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Diversity, host association, and community structure of helminth parasites in six freshwater fish species of Dhar district, Madhya Pradesh, India

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Abstract
The helminths of freshwater fishes are a genuine part of aquatic biodiversity, yet for much of central India we still know very little about which parasites occur in which hosts, or how these assemblages are put together. The present study was undertaken to address this gap for Dhar district, Madhya Pradesh. We examined the diversity, host associations, abundance, and pooled community structure of helminth parasites in six freshwater fish species drawn from two water bodies, Munj Talab and Jeerabad Dam. Fishes were collected between November 2023 and October 2025. Of the 680 fishes obtained, 540 were found suitable and were taken up for detailed parasitological examination. Helminths were recovered by external and internal examination, then preserved, stained, mounted, and identified on the basis of morphological characters. In all, 336 fishes carried infection, giving an overall prevalence of 62.22%. A total of 968 helminth individuals were recovered, representing nine genus-level taxa, three trematodes, two cestodes, three nematodes, and one acanthocephalan. Numerically, nematodes led the assemblage (330 individuals; 34.09%), followed by trematodes (303; 31.30%), cestodes (245; 25.31%), and acanthocephalans (90; 9.30%). *Camallanus* sp. was the single most abundant taxon (148; 15.29%), whereas *Clinostomum* sp. was the least abundant (80; 8.26%). Among the hosts, *Channa striata* and *Channa punctata* each yielded six recorded taxa, while *Cirrhinus mrigala* yielded only one. Infection status differed significantly across the six host species ($\chi^2 = 39.706$, df = 5, $p < 0.001$; Cramér's V = 0.271). For the pooled assemblage, the Shannon diversity index was 2.177, Simpson dominance 0.116, Simpson diversity 0.884, and Pielou's evenness 0.991. Taken together, these values describe a diverse and remarkably even helminth assemblage, in which the predatory snakeheads carried broader host associations than the cyprinids examined alongside them. The study offers baseline information that should prove useful for fish-parasite biodiversity assessment and for the monitoring of freshwater fish health in Dhar district.

Keywords: Fish parasitology, helminth assemblage, host–parasite association, parasite richness, community diversity, snakehead fishes, Dhar District

Introduction

Freshwater ecosystems occupy only a small fraction of the earth's surface, and yet they hold a disproportionately large share of its biological diversity. They also do a great deal of work on our behalf, supplying food and water, sustaining livelihoods, and providing a range of ecological services. All of this comes under steady pressure from habitat alteration, pollution, biological invasions, altered flow regimes, and the shifts that accompany a changing climate (Dudgeon *et al*., 2006; Reid *et al*., 2019) [9, 33]. Fishes sit at the centre of these systems, linking trophic levels and underpinning inland fisheries. Their parasites form a second, quieter layer of freshwater biodiversity, one that is easy to overlook but no less real.

It is worth stating plainly that parasites are not merely agents of disease. They take part in food-web processes, exert influence on host populations, and add a substantial amount of biological diversity to aquatic systems. Whether a parasite is transmitted at all depends on a host's diet, its use of habitat, its movements, its age and body size, and on whether the necessary intermediate or paratenic hosts happen to be present (Lafferty *et al*., 2008; Marcogliese, 2002; Poulin & Morand, 2000) [13, 20, 29]. Helminths with complex life cycles are especially telling in this respect, because their transmission hinges on ecological contact among several organisms. Their presence can therefore point to trophic links that a conventional fish survey would miss entirely (Marcogliese, 2005) [21].

Freshwater fishes tend to carry helminths from four main groups: the trematodes, cestodes, nematodes, and acanthocephalans. Each has gone its own way. They are built differently, they hold on to the host by different means, they settle in different places inside it, and they get from one host to the next by different routes. Trematodes and cestodes usually need one or more intermediate hosts to complete the journey. Many fish nematodes make the trip through aquatic invertebrates or smaller vertebrates. Acanthocephalans grip the intestinal wall with a hooked proboscis and are usually taken up through crustacean intermediate hosts (Anderson, 2000 [3]; Amin *et al*., 2021). It is this very divergence that lets several helminth taxa live in one fish community side by side, without any one crowding out the rest.

