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Helminth infection in *Wallago attu* from the Godavari River in Nashik

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ABSTRACT

Helminth infection in predatory freshwater fish provides information on host exposure and parasite diversity, but local estimates depend on consistent denominators and defensible identification. This study analysed *Wallago attu* examinations from three Godavari River reaches in Nashik, Maharashtra, during June 2022 to May 2024. Infection prevalence, mean intensity, mean abundance and major-group composition were calculated from the survey summaries. Proportions were accompanied by 95% Wilson confidence intervals. Pearson chi-square tests assessed five host and sampling comparisons, with Holm adjustment for multiple testing. Of 789 fish examined, 58 were infected and 75 helminths were recovered. Overall prevalence was 7.35% (95% confidence interval 5.73–9.39%), mean intensity was 1.29 helminths per infected fish, and mean abundance was 0.095 helminths per examined fish. Thirteen taxa or operational morphotypes were recorded: eight cestodes, three nematodes and two trematodes. Cestodes accounted for 50 of the 75 worms. Prevalence increased from 4.01% in monsoon to 11.27% in summer; the seasonal association remained significant after adjustment (adjusted p = 0.0381). Larger fish also had higher prevalence (adjusted p = 0.0083). Differences among reaches, sexes and study years were not significant. The examined assemblage combined low pooled infection burden with cestode-dominated morphotype richness. These findings provide a descriptive baseline for the Nashik survey, while voucher-linked taxonomy and fish-level records remain necessary for resolving species identities and jointly assessing ecological predictors.

Keywords: *Wallago attu*; helminths; Godavari River; Nashik; prevalence; cestodes; seasonal variation.

INTRODUCTION

Wallago attu is a large silurid predator that participates in freshwater food webs and regional fisheries. A Godavari-basin gut-content study documented substantial consumption of animal material, including small fishes, making trophic acquisition of helminths biologically plausible.[1] Tapeworm revisionary work and surveys of larval trematodes have established that Indian freshwater fish support varied parasite assemblages, although host identity alone cannot validate a parasite name. [2,3]

For the Nashik reach of the Godavari, a useful baseline must distinguish the proportion of fish infected from the number of worms carried and the number of

taxonomic forms recognised. These quantities describe different features of transmission. A river sample can contain several uncommon morphotypes while most fish remain parasite-negative. Conversely, a numerically dominant parasite can contribute substantially to burden without increasing taxonomic richness.

Studies of *Isoparorchis hypselobagri* in *Wallago attu* have demonstrated temporal variation in infection outside Maharashtra.[4] Such observations establish a reason for repeated local sampling, rather than a universal seasonal pattern. Research on Godavari water quality also documents variation across space and time; these environmental patterns provide context but cannot establish a causal explanation for infection in the present fish sample.[5]

Taxonomy is another constraint. Revisions of *Gangesia* and subsequent molecular work have changed accepted species limits and illustrated the value of voucher-linked evidence.[6,7,8,9] The present study therefore retained operational morphotypes where identification was incomplete. Its objectives were to quantify pooled helminth infection, describe higher-group composition, and evaluate the reported seasonal, spatial and host-related contrasts in the two-year Nashik dataset.

MATERIALS & METHODS

Study area and survey design

The observational survey covered upstream (S1), midstream (S2) and downstream (S3) sectors of the Godavari River in Nashik. The study presentation identified these sectors as Gangapur Dam to Gangapur Gaon, Ramkund to Tapovan, and Dasak Panchak to Odha, respectively. Sampling summaries covered June 2022–May 2024. Figure 1 provides photographic context for the host and river setting; the images are independent of the survey examinations.



Figure 1. Wallago attu and the Godavari River in Nashik

Host examination and morphological assessment

The analytical dataset comprised 789 host examinations, 58 infected hosts and 75 recovered helminth individuals. Each positive examination detected at least one helminth. Host summaries included total length, body mass and sex. Total length ranged from 23.5 to 89.0 cm (mean ± standard deviation 54.8 ± 11.2 cm), and body mass ranged from 385 to 2,950 g (1,560 ± 420 g). The sample included 401 males and 388 females. The reported size comparison used classes of <45 cm and ≥45 cm. The survey workflow involved dissecting and examining the digestive tract and associated visceral sites. We assessed flatworms as stained preparations and nematodes as cleared mounts. Identification considered attachment structures, body form, internal anatomy, developmental stage and organ of recovery. The inventory included intestinal cestodes, mesenteric or serosal nematode larvae, intestinal adult nematodes and swim-bladder or encysted trematodes. *We interpreted Isoparorchis identifications in the context of the genus revision, while treating clinostomid material* cautiously because closely related forms require detailed morphological and molecular

discrimination. [10,11] Thirteen working units were retained. The terms "taxon" and "morphotype" refer to the resolution of the morphological record; they do not imply 13 molecularly confirmed species. The qualifiers "sp.", "gen. sp." and "cf." were preserved where genus, family or tentative species-level placement was the defensible limit. No formal new-species descriptions or sequence-based identifications are made here.

Statistical analysis

Infection indices followed standard quantitative-parasitology definitions. [12,13] With N denoting examined hosts, I infected hosts, and W recovered worms, prevalence was 100I/N, mean intensity was W/I, and mean abundance was W/N. Richness was the count of working taxonomic units. We calculated higher-group percentages separately for the 13 units and 75 worm individuals. We did not interpret these two percentage distributions as host prevalence. We defined two hydrological years: June 2022–May 2023 and June 2023–May 2024. The seasonal classifications used in the count tables were monsoon (June–September), winter (October–February) and summer (March–May). Month-specific estimates pooled the corresponding months across both years. Because seasonal denominators differed, comparisons used infection proportions rather than positive-host counts alone. We used the Wilson score method with $z = 1.96$ to calculate nominal 95% confidence intervals for prevalence. [14, 15] Pearson chi-square tests without continuity correction compared infected and uninfected counts across study year, season, reach, size class and sex. The smallest expected cell count was 15.66, supporting the asymptotic calculations. All five omnibus p-values were adjusted together by the Holm procedure. Cramér's V described association strength; for two-category comparisons it equals the absolute phi coefficient. Statistical significance was assessed at adjusted $p < 0.05$. Selected odds ratios used the infected/uninfected cross-products and log-scale 95% confidence intervals. They describe unadjusted contrasts and are not multivariable causal estimates. Monthly proportions were descriptive and were not tested with 12 separate significance tests. Fish-level worm counts were unavailable for resampling intensity intervals or fitting burden models. We did not recalculate environmental correlations and diversity indices without their underlying observation matrices.

RESULT

Pooled infection and sample denominators

Among 789 examined fish, 58 were positive, and 731 were negative for detected helminths. Table 1 summarises the pooled indices. The prevalence estimate was 7.35%, with a 95% Wilson interval of 5.73–9.39%. The 75 worms recovered corresponded to 1.29 worms per infected fish and 0.095 worms per examined fish. We calculated these metrics from worm individuals, not from the 13-unit inventory.

Table 1. Pooled infection indices for Wallago attu examined during June 2022–May 2024.

Measure	Estimate or count	Definition
Hosts examined	789	Survey denominator
Hosts infected	58	At least one helminth detected
Hosