specific symptoms such as general malaise, fever, urticaria, anorexia, nausea, vomiting, diarrhea, and epigastric discomfort emerge 24-48 hours after eating larvae of *G. spinigerum* in humans. However, no symptoms in fish have yet been documented.

2.2.3 Clinostomum spp.

Clinostomum trematodes are worldwide parasites that infect fish, amphibians, reptiles, and snails as intermediate hosts. It has three hosts and various phases in its life cycle (McAllister et al., 2009). Despite the widespread geographic distribution of this genus, the question of how many species it contains and how their host preferences differ from one another has not been settled (Calhoun et al., 2019). Adult flukes are found in the digestive system, esophagus, throat, and/or mouth of fish-eating birds, most often Charadriiformes and Ciconiiformes (Kanev et al., 2002), or less commonly, within reptiles, mammals, or even humans (Hara et al., 2014). To date, various species of *Clinostomum* have been reported from over 40 species of

birds from six continents, from great blue herons (*Ardea herodias*) to African darters (*Anhinga rufa*). Eggs are laid by definitive hosts in an aquatic environment, where they hatch into miracidia and mature into sporocysts after being ingested by rams horn snails (usually of the genus *Helisoma*) (Smyth, 1980). There have been reports of individuals belonging to other snail genera and families (such as *Lymnaea, Radix, Bulinus,* and Biomphalaria) serving as hosts, but on a far less frequent basis (Pinto et al., 2014; Rosser et al., 2016). Sporocysts are responsible for the release of free-swimming cercariae, which are capable of infecting a wide variety of freshwater fish and amphibian species (McAllister et al., 2009), within which they form loosely encysted metacercariae (Kanev et al., 2002). Once an amphibian or fish infected with the parasite is consumed by an appropriate definitive host, the metacercariae may survive in the second intermediate host for up to four years before maturing into adults (Bruni and Angelini, 2016).

There have been reports of clinostome metacercaria in freshwater fish all over the globe. Clinostome metacercaria are large and visible to the unaided eye. Several genera and species of fish use the excysted progenetic larval metacercaria of *Clinostomum piscidium* as an infecting stage. Additionally, the digenetic trematode of the genus *Clinostomum* is found in a variety of freshwater fish species and spreads zoonotic infections. Consuming raw fish allows Clinostomum sp., an accidental host, to enter people. In Japan, at least 19 of these incidents have been documented (Hara et al., 2014). Human infection with clinostome has also been reported in Israel, India, and Korea (Chung et al., 1995; Yamashita, 1938). In Thailand and Korea, cases of pharyngitis and lacramalitis attributed to *Clinostomum* sp. have been documented (Chauhan et al., 2021). An ophthalmological examination of a man with discomfort in the frontal sinus region for two to three months found a white spot at the right lower inner eyelid, moderate inflammation, and conjunctivitis in one case report from Thailand that demonstrated how this worm affected the eye. The patient fully recovered after the worm was removed from the lacrimal opening (Tiewchaloern et al., 1999). In addition, metacercariae have also been reported in the stools of humans and cause serious digestion problems, respiratory disorders upon entry into the lungs, and many other severe consequences (Park et al., 2009; Zimik et al., 2019).

In Thailand, C. piscidium metacercariae were discovered in the body cavity of T. pectoralis (see(Tansatit et al., 2014)). The parasites were identified in the abdominal cavity, either free or adhered to adipose tissue and the exterior surface of the viscera of affected fish. The infected fish seemed starving and had a much lower body weight than the uninfected fish. On the hepatic surface, gross pathology results indicated a few white migratory trails. The track exhibited histologically core necrosis and hemorrhage of hepatic and pancreatic cells surrounded by a layer of macrophages and epithelioid cells, encircled by a rim of lymphocytes, eosinophilic granular cells, and fibroblasts (Tansatit et al., 2014). Clinostomum piscidium is one of the most severe issues in pond fish culture, causing weight loss, reduced growth, and loss of productivity (Paperna, 1991). The fish become susceptible to additional health problems because of parasitism, which can lead to death. Clinostomum sp. requires a molluscan host, a fish (as the second intermediate host), and a definitive host, which is often a piscivorous bird, in order to complete its life cycle (Dabrowski, 2012). The first intermediate host of this parasite, Lymnaea lutiola, is a snail, and the second intermediate host, Ophiscephalus punctatus, is a serpent-head fish, where the metacercariae move actively inside its body cavity. Fish-eating birds like the Bulbulcus ibis and Egretta sp. are the ultimate hosts (Tansatit et al., 2014).



Figure 3 Picture of *Clinostomum* spp. (Source: Internet, Accessed on 2 April, 2023) Clinostomids are one of the digenean that are found the most often. During their life cycle (Figure 4), gastropods serve as the first invertebrate intermediate host, while various fish species are second intermediate hosts (Laimgruber et al., 2005). When the trematode eggs hatch, free-swimming miracidia are released; these miracidia aggressively infect snails and then proliferate inside a sac-like sporocyst to create many rediae. These stages mature into cercariae released from the snails and either actively infect new definitive hosts or form encysted metacercariae (Dias et al., 2003). It may be found encysted in fish muscle with a thin cyst wall, or it can move freely throughout the fish body cavity with no cyst wall (Waikagul and Thaenkham, 2014). Due to this thin cyst wall, it is recommended not to use pepsin-HCl artificial digestion techniques; thus, it may damage the metacercariae of *Clinostomum* spp. (Sohn, 2009). Metacercariae are readily released when the cyst wall is extremely thin and just a little amount of pressure is applied to the coverslip with muscle compression (Sohn, 2009). Advantages of the compression method include knowing metacercariae's exact location and infection site in fish examined and economical.



Figure 4 Life cycle of *Clinostomum* spp.

2.3 Diagnosis of fish parasites

The classification of fish parasites often uses a wide variety of diagnostic approaches. Among them are molecular diagnosis, histological diagnosis, and microscopic diagnosis is most common (Eissa et al., 2017).

2.3.1 Microscopic diagnosis

It is essential to promptly diagnose illnesses that affect fish to stop the further spread of the disease and maintain the overall health of the fish population. Microscopy is a crucial instrument for determining the nature of fish illnesses. The equipment's quality, the expert's experience, and the speed with which the procedure may be carried out all impact the accuracy of the results (Bruno et al., 2006). The light microscope is the most commonly used in illness diagnosis. Scrapings from the fish may be prepared for the examinations. Analyses of stained microorganisms and slides of histology specimens may also be performed using light microscopy.

2.3.2 Histological diagnosis

The symptoms of infected fish are not readily evident based on the fish's external appearance or their behavior in their natural environment. The first step of the test consists of a visual inspection of the fish's outsides for any signs of sickness (Khan, 2009). To receive nourishment, pathogens decompose the body's tissues or absorb food already digested from the intestines. The hyperplasia that occurs in the gills takes place between the gill lamellae. These parasites consume the freshly generated cells and cause harm to the gills. In histopathology, tissue sections are often examined to screen for damaged areas. However, the tissue is fixed for subsequent tests. Investigations of hematology have been gaining an ever-increasing amount of relevance in the field of applied fish pathology. Examining smears is the foundation of any hematological analysis; nevertheless, estimates of hemoglobin and total protein, serum electrophoresis, and several other biochemical measurements Fish also performed. pathogens also identified using are may be immunohistochemistry techniques applied to sections of tissue (Duraiyan, 2012).

2.3.3 Molecular diagnosis

Parasites in otherwise asymptomatic fish have been detected using molecular diagnostic methods in an effort to stave off epidemics. Two "primers" designate the site at which a thermostable DNA polymerase will begin replicating a DNA sequence, resulting in an amplification of a specified portion of the genome. Detection and quantification of *Clinostomum* spp. an internal parasite affecting fish worldwide has

utilized PCR (Aohagi et al., 1992). However, molecular analysis of *Clinostomum* spp. In Thailand is lacking.



CHULALONGKORN UNIVERSITY

Chapter 3: Materials and Methods

3.1 Ethical approvement

The protocols for this study were designed in accordance with Chulalongkorn University's animal ethical standards, protocol numbers IBC 223103 and IACUC 2231043.

3.2 Study area

From February to October 2022, a total of 4- to 8-month-old 262 live specimens of *T. pectoralis* were collected from aquaculture farms located in Samut Prakan, Samut Songkhram, Samut Sakhon, and Kanchanaburi province in Thailand (Figure 5). These provinces are the primary sources of supplies to the market and are abundant with snakeskin gourami fish farms. These areas are most productive with snakeskin fish farming, and previous cases of *Clinostomum* spp. have been reported previously.



Figure 5 Sample collection areas located in different provinces of Thailand.

3.3 Sample size estimation

In this present study, we used Epitools (<u>https://epitools.ausvet.com.au</u>) online server for calculating the sample size for the prevalence study. These tools may be used to estimate population means and proportions, discover significant differences between two means or proportions, and calculate sample sizes needed to do so, as well as to determine the real prevalence of an animal at the herd level (Reiczigel et al., 2010).

3.4 Collection of parasites

The fish were transported in aerated polyethylene to the Parasitology Unit of the Faculty of Veterinary Science at Chulalongkorn University, Thailand, where they were kept in aquariums with the appropriate aeration. Tricaine methane sulphonate (250 mg/l) was used for euthanizing the fish to die. The fish were examined for parasites using an established methodology (Fernando, 1972). First, each fish will be measured in terms of overall length and weight. The external characteristics will determine the sexes of the fish. Necropsy was done, all internal organs were present, and the exposed body cavity was visually inspected for parasites. After counting the parasites, specific morphological and molecular examination samples were processed.

3.5 Prevalence study of the parasites MICHELLE

Analysis of parasite prevalence is not simple. Parasites are generally not distributed, either in the fish or in the population. Negative binomials are often found to describe the distribution of parasites, so non-parametric statistics are essential. Further, fish populations are not randomly distributed, so the fish sample may not represent the population. In the present study, the prevalence was determined as a percentage based on the ratio of the number of infected fish to the total number of fish investigated. By dividing the total number of parasites collected by the total number of infected fish, the mean intensity of parasite infection was calculated.

3.6 Muscle compression techniques for metacercariae collection

The flesh from the muscles and fins of the representative fish samples was collected to check the presence of the metacercariae of *Clinostomum* spp. After that, each sample was compressed between two glass slides. This step was repeated 2-3 times to increase the detection rate of the metacercariae. Afterward, each sample was placed under a stereomicroscope to observe and identify the metacercariae.

3.7 Morphological identification

3.7.1 Semichon's carmine staining

Necropsy was done, all internal organs were present, and the exposed body cavity was visually inspected for parasites. Their visceral organs were dissected and placed on a petri plate, where they were rinsed with 0.85 % NaCl (NSS) and checked for parasites. After counting the parasites, specific samples were processed for light microscopic examination. The metacercariae flattened between two glass slides for carmine compression. At first, the parasite specimens were fixed in alcohol-formalin acetic acid (AFA) overnight before being rinsed in distilled water. After that, they were stained with Semichon's carmine for 24 hours or until overstain, and the specimens were destained in a mixture of 70% ethanol and 1% HCL solution 2-3 times. The samples were then dehydrated in graded series of ethanol (50%, 70%, 80%, 90%, and 95%) for 30 mins and after that with 100% for 30 mins two times. Followed by counterstain with a fast green, cleaned in xylene, mounted in permouth, then viewed and photographed using an Olympus stereomicroscope CX31.

3.7.2 Scanning electron microscopic examination

Parasites were post-fixed in 1% OsO_4 (Ted Pella Inc., USA) for two hours after being fixed overnight in 2.5% glutaraldehyde in 0.1 M phosphate buffer solution (Servicebio, China) in pH 7.2 for scanning electron microscopy. After that, specimens were rinsed twice with phosphate buffer and once with distilled water for 10 minutes each. Metacercaria was dehydrated with graded series of ethanol (30%, 50%, 70%, 95%, and 100% for 15 minutes each and three changes at 100%). Then it dried with CO_2 using the critical point technique (critical point dryer, Leica model EM CPD300, Austria). After that, mounting and gold (sputter coater, Balzers model SCD 040, Germany) coating was applied to the samples, and a scanning electron microscope (JSM-IT300, Japan) was used.

3.8 Histopathological analysis

Tissues from the liver, spleen, and intestine that had been infected with metacercaria were thoroughly cleaned with water before being preserved in buffered formalin for around 24 hours for histological analysis. The specimens were thoroughly cleaned, then dehydrated in a series of ethyl alcohols (50, 70, 90, and 100%) and acetone before being cleaned with methyl benzoate (Jithila and Prasadan, 2019). Samples were dehydrated in a graded ethanol series, and then they were paraffin-embedded. Wax was melted and stored in blocks called paraffins at 58°C. The Microtec rotatory microtome (Germany) was used to cut serial slices of 5 m thickness, which were subsequently stained with Heidenhain's Hematoxylin and Eosin to study the histopathology and cellular infiltration at the attachment site. An Olympus CX31 light microscope was used to view the DPX-mounted sections, and a Nikon Y-TV55 camera linked to the microscope was used to capture pictures.

3.9 Molecular identification

3.9.1 Deoxyribonucleic acid extraction and polymerase chain reaction

Prior to being kept in 70% ethanol until DNA extraction, all of the metacercarial specimens were washed in saline. Using a Nucleospin DNA extraction kit and according to the manufacturer's instructions, genomic DNA was isolated from samples. The ITS1-5.8S rDNA-ITS2 and 18S rDNA sequences were amplified using the primer pairs specified in Table 4, respectively. A total of 25 µl were used for the PCR reaction, which included 1 µl of each primer, 4 µl of genomic DNA, 12.5 µl of the Go Tag® Master Mix (Madison, USA), and 6.5 µl of distilled water. The early steps of the PCR cycle condition were carried out with denaturation at 94 °C for 5 minutes, followed by 40 cycles of 94 °C for 30 seconds, annealing at a specific primer 65 °C/60°C (65 °C for 18s rDNA and 60°C for ITS1-5.8S rDNA-ITS2) for 30 seconds, and 72°C for 1 minute; with a final step of 72°C for 7 minutes. The purification of PCR products was conducted through the utilization of a 1.5% agarose gel. The anticipated PCR product was purified using a commercially available kit in accordance with the manufacturer's protocol (NucleoSpin® Gel and PCR Clean-up, Macherey-Nagel, Düren, Germany). Subsequently, sequencing of the purified product was performed in both directions by a commercial DNA sequencing service provider

(Celemics, Korea). The primer set was devised utilizing the Pimer3plus server to enhance the amplification of the 18S rDNA coding and ITS1-5.8S rDNA-ITS2 non-coding region of the parasites (Kumar and Chordia, 2015). Initially, newly acquired sequences of the 18S rDNA (Table 2) and ITS1-5.8S rDNA-ITS2 (Table 3) genes of *Clinostomum* spp. were aligned with sequences sourced from the Genbank database using MEGA 11. The final comparisons were then edited and evaluated by Bioedit v.7.0.5.3 (Hall, 1999) and TBtools (Chen et al., 2020).