Of everything that shapes a parasite assemblage, none counts for more than the identity of the host. A fish that lives in a different place, or eats different things, meets a different set of infective stages. Predators are the clearest case. Because their prey can run from insects and molluscs to crustaceans, amphibian larvae, and smaller fishes, they end up gathering a wider spread of trophically transmitted

parasites. This is why comparative studies have linked parasite richness to a host's body size, its trophic position, how varied its diet is, how much habitat it ranges over, and, not least, how hard anyone looked for the parasites in the first place (Bell & Burt, 1991; Luque *et al*., 2004; Luque & Poulin, 2008; Price & Clancy, 1983) [4, 14, 17, 30]. None of this holds as a rule, though. What hosts happen to be around locally, and the conditions of the moment, can push the pattern one way or the other.

To describe a parasite community, researchers reach for a small set of measures that complement one another. Taxon richness is the plain count of how many taxa turn up. Abundance is how many individuals were found, and relative abundance is each taxon's slice of the total. Diversity indices take this a step further, rolling richness and how the individuals are distributed into one number. Shannon's index climbs as both richness and evenness increase; Simpson dominance picks up on how far a handful of common taxa run the show; and Pielou's index asks a narrower question, namely how evenly the individuals are shared out among the taxa on record (Magurran, 2004; Pielou, 1966; Simpson, 1949) [18, 24, 36]. No single figure means much on its own. Each has to be weighed against how the sampling was done and how finely the parasites could be told apart (Poulin, 2019; Walther *et al*., 1995) [27, 39].

Freshwater fish helminths have been recorded from various parts of India, but the map still has plenty of gaps. A checklist from Meghalaya brought to light a good deal of helminth richness among the fishes of the north-east, and taxonomic and molecular work keeps turning up diversity that remains unsettled among Indian fish parasites (Jyrwa *et al*., 2016; Rana & Kaur, 2021) [12, 32]. Regional inventories earn their place precisely here: they are the raw evidence that later taxonomic, ecological, and conservation work has to stand on. And they count for even more where parasites have shown up only as odd, scattered host records.

Dhar district contains a mix of urban lakes, rural reservoirs, seasonal streams, and fishery resources, but the helminth fauna of its freshwater fishes has never been described in any systematic, community-level way. Against this background, the present study examined six common freshwater fish species from Munj Talab and Jeerabad Dam. Our aims were to document the genus-level helminth taxa, to set out their recorded host associations, to compare taxon richness among the fish species, to quantify abundance at the level of both taxon and group, and to describe the pooled helminth community using standard diversity indices. Going in, we expected the predatory *Channa* species to carry broader helminth associations than the cyprinids, simply because they are exposed to a wider range of animal prey.

Materials and Methods

1. Study design and study area

This was a field-based, observational study carried out from November 2023 to October 2025 in two freshwater habitats of Dhar district, Madhya Pradesh, India. The first, Munj Talab, also known as Munj Sagar, is an urban to semi-urban lentic water body lying at roughly 22.601° N and 75.302° E. It takes in seasonal runoff and holds water through most of the year. The second, Jeerabad Dam, is a rural freshwater reservoir at approximately 22.318° N and 75.026° E; it is bordered largely by agricultural land and natural vegetation, and its water level rises and falls with the seasons.

The two sites were chosen because they support local fisheries, hold the commonly available cyprinid and channid fishes, and between them represent two rather different freshwater settings within the district. We did not measure water quality, the density of intermediate hosts, or the degree of habitat disturbance in any quantitative way. For that reason, the sites are best regarded as sampling locations rather than as experimentally controlled environmental categories.

