

Global Burden of Clinostomum complanatum in Freshwater Fish: A Systematic Review and Meta-Analysis of Prevalence and Pathological Effects

Mengesha Ayehu Getnet

Mengeshaayehu126@gmail.com

University of Gondar

Melkie Dagnaw Fenta

University of Gondar

Asnakew Mulaw Berihun

University of Gondar

Wilmien Luus Powell

University of Limpopo

Moges Maru Alemayehu

University of Gondar

Tameru Gedefaw

University of Gondar

Zenebe Jemere

University of Gondar

Zewdu Seyoum Tarekegn

University of Gondar

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Abstract

Background

Clinostomum complanatum is a trematode parasite that infects a wide range of freshwater fish hosts, causing significant pathological damage, reduced fish productivity, and economic losses. Despite its considerable economic and health impact, its global burden remains poorly quantified.

Objective

This study aimed to evaluate the global burden of *C. complanatum* infection in fish, with particular emphasis on prevalence patterns, habitat associations, and pathological impacts.

Methods

A systematic review and meta-analysis following PRISMA 2020 guidelines included 30 studies reporting *C. complanatum* prevalence in 70 freshwater fish species from 18 families. Pooled prevalence was estimated using random-effects models in R. Heterogeneity was assessed with Cochran's Q and I^2 statistics, subgroup analyses were performed, and publication bias was evaluated using Egger's regression test.

Results

Prevalence of *C. complanatum* varied widely among freshwater fish species, reaching 100% in *Squalidus chankaensis* and remaining undetected in several fish species (*Cobitis biwae*, *Hypomesus transpacificus*, *Salangichthys microdon*, and *Silurus asotus*). The pooled global prevalence was 28.7% (95% CI: 22.0–36.5%), with extremely high heterogeneity ($I^2 = 99.0\%$). Significant differences were observed by fish family, country, continent, and habitat type, with the highest prevalence in Percidae (97%), Osphronemidae (67%), and Gobionidae (65%). Africa (49%) and Europe (46.0%) showed the highest regional prevalence, and aquaculture systems had higher infection rates (45.0%) than natural habitats. No effects of publication year, season, or host sex were detected, and no publication bias was evident. Metacercariae predominantly encysted in muscle, buccal, and branchial tissues, forming yellow-grub cysts associated with muscle degeneration and inflammatory responses. The internal transcribed spacer (ITS) region was the most commonly used molecular marker, although molecular diagnostics were underutilized.

Conclusion and Recommendation:

In conclusion, *C. complanatum* represents a widespread but highly heterogeneous threat to freshwater fish health, and aquaculture productivity. Routine incorporation of molecular diagnostics, standardized surveillance protocols, and targeted control strategies particularly in aquaculture systems are strongly recommended to reduce infection burden, economic losses, and zoonotic risk.

1. INTRODUCTION

Freshwater fishes are integral components of aquatic ecosystems and constitute a major source of high-quality animal protein for human populations [21, 57, 61]. However, fish production is threatened by various types of infectious diseases, among which parasitic infections are among one of the particular concerns [33, 52, 36, 46]. From those diverse parasites infecting freshwater fish, digenean trematodes are notable due to their complex life cycles, broad host ranges, and zoonotic relevance [35, 13, 49]. Among digenean trematodes, *Clinostomum complanatum* is a widely distributed species of the family Clinostomidae that infects a wide range of freshwater fish species [30, 55].

The *Clinostomum complanatum* life cycle involves piscivorous birds as definitive hosts and freshwater fish as second intermediate hosts, in which the metacercarial stage develops [40, 61]. Infection with *C. complanatum* can impair fish condition, reduce productivity, cause illness, and reduce commercial acceptability; however, its effects on freshwater fisheries are generally context-dependent and are often intensified by anthropogenic pressures such as habitat modification, pollution, altered host assemblages, and aquaculture intensification, rather than constituting a universal threat to fisheries sustainability [34, 10, 39].

In fact, *C. complanatum* possesses a complex indirect life cycle involving both aquatic and terrestrial hosts. Adult worms inhabit the oral cavity, pharynx, or esophagus of piscivorous birds, where they reproduce and release eggs into aquatic environments via feces [63, 40]. Following hatching, free-swimming miracidia infect freshwater gastropods that serve as first intermediate hosts. Within snails, the parasites undergo asexual multiplication through sporocyst and redial stages, producing cercariae that are subsequently released into the water column [29]. These cercariae actively penetrate freshwater fish or, less commonly, amphibians, encysting as metacercariae in tissues such as skeletal muscle, gills, fins, or body cavities [36, 61]. The life cycle is completed when infected prey are consumed by piscivorous birds.

The prevalence of *C. complanatum* infection in freshwater fish varies considerably across studies and regions. This variation reflects differences in geographical location, fish species composition, ecosystem type, availability of intermediate snail hosts and definitive avian hosts, seasonal dynamics, water quality, and sampling strategies [54, 7]. The parasite is particularly widespread in freshwater systems that support abundant snail populations and piscivorous birds [6, 7].

Metacercariae of *C. complanatum* encyst in multiple fish tissues, including skeletal muscle, skin, gills, fins, head, and visceral organs [35]. These infections can result in tissue degeneration, inflammatory responses, fibrosis, and behavioral alterations in fish hosts [57, 64]. The severity of pathological effects is influenced by parasite intensity, host species, and environmental factors, and is commonly associated with the condition known as “yellow grub disease,” characterized by conspicuous yellow cysts within edible tissues [64]. This condition has notable economic implications, as visibly infected fish are frequently rejected by consumers or sold at reduced prices, leading to financial losses in both aquaculture and capture fisheries [18, 40].

Traditionally, identification of *C. complanatum* metacercariae in fish has relied on morphological characteristics. Metacercarial cysts are typically round to oval, yellowish, and visible to the naked eye, each containing a single parasite [1, 6]. Upon excystation, metacercariae exhibit a dorsoventrally flattened, linguiform body with well-developed oral and ventral suckers [22]. While morphological identification remains widely used, advances in molecular diagnostics particularly PCR amplification and sequencing of internal transcribed spacer

regions (ITS-1 and ITS-2) and mitochondrial cytochrome oxidase subunit I (mt-COI) have substantially improved the accuracy of species-level identification [8].

Despite the growing body of literature on *C. complanatum* infections in freshwater fish, current knowledge remains fragmented and inconsistent. Published studies differ substantially in study design, diagnostic approaches, host species investigated, and the reporting of key epidemiological indicators such as prevalence and infection intensity. Consequently, there is no consolidated quantitative synthesis describing global patterns of distribution, prevalence, habitat-related risk factors, or pathological outcomes. This lack of integration limits cross-study comparability, weakens evidence-based risk assessment, and hampers the development of standardized surveillance, prevention, and management strategies. Given the economic importance of freshwater fisheries, the impact of *C. complanatum* on fish health and marketability, and its recognized zoonotic potential, a comprehensive synthesis is urgently needed. Therefore, this study conducted a systematic review and meta-analysis to summarize global evidence on the prevalence, geographic distribution, host range, infection intensity, parasite predilection sites, and pathological effects of *C. complanatum* in freshwater fish.

2. METHODS

2.1. Study Design

This study was conducted as a systematic review and meta-analysis in accordance with the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) 2020 guidelines [47]. The completed PRISMA checklist is provided as Supplementary Material S1.

2.2. Information Sources and Literature Search Strategy

A comprehensive systematic literature search was performed to identify all relevant peer-reviewed studies reporting the prevalence, pathological effects, and biological characteristics of *C. complanatum* in freshwater fish. The initial search was conducted on 7 April 2025, followed by an updated search on 7 June 2025 to capture newly published studies. Electronic databases searched included PubMed, Web of Science, Google Scholar, and HINARI. In addition, manual searches and snowballing were conducted by screening the reference lists of relevant articles to identify additional eligible studies. Searches combined controlled vocabulary, where applicable, with free-text terms using Boolean operators, truncation, and quotation marks. The following search string was applied: “*Clinostomum complanatum*” AND “prevalence OR epidemiology OR infection” AND “pathology OR histopathology OR lesion*” AND “fish OR freshwater fish OR aquaculture” AND “morphology OR morphological identification OR molecular OR PCR OR gene*”. Searches were restricted to the title, abstract, and keywords where possible. Moreover, the same terms were used and results were screened manually for relevance.

2.3. Study Selection and Eligibility Criteria

All retrieved records were imported into reference management software and duplicates were removed prior to screening. Study selection followed a structured two-stage screening process. Titles and abstracts were independently screened by two reviewers (MA and AM) to identify potentially relevant studies, followed by full-text assessment of eligible articles. Discrepancies were resolved through discussion or consultation with a third reviewer (MD).

2.4. Inclusion and Exclusion Criteria

Studies were eligible for inclusion if they reported the prevalence of *C. complanatum* and provided original observational or cross-sectional data on *C. complanatum* infection. Eligible studies involved wild, farmed, or captive freshwater fish from any geographic region and specified the freshwater habitat type (river, lake, or aquaculture system). Parasite identification had to be confirmed using morphological and/or molecular diagnostic methods [1, 2, 8, 18], and studies were required to report mean intensity of infection. In addition, studies had to clearly specify the geographic location (country and continent). No restriction was applied to the year of publication; however, only studies published in English were considered. Furthermore, included studies were required to report the anatomical distribution of the parasite within fish tissues, describe pathological or histopathological alterations associated with *C. complanatum* infection, or provide biologically relevant information related to host pathology [16, 28, 35, 64].

Studies were excluded if they did not present original primary data, including review articles, editorials, opinion papers, conference abstracts, or short communications lacking quantitative results. Studies involving experimental infections or laboratory-based trials, and studies focusing on non-fish hosts were also excluded. Articles that lacked sufficient diagnostic detail to confirm *C. complanatum* at the species level—such as inadequate morphological descriptions or the absence of validated molecular identification—were excluded. Studies that did not provide extractable quantitative prevalence data (e.g., numerical values expressed as n/N) were not included in the quantitative synthesis. To prevent data duplication, studies reporting overlapping datasets from the same host populations or geographic locations were excluded, with only the most comprehensive or most recent publication retained. Preprints, unpublished manuscripts, and other non-peer-reviewed sources were excluded to ensure data quality and reliability.

2.5. Data Extraction and Management

Following full-text eligibility assessment, data were extracted using a standardized extraction form. One reviewer (MA) performed the primary data extraction from text, tables, and figures, while a second reviewer (MD) independently cross-checked the extracted data to ensure accuracy and consistency. Any discrepancies were resolved by consensus. For each included study, the following information was extracted and compiled into an electronic database: study characteristics (authors, year of publication, journal), geographic information (country and freshwater habitat type), host-related data (fish species, number examined, number infected), parasite-related data (anatomical site of infection, prevalence, and mean intensity), methodological details (parasite detection and identification methods, including morphological and molecular approaches and genes targeted), and reported pathological or histopathological findings.

2.6. Definitions of Parasitological Parameters

Parasitological terminology followed standard definitions. Prevalence was defined as the proportion of infected fish among those examined, expressed as a percentage. Parasitic intensity was defined as the number of parasites recovered from each infected (positive) fish host, and mean intensity was calculated as the total number of parasites divided by the number of infected fish [12].

2.7. Data Synthesis and Meta-Analysis

Quantitative synthesis and meta-analysis were conducted using R software (version 4.0.2; R Core Team, 2020). Pooled prevalence estimates were calculated using a random-effects model to account for expected heterogeneity among studies conducted under varying ecological conditions, sampling procedures, and diagnostic approaches [45, 11]. Studies reporting zero events were retained in the analysis, and appropriate variance stabilization was applied.

Between-study heterogeneity was assessed using Cochran's Q test, the I^2 statistic, and the between-study variance (τ^2), which was estimated using maximum likelihood methods [25]. Potential sources of heterogeneity were explored through subgroup analyses based on continent, country, fish family, habitat type (aquaculture versus wild freshwater systems), and diagnostic method. Results were expressed as pooled prevalence estimates with 95% confidence intervals and visualized using forest plots.

2.8. Quality Assessment of Included Studies

The methodological quality of the included studies was assessed using the Joanna Briggs Institute (JBI) Critical Appraisal Checklist for Prevalence Studies. Eight quality domains were evaluated: appropriateness of the sample frame, sampling method, sample size adequacy, clarity of study setting and subjects, data coverage, validity of diagnostic methods, reliability of measurement, and appropriateness of statistical analysis. Each criterion was scored as "Yes" or "No", yielding a maximum possible score of eight. Based on the proportion of affirmative responses, studies were categorized as high ($\geq 80\%$), moderate (60–79%), or low ($< 60\%$) quality [44].

3. RESULTS

3.1. Study Selection

In total, 30 papers investigating the prevalence, geographical distribution, infection intensity, and pathological effects of *C. complanatum* in freshwater fish were included after the screening process (Fig. 1).

3.2. Geographical Occurrence, Distribution, and Parasite Intensity of the Included Studies

As presented in Table 1, without considering geographical or global restriction, the current scientific paper reviewed 30 papers, including data on the geographical distribution of *C. complanatum*, which demonstrates that the parasite is widely distributed across the globe [6, 7, 30, 55].

Moreover, this paper explored data on the parasitic burden of *C. complanatum*, such as parasitic intensity in infected fish, and compared the intensity levels reported among the included studies. Parasitic intensity is defined as the number of parasites recovered from each infected (positive) fish host, and mean intensity is the average number of parasites per infected fish; mean intensity is calculated as the total number of parasites divided by the number of infected fish [12, 59]. These findings reflect the extent of infestation and the potential damage caused by the parasite to fish health.

In Korea, within aquaculture systems, the intensity of *C. complanatum* was reported to be 216.6, which was the highest among all studies reviewed [32]. The second highest intensity was recorded in Croatia (Europe), where

fish from river systems showed a mean intensity of 37.5 [24]. However, the lowest intensity was reported in Türkiye, where fish from stream habitats exhibited an intensity of only 0.3 [8].

Table 1
Occurrence, prevalence, mean intensity, and molecular markers of *Clinostomum complanatum* reported worldwide

Country	Continent	Freshwater type	Positive / Examined (P/N)	Prevalence (%)	Mean intensity	Gene used for molecular detection	Reference
Egypt	Africa	–	187 / 520	35.94	–	COI mtDNA	[57]
Egypt	Africa	River	160 / 400	40.0	5.0	–	[18]
Egypt	Africa	–	175 / 250	70.0	–	ITS rRNA	[18]
Iran	Asia	River	39 / 849	4.6	3.9	–	[3]
Japan	Asia	Aquaculture	227 / 1860	12.2	4.7	–	[5]
Japan	Asia	Aquaculture	42 / 226	18.6	–	–	[4]
Japan	Asia	River	140 / 323	43.34	–	–	[4]
Türkiye	Asia	River	9 / 79	11.4	6.0	–	[9]
Türkiye	Asia	Stream	73 / 216	33.8	7.5	ITS	[8]
Türkiye	Asia	–	14 / 25	56.0	27.14	–	[46]
Türkiye	Asia	–	3 / 403	0.74	–	–	[61]
Iraq	Asia	–	26 / 959	2.7	2.3	ITS-2, mt-COI, ITS1-5.8S-ITS2, 28S rDNA	[2]
Korea	Asia	Aquaculture	398 / 741	26.8	4.76	–	[32]
Korea	Asia	Aquaculture	234 / 276	84.8	216.6	–	[32]
Korea	Asia	River	811 / 1578	51.4	9.8	–	[62]
India	Asia	River	66 / 150	44.0	8.77	–	[26]
India	Asia	Aquaculture	1242 / 1484	83.7	11.7	–	[31]
India	Asia	Aquaculture	80 / 364	21.98	2.27	V4-18S	[58]
India	Asia	Aquaculture	89 / 250	35.6	3.06	ITS1 + 5.8S + ITS2	[59]
Saudi Arabia	Asia	Aquaculture	398 / 721	55.2	15.0	–	[28]
Iran	Asia	River	53 / 112	47.3	6.34	–	[36]
Iran	Asia	River	11 / 224	5.0	3.2	ITS	[37]
Note: P = number of positive samples; N = total number of examined samples. The symbol (–) indicates that the information was not reported in the original study.							

Country	Continent	Freshwater type	Positive / Examined (P/N)	Prevalence (%)	Mean intensity	Gene used for molecular detection	Reference
Iran	Asia	River	5 / 97	4.12	1.25	–	[23]
Brazil	South America	River	1129 / 2920	38.7	15.4	–	[17]
Brazil	South America	River	1120 / 2682	41.75	–	–	[16]
Brazil	South America	River	13 / 1582	0.82	9.3	–	[60]
Slovakia	Europe	River	142 / 270	47.4	4.66	–	[20]
Italy	Europe	–	12 / 30	40.0	2.0	–	[22]
Italy	Europe	Lake	21 / 112	18.75	1.4	ITS	[41]
Croatia	Europe	River	13 / 81	16.5	37.5	–	[24]
France	Europe	River	32 / 33	97.0	5.8	28S rRNA	[55]
Note: P = number of positive samples; N = total number of examined samples. The symbol (–) indicates that the information was not reported in the original study.							

3.3. Cumulative prevalence of *Clinostomum complanatum* in various fish species

The present work synthesized cumulative prevalence data of *C. complanatum* across multiple fish species (Table 2) and revealed considerable variation among host taxa. Notably higher prevalence was observed in *Squalidus chankaensis* (100%), *Squalidus japonicus coreanus* (98.7%), *Perca fluviatilis* (97%), *Acheilognathus rhombea* and *Microphysogobio yaluensis* (88.89% each), *Trichogaster fasciatus* (83.69%), and *Acheilognathus koreensis* (74.26%) respectively. Moderate prevalence (20–59%) was recorded across a broad range of taxa, including *Acheilognathus yamatsutae* (57.55%), *Loricariichthys platymetopon* (58.97%), *Rhodeus uyekii* (58.33%), *Aphanius dispar* (55.20%), *Cobitis elongatoides* (52.59%), *Oreochromis niloticus* (44.62%), *Parauchenipterus galeatus* (42.57%), *Pseudosphromenus cupanus* (44.00%), and *Capoeta capoeta gracilis* (47.32%). In contrast, low prevalence (< 20%) characterized many species, including *Capoeta trutta* (1.84%), *Cyprinion macrostomum* (1.54%), *Planiliza abu* (1.37%), *Hoplias malabaricus* (2.45%), *Loricaria* sp. (2.56%), and *Rhodeus ocellatus* (0.86%), as well as several taxa in which no infections were detected (e.g. *Cobitis biwae*, *Hypomesus transpacificus*, *Salangichthys microdon*, and *Silurus asotus*). Overall, these findings indicate pronounced host-specific differences in susceptibility, with a limited number of species acting as highly competent intermediate hosts, while many others exhibit sporadic or negligible infection levels.

Table 2
Cumulative (pooled) prevalence of *Clinostomum complanatum* in various fish species

Fish species	ΣN (examined)	ΣP (infected)	Cumulative prevalence (%)	References
<i>Alburnus sellal</i>	61	3	4.9	[2]
<i>Capoeta trutta</i>	217	4	1.8	[2]
<i>Capoeta umbla</i>	160	8	5.0	[2]
<i>Carasobarbus kosswigi</i>	5	1	20.0	[2]
<i>Cyprinion macrostomum</i>	324	5	1.5	[2]
<i>Garra rufa</i>	96	17	17.7	[2, 46, 37]
<i>Planiliza abu</i>	73	1	1.37	[2]
<i>Squalius lepidus</i>	61	3	4.9	[2]
<i>Alburnoides bipunctatus</i>	101	8	7.9	[2]
<i>Capoeta gracilis</i>	103	25	24.3	[3]
<i>Cobitis cf. taenia</i>	101	5	4.9	[3]
<i>Squalius cephalus</i>	242	17	7.0	[3, 61, 37, 24]
<i>Carassius gibelio langsdorfi</i>	378	114	30.2	[3]
<i>Carassius cuvieri</i>	41	18	43.9	[3]
<i>Cyprinus carpio</i>	144	33	22.9	[3, 24]
<i>Pseudorasbora parva</i>	281	54	19.2	[3, 32]
<i>Rhodeus ocellatus</i>	233	2	0.86	[3]
<i>Rhodeus lanceolatus</i>	529	53	10.0	[5]
<i>Hypomesus transpacificus</i>	220	0	0.0	[5]
<i>Salangichthys microdon</i>	106	0	0.0	[5]
<i>Cobitis biwae</i>	40	0	0.0	[5]
<i>Silurus asotus</i>	25	0	0.0	[5]
<i>Leuciscus hakonensis</i>	20	0	0.0	[5]
<i>Ischikavia steenackeri</i>	12	0	0.0	[5]
<i>Zacco platypus</i>	257	80	31.1	[5, 32]
<i>Gnathopogon elongatus elongatus</i>	4	0	0.0	[5]
Notes: ΣP denotes the total number of infected fish, and ΣN denotes the total number of fish examined.				