Scientific Name	Description	Accession No.
Clinostomum sp.	18S small subunit ribosomal	MW539004.1
2	RNA gene	
Clinostomid sp.	185 small subunit ribosomal	AY829252.1
Le contra de la co	RNA gene	
Clinostomum sp.	185 small subunit ribosomal	AY222094.1
	RNA gene	
24		
Clinostomum piscidium	185 small subunit ribosomal	FJ970655.1
จุหา	RNA gene	
C		
Clinostomum brieni	185 small subunit ribosomal	MH606189.1
	RNA gene	
Clinostomum	18S small subunit ribosomal	KF811012.1
complanatum	RNA gene	
Clinostomum sinensis	185 small subunit ribosomal	MK490986.1
	RNA gene	
Clinostomum giganticum	185 small subunit ribosomal	FJ970654.1
	RNA gene	

Table 2 List of 18S rDNA gene used for primer design.

Clinostomum	185 small subunit ribosomal	MF398350.1
marginatum	RNA gene	

Table 3 List of ITS1–5.8S rDNA-ITS2 gene used for primer design.

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		spacer 2 region	

Table 4 List of primers used in this research.

Gene	Forward Primer	Reverse Primer	Product	Reference
			size	
			(bp)	
18S	ATTCCGGAGGGAGCCCTG	ATCAACCCAGTCAGCACCC	395	Present
rRNA				study
ITS	CACCGCCCTGGCGTAATA	CGACACTTCGAACGATTTCTAGA	801	Present
				study

3.9.2 DNA sequencing and phylogenetic tree analysis

The PCR product was subjected to purification using a commercially available kit, following the manufacturer's instructions (NucleoSpin® Gel and PCR Clean-up, Macherey-Nagel, Düren, Germany), prior to being sent to a professional DNA sequencing service (Celemics, Korea). The alignment of sequences was performed through the utilization of ClustalW multiple alignments, which was executed on BioEdit version 7.0.5.3. The identity of the aligned sequences was assessed by comparing them with available sequences in the GenBank database, utilizing the Basic Local Alignment Search Tool (http://www.ncbi.nlm.nih.gov/BLAST/). The construction of phylogenetic trees was carried out through the utilization of the maximum likelihood method, accompanied by a bootstrap method test of phylogeny consisting of 1000 bootstrap replications. The nucleotides substitution type and the Poisson substitution model were employed, and the computation of pairwise distance homology was executed. The software program utilized was the MEGA X software program (Newman et al., 2016).

3.10 Statistical analysis

The independent sample t-test was utilized to compare the data obtained from the infected and non-infected fish. A significance level of 0.05 was adopted, which a P-value was deemed statistically significant. The statistical analysis was conducted using Microsoft Excel.
Chapter 4: Results

4.1 Study area

All the fish were collected from Samut Prakan, Samut Songkhram, Samut Sakhon, and Kanchanaburi provinces in Thailand. The fish were cultured in the earthen ponds (Figure 6), and the population density was 10,000-15,625 fingerlings per rai (1 rai = 0.395 acres). Water used for the fish farms was supplied from a nearby irrigation canal. The age of the fish during stocking in the grow-out pond was mainly between 3-4 months. In most cases, the farmers provided in-house produced fry to culture the fish and culture approximately 8-9 months marketable size. Farmers often collect the fish when they reach a size of 5 to 6 fish/kg to sell in the market.



Figure 6 Pictures of culture pond of snakeskin gourami from different locations of Thailand.

4.2 Sample size estimation

The fish's sample size was estimated using an online statistical prediction tool Epitools (<u>https://epitools.ausvet.com.au</u>). Here, we set the different parameters in the study to estimate the total sample size. At first, we selected the section "Sample

size to estimate a true prevalence with an imperfect test" and set the parameters as follows Assumed true prevalence = 0.4; Assumed sensitivity = 1; Assumed specificity = 1; Desired precision = 0.05 and Confidence level = 0.90 (Figure 7). The tool after that calculating the sample size required for our study was 260 (Figure 7). The aforementioned software application generates the necessary sample size for accurately approximating the actual prevalence, while maintaining the desired level of precision and confidence. Tables containing sample sizes for various prevalence, precision, sensitivity, and specificity values are also generated.

EPITOOLS	Home Prevalence -	Freedom • Studies •	Diagnostics -	Sampling 👻				
Estimating prevalence								
Sample size to estimate a tr	ue prevalence w	ith an imperfe	ct test					
Assumed true prevalence 0.4			Home	Prevalence *	Freedom +	Studies *	Diagnostics *	Sampling +
Assumed sensitivity)	EPITOOL	S						
Assumed specificity)			Sensitivity				1	
Desired amplicing			Desired precision				0.0	15
Desired precision			Confidence				0.9	9
Confidence level 0.9	~							
Submit	1. A.							
	Deville							
	Results							
	Sample size	required for specified inpu	its					
	<u> </u>							
1 Contraction of the second se		Samp	ole size			_ L	260	

Figure 7 Estimation of the sample size of the study by Epitools.

4.3 Collection and prevalence study of the parasites

At first, a necropsy of the fish was done to collect the parasites. Each fish species' body weight and length were estimated, and sexes were determined before the necropsy procedure. Figure 8 provides illustrations of both the male and female snakeskin gourami. The metacercaria of the parasite was retrieved from the intraabdominal cavity of the fish, specifically from the exterior of the intestinal and hepatic regions (Figure 9). In this study, 35 out of the 262 *T. pectoralis* were infected with metacercaria of *C. piscidium*. The total number of male and female fish was 46 and 216, respectively. The overall prevalence of infection was 13.35%, out of which 42.85% infection was recorded in farm No. 12 in Kanchanaburi was the highest, followed by Farm 2 in Samut Songkhram, where the prevalence was 41.66% (Table 5). Whereas, in some farms in Samut Songkhram (Farm 5 and Farm 8) and Samut Sakhon (Farm 9) the prevalence was the lowest (0.00%) (Table 5). The total number of infected and non-infected male were 5 and 41, respectively. Whereas a total number of 30 females were found infected, and 186 females were found noninfected. Significant (P<0.05) differences exist between infected and non-infected males and female's snakeskin gourami. The infection intensities were highest at 3 \pm 0.00 in females in Samut Prakarn (Farm 11) and 4 ± 0.00 in the males of *T. pectoralis* collected from farm No. 4 in Samut Songkhram (Table 5). The infection and intensity percentage were significantly higher in the female fish than in the male collected from all the farms. The between body weight and body length of infected and noninfected females of *T. pectoralis* were highest 194 ± 0.00 gm and 252.33±23.41 gm and 20±0.00 cm and 18.50±0.86 cm, respectively (Table 6). The relationship between body weight and body length of infected and non-infected male fish from the study was statistically significant (P<0.05). However, in females, the relationship between body weight and body length between infected and non-infected fish was found non-significant (P>0.05) in this study. The number of males and females infected and non-infected is given in Figure 10 and Figure 11, respectively.



Figure 8 Pictures of *Trichopodus pectoralis* (A) Male and (B) Female fish.



Figure 9 (A-F) Collection of the metacercariae of *Clinostomum piscidium* in different organs of the fish.

Table 5 Prevalence and intensities of infection with metacercariae of Clinostomumpiscidium in male and female Trichopodus pectoralis.