2. Fish collection and host composition

Fishes were caught using nets and traps suited to each site, with the help of the fishers who work these waters. Every specimen was labelled by site and by collection period, then brought back for examination. The catch came to 680 fishes in all. Those that were damaged, immature, poorly preserved, or otherwise not fit for study were set aside, and this left 540 fishes for close parasitological work. The final sample worked out to 90 individuals each of Labeo rohita, Catla catla, Cirrhinus mrigala, Labeo calbasu, Channa striata, and Channa punctata. Identification of the fishes themselves followed standard regional taxonomic references (Talwar & Jhingran, 1991) [38].

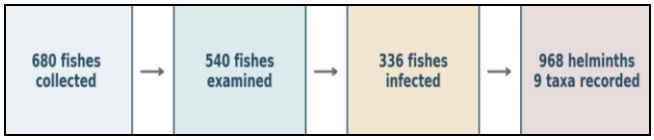

Fig 1: Study workflow showing fish collection, selection, infection records, and helminth recovery. The figure summarises the complete dataset used in the present article.

3. Parasitological examination

Each fish was examined externally first, for any visible parasite, lesion, or unusual structure. Nothing was skipped over: the body surface, the fins, the mouth, the opercular region, and the gills were all checked. The fish was then dissected, and the body cavity, gastrointestinal tract, liver, musculature, and other relevant tissues were gone through one by one. The intestinal tract was slit open along its whole length and its contents examined in saline. Helminths, once found, were teased out gently with fine forceps, needles, or pipettes; each was counted and set down on record, along with the host it came from and the main site of infection.

How a parasite was washed and preserved depended on which group it belonged to. Trematodes and cestodes were flattened where that was needed, then fixed, stained, dehydrated, cleared, and mounted for study under the microscope. Nematodes were fixed and cleared so that the buccal capsule, oesophagus, reproductive structures, tail, and cuticle came into view. Acanthocephalans were processed to expose the proboscis, the hooks, the trunk spines, and the reproductive structures. Throughout, collection and preservation followed established parasitological procedure (Pritchard & Kruse, 1982) [31].

4. Morphological identification and taxonomic resolution

Identification rested on morphological comparison. We drew on body form, on the structures used for attachment, on digestive and reproductive characters, on scolex morphology, on the make-up of the buccal capsule, on the armature of the proboscis, and on where in the host the

parasite had settled. Standard helminth references and taxonomic works were consulted throughout, among them Yamaguti (1958, 1959), Soota (1983), and Moravec (2010) [23, 37, 41, 42]. We chose to stop at the genus level on purpose: molecular confirmation and a full set of species-level diagnostic measurements were not to be had for every form we recovered. Everything reported here as a diversity measure therefore refers to helminth taxa, not to confirmed species.

5. Community descriptors and statistical analysis

Prevalence, mean intensity, and mean abundance were calculated according to the definitions of Bush *et al*. (1997) [6]. Prevalence is the percentage of examined fishes found to be infected. Mean intensity is the number of helminths recovered divided by the number of infected fishes, while mean abundance is the number recovered divided by the total number of fishes examined.

A binary host–parasite association matrix was assembled from the recorded occurrence of each helminth taxon in each host species, with a recorded association coded as 1 and an unrecorded one as 0. Host-level taxon richness was then taken as the number of helminth taxa recorded in each fish species. The network that follows from this is, by construction, a presence–absence network; it says nothing about the abundance of any given parasite taxon within a given host.

For the pooled assemblage, relative abundance was calculated as, $n_i/N \times 100$ where n_i is the number of individuals of taxon i and N the total number of helminths recovered. Shannon diversity was calculated as $H' = -\Sigma p_i ln(p_i)$ Simpson dominance as $D = \Sigma p_i^2$, Simpson diversity as $1 - D$, , and Pielou's evenness as $J' = H'/ln(S)$, where p_i is the proportional abundance of taxon *i* and *S* the pooled taxon richness. Natural logarithms were used throughout. These indices describe the pooled recovered assemblage; we have not treated them as direct measures of water quality or of ecosystem stability.