Fish species	ΣN (examined)	ΣP (infected)	Cumulative prevalence (%)	References
<i>Carassius</i> spp.	825	423	51.3	[4, 32]
<i>Aphanius dispar</i>	721	398	55.2	[28]
<i>Squalius cii</i>	79	9	11.4	[9]
<i>Alburnus escherichii</i>	216	73	33.8	[8]
<i>Cichlasoma paranaense</i>	56	6	10.7	[60]
<i>Gymnotus carapo</i>	88	7	7.95	[60]
<i>Squalidus japonicus coreanus</i>	77	76	98.7	[62]
<i>Squalidus chankaensis</i>	51	51	100.0	[62]
<i>Squalidus gracilis majimae</i>	31	5	16.1	[62, 32]
<i>Hemibarbus longirostris</i>	77	20	26.0	[62]
<i>Hemibarbus labeo</i>	8	2	25.0	[62]
<i>Acheilognathus majusculus</i>	194	132	68.0	[62]
<i>Acheilognathus koreensis</i>	136	101	74.3	[62, 32]
<i>Acheilognathus rhombeus</i>	35	23	65.7	[62]
<i>Acheilognathus yamatsutae</i>	106	61	57.5	[32]
<i>Trichogaster fasciatus</i>	1484	1242	83.7	[31]
<i>Channa punctatus</i>	614	169	27.5	[58, 59]
<i>Capoeta capoeta gracilis</i>	112	51	47.3	[36]
<i>Acanthobrama mossulensis</i>	61	3	4.76	[37]
<i>Perca fluviatilis</i>	33	32	97.0	[55]
<i>Cobitis bilineata</i>	30	12	40.0	[22]
<i>Cobitis elongatoides</i>	270	142	52.6	[20]
<i>Loricariichthys platymetopon</i>	1728	1019	58.9	[17, 16]
<i>Parauchenipterus galeatus</i>	2619	1115	42.6	[17, 16]
<i>Hoplosternum littorale</i>	1010	109	10.8	[17, 16]
<i>Hoplias malabaricus</i>	204	5	2.45	[17]
<i>Loricaria</i> sp.	39	1	2.56	[17]
Notes: ΣP denotes the total number of infected fish, and ΣN denotes the total number of fish examined.				

3.4. Meta-analysis for pooled prevalence, heterogeneity and publication bias

The current article has done the meta-analysis from the included 30 studies. The pooled prevalence under the random-effects model, which accounts for between-study variation, estimated a lower prevalence of 28.7% (95% confidence interval: 22.0–36.5%). As Fig. 2 (forest plot) shows Heterogeneity across studies was extremely high ($\tau^2 = 0.95$ [0.98–3.48]; $\tau = 0.98$ [0.99–1.87]; $I^2 = 99.0\%$ [98.8–99.1%]; $H = 9.80$ [9.18–10.46], and the Q statistic ($Q = 2881$, $df = 30$, $p < 0.0001$) confirmed strong evidence of heterogeneity. Despite this variability, publication bias was not detected, as indicated by Egger's regression test ($z = -0.55$, $p = 0.5791$), with no evidence of funnel plot asymmetry (limit estimate = -0.72; 95% CI: -1.64 to 0.21) (Fig. 3).

3.5. Subgroup meta-analysis revealed prevalence *Clinostomum complanatum* infection

3.5.1. Subgroup analysis across fish families

The subgroup meta-analysis revealed substantial variation in the pooled prevalence of *C. complanatum* across fish families, forming a clear gradient from high to low infection levels. The highest prevalence was observed in Percidae (97%), followed by Osphronemidae (67%), Gobionidae (65%), and Aphaniidae (55.20%), indicating strong host-family associations with infection risk. Moderate prevalence was recorded in Acheilognathidae (39.29%), Cichlidae (37.30%), Auchenipteridae (30.33%), and Channidae (28.27%), with considerable between-study heterogeneity. Lower prevalence estimates were observed in Loricariidae (15.89%), Cobitidae (16.07%), and Cyprinidae (13.75%), despite the latter contributing the largest number of studies. The lowest prevalence occurred in Callichthyidae (10.79%), Gymnotidae (7.95%), Erythrinidae (2.45%), Siluridae (1.92%), Mugilidae (1.37%), Salangidae (0.47%), and Osmeridae (0.23%). The test for subgroup differences was highly significant ($Q = 481.97$, $df = 17$, $p < 0.0001$), confirming that fish family is a major source of heterogeneity in *C. complanatum* prevalence (Table 3).

Table 3
Subgroup meta-analysis of *Clinostomum complanatum* prevalence by fish family

Fish family	Prevalence (%)	95% CI (%)	τ^2 (Tau ²)	τ (Tau)	Test for subgroup differences
Cyprinidae	13.75	7.97–22.66	2.1426	1.4638	
Mugilidae	1.37	0.19–9.09	—	—	
Cobitidae	16.07	2.70–56.89	3.4223	1.8499	
Acheilognathidae	39.29	8.60–81.66	5.6733	2.3819	
Osmeridae	0.23	0.01–3.51	—	—	
Salangidae	0.47	0.03–7.02	—	—	
Siluridae	1.92	0.12–24.36	—	—	
Gobionidae	65	15.04–95.00	7.3545	2.7119	Q = 481.97, df = 17, p < 0.0001
Aphaniidae	55.20	51.55–58.80	—	—	
Cichlidae	37.30	15.90–65.19	1.3170	1.1476	
Gymnotidae	7.95	3.84–15.76	—	—	
Osphronemidae	67	24.31–92.70	1.7450	1.3210	
Channidae	28.27	16.92–43.28	0.2105	0.4588	
Percidae	97	81.39–99.57	—	—	
Loricariidae	15.89	1.78–66.32	3.9298	1.9824	
Auchenipteridae	30.33	3.53–83.84	3.1895	1.7859	
Callichthyidae	10.79	9.02–12.86	0.0000	0.0000	
Erythrinidae	2.45	1.02–5.75	—	—	

3.5.2. Subgroup analysis across countries

Country-level random-effects analysis revealed substantial geographic heterogeneity in the prevalence of *C. complanatum*. Very high pooled prevalence were observed in France (97%), India (66%), Korea (56%), Saudi Arabia (55%), Slovakia (53%), and Egypt (45%), whereas markedly lower prevalence was reported in Iraq (3%), Iran (8%), Turkiye (14%), Japan (17%), and Croatia (16%). Several countries, including Brazil and Turkiye, showed wide confidence intervals and high τ^2/τ values, indicating pronounced between-study heterogeneity (Table 4). Overall, the significant test for subgroup differences (Q = 635.58, p < 0.0001) confirms strong country-level variation in infection prevalence, highlighting the influence of geographic and ecological factors on *C. complanatum* distribution.

Table 4
Subgroup meta-analysis of *C. complanatum* prevalence by Country

Country	Prevalence (%)	95% CI	τ^2 (Tau-squared)	τ (Tau)	Test for Subgroup Differences
Egypt	44.62	[0.2839–0.6954]	0.5859	76.55%	Q (Between Groups) = 635.58, df = 13, p < 0.0001
Iraq	27.1	[0.0185–0.0395]	--	--	
Japan	16.98	[0.0963–0.4400]	0.764	87.41%	
Turkiye	13.69	[0.0187–0.5851]	4.6666	216.02%	
Brazil	31.49	[0.0089–0.7332]	6.3687	252.36%	
Slovakia	52.59	[0.4663–0.5848]	--	--	
Italy	23.24	[0.1181–0.5158]	0.464	68.12%	
Iran	8.35	[0.0181–0.4790]	2.8585	169.07%	
Croatia	16.05	[0.0955–0.2571]	--	--	
Korea	55.61	[0.3974–0.8426]	0.844	91.87%	
India	65.70	[0.2080–0.7524]	1.5439	124.25%	
Saudi Arabia	55.2	[0.5155–0.5880]	--	--	
France	96.97	[0.8139–0.9957]	--	--	

3.5.3. Analysis stratified by continent and freshwater type

Table 5 shows subgroup analysis demonstrated significant heterogeneity in *C. complanatum* prevalence across both continents and freshwater types. By continent, the highest pooled prevalence was observed in Africa (49%) and Europe (46%), followed by Asia (28%), while South America showed the lowest estimate (14%) with wide confidence intervals and high heterogeneity. The test for subgroup differences confirmed a significant continental effect (Q = 63.73, p < 0.0001). Regarding freshwater type, aquaculture systems exhibited the highest pooled prevalence (45%), whereas stream (34%), rivers (25%) and unstated freshwater types (20%) showed lower estimates. Single-study categories (streams and lakes) yielded moderate prevalence but were not pooled. Overall, freshwater type significantly influenced prevalence patterns (Q = 10.38, p = 0.035), indicating that both geographic region and habitat type contribute to variability in *C. complanatum* occurrence.

Figure 4 shows the global distribution of studies on *Clinostomum complanatum* in freshwater fish, revealing marked geographic heterogeneity in prevalence. Most studies originated from Asia particularly Japan, Korea, India, Iran, Egypt, and Türkiye where infection burdens were generally higher. Prevalence ranged from < 1% in some freshwater systems (Brazil and Türkiye) to > 80–97% in fish markets and localized river systems in India, Korea, and France. Overall, the pooled prevalence indicates a globally distributed but highly uneven infection pattern, influenced by local ecological conditions, host species, and sampling sources.