Localities	Sex of Fish	No. of examined fish	Total number of recovered parasites	No. of infected fish	Prevalence (%)	Mean intensity of parasite (mean ± SD)	Significance
Farm No:	Female	27	2	2	7.40	1 ± 0.00	p < 0.001
1	Male	3	1	1	33.33	1 ± 0.00	ρ < 0.001
Farm No:	Female	24	25	10	41.66	2.5 ± 1.2	p < 0.001

2	Male	5	1	1	20	1 ± 0.00		
Farm No:	Female	22	-	-	-	-		
3	Male	3	-	-	-	-	-	
Farm No:		00	F	4	47.20	1.25 ±		
4	Female	23	5	4	17.39	0.43	p < 0.001	
	Male	5	4	1	20	4 ± 0.00		
Farm No:	Female	9	-	-	-	-		
5	Male	6		Mer.	-	-	-	
Farm No:	Female	17	5	4	23.52	1.25 ± 0.4	r < 0.001	
6	Male	5	1///	1	20	1 ± 0.00	p < 0.001	
Farm No:	Female	13	1///	1	7.69	1 ± 0.00		
7	Male	2			-	-	p < 0.001	
Farm No:	Female	14			-	-		
8	Male	3)	-	-	
Farm No:	Female	26	-		-	-		
9	Male	5 จุฬ	าลงกรณ์ม	หาวิทยาล้	<i>้</i> ย	-	-	
Farm No:	Female	26 CHUL	A <u>longkor</u>	N ¹ UNIVER	3.84	1 ± 0.00		
10	Male	5	-	-	-	-	p < 0.001	
Farm No:	Female	8	3	1	12.5	3 ± 0.00		
11	Male	3	-	_	-	-	p < 0.001	
Earm No.	Femalo	7	5	3	12.85	1.66 ±		
12	Female /	1			42.03	0.94	p < 0.001	
12	Male	1	1	1	100	1 ± 0.00		

Locality	Sex	Status of infection	No. of fish	Body weight (mean ± S.D., gm)	Total length (mean ± S.D., cm)
	Female	Non- infected	25	143.84±14.16	18.36±1.76
		Infected	2	110	14.5±0.5
Farm NO. 1	Male	Non- infected	2	153±4.00	18±2
		Infected	1	141	19
Farm No. 2	Female	Non- infected	14	102.93±19.38	16.07±1.43
		Infected	10	113.60±30.63	15.80±1.77
	Male	Non- infected	4	104.25±10.15	16.50±0.86
		Infected	1	84	14
	Female Male	Non- infected	22 ₁₅ ณ์ม	46.50±7.42	12.18±1.52
Form No. 3		Infected	ONGKOR	n University	-
Farm NO. 3		Non- infected	3	38.67±3.39	10.66±1.24
		Infected	-	-	-
Farm No. 4	Female	Non- infected	19	164.15±31.30	18.05±1.87
		Infected	4	142.25±36.88	16.75±3.11
	Male	Non- infected	4	104.75±17.65	14.50±2.17
		Infected	1	104	14

Table6 Relationship between body weight and total length of Trichopoduspectoralis infected with Clinostomum piscidium.

	Female	Non-	9	252.33±23.41	18.50±3.09	
		Infected	-	-	-	
Farm No. 5		Non-			40.445	
	Male	infected	6	21.44±1.34	19±1.15	
		Infected	-	_	-	
		Non-	13	110 23+8 65	15 02+1 07	
	Female	infected	1.5	119.25±0.05	10.92±1.97	
Earm No. 6		Infected	4	115.5±8.07	14.50±2.06	
		Non-		115 25 9 61	15 25 2 48	
	Male	infected 🚽	4 115.25±8.61		13.23±2.40	
		Infected	1///	114	14	
		Non-	12	162.75±7.27	10 50 0 07	
	Female	infected			10.00±0.00	
		Infected	1	137	15	
Farm NO. 7	Male	Non-	A fireeeee			
		infected	Leader V	165.50±0.5	17.50±0.5	
		Infected	-	-	-	
	Female	Non-	10~01	107 42 5 47	13 28+1 03	
		infected	11413688	107.42±3.47	15.20±1.05	
Earm No. 9		Infected	UNGKUR	M UNIVERSITY	-	
		Non-	2	101 22 1 60	12 66 0 47	
	Male	infected	3	101.33±1.09	12.66±0.47	
		Infected	-	_	-	
		Non-	26	202 72 22 01	10 52 1 92	
Fame Na 0	Female	infected	20	202.73±33.81	19.53±1.82	
		Infected	-	-	-	
Failli NO. 9		Non-	Б	194,13.46	10,167	
	Male	infected		104113.40	19±1.67	
		Infected	-	-	-	

	Female	Non- infected	25	201.04±36.61	19.24±1.06	
Earry No. 10		Infected	1	194	20	
Farm NO. 10		Non-	г	200.20.45.10	20.244	
	Male	infected	5	200.20±45.19	ZU±Z.44	
		Infected	-	-	-	
		Non-	7	60 14 11 55	13.85±1.80	
	Female	infected	1	00.14±11.55		
Earm No. 11		Infected	1	65	12	
1 4111 NO. 11	Male	Non-	3	60 66+11 58	15+2 44	
		infected 🚽		00.00111.50	13±2.77	
		Infected			-	
	Female	Non-		73 75 11 08	14 25+1 02	
Farm No. 12		infected		15.1511.70	14.2J±1.72	
		Infected	3	81±5.56	14.33±1.69	
		Non-	Altecceo		_	
	Male	infected	-9200	and and a		
		Infected	1	58	14	

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Figure 10 Number of male infected fish with metacercaria and non-infected fish.

Figure 11 Number of infected female fish with metacercaria and non-infected fish. 4.4 Morphological identification

The parasite was slightly yellowish in color; its body was linguliform and dorsoventrally flattened with round anterior and posterior ends (Figure 12 A). A total of ten parasite was checked for morphological analysis where the minimum and maximum length of the fluke was determined 0.086 and 0.63 mm, respectively. While the minimum and maximum width at the middle and posterior one-third of the body was about 0.025 and 0.035 mm, respectively. The oral sucker was at the anterior tip, slightly oval, measured (0.014-0.024) × (0.011-0.025) mm in diameter. The ventral sucker was situated at the anterior one-third of the body, more significant than the oral sucker, oval-shaped, and measured (0.053-0.148) × (0.042-0.074) mm in diameter. The pharyngeal structure exhibited a limited length and expanded into the pharyngeal bulb. The paired testes were positioned in a tandem arrangement along the median longitudinal axis, specifically located at the posterior one-third of the body. The testis located anteriorly exhibited a triangular shape with lobulated margins, positioned slightly to the left of the median axis. The testis located posteriorly exhibited a symmetrical Y-shape and was positioned along the median

axis. The anatomical structures observed in Figure 12 B include the cirrus pouch and the ovary, which are in proximity to each other with the oval cirrus pouch positioned anteriorly to the ovary. The oval-shaped ovary was situated in a posterior position relative to the cirrus pouch on its left. The elongated sac of the uterus was situated towards the posterior aspect of the margin of the ventral sucker. The caudal region of the specimen exhibited the excretory orifice, serving as the aperture of the excretory vesicle (as depicted in Figure 12). Table 7 presents a comparison of the primary morphological characteristics of the metacercaria studied with those reported in other studies on *C. piscidium* metacercariae.



Figure 12 Light micrographs of the same metacercaria of *Clinostomum piscidium*. A) The whole mount (Semichon's carmine stained). B) Details of a whole mount: Oral sucker (Os), Ventral sucker (Vs), Pharyngeal bulb (Pb), Anterior testis (Ant. te.), Posterior testis (Post te.), Uterine sac (Us), Ovary (Ov), Cirrus pouch (Cp), and Excretory pore (Ep).

The host-isolated metacercaria was characterized by their oval shape with a body length of 500 μ m (Figure 13A). The metacercaria taken from the hosts had a tiny oral sucker encircled by a conspicuous oral collar, as shown by scanning electron microscopy (Figure 13 (B-D)). Located in the anterior portion of the body, the

rectangular ventral sucker is much bigger than the oral sucker (Figure 13E). The cirrus pouch is curved and overlaps the anterior testis's right border; the ejaculatory duct is narrow, and the cirrus is noticeable (Figure 13F). The excretory pores, also known as the aperture of the excretory bladder, were located at the end of the posterior region (Figure 13G).