Whether infection status differed among the six-host species was tested with a Pearson chi-square applied to the counts of infected and uninfected fishes, and the effect size was expressed as Cramér's V. Statistical significance was set at $p < 0.05$. The final 6 × 2 table gave $\chi^2 = 39.706$ with 5 degrees of freedom, $p = 1.71 \times 10^{-7}$, and Cramér's V = 0.271.

Results

1. Fish examination and overall infection

Of the 540 fishes examined, 336 were infected and 204 were not, which places overall prevalence at 62.22%. Altogether 968 helminth individuals were recovered. Mean intensity worked out to 2.88 helminths per infected fish and mean abundance to 1.79 helminths per fish examined. Infection status differed significantly among the six-host species ($\chi^2 = 39.706$, df = 5, $p < 0.001$), with a Cramér's V of 0.271, which points to a moderate host-related association.

Table 1: Host composition, infection characteristics, parasite recovery, and recorded taxon richness.

Fish species	Family	Examined	Infected	Prevalence (%)	Helminths recovered	Mean intensity	Taxon richness
Labeo rohita	Cyprinidae	90	48	53.33	118	2.46	2
Catla catla	Cyprinidae	90	54	60.00	138	2.56	2
Cirrhinus mrigala	Cyprinidae	90	36	40.00	81	2.25	1
Labeo calbasu	Cyprinidae	90	60	66.67	165	2.75	2
Channa striata	Channidae	90	66	73.33	212	3.21	6
Channa punctata	Channidae	90	72	80.00	254	3.53	6
Total	-	540	336	62.22	968	2.88	9 pooled

2. Helminth taxonomic composition

Nine genus-level helminth taxa, belonging to four major groups, were recorded. Trematoda and Nematoda contributed three taxa apiece, each accounting for 33.33% of the pooled taxon richness; Cestoda contributed two taxa (22.22%), and Acanthocephala a single taxon (11.11%). The picture shifts when one counts individuals rather than taxa. Here Nematoda came out ahead with 330 helminths (34.09%), followed by Trematoda with 303 (31.30%), Cestoda with 245 (25.31%), and Acanthocephala with 90 (9.30%).

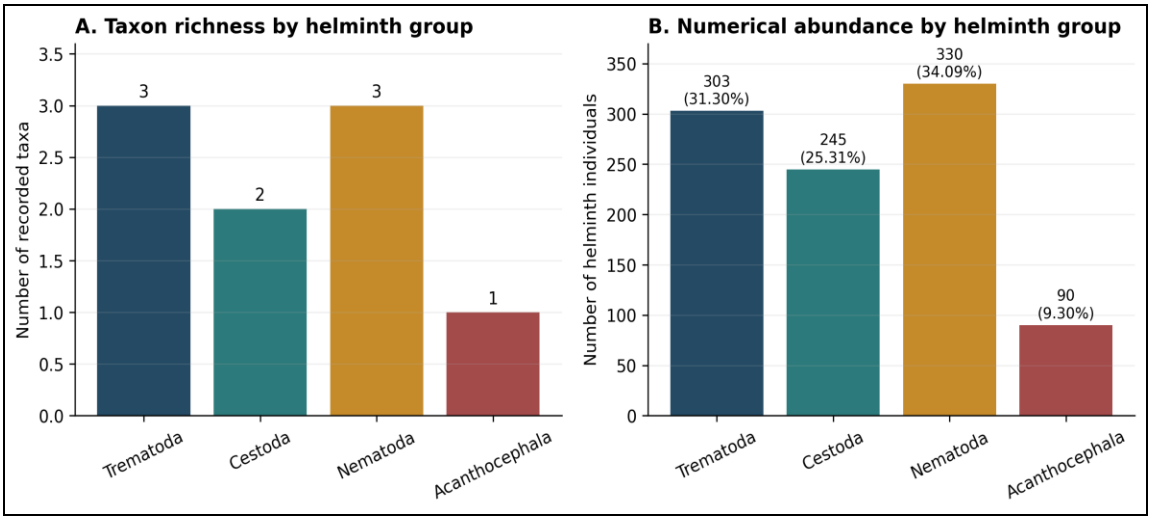

Fig 2: Composition of the pooled helminth assemblage. (A) Number of recorded taxa in each helminth group. (B) Number and percentage of helminth individuals recovered from each group.

3. Recorded host associations and host-level richness

The helminth taxa were far from evenly spread across the six hosts. *Bothriocephalus* sp. turned up in three cyprinid hosts, while a cluster of taxa was shared between the two *Channa* species. *Channa striata* and *C. punctata* each carried six recorded taxa. *Labeo rohita*, *C. catla*, and *L. calbasu* each carried two, and *C. mrigala* just one. It should be stressed that the matrix records observed occurrence only, and must not be read as a statement of complete host specificity.

Table 2: Presence–absence matrix of recorded associations between fish hosts and helminth taxa.

Helminth taxon	*L. rohita*	*C. catla*	*C. mrigala*	*L. calbasu*	*C. striata*	*C. punctata*
Allocreadium sp.	✓	-	✓	-	-	-
Genarchopsis sp.	-	-	-	-	✓	✓
Clinostomum sp.	-	✓	-	-	-	✓
Senga sp.	-	-	-	-	✓	✓
Bothriocephalus sp.	✓	✓	-	✓	-	-
Camallanus sp.	-	-	-	-	✓	✓
Procamallanus sp.	-	-	-	✓	✓	-
Neocamallanus sp.	-	-	-	-	✓	✓
Pallisentis sp.	-	-	-	-	✓	✓

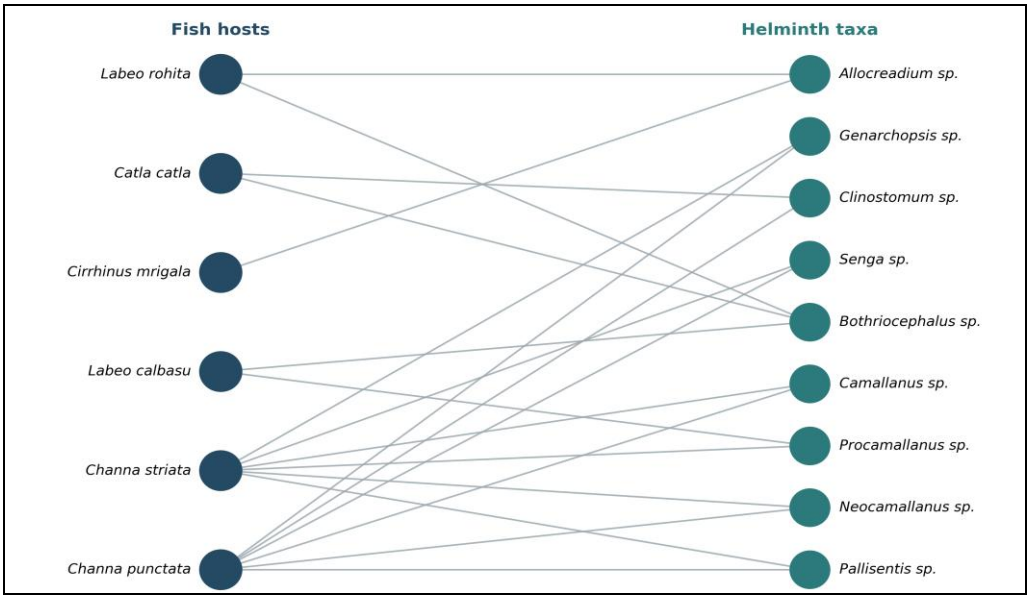

Fig 3: Presence–absence host–parasite association network. Lines show the recorded occurrence of a helminth taxon in a fish host. Link width does not represent abundance or infection intensity.