Table 5
Subgroup analysis of *Clinostomum complanatum* prevalence by continent and freshwater type

Subgroup factor	Category	Pooled proportion (95% CI)	Tau ²	Tau	Test for subgroup differences
Continent	Africa	0.49 (0.28–0.70)	0.59	0.77	Q = 63.73, df = 4, $p < 0.0001$
	Asia	0.28 (0.15–0.45)	2.83	1.68	
	South America	0.14 (0.01–0.73)	6.37	2.52	
	Europe	0.46 (0.15–0.80)	3.01	1.73	
Freshwater type	Not stated	0.20 (0.04–0.61)	5.02	2.24	Q = 10.38, df = 4, $p = 0.035$
	River	0.25 (0.12–0.45)	3.19	1.78	
	Aquaculture	0.45 (0.24–0.68)	1.90	1.38	
	Stream	0.34 (0.28–0.40)	–	–	
	Lake	0.19 (0.13–0.27)	–	–	

3.5.4. Subgroup analysis based on publication year, season and sex

Subgroup analyses indicated no significant effects of publication year, season, or host sex on the pooled prevalence of *C. complanatum*. Prevalence estimates were comparable across publication periods, with slightly higher values reported before 1999 (43%) than during 2000–2013 (18%) and after 2013 (29%); however, subgroup differences were not statistically significant ($Q = 2.11$, $p = 0.347$) (Table 8). Similarly, prevalence remained consistent across seasons, ranging from 43% to 47%, with no evidence of seasonal variation ($Q = 0.10$, $p = 0.992$). Host sex also showed no significant influence, as prevalence in females (36.0%) and males (31.4%) did not differ significantly ($Q = 0.09$, $p = 0.761$) as shown on Fig. 5 (forest plot) and Table 6. Overall, these findings suggest that temporal factors, seasonal variation, and host sex do not substantially contribute to heterogeneity in *C. complanatum* prevalence.

Table 6

Subgroup analysis of *Clinostomum. complanatum* prevalence according to publication year, season, and host sex

Subgroup factor	Category	Pooled proportion (95% CI)	Tau ²	Tau	Test for subgroup differences
Publication year	Before 1999	0.43 (0.21–0.69)	1.72	1.31	Q = 2.11, df = 2, <i>p</i> = 0.347
	2000–2013	0.18 (0.06–0.45)	3.02	1.74	
	After 2013	0.29 (0.15–0.49)	3.38	1.84	
Season	Winter	0.47 (0.26–0.70)	1.77	1.33	Q = 0.10, df = 3, <i>p</i> = 0.992
	Spring	0.43 (0.20–0.70)	2.83	1.68	
	Summer	0.43 (0.21–0.68)	2.11	1.45	
	Autumn	0.47 (0.26–0.69)	1.42	1.19	
Sex	Female	36% (14.2–65.8)	1.89	–	Q = 0.09, df = 1, <i>p</i> = 0.761
	Male	31.4% (20.8–44.4)	0.30	–	

3.6. Parasitic Distribution and Pathological Effect in Fish

As indicated in Table 7, this article explored the distribution and preferred infection sites of *C. complanatum* within different fish body parts. The most commonly affected tissues were the musculature, branchial cavity/gills, and buccal cavity. Pathologically, infected fish frequently exhibited external nodular swellings resulting from the presence of one to two cysts, commonly appearing as yellow grubs. Most of the included studies reported that muscular degeneration and inflammatory cell infiltration particularly involving macrophages and eosinophils were the predominant pathological alterations induced by this parasite.

Table 7
Parasite distribution sites and pathological effects associated with *Clinostomum complanatum*

Parasite infection site(s)	Pathological effects	Reference
Buccal cavity, branchial cavity/gills	NS	[57]
Buccal cavity, muscle	Infiltration of inflammatory cells (macrophages and eosinophils), muscle hyalinization, and degenerative changes in muscle tissue	[40]
Muscle, pharynx, mesentery	NS	[2]
Fins, muscle, inner wall of operculum, gill arches, lips, upper jaw, body cavity, palate	NS	[46]
Dermis and lower muscular tissue	NS	[22]
Under mouth, behind opercula, muscles around gills	Inflammatory cell infiltration with mild hemorrhage in muscle fibers; hyaline degeneration indicative of myositis	[36]
Muscle, buccal cavity, suboperculum, gill cavity, pharynx	NS	[37]
Base of anal fin, base of pectoral fin, between pectoral and pelvic fins, under pectoral fin	NS	[23]
Under skin and in muscle of perch	NS	[55]
Muscle tissues, operculum	Necrotic and fibrotic muscle tissue surrounding the parasite; immune cell infiltration; severe tissue damage and cellular degeneration; excysted metacercariae on operculum	[26]
Buccal cavity, branchial cavity	NS	[9]
Anterior digestive tract, branchial cavity, supraorbital region, hypaxial musculature near paired fins, buccal cavity, pharynx, oesophagus, base of gill arches	Muscle fiber hypercontraction, mucosal epithelial thinning, muscle fiber atrophy with endomysial fibrosis, segmental necrosis, macrophage invasion of damaged fibers	[24]
Buccal cavity, gills, muscle, skin	Inflammatory reaction in host tissue adjacent to cysts	[40]
Under skin, brain	NS	[3]
Muscle, gills, pharynx	NS	[4]
Gills, peritoneal cavity, viscera	NS	[31]
Kidney, muscle, buccal cavity	Heavy immune cell infiltration; necrosis and fibrosis of infected muscle; encysted metacercariae in kidney with inflammation and tissue damage	[58]
Muscle, buccal cavity, kidney	NS	[59]
Near eye, gills, muscle, liver, kidney	Cellular degeneration near eyes and gills; degenerative muscle fibers; degenerative	[28]
Notes: NS = not stated.		

Parasite infection site(s)	Pathological effects	Reference
	changes in liver and kidney; vacuolated cells replacing necrotic muscle cells	
Muscle, gills	NS	[5]
Skin, fins, abdominal cavity, gills, eyes, buccal cavity, skeletal muscle	Degenerative muscle changes around excysted metacercariae; inflammatory cell infiltration including eosinophilic granular cells; fibrotic connective tissue around cysts	[8]
Body surface, fins, abdominal cavity, gills, eyes	NS	[41]
Notes: NS = not stated.		

3.7. Assessment of Study Quality

In this review, the methodological quality of the included studies was independently evaluated by two authors using the Joanna Briggs Institute (JBI) critical appraisal checklist designed for studies reporting prevalence data (Munn et al., 2020). This checklist comprises eight items that assess various aspects of study quality (Table 8). Each study was rated by authors M.A. and M.D. as Yes = 1, No = 0, or Unclear = 0. Any differences in scoring were resolved through discussion, and when necessary, by consultation with two additional authors (MM and AM), after which consensus was achieved.

Studies scoring 7–8 “Yes” responses (> 75%) were deemed high quality, reflecting strong methodological rigor and fulfillment of most checklist items. Those with 5–6 “Yes” responses (50–75%) were considered moderate quality, indicating adequate but improvable methodological standards. Studies receiving four or fewer “Yes” responses (< 50%) were classified as low quality, showing substantial methodological weaknesses and were excluded from further analysis. The final inclusion criterion required a study to achieve a minimum score of 60% to be considered acceptable for analysis.

Table 8
Quality assessment of included studies

Article	Q1	Q2	Q3	Q4	Q5	Q6	Q7	Q8	Total score	Percentage (%)	Quality rating
Salem et al., 2021 [57]	Yes	Yes	Yes	Yes	Yes	No	No	Yes	6	75	Moderate
Abdullah et al., 2023 [2]	Yes	Yes	No	Yes	Unclear	Yes	Yes	Yes	6	75	High
Aghlmandi et al., 2018 [3]	Yes	Yes	Yes	Yes	Yes	No	Yes	Yes	7	87	High
Aohagi et al., 1992 [5]	Yes	Yes	Yes	Yes	No	Yes	Yes	Yes	7	87	High
Aohagi & Shibahara, 1994 [4]	Yes	Yes	Yes	Yes	Yes	No	No	Yes	5	75	Moderate
Aydoğdu & Torcu Koç, 2015 [9]	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	7	80	High
Aydoğdu et al., 2025 [8]	Yes	Yes	Yes	Yes	Yes	No	Yes	No	6	75	Moderate
Dias et al., 2003 [17]	Yes	Yes	Yes	Yes	Unclear	Yes	Yes	Yes	7	87	High
Dias et al., 2006 [16]	Yes	Yes	Yes	Yes	Yes	No	Yes	Yes	7	87	High
Fedorčák et al., 2019 [20]	Yes	Yes	Yes	Yes	Yes	No	Yes	Yes	7	87	High
Gaglio et al., 2016 [22]	Yes	Yes	Yes	No	Unclear	Yes	Yes	Yes	6	75	Moderate
Gholami et al., 2011 [23]	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	8	100	High
Gjurčević et al., 2022 [24]	Yes	Yes	Yes	Yes	Yes	No	Yes	Yes	7	87	High
Jeong et al., 1995	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	7	80	High
Notes: Q1–Q8 corresponds to the following quality assessment criteria: Q1: Appropriate sample frame; Q2: Appropriate sampling method; Q3: Adequate sample size; Q4: Detailed description of subjects and setting; Q5: Sufficient coverage in data analysis; Q6: Valid identification methods; Q7: Standard and reliable measurement; Q8: Appropriate statistical analysis. “Yes” = 1 point; “No” or “Unclear” = 0 points.											