Figure 13 *Clinostomum piscidium* images from scanning electron microscopy. (A) Entire metacercariae body; scale bar = 500 μ m. (B-C) The oral sucker collar is seen on metacercariae from the anterior end; scale bar = 100 μ m. (D) Oral collar, showing ventral constriction; scale bar = 50 μ m, sensilla (arrow) (E) Ventral sucker of metacercariae; scale bar = 50 μ m, (F) Cirrus pouch of the worm; scale bar = 10 μ m, and (G) Excretory pore of the metacercariae; scale bar = 10 μ m.

Morphological	Southwall 8	Singh at al	Tangatit at al	Drocopt study
Morphological	Southwell &	Singh et at.,	Tansatit et al.,	Present study
characteristics	Prashad, 1918	2010	2014	
Body length	2.8-5.2	2.27-3.36	2.4-4.2	0.086-0.63
(mm)				
Body width	1.4-1.8	1.17-1.26	1.2-1.7	0.025-0.035
(mm)				
Size of oral	0.18 in diameter	(0.14-0.18) ×	(0.09-0.20) ×	(0.014-0.024) ×
sucker (mm)		(0.23-0.3)	(0.25-0.35)	(0.011-0.025)
Size of ventral	0.6 × 0.48	(0.60-0.68) ×	(0.48-0.7) ×	(0.053-0.148)
sucker (mm)		(0.7 -0.8)	(0.62-0.85)	× (0.042-0.074)
Shape of ovary	Oval or bean	Globular	Oval	Oval, Globular
Shape of ant.	Lobed	Lobed	Triangle,	Triangle,
testis			Lobed	Lobed
Shape of post.	Y-shaped	Y-shaped	Y-shaped	Y-shaped
testis			3	
Host species	Nandus nandus,	Colisa	T. pectoralis	T. pectoralis
	T. fasciatus	fasciata	201	
Microhabitat	Body cavity	Body cavity	Body cavity	Body cavity
Metacercariae	Non encysted	Non	Non encysted	Non encysted
form		encysted		

Table 7 Comparison of morphological characteristics of *Clinostomum piscidium* metacercariae found in the present study and described previously.

4.5 Histopathological analysis

The histopathology of Metacercaria infected liver, spleen, and intestine tissues was examined. In this study, gross pathological findings were observed on the liver. The hepatic tissue exhibited a slightly yellowish color, and uninfected piscine specimens demonstrated a typical configuration of hepatocytes arranged in cords or plates, as depicted in Figure 14A. The observation of the multiplication of bile ducts in a conventional arrangement encircling the portal vein of the liver was made (refer to Figure 14B). The non-encysted form of metacercariae of *C. piscidium* was observed to

be either freely moving or attaching to the adipose tissue. The migratory track of the metacercaria was observed in the liver and spleen of the infected fish (Figure 14 (C-D)). The liver of the non-infected fish exhibited no notable histopathological alterations and exhibited the presence of hepatopancreatic tissue surrounding a portal vein (Figure 14A). The hepatic tissue of *T. pectoralis* was observed to contain metacercariae of C. piscidium, which were characterized by a migratory path and successive layers of macrophages and epithelioid cells near the migratory route (Figure 14C). Furthermore, the liver exhibited the presence of inflammatory cells, as depicted in Figure 14E. Additionally, eosinophilic cells were observed in the cytoplasm surrounding the bile duct of the liver cell (Figure 14F). The metacercariae of C. piscidium were observed to be affixed to the serosal surface of the intestine. Additionally, the presence of eosinophilic granular cells in close proximity to the epithelial cells within the infected intestine was noted (Figure 14G). The infected spleen of *T. pectoralis* exhibited the presence of numerous melano-macrophage centers (Figure 14H).





Figure 14 Light micrographs of visceral organs of *Trichopodus pectoralis* non-infected (A-B) and infected (C-H) with *C. piscidium* (H&E stained). A) Liver of non-infected fish shows normal arrangement of hepatocytes (Hc) into cords or plates. Hepatopancreas (Pa) lies around a portal vein (Pv). (B) Normal arrangement of bile duct (Bd) proliferation around the portal vein of the liver cell, (C) Liver of infected fish shows migratory track (Mt), macrophages (Mp) near the migratory track, (D) Spleen of infected fish shows migratory track where the red blood cells are absent and changes in the necrotic tissue, (E) Inflammatory cells (Ic) in the periphery (asterisk) of the liver cells, (F) Eosinophilic cells (asterisk) in the cytoplasm around the bile duct of the

liver cell, (G) Eosinophilic granular cells (Eg) (asterisk) near the epithelial cells (Ec) in the infected intestine, and (H) Many melano-macrophage centers (MMc) in the infected spleen.

4.6 Molecular identification

A partial fragment of the 18S rDNA gene was generated using PCR amplification (Figure 15). After sequencing, a contig of 395 bp lengths was formed, for which GenBank Accession No. OP793985, OP793986, OP793987, OP793988, OP793989, OP793990, OP793991, OP793992, OP793993, and OP793994 were obtained. A phylogenetic tree was created using *Schistosoma spindale* as an outgroup and various clinostomid trematode isolates from diverse geographic locations. (Figure 16). To determine the evolutionary history, the Kimura 2 parameter model and the Maximum Likelihood method were used (Mahadani et al., 2022). The branches indicate the percentage of trees in which the linked taxa are grouped (Figure 16). Initial tree(s) for the heuristic search were produced automatically by performing the Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances calculated using the Maximum log-likelihood value. The branch lengths are expressed in terms of substitutions per site, and the tree is shown to scale.

The phylogenetic tree indicated that our isolate had 99% similarity with *Clinostomum piscidium* (FJ970655), *Clinostomum* sp. (AY222094), *Clinostomum* sp. (MW539004), and *Clinostomid* sp. (AY829252) from India, Australia, and the United States, respectively (Figure 16) (Table 8). Another group containing *C. complanatum* (MK490986) from China, *C. complanatum* (MK811210) from the USA, and *C. complanatum* (AY245701) of Israel origin under the same clade showed 97% similarity (Figure 16). According to the evolutionary tree, *C. breini* (KF811009) may have developed earlier. Additionally, it should be highlighted that *S. spindale* (Z11979) fell within the out-group, while *C. marginatum* (MF398350) and *C. tataxumui* (MF398349) are branched under the distinct clade.

Species Name	Accession No.	Identity (%)
Clinostomum sp.	MW539004	100
Clinostomid sp.	AY829252	100
Clinostomum sp.	AY222094	100
Clinostomum piscidium	FJ970655	98.93
Clinostomum brieni	MH606189	98.12
Clinostomum brieni	MH606188	98.12
Clinostomum complanatum	KF811012	98.12
Clinostomum brieni	MH606187	97.86
Clinostomum complanatum	FJ609420	97.59
Clinostomum complanatum	AY245701	97.59
Clinostomum brieni	KF811009.1	97.59
Clinostomum giganticum	FJ970654	97.05
Clinostomum marginatum	MF398350	96.51
Clinostomum tataxumui	MF398349	96.51
Clinostomum marginatum	AY245760	96.51
Clinostomum sp. จุหาลงกรณ์ม	AY222095	96.51
Trematoda sp. CHULALONGKOR	KX172121	96.60
Schistosoma spindale	Z11979	90.74

Table 8 Sequence identity matrix (%) amongst the *Clinostomum* spp. based on the partial sequence of the 18S rDNA gene.