4. Taxon abundance and pooled community structure

The most abundant taxon was *Camallanus* sp., with 148 individuals, or 15.29% of all helminths recovered. Next came *Bothriocephalus* sp. (137; 14.15%) and *Genarchopsis* sp. (120; 12.40%). At the other end of the scale, *Clinostomum* sp. was the least abundant (80; 8.26%). The rounded relative abundances summed to approximately 100%.

Table 3: Taxonomic group, numerical abundance, and relative abundance of the recorded helminth taxa.

Helminth taxon	Group	Individuals (n)	Relative abundance (%)	Rank
Allocreadium sp.	Trematoda	103	10.64	5
Genarchopsis sp.	Trematoda	120	12.40	3
Clinostomum sp.	Trematoda	80	8.26	9
Senga sp.	Cestoda	108	11.16	4
Bothriocephalus sp.	Cestoda	137	14.15	2
Camallanus sp.	Nematoda	148	15.29	1
Procamallanus sp.	Nematoda	85	8.78	8
Neocamallanus sp.	Nematoda	97	10.02	6
Pallisentis sp.	Acanthocephala	90	9.30	7
Total	Four groups	968	100.00	-

The pooled assemblage held nine taxa and 968 individuals. The Shannon diversity index came to 2.177, Simpson dominance to 0.116, Simpson diversity to 0.884, and Pielou's evenness to 0.991. Low dominance together with high evenness tells us that the recovered individuals were spread fairly uniformly across the nine taxa, even though *Camallanus* sp. stood out as the single most abundant one.

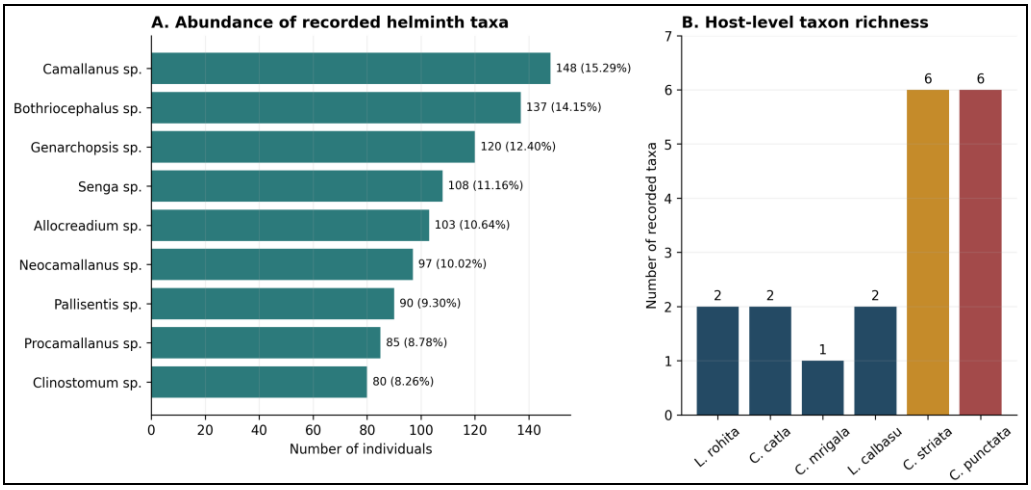

Fig 4: Taxon abundance and host-level richness. (A) Numerical and relative abundance of the nine recorded helminth taxa. (B) Number of helminth taxa recorded from each fish species.

Discussion

1. Diversity and composition of the helminth assemblage

The present study turned up 968 helminth individuals across nine genus-level taxa, drawn from six freshwater fish species, and all four major endohelminth groups were represented. That breadth tells us the two water bodies support several distinct routes of transmission at once, some involving direct exposure to the environment, others intermediate hosts, and still others trophic transfer from prey to predator. The finding sits comfortably alongside earlier work showing that tropical freshwater fishes can maintain taxonomically varied helminth communities wherever suitable hosts and infective stages come together (Choudhury & Dick, 2000 [7]; Salgado-Maldonado *et al*., 2020) [34].