Article	Q1	Q2	Q3	Q4	Q5	Q6	Q7	Q8	Total score	Percentage (%)	Quality rating
[32]											
Jithila et al., 2019 [26]	Yes	Yes	Yes	Yes	Yes	No	No	Yes	5	87	High
Kalantan et al., 1987 [28]	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	7	87	High
Khan et al., 2018 [31]	Yes	Yes	Yes	Yes	Yes	No	No	Yes	6	75	Moderate
Kim & Nagasawa, 1996 [32]	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	8	100	High
Mahdy et al., 2024 [40]	Yes	Yes	Yes	Yes	Yes	No	Yes	Yes	6	75	High
Mahdy et al., 2023 [40]	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	8	100	High
Malek & Mobedi, 2001 [36]	Yes	Yes	Yes	No	Yes	No	Yes	Yes	6	75	Moderate
Maleki et al., 2018 [37]	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	8	100	High
Menconi et al., 2020 [41]	Yes	Yes	Yes	Yes	Unclear	No	Yes	Yes	6	75	Moderate
Özil et al., 2022 [46]	Yes	Yes	Yes	Yes	No	Yes	Yes	Yes	7	87	High
Rochat et al., 2025 [55]	Yes	Yes	Yes	Yes	No	No	Yes	Yes	6	75	High
Shareef et al., 2012 [58]	Yes	Yes	Yes	Yes	Unclear	Yes	Yes	Yes	7	87	High
Sharma & Chaudhary, 2011 [59]	Yes	Yes	Yes	Yes	No	No	Yes	Yes	6	75	High
Silva-Souza &	Yes	Yes	Yes	Yes	Yes	No	Yes	Yes	6	75	High
Notes: Q1–Q8 corresponds to the following quality assessment criteria: Q1: Appropriate sample frame; Q2: Appropriate sampling method; Q3: Adequate sample size; Q4: Detailed description of subjects and setting; Q5: Sufficient coverage in data analysis; Q6: Valid identification methods; Q7: Standard and reliable measurement; Q8: Appropriate statistical analysis. “Yes” = 1 point; “No” or “Unclear” = 0 points.											

Article	Q1	Q2	Q3	Q4	Q5	Q6	Q7	Q8	Total score	Percentage (%)	Quality rating
Ludwig, 2005 [60]											
Şimşek et al., 2018 [61]	Yes	Yes	Yes	Yes	No	No	Yes	Yes	6	75	High
Sohn & Cho, 2019 [62]	Yes	Yes	Yes	Yes	No	Yes	Yes	Yes	7	87	High
Notes: Q1–Q8 corresponds to the following quality assessment criteria: Q1: Appropriate sample frame; Q2: Appropriate sampling method; Q3: Adequate sample size; Q4: Detailed description of subjects and setting; Q5: Sufficient coverage in data analysis; Q6: Valid identification methods; Q7: Standard and reliable measurement; Q8: Appropriate statistical analysis. “Yes” = 1 point; “No” or “Unclear” = 0 points.											

4. DISCUSSION

This systematic review and meta-analysis provides a comprehensive and globally relevant synthesis of the epidemiology, host associations, and pathological effects of *C. complanatum* infection in fish. By integrating evidence from 30 studies spanning multiple countries, freshwater habitats, and host taxa, this work offers one of the most detailed global assessments of *C. complanatum*.

One of the most striking outcomes of this article is the extreme interspecific variability in infection prevalence, ranging from complete absence to near-universal infection within certain host species. Exceptionally high prevalence values were consistently observed in cyprinid fishes such as *Squalidus chankaensis*, *Squalidus japonicus coreanus*, *Acheilognathus rhombea*, and *Microphysogobio yaluensis*, as well as in non-cyprinid taxa including *Perca fluviatilis*. These findings align closely with earlier studies identifying cyprinids as highly competent second intermediate hosts for *C. complanatum* [13, 34].

The high susceptibility of cyprinids can be largely attributed to their ecological traits. Many cyprinid species exhibit benthic or benthopelagic feeding strategies and inhabit shallow, slow-flowing waters where cercariae released from infected snail intermediate hosts are most concentrated. Experimental and field-based studies have demonstrated that cercarial encounter rate is a primary determinant of infection success in digenean trematodes [14, 52]. In addition, cyprinid muscle tissue appears particularly suitable for metacercarial encystment, facilitating parasite survival and trophic transmission to piscivorous bird definitive hosts.

In contrast, several species such as *Hypomesus transpacificus*, *Salangichthys microdon*, *Cobitis biwae*, and *Silurus asotus* consistently exhibited zero prevalence across studies. Rather than reflecting inherent resistance, this pattern likely results from ecological separation and reduced exposure to infective stages. Pelagic or fast-swimming species may experience limited contact with substrate-associated cercariae, while habitat specialists may rarely overlap spatially or temporally with infected snail populations [52, 38]. Seasonal sampling bias and fine-scale spatial heterogeneity in snail distribution may further obscure true infection risk in these taxa.

Importantly, the coexistence of highly infected and uninfected species within the same geographic regions, particularly in East Asia, strongly supports the conclusion that host ecology and behavior exert greater influence

on infection risk than geography alone. This observation is consistent with ecological parasitology frameworks emphasizing host–parasite–environment interactions as the dominant drivers of transmission dynamics [39, 51].

At higher taxonomic levels, marked variation in prevalence was evident among genera and families. Genera such as *Perca*, *Microphysogobio*, *Nycticorax*, and *Ardea* were strongly associated with infection, whereas *Gnathopogon*, *Hypomesus*, *Leuciscus*, and *Silurus* consistently lacked detectable metacercariae. Similarly, families including Percidae, Gobiidae, and Acanthidae exhibited high prevalence, while Salangidae and Siluridae showed no evidence of infection despite moderate to large sample sizes.

These patterns indicate that host compatibility with *C. complanatum* is governed primarily by ecological niche, trophic interactions, and exposure pathways rather than strict phylogenetic relatedness. Comparable conclusions have been drawn in broader comparative studies of digenean trematodes, which demonstrate that transmission success is more closely linked to ecological overlap with intermediate and definitive hosts than to host taxonomy per se [56, 42].

The meta-analysis revealed pronounced geographic heterogeneity in *C. complanatum* prevalence, with the highest pooled estimates observed in Africa and Europe, followed by Asia, and substantially lower values in South America. These findings are consistent with global patterns of trematode transmission, which are strongly influenced by climatic conditions, freshwater productivity, snail host diversity, and migratory routes of piscivorous birds [39, 27].

Warm, nutrient-rich freshwater ecosystems common in parts of Africa and Europe support dense snail populations and attract large numbers of definitive avian hosts, thereby facilitating parasite persistence and amplification. In contrast, the lower prevalence estimates reported from South America are likely influenced by limited sampling coverage rather than true absence, as underrepresentation of certain geographic regions remains a well-recognized limitation in global parasitological syntheses [50].

Extremely high heterogeneity observed across studies ($I^2 = 99\%$) is characteristic of ecological meta-analyses and reflects genuine biological and environmental variation rather than analytical shortcomings [25, 53]. This underscores the importance of cautious interpretation of pooled prevalence values and validates the use of random-effects models in parasite epidemiology.

Freshwater habitat type emerged as a major moderator of infection prevalence, with aquaculture systems exhibiting the highest pooled prevalence of *C. complanatum*. This finding is consistent with numerous studies demonstrating that aquaculture environments create ideal conditions for parasite transmission due to high host density, organic enrichment, reduced water exchange, and proliferation of snail intermediate hosts [48, 19].

Moreover, aquaculture ponds frequently attract piscivorous birds, which act as definitive hosts and contribute to sustained environmental contamination with parasite eggs. In contrast, natural freshwater systems generally exhibit greater ecological complexity and biodiversity, resulting in dilution effects that can reduce transmission efficiency [27]. These results highlight aquaculture systems as key hotspots for *C. complanatum* transmission and emphasize the need for targeted parasite management strategies in cultured fish production.

Substantial variation in infection intensity was observed across studies, with the highest mean intensities reported in aquaculture systems, particularly in East Asia. High parasite burdens have been repeatedly linked to increased tissue damage, impaired growth, and elevated mortality risk, especially under stressful environmental or husbandry conditions [28, 24].

Consistent with previous histopathological investigations, this review confirms that the musculature, branchial cavity, and buccal cavity are the principal predilection sites for *C. complanatum* metacercariae. Muscle tissue was the most frequently affected site, likely because it provides a stable, nutrient-rich, and relatively immune-privileged environment for encysted larvae [15]. Localization within edible muscle tissue not only enhances trophic transmission but also increases zoonotic risk and contributes directly to economic losses through market rejection of visibly infected fish [13, 56].

Histopathological changes including muscle fiber degeneration, necrosis, granuloma formation, and inflammatory cell infiltration were consistently reported and are known to compromise fish mobility, respiration, and feeding efficiency [43, 37].

A major limitation identified in this review is the continued reliance on morphological identification, with fewer than one-third of studies incorporating molecular confirmation. Given the existence of closely related clinostomid species, molecular characterization using ITS rDNA and mitochondrial COI markers is essential for accurate species delineation and for resolving cryptic diversity [8, 2]. Limited molecular application likely contributes to misidentification, underestimation of prevalence, and incomplete understanding of transmission pathways.

Additionally, inconsistent reporting of host sex, seasonality, and ecological variables limits the ability to assess their contributions to infection dynamics. Although subgroup analyses did not detect significant effects of these factors at the global scale, their importance at local or regional levels should not be discounted.

Overall, the findings support the conclusion that *C. complanatum* infection can impair fish health and substantially reduce commercial value, particularly in aquaculture systems. However, its impact on freshwater fisheries is highly context-dependent and strongly influenced by anthropogenic pressures such as habitat modification, pollution, and aquaculture intensification. As previously emphasized, parasite impacts are rarely uniform across systems and should be interpreted within their ecological and management contexts [34].

5. CONCLUSION AND RECOMMENDATIONS

This study demonstrates that *C. complanatum* is a widely distributed fish-borne trematode with a substantial and highly heterogeneous global infection burden. Prevalence varied markedly among freshwater fish species, reaching 100% in *S. chankaensis* while remaining undetected in several taxa, and the pooled global prevalence was 28.7%. Significant variation by fish family, geographic region, and habitat type highlights the strong influence of ecological conditions and management practices on transmission dynamics. Higher prevalence in aquaculture systems, together with the frequent encystment of metacercariae in muscle, buccal, and branchial tissues causing yellow-grub lesions, underscores the parasite's impact on fish health, marketability, and zoonotic risk. To improve epidemiological accuracy and risk assessment, routine incorporation of molecular diagnostics particularly ITS-based sequencing alongside standardized study designs is strongly recommended. Control efforts should prioritize aquaculture systems through integrated parasite management, including snail

control, improved pond hygiene, optimized stocking densities, and non-lethal management of piscivorous birds. In parallel, public health education on safe fish consumption is essential to reduce economic losses and zoonotic transmission.