Figure 15 PCR Amplification of 18S rRNA of *Clinostomum* sp. Here, Lane M – DNA Ladder; Lane N - Negative Control; Lane 1 to 6 – Samples and Lane P – Positive control.



Figure 16 Based on a partial 18S rDNA sequence, the evolutionary relationships between clinostomids were determined using the maximum likelihood method. The percentage of replicate trees in which the related taxa grouped in the bootstrap test (1000 replicates) is displayed above the branches.

Furthermore, with the accession number OP782661, an 801 bp fragment of the *C. piscidium* ITS1-5.8S rDNA-ITS2 gene was uploaded to GenBank to facilitate molecular research. The partial sequence showed 100% homology with *C. piscidium* (KY312848) isolated from India (Table 9). In addition, for the phylogenetic analysis, additional sequences with lower similarity (96-99%) were employed (Table 9). The isolated *C. piscidium* from *Colisa fasciata* and the current species were closely linked in phylogenetic analysis, putting them in the same clade with a high bootstrap value (Figure 17). In most cases, the comparison that constitutes the rate of evolution study is one in which the evolutionary change corresponds to a change in the relative position of a species. In addition, the results of this research imply that the ITS-1 and ITS-2 regions may be more accurate for the interspecific distinction of *Clinostomum* species than initially assumed.

Species Name	Accession No.	Identity (%)
Clinostomum piscidium _ALONGKOR	KY312848	100
Clinostomum philippinense	KP110570	99.52
Clinostomum sp.	MT446431	99.52
Clinostomum sp.	KY865653	98.25
Clinostomum tilapiae	KY649356	98.25%
Clinostomum phalacrocoracis	KP110569	98.09%
Clinostomum cutaneum	KP110564	97.93%
Euclinostomum heterostomum	KY312847	97.46%
Clinostomum chabaudi	MW528863	96.98%

Table 9 Sequence identity matrix (%) amongst the *Clinostomum* spp. based on the partial sequence of ITS gene.



Figure 17 The phylogenetic tree of ITS gene constructed by maximum likelihood displays *C. piscidium* (OP782661) from *Trichopodus pectoralis* clustering next to the Indian group of *C. piscidium*. GenBank accession numbers are provided before species names, and the numbers on the nodes reflect bootstrap confidence levels.



Chapter 5: DISCUSSION, CONCLUSIONS AND RECOMMENDATIONS

5.1 Discussion

In the present study, the overall prevalence of C. piscidium infection in T. pectoralis was rather high (13.35%) compared to the previous research by Tansatit et al. (2014) which was 43.95 %. It was discovered that there was a connection between the sex of the hosts and the level of parasite infection and intensity. Female fish were more prone to contracting the disease than male fish. From all the farms, it was found that the rate of infection and the severity of worms were higher in the females than in the males. Records on greater infectivity in female hosts are also reported by Tansatit et al. (2014), who observed that the prevalence of C. piscidium in T. pectoralis was higher in females than males. Both the prevalence and the degree of endoparasite infections were higher in female Channa punctatus than in males (Alam et al., 2011). Gholami et al. (2011) also reported a higher rate of C. complanatum infection was seen in female Aphanius dispar (1.33%) compared to male A. dispar (1%), who had a lower rate (Gholami et al., 2011). On the contrary, there have been reports of men having stronger infectivity than females. Ochieng et al. (2012) reported a more significant C. tilapia infection in males Oreochromis niloticus than female fish (Ochieng, 2012). The factors that contribute to differences in parasite infectivity between sexes are unclear. Female hosts may have a higher incidence and severity of parasite infection owing to physiological and biological characteristics that make females more sensitive and enable parasites to live longer. On the other hand, male fish could be better able to fight off parasites and infection (Siddigui and Nizami, 1982). Possible behavioral variations between sexes contribute to the disparity in infection rates (Thompson & Kavaliers, 1994).

The parasites recovered from the body cavity of *T. pectoralis* showed morphological traits that differed from the metacercaria of *C. piscidium* previously reported by Southwell and Prashad (1918), Singh et al. (2010), and Tansatit et al. (2014). The form of the anterior and y-shaped posterior testis distinguishes this species. The anterior testis, ovary, and posterior testis shape were identical to the earlier research published by Tansatit et al. (2014) in *T. pectoralis*. However, the size of the body length, body width, oral sucker and the ventral sucker were found different from the

previous study. The metacercariae of *C. piscidium* were described for the first time in *Nandus* nandus in India (Southwell and Prashad, 1918). In Thailand, Charoenpornsook (1985) reported the finding of this metacercariae from the body cavity of *T. pectoralis* and *T. micropterus*. In this investigation, *C. piscidium* metacercariae were exclusively found in the fishes' abdominal cavities. Similar findings were also found in *N. nandus* (see(Southwell and Prashad, 1918)), *Colisa fasciata* (see(Singh et al., 2010)), and *M. aculeatus* (see(Khanum et al., 2011)). These indicate the highly specific microhabitat of the parasite in their hosts.

Morphological examination by scanning electron microscope showed that the metacercariae of the *C. piscidium* were found to be oval. However, the previous study described it as a rod-shaped structure (Tansatit et al., 2014). Moreover, the cuticular spines were seen in this work; nonetheless, the Clinostomidae family is distinguished by its lack of a cuticle protective mechanism (Woodyard et al., 2017). Notably, most cuticular spines might be destroyed during the staining and experimental process and not be seen on a permanent slide (Caffara et al., 2014).

The current study reveals significant histopathological impairment in the liver of T. pectoralis due to the presence of migratory tracks caused by the fluke and host response through chronic inflammation. The manifestation of granuloma formation was identified through the infiltration of macrophages and epithelioid cells along the outer perimeter of the track. This action was taken to isolate the affected area. The histopathological examination of liver damage in Channa punctata, following parasitization with encysted metacercaria of Euclinostomum heterostomum, exhibited a broad expanse of metacercariae cysts and impaired hepatic tissue (Kaur et al., 2012). The formation of tracks in the hepatic parenchyma may be attributed to two primary mechanisms. The first mechanism involves the prehensile action of the oral sucker, which causes mechanical damage. The second mechanism involves the mechanical abrasion caused by spines on the fluke's tegument after they have burrowed and migrated in the liver. Furthermore, it is plausible that the detrimental impact on the hepatic parenchyma could be attributed to the noxious properties of the excretory-secretory (ES) substances produced by the parasite. The cysteine protease present in the ES products released by the metacercaria of clinostomids has been identified as the agent responsible for the degradation of host proteins (Shareef and Abidi, 2013; Shareef et al., 2010). These products comprise an enzyme that is indispensable for the advancement of the nascent flukes' locomotion and maturation. These compounds are utilized to infiltrate the host tissue and acquire nutrients for their own sustenance (Kasny et al., 2009). Increased eosinophils often accompany infection with metacercariae of different digenea (Adeyemo and Agbede, 2010; Prasanna and Chikkam, 2013). Oreochromis niloticus, which was parasitized by C. tilapia metacercariae, had an increase in eosinophilic granular cells in the gills, according to Adeyemo & Agbede (2008). Tetracotyle metacercariae infection of Mastacembelus armatus resulted in an increase in eosinophilic granular cells in the area between the host tissue and the parasite (Prasanna and Chikkam, 2013). According to Milbourne and Howell (1993), the ES product from the fluke has similar biological properties to interleukin-5 (IL-5), a cytokine that stimulates myeloid precursor cells to differentiate and activate eosinophils. According to this study, eosinophilic granular cells in the liver and intestine's periphery represent the host immune system's reaction to the ES antigen on the metacercariae. Due to the mechanical harm and toxicity brought on by ES products, infection with C. piscidium metacercariae may impair the host's ability to function their liver and pancreas. This may occur because ES product causes toxicity. The liver is thought to be the most significant digestive gland in fish since it performs various functions that are crucial to their survival. It significantly affects the metabolism of carbohydrates, proteins, and lipids as well as the glycogen store. Furthermore, here is where the detoxification process is carried out (Akiyoshi and Inoue, 2004). The extensive necrosis of the hepatic and pancreatic tissues may potentially interfere with metabolic processes, leading to a disruption of the host's overall metabolic function and a subsequent reduction in growth potential. The presence of melano-macrophages was detected in the spleen of the affected fish. There may be a correlation between heightened levels of pigmented macrophages and stress and a lack of food (Shinya et al., 2002). Clinostomidae parasites are cosmopolitan, possibly zoonotic flukes that have been little researched in Thailand using molecular taxonomic methods. Mainly, morphological distinctions across the several phases of parasite growth have made