Trematoda and Nematoda tied for the greatest taxon richness at three taxa each, yet it was Nematoda that dominated numerically, a reminder that equal richness need not translate into equal numerical weight. Nematodes made up 34.09% of individuals against the trematodes' 31.30%. The presence of *Camallanus*, *Procamallanus*, and *Neocamallanus* speaks to the importance of aquatic food resources that can serve as intermediate or paratenic hosts. Integrative studies of camallanids have shown, too, that morphological similarity can mask a good deal of underlying variation, which only strengthens the case for careful taxonomic resolution in later work (Ailán-Choke *et al*., 2020) [1].

Cestodes accounted for two taxa and a quarter of the individuals (25.31%). *Bothriocephalus* sp. occurred in three cyprinid hosts, giving it the widest recorded host distribution in our matrix, while *Senga* sp. was confined to the two *Channa* species within the host set we examined. Patterns of this kind are consistent with trophic transmission, though our data cannot pin down the exact intermediate hosts, nor establish genuine host specificity. The one acanthocephalan, *Pallisentis* sp., was found in both snakeheads. *Pallisentis* is a significant element of Indian freshwater fish helminthology, and recent morphological and molecular studies make clear that identifying it to species demands detailed proboscis, trunk, reproductive, and sequence data (Amin *et al*., 2021; Rana & Kaur, 2021) [32]. This is exactly why the conservative, genus-level reporting adopted here is the appropriate course.

2. Host association and the role of predatory fishes

Host-level richness was strikingly uneven. *Channa striata* and *C. punctata* each supported six recorded taxa, whereas the four cyprinids managed only one or two. The two *Channa* species also returned the highest prevalence and the largest total parasite recovery. This fits the general expectation that predatory fishes meet more trophically transmitted parasite stages by way of their animal prey. Food-web transmission is, after all, a principal channel connecting fish hosts to trematodes, cestodes, nematodes, and acanthocephalans alike (Marcogliese, 2002) [20].

Comparative studies of fish parasites have repeatedly tied parasite richness to host body size, diet, trophic level, habitat range, and sampling effort (Luque *et al*., 2004; Luque & Poulin, 2007, 2008) [14, 16, 17]. A predator can integrate parasite stages from several lower trophic levels, whereas planktivorous, herbivorous, or detritivorous fishes tend to encounter a narrower slice of what is available. In our case that ecological reading is plausible, since *Channa* species routinely take aquatic invertebrates, amphibian larvae, and smaller fishes. But we did not measure diet directly. The honest way to put it, then, is that the higher richness is associated with a predatory feeding ecology, not that di*et al*one has been shown to cause it.

The network also shows several taxa shared between the two *Channa* species. Shared diet, overlapping habitat use, phylogenetic proximity, and exposure to the same intermediate hosts could all feed into this pattern. Network analyses have shown that host and parasite identity can structure associations at several scales, but any reliable estimate of specialisation would need broader host sampling and taxon-specific abundance data (Brian & Aldridge, 2024; Dallas *et al*., 2017) [5, 8]. The present network is therefore best treated as a regional occurrence network, not as a finished measure of host range.

3. Numerical abundance and community organisation

Although *Camallanus* sp. was the most abundant taxon, it still amounted to only 15.29% of the assemblage. The next two, *Bothriocephalus* sp. and *Genarchopsis* sp., contributed 14.15% and 12.40% respectively, and even the least abundant taxon, *Clinostomum* sp., held 8.26%. It is this narrow spread, from roughly 8% to 15%, that accounts for the low Simpson dominance and the high evenness.

A Shannon value of 2.177 signals substantial diversity for an assemblage of nine recorded taxa. Simpson dominance of 0.116 confirms that the assemblage was not concentrated in any one taxon, and Simpson diversity of 0.884 says the same thing from the opposite direction. Pielou's evenness of 0.991 sits almost at the theoretical ceiling of 1.0. Together they describe a pooled assemblage that is highly even. Indices such as these are in wide use for community comparison, but they remain sensitive to taxonomic resolution, to sampling effort, and to the level at which the data are pooled (Magurran, 2004; Poulin, 2019) [18, 27].