Declarations

Ethical consideration

Not applicable

Consent for publication

All authors (Mengesha Ayehu, Melkie Dagnaw, Asnakew Mulaw, Wilmien Luus Powell, Moges Maru, Tameru Gedefaw, Zenebe Jemere, Zewdu Seyoum), have given consent for the publication of this paper

Competing interests

We declare that no conflict of interest.

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Author Contribution

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Data Availability

All authors are ready to give the available data to the readers by requesting via email and any communication platform.

References

1. Abdallah KFM, Eissa SIAM. Ultrastructure of *Clinostomum* metacercariae in fish. Parasitol Res. 2021;120:3101–10.

2. Abdullah KFM, Eissa IAM. *Clinostomum complanatum* and *Clinostomum phalacrocoracis* in *Oreochromis niloticus*: morphological and molecular characterization. Egypt J Aquat Biol Fish. 2023;25(2):1–18.
3. Aghlmandi MR, Zeinalzadeh R, Tavakoli M. Prevalence and intensity of *Clinostomum complanatum* metacercariae in freshwater fish from Iran. J Parasit Dis. 2018;42(3):367–73.
4. Ahdogi Y, Shibahara T. Studies on trematode metacercariae of freshwater fishes in Japan. Jpn J Parasitol. 1994;43(1):17–26.
5. Ahdogi Y, Yoshihara S, Ogawa K, et al. Distribution and prevalence of *Clinostomum complanatum* metacercariae in freshwater fish of Japan. Jpn J Parasitol. 1992;41(6):451–8.
6. Aksit D, Simsek E, Aydogdu A. *Clinostomum complanatum* infections in freshwater ecosystems. Acta Parasitol. 2023;68:101–10.
7. Aktop A, Innal D, Ozil A. Distribution of metacercarial infections in freshwater fish. Turk J Vet Anim Sci. 2021;45:512–20.
8. Aydogdu A, Simsek E, Innal D. Molecular identification of *Clinostomum complanatum* using ITS and mt-COI. Parasitol Int. 2025;98:102801.
9. Aydogdu A, Torcu Koç H. Prevalence of *Clinostomum complanatum* metacercariae in fish from Turkey. Turk J Zool. 2015;39:865–74.
10. Barber I, Hoare D, Krause J. Effects of parasites on fish behaviour. Adv Study Behav. 2016;48:1–68.
11. Barendregt JJ, Doi SA, Lee YY, Norman RE, Vos T. Meta-analysis of prevalence. J Epidemiol Community Health. 2013;67(11):974–8.
12. Bush AO, Lafferty KD, Lotz JM, Shostak AW. Parasitology meets ecology on its own terms: Margolis et al. revisited. J Parasitol. 1997;83(4):575–83.
13. Chai JY, Lee SH. Fish-borne zoonotic heterophyid infections: heterophyidiasis. In: Sohn WM, editor. Foodborne parasitic zoonoses: fish and plant-borne parasites. Springer; 2002. pp. 157–74.
14. Combes C, Gabrion C, Theron A. Relationship between transmission success and cercarial behavior in trematodes. Parasitol Today. 2002;18(3):91–3.
15. Cribb TH, Bray RA, Barker SC, Cribb BW. Metacercarial site specificity in the trematode *Clinostomum complanatum*. Int J Parasitol. 2002;32(11):1373–7.
16. Dias GB, de Souza MA, Silva RM. Pathological alterations induced by *Clinostomum complanatum* metacercariae in freshwater fish. Braz J Biol. 2006;66(4):1119–23.
17. Dias GB, Lopes NP, Silva SS. Occurrence of *Clinostomum complanatum* in Brazilian rivers. Parasitol Res. 2003;89(5):382–6.
18. Eissa IAM, Abdallah KFM. Morphological and molecular characterization of *Clinostomum complanatum*. Egypt J Aquat Biol Fish. 2021;25:1–18.
19. Elsheikha HM, Khan RA. Trematode infections in aquaculture systems. Aquaculture. 2011;318(3–4):274–83.
20. Fedorčák J, Špakulová M, Hruzová Z. Metacercariae of *Clinostomum complanatum* in freshwater fish from Slovakia: prevalence and intensity. Acta Parasitol. 2019;64(2):401–6.
21. Food and Agriculture Organization of the United Nations. The state of world fisheries and aquaculture. Rome: FAO; 2020.

22. Gaglio G, Brianti E, Giannetto S. Morphological features of *Clinostomum complanatum* metacercariae. Parasitol Res. 2016;115:3585–92.
23. Gholami Z, Kazemi B, Ahmadzadeh N. Prevalence of *Clinostomum complanatum* in fishes from Iranian rivers. J Helminthol. 2011;85(3):315–20.
24. Gjurčević E, Bradarić I, Šolić I, Kusak J. Prevalence and intensity of *Clinostomum complanatum* in fish from Croatian rivers. Acta Parasitol. 2022;67(1):45–53.
25. Higgins JP, Thompson SG. Quantifying heterogeneity in a meta-analysis. Stat Med. 2002;21(11):1539–58.
26. Jithila PB, Krishnan LK, Kumari B. Prevalence of *Clinostomum complanatum* in freshwater fish in India. Int J Zool Res. 2019;15(2):67–74.
27. Johnson PTJ, De Roode JC, Fenton A. Why infectious disease research needs community ecology. Science. 2015;349(6252):1259504.
28. Kalantan N, Kamel B, Abu-Samra M. Histopathological effects of *Clinostomum complanatum* metacercariae in fish muscles from Saudi Arabia. J Egypt Soc Parasitol. 1987;17(3):833–42.
29. Kanev I, Radev V, Fried B, Family Clinostomidae, Lühe. 1901. In: Gibson DI, Jones A, Bray RA, editors. Keys to the Trematoda. Vol 1. Wallingford: CAB International; 2002. pp. 113–120.
30. Khan MK, Saifullah MK. Prevalence of *Clinostomum complanatum* in freshwater fish. Pakistan J Zool. 2017;49:123–30.
31. Khan RA, Iqbal S, Telford SR. Prevalence of trematodes in fish from Pakistan: pathological and epidemiological aspects. J Fish Biol. 2018;92(5):1286–97.
32. Kim KC, Nagasawa K. Studies on *Clinostomum complanatum* metacercariae in Korea. J Parasitol. 1996;82(3):375–81.
33. Lafferty KD, Allesina S, Arim M, et al. Parasites in food webs: the ultimate missing links. Ecol Lett. 2008;11:533–46.
34. Lafferty KD, Kuris AM. How environmental stress affects parasites. Limnol Oceanogr. 1999;44:925–31.
35. Li Y, Wang G, Nie P. Pathological effects of *Clinostomum complanatum* metacercariae in fish. Fish Shellfish Immunol. 2018;72:201–8.
36. Malek M, Mobedi I. Occurrence and pathology of *Clinostomum complanatum* in freshwater fish. J Helminthol. 2001;75:201–6.
37. Maleki A, Makki M, Danesh M. Prevalence and histopathological study of *Clinostomum complanatum* metacercariae in Iranian fish species. J Fish Dis. 2018;41(4):609–16.
38. Marcogliese DJ. Parasite diversity and environmental degradation: a meta-analysis. Int J Parasitol. 2016;46(9):593–602.
39. Marcogliese DJ. Parasites: small players with crucial roles in the ecological theater. EcoHealth. 2005;2(2):151–64.
40. Menconi V, Bertolini S, Gaglio G. Life cycle and pathology of *Clinostomum complanatum*. Parasitol Res. 2023;122:987–98.
41. Menconi V, Gaglio G, Bertolini S. Infection patterns of *Clinostomum complanatum* in Italian lakes. Parasitol Res. 2020;119(3):823–30.

42. Morand S, Krasnov BR, Poulin R. Micromammals and their parasites: is host specificity linked to parasite speciation? *Evol Ecol.* 2015;29(1):41–62.
43. Moravec F. Metazoan parasites of fishes: their development and transmission. 2nd ed. Dordrecht: Springer; 2009.
44. Munn Z, Moola S, Lisy K, Riitano D, Tufanaru C. Methodological guidance for systematic reviews of observational epidemiological studies reporting prevalence and incidence data. *Int J Evid Based Healthc.* 2020;13(3):147–53.
45. Nyaga VN, Arbyn M, Aerts M. Metaprop: a Stata command to perform meta-analysis of binomial data. *Arch Public Health.* 2014;72(1):39.
46. Özil A, Aktop A, Innal D. Helminth parasites of freshwater fish and their ecological significance. *Turk J Zool.* 2022;46:321–33.
47. Page MJ, McKenzie JE, Bossuyt PM, et al. The PRISMA 2020 statement: an updated guideline for reporting systematic reviews. *BMJ.* 2021;372:n71.
48. Paperna I. Parasites, infections and diseases of fish in Africa: an update. CIFA Technical Paper No. 31. Rome: FAO; 1996.
49. Park CW, Kim JS, Joo KH. Human infection with *Clinostomum complanatum*: a case report. *Korean J Parasitol.* 2009;47:401–4.
50. Poulin R, Leung TLF. Taxonomic patterns in parasite diversity: an overview. *Int J Parasitol Parasites Wildl.* 2011;1(1):1–8.
51. Poulin R, Mouritsen KN. The dynamics of parasite transmission: host behavior and environmental heterogeneity. *Parasitology.* 2006;132(4):563–74.
52. Poulin R. Evolutionary ecology of parasites. 2nd ed. Princeton: Princeton University Press; 2014.
53. Poulin R. The evolution of life histories of parasitic trematodes: a plea for the importance of ecological and behavioral factors. *Parasitol Today.* 1996;12(6):198–202.
54. Rizvi AN, Afsar N, Khan A. Seasonal prevalence of *Clinostomum complanatum* in freshwater fish. *J Parasit Dis.* 2020;44:456–62.
55. Rochat E, Gaglio G, Brianti E. Emerging patterns of *Clinostomum* infections in freshwater fish. *Parasites Vectors.* 2025;18:45.
56. Rohde K. Ecology and biogeography of marine parasites. *Adv Mar Biol.* 2005;48:1–84.
57. Salem MM, Mahmoud MS, Abdel-Baki AS. Occurrence of *Clinostomum complanatum* in freshwater fish: prevalence and morphological characterization. *J Parasit Dis.* 2021;45(3):422–8.
58. Shareef MA, Al-Mashhadani MA, Jabbar M. Molecular detection of *Clinostomum complanatum* in Indian fish. *J Fish Dis.* 2012;35(10):785–92.
59. Sharma R, Chaudhary R. Prevalence and pathological effects of *Clinostomum complanatum* in freshwater fish. *Int J Fish Aquat Stud.* 2011;1(3):123–9.
60. Silva-Souza AG, Ludwig A. Low prevalence of *Clinostomum complanatum* in Brazil. *Rev Bras Parasitol Vet.* 2005;14(1):28–32.
61. Simsek E, Innal D, Aydogdu A. Prevalence and pathology of *Clinostomum complanatum* in freshwater fish. *Parasitol Res.* 2018;117:2157–64.