their identification more complex (Choudhary et al., 2022). Thus, to ensure more accuracy in identifying *Clinostomum* species, morphological identification has been advised to be paired with DNA evidence (Briosio-Aguilar et al., 2019); this is what the current research has done. We presented comprehensive morphological descriptions for identifying the metacercaria of *C. piscidium* and related sequencing data, which may be utilized in future research on diagnostics, freshwater conservation management plans, and public health concerns in Thailand. Although *Clinostomum* spp. is commonly recognized as a zoonotic parasite, it should be highlighted that many medical reports are predicated on this assumption rather than presenting proof of the parasite's identification (Park et al., 2009; Rahmati et al., 2020). As a result, the presence of infectious metacercariae in snakeskin gourami in the current research should be regarded as a potential risk.

This study also aimed to find the cercaria of *Clinostomum* sp. in their first intermediate host, freshwater snail (Figure 18). However, this study recovered no cercaria from the snail for further experiments. In addition, 20 representative samples from both infected and non-infected were processed for the muscle compression experiment to recover the parasite from the muscle and skin of the fish. As a result of the low parasite infestation, this study did not find any parasites in the muscle of the fish.

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Figure 18 Collection of the snail (A) and checking for the presence of cercariae in the first intermediate host (B).

Clinostomid parasites have low host specificity and may infect a wide range of hosts, causing damage and impairment and, in extreme instances, death (Aghlmandi et al.,

2018; Dang, 2021; Montes et al., 2020; Sutili et al., 2014). Even though just a single species was studied in this work, it is evident that additional research into the prevalence of this parasite and its effects on the health of fish hosts is required. Fisheating birds serve as definitive hosts in nature, but morphological evidence alone is often insufficient to connect the metacercaria and adult stages (Jousson et al., 1998; Rosser et al., 2018; Shamsi et al., 2013). For future research purposes, the current work established a relationship between metacercariae of *Clinostomum* spp. and *Clinostomum piscidium*, which are often indistinguishable. Body size and shape, sucker ratio, and, most noticeably, genital complex structure are only some morphological changes that occur throughout the metacercariae's metamorphosis into an adult (Choudhary et al., 2022). Notably, most of the cuticular spines might be destroyed during the staining and experimental process and not be seen on a permanent slide (Caffara et al., 2014).

The fish were confined in an intensive aquaculture environment in the present investigation. The snails noticed inside the pond could be another source of infection (Bera et al., 2021). The co-habituating cercariae of the snail may be able to identify the second intermediate host in the aquaculture system. The metacercariae of *Clinostomum* spp. show broad host specificity, according to fish from various zoogeographical regions and families, which makes the current research results relevant owing to the possible effects on key farmed fish and public health. Moreover, due to severe infection with *Clinostomum* metacercariae, amphibians have also been linked to muscular dystrophy and scoliosis (Belló et al., 2000; Perpiñán et al., 2010).

Previous studies have documented the occurrence of localized hemorrhage resulting from *C. piscidium* infection in *T. pectoralis* (Tansatit et al., 2014). The study reported that fish that were infected with clinostomatid metacercaria exhibited a delayed development (Roberts, 1986). In host tissue, a distinction has been made between encysted and non-encysted metacercariae of clinostomids. The metacercariae of the *C. piscidium* species possess the unique ability to endure within the cavity of the second intermediate host without encystment (Tansatit et al., 2014). The non-cysted metacercaria of this species possess the capability to cause significantly greater

harm to the host fish due to its unrestricted mobility within the visceral organs (Echi et al., 2012). The present study reveals that C. piscidium metacercariae were solely retrieved from the abdominal cavity of the fish that were infected. Similar observations were found in both Nandus nandus and Colisa fasciata ("Notes from the Bengal Fisheries Laboratory. Parasites of Indian fishes, with a note on careinoma in the Climbing Perch," 1918; Singh et al., 2010). These findings offer proof of the distinct microenvironment that the parasite inhabits within its host organisms. The hepatic parenchyma of the host may suffer damage due to the toxic impact of the excretory-secretory (ES) secretions of the parasite, C. piscidium, in the event of an infection. The cysteine protease, which has the ability to degrade host proteins, has been identified as the ES product secreted by the metacercaria of clinostomids (Shareef et al., 2010; Shareef and Abidi, 2013). The mentioned products consist of enzymes that are essential for the advancement of undeveloped flukes during their migration and growth. The compounds are utilized to infiltrate the host tissue and acquire nutrients for self-sustenance (Kasny et al., 2009). Infection with metacercariae of various digenean is often accompanied by increased eosinophils (Adeyemo and Agbede, 2010). The infection with metacercariae of C. piscidium may compromise the host's liver and pancreas function because of the mechanical damage and toxicity caused by ES products. Consequently, severe necrosis of hepatic and pancreatic tissues may disrupt metabolic processes, disrupting the metabolism and leading to stunted development of the fish (Tansatit et al., 2014).

For the molecular characterization of trematodes from the piscine (second intermediate host), including clinostomids and allocreadiids, PCR amplification utilizing rDNA markers has proven effective (Olson et al., 2003). Molecular markers of mitochondrial and ribosomal origins may also help recognize a new species, such as *C. tataxumui*, and verifying *C. complanatum* in Mexico's freshwater fish and fisheating birds (Sereno-Uribe et al., 2013). Recently, scientists used an internal transcribed spacer 1 (ITS1) region to validate *C. marginatum* and matched it to adult and larval specimens from various hosts and geographic areas (Calhoun et al., 2019). Our *Clinostomum* sp. isolates from *T. pectoralis* showed the most genetic resemblance to *C. piscidium* from banded gourami (*Colisa fasciata*) (FJ970655) of

Indian origin in a phylogenetic tree based on the 18S rDNA sequence. In addition, the *Clinostomum sp.* (AY222094) isolated from *Hypseleotris galii* (Murray cod) from Australia demonstrated a powerful association with the 99% sequence similarity matrix. Previous findings on *C. complanatum* from China, the United States of America, and Israel were all placed in a different group within the same clade as our isolate, which shared 97% of their sequence similarities. In conclusion, the 18S rDNA gene-based phylogenetic tree (Figure 3) and sequence identity matrix (Table 3) would be able to identify *C. breini, C. margunatum,* and *C. tataxumui* and placed them in a different clade, which corroborated the conclusions of the earlier research (Gustinelli et al., 2010; Caffara et al., 2014; Wang et al., 2017).