It would be a mistake to take these figures, on their own, as proof that Munj Talab and Jeerabad Dam are environmentally stable or free of pollution. Parasite diversity can indeed track food-web complexity and host diversity, but it also responds to fishing, to pollution, to habitat alteration, and to the loss or gain of particular hosts (Marcogliese, 2005, 2023; Wood & Lafferty, 2015) [21, 22, 40]. Any environmental interpretation would call for independent data on water quality, habitat condition, intermediate-host abundance, and change over time. For now the indices are best confined to describing the structure of the helminth assemblage we recovered, and nothing more.

4. Regional significance and taxonomic considerations

What the study offers is a consolidated account of fish helminths from a district where community-level information had been thin on the ground. Regional datasets earn their keep because parasite distributions are bound up with the distributions of their hosts and intermediate hosts. The occurrence records set out here can feed into future taxonomic surveys, into fish-health monitoring, and into comparisons across the freshwater systems of central India. They also add to the wider effort to document fish–helminth associations and make them available for ecological analysis (García-Prieto *et al*., 2022; Jyrwa *et al*., 2016) [11, 12].

Working at the level of genus is at once a strength and a limitation. It keeps us from making species assignments the evidence cannot support, but it may also lump together more than one cryptic or closely similar species. Since taxonomic resolution feeds directly into community metrics and into inferred host range (Poulin & Leung, 2010) [28], future work should retain voucher specimens, record the full suite of morphometric characters, and bring in molecular markers wherever possible. Molecular confirmation would be particularly valuable for the camallanids, the acanthocephalans, and the larval trematodes. It would sharpen species-level comparisons without in any way diminishing the value of the present baseline inventory.

From a fisheries standpoint, the recovery of 968 helminths from common food and predatory fishes simply confirms that parasitism is a normal part of the local fish community. The present article makes no claim about disease severity or economic loss, since clinical outcomes and controlled comparisons lay outside its scope. Even so, systematic parasite monitoring can help flag changes in host exposure and can supply material for later fish-health assessment. Parasite biodiversity, in other words, deserves to be considered alongside fish biodiversity, rather than being noticed only when visible disease appears (Scholz & Choudhury, 2014) [35].

5. Study limitations

Several limitations should be kept in view. Parasites were identified morphologically to genus, without molecular confirmation. The host–parasite matrix records occurrence but not taxon-specific abundance within each fish species, which is why weighted host-network measures and host-specific diversity indices could not be computed. Only six fish species and two freshwater habitats were covered. Intermediate-host abundance, fish diet, water quality, and habitat disturbance were not measured in quantitative terms. The pooled diversity indices cannot serve as direct indicators of ecosystem stability. And finally, the findings speak for the hosts and sites actually studied; they should not be extended to all fishes or all water bodies of Dhar district without further sampling.

Conclusion

This study documented 968 helminth individuals across nine genus-level taxa from six freshwater fish species of Dhar district, Madhya Pradesh. Trematodes and nematodes were richest in taxa, while nematodes were the most abundant group numerically. *Camallanus* sp. was the most abundant single taxon, and yet its share stayed below one-sixth of the whole assemblage. *Channa striata* and *C. punctata* carried the broadest recorded helminth associations, six taxa each, whereas *Cirrhinus mrigala* carried just one. The pooled community proved highly diverse, low in dominance, and very even. These results provide baseline information on the freshwater fish helminths of Dhar district and underline how strongly host identity and trophic ecology shape parasite associations. Species-level identification, molecular confirmation, wider host coverage, and environmental measurement all belong on the agenda for future studies.

Declarations

Animal handling statement

Fish collection, handling, transport, dissection, parasite recovery, and tissue examination were all carried out in keeping with applicable institutional procedures and accepted animal-research practice. Handling time was kept to a minimum, and every examination followed established fish-parasitology and laboratory methods.

Conflict of interest

The authors declare no conflict of interest.

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