62. Sohn WM, Cho SH. Prevalence of *Clinostomum complanatum* in Korean river fish. Korean J Parasitol. 2019;57(5):507–13.
63. Ukoli FMA. On the biology of *Clinostomum complanatum*. J Helminthol. 1966;40:129–44.
64. Wang GX, Nie P, Li Y. Histopathological effects of *Clinostomum* metacercariae in fish. Vet Parasitol. 2017;238:50–7.

Figures

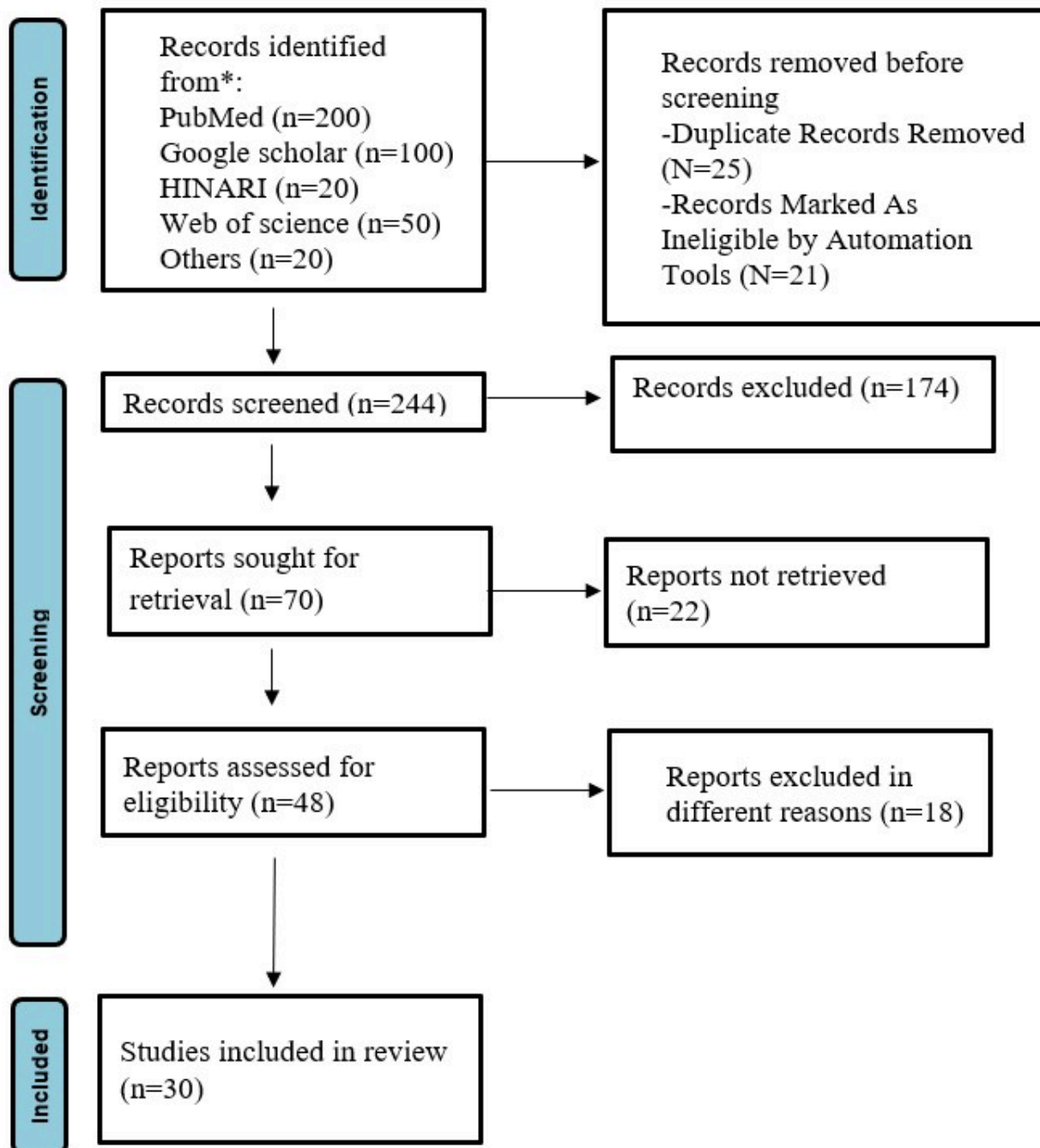


Figure 1

PRISMA flow diagram illustrating the selection process of included and excluded studies [47].