In addition, our findings imply that ITS-1 and ITS-2 sequences, rather than 28S sequences, may be more effective for discriminating between closely related species that belong to the family Clinostomidae. Previous research has supported this hypothesis (Curran et al., 2006; Lotfy et al., 2010; Phalee and Wongsawad, 2014). Figure 4 makes it very evident that our *C. piscidium* isolate from the snakeskin gourami grouped into the same cluster as an Indian isolate of *C. piscidium*. In this work, we report the first genetic identification of *C. piscidium* metacercariae from one of Thailand's most important commercial species, *T. pectoralis*. Regarding the solid genetic relationship between *Clinostomum* species, the phylogenetic analysis led us to recognize *C. piscidium* as a distinct parasite for snakeskin gourami based on a comparison of molecular data.

5.2 Conclusion and Recommendations

Snakeskin gourami (Trichopodus pectoralis) is a popular and economically valuable species in the commercial aquaculture industry in Thailand. However, the intensive culture practices employed in this industry make the snakeskin gourami highly susceptible to various parasitic diseases, particularly digenean trematodes. Among these parasites, Clinostomum spp. are economically important parasites that affect freshwater fishes, snails, and birds worldwide. Efficient control and preventative strategies for these parasitic infections require accurate identification of the parasites down to the genus and species level. However, before the available information, no studies have been conducted to establish the molecular identification of *Clinostomum* spp. in snakeskin gourami in Thailand. This knowledge gap underscores the need for further research to enhance our understanding of the prevalence, distribution, and genetic diversity of *Clinostomum* parasites in snakeskin gourami populations. To reduce the economic losses caused by *Clinostomum* infection in fish, preventive measures must be taken through the culmination of snails to prevent the disease in fish, or research on vaccine development and chemotherapeutics needs special attention since snakeskin gourami is a highly valued economic fish of Thailand.

In addition, it is crucial to encourage education and training among aquaculture farmers, industry participants, and relevant authorities. By educating farmers about the dangers of *Clinostomum* spp. infections and providing them with information and tools on disease prevention, detection, and management, we may help to reduce the incidence and spread of these diseases.

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APPENDIX A

Table List of 18S rDNA gene used for primer design.

Scientific Name	Description	Accession No.
Clinostomum sp.	185 small subunit ribosomal RNA gene	MW539004
Clinostomid sp.	185 small subunit ribosomal RNA gene	AY829252
Clinostomum sp.	185 small subunit ribosomal RNA gene	AY222094
Clinostomum piscidium	185 small subunit ribosomal RNA gene	FJ970655
Clinostomum brieni	185 small subunit ribosomal RNA gene	MH606189
Clinostomum complanatum	185 small subunit ribosomal RNA gene	KF811012
Clinostomum sinensis	18S small subunit ribosomal RNA gene	MK490986
Clinostomum giganticum	185 small subunit ribosomal RNA gene	FJ970654
Clinostomum marginatum	18S small subunit ribosomal RNA gene	MF398350

APPENDIX B

List of ITS1–5.8S rDNA-ITS2 gene used for primer design.

Scientific Name	Description	Accession No.
Clinostomum piscidium	internal transcribed spacer 1	KY312848
	and internal transcribed	
	spacer 2 region	
Clinostomum piscidium	internal transcribed spacer 1	KY290511
	and internal transcribed	
	spacer 2 region	
Clinostomum tilapiae	internal transcribed spacer 1	KY649356
	and internal transcribed	
	spacer 2 region	
Clinostomum	internal transcribed spacer 1	MH845235
complanatum	and internal transcribed	
	spacer 2 region	
Clinostomum	internal transcribed spacer 1	MK796829
complanatum	and internal transcribed	
ຈາກ	spacer 2 region	
Clinostomum piscidium	internal transcribed spacer 1	KY304779
	and internal transcribed	
	spacer 2 region	

APPENDIX C

Table List of primer set used in this study.

Gene	Forward Primer	Reverse Primer	Product	Reference
			size	
			(bp)	
18S	ATTCCGGAGGGAGCCCTG	ATCAACCCAGTCAGCACCC	395	Present
rRNA		11/22		study
ITS	CACCGCCCTGGCGTAATA	CGACACTTCGAACGATTTCTAGA	801	Present
				study
	จุฬาลงก Chulalon	รณ์มหาวิทยาลัย Igkorn University		

APPENDIX D

Table Sequence identity matrix (%) amongst the clinostomids based on the partial sequence of 18S rDNA gene.

Species Name	Accession No.	E-value	Identity (%)
Clinostomum sp.	MW539004	0.00	100
Clinostomid sp.	AY829252	0.00	100
Clinostomum sp.	AY222094	0.00	100
Clinostomum piscidium	FJ970655	0.00	98.93
Clinostomum brieni	MH606189	0.00	98.12
Clinostomum brieni	MH606188	0.00	98.12
Clinostomum complanatum	KF811012	0.00	98.12
Clinostomum brieni	MH606187	5e-180	97.86
Clinostomum complanatum	FJ609420	6e-179	97.59
Clinostomum complanatum	AY245701	6e-179	97.59
Clinostomum brieni	KF811009.1	2e-178	97.59
Clinostomum giganticum	FJ970654	5e-175	97.05
Clinostomum marginatum	MF398350	1e-171	96.51
Clinostomum tataxumui	MF398349	1e-171	96.51
Clinostomum marginatum	AY245760	1e-171	96.51
Clinostomum sp.	AY222095	1e-171	96.51
Trematoda sp.	KX172121	3e-147	96.60
Schistosoma spindale	Z11979	3e-137	90.74

APPENDIX E

Table Sequence identity matrix (%) amongst the clinostomids based on the partial sequence of ITS gene.

Species Name	Accession No.	E-value	Identity (%)
Clinostomum piscidium	KY312848	0.00	100
Clinostomum philippinense	KP110570	0.00	99.52
Clinostomum sp.	MT446431	0.00	99.52
Clinostomum sp.	KY865653	0.00	98.25
Clinostomum tilapiae	KY649356	0.00	98.25%
Clinostomum phalacrocoracis	KP110569	0.00	98.09%
Clinostomum cutaneum	KP110564	0.00	97.93%
Euclinostomum heterostomum	KY312847	0.00	97.46%
Clinostomum chabaudi	MW528863	0.00	96.98%
Schistosoma spindale	Z11979		



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APPENDIX F

Table Sex, weight and length of studied fishes

Location	No.	Ν	Number Weight (g) Total len		Weight (g)		ngth (cm)
		of fish					
		Male	Female	Range	Mean±S.D.	Range	Mean±S.D.
				(g)		(cm)	
Samutsongkram	Farm-	3	27	101-	142.1±15.47	14-21	18.1±1.92
	1			174			
Samutsongkram	Farm-	5	24	74-184	106.13±23.28	13-19	15.96±1.51
	2	- Canada					
Samutsongkram	Farm-	3	22	36-63	45.56±7.36	9-15	11.88±1.50
	3				2		
Samutsongkram	Farm-	5	23	76-230	150.39±36.98	12-20	17.21±2.48
	4		Tao ta A				
Samutsongkram	Farm-	6	9	144-	226±41.77	18-24	20.46±1.69
	5	à	1919498	296			
Samutsongkram	Farm-	5	17	101-	117.59±8.39	11-18	15.45±2.1
	6			131	9		
Samutsongkram	Farm-	2	13	137-	160.73±8.82	15-20	18.13±1.13
	7	19113	гичиі	173	B		
Samutsongkhram	Farm-	A3 ONG	14 RN U	97-113	106.35±5.37	12-15	13.17±0.95
	8						
Samutsakorn	Farm-	5	26	153-	199.70±31.67	17-25	19.45±1.78
	9			223			
Samut Prakarn	Farm-	5	26	140-	200.67±36.99	17-22	19.38±1.38
	10			298			
Samut Prakarn	Farm-	3	8	48-87	60.72±10.63	10-18	14.00±2.00
	11						
Kanchanaburi	Farm-	1	7	57-89	74.5±10.91	11-16	14.25±1.61
	12						

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