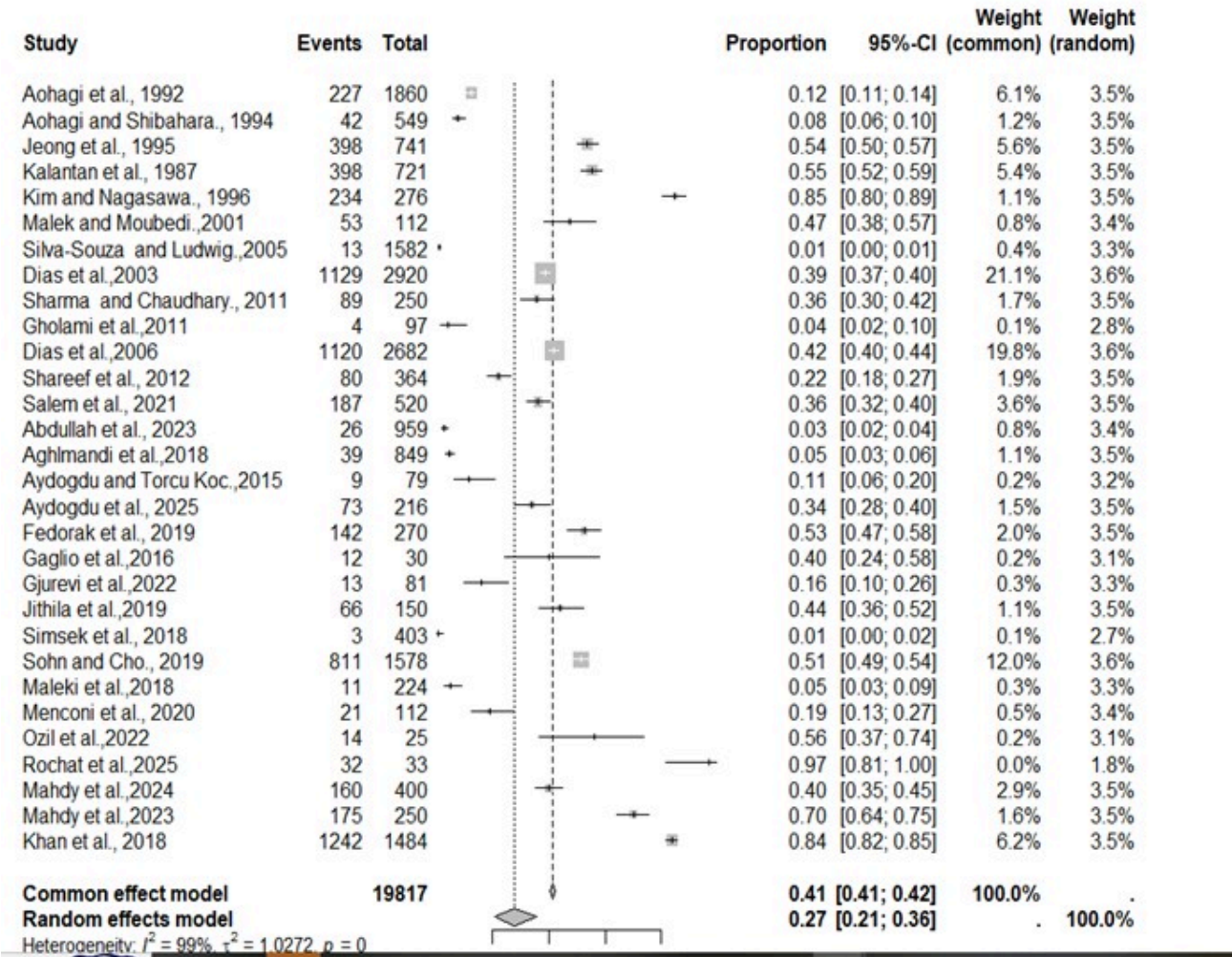


Figure 2
Forest plot for the prevalence of *C. complanatum* among Fish

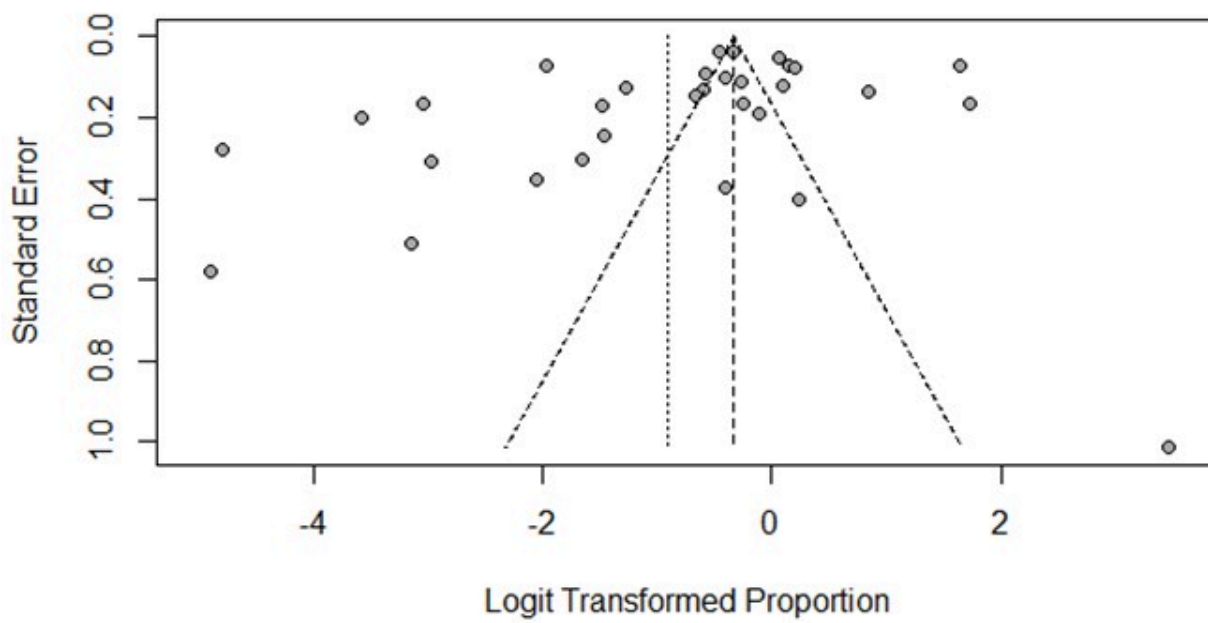


Figure 3

Funnel plot with pseudo 95% confidence limits of pooled prevalence of *Clinostomum complanatum* in freshwater fish globally

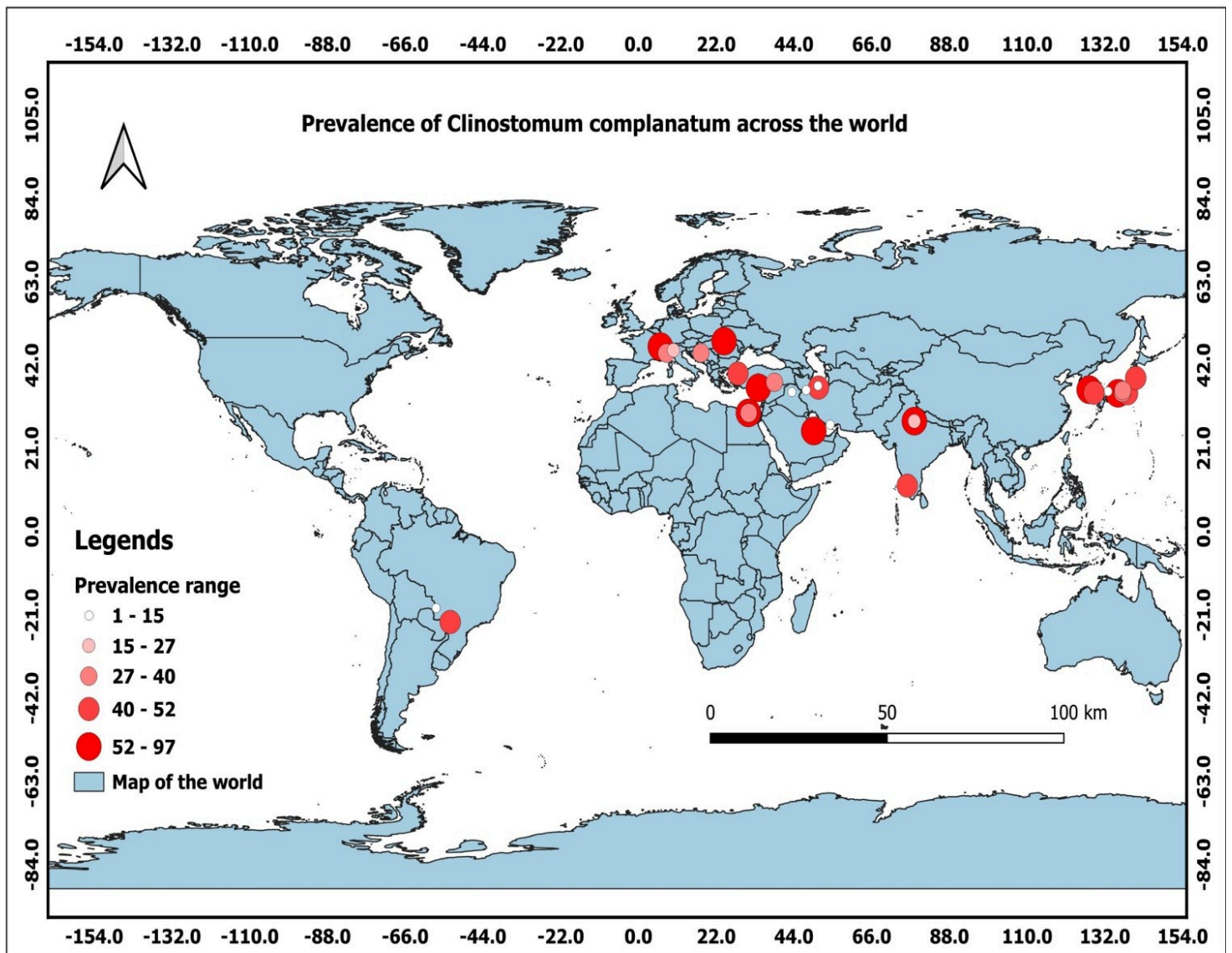


Figure 4

Distribution of studies and pooled prevalence of *C. complanatum*

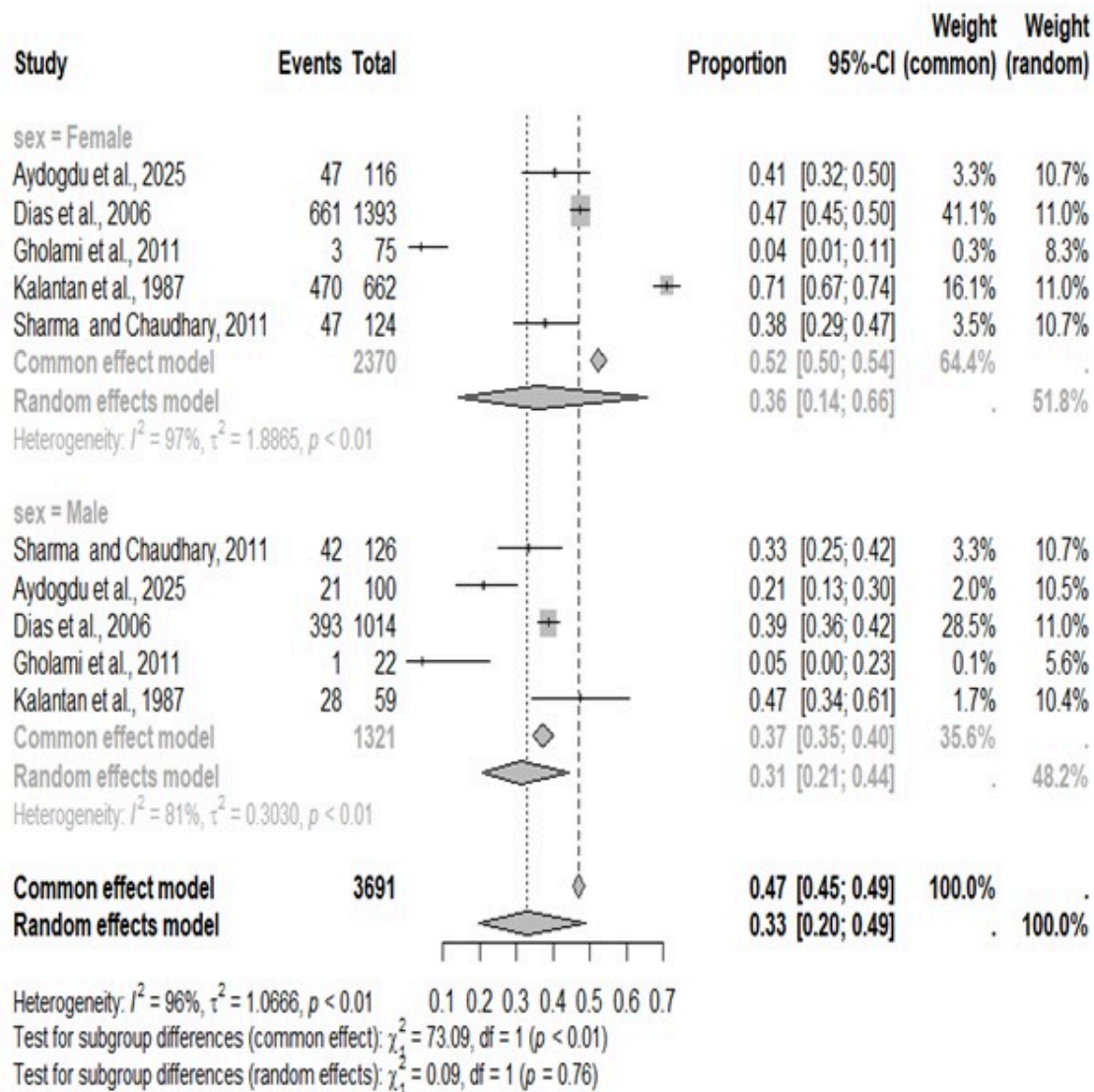


Figure 5

Forest plot for the prevalence of *C. complanatum* among fish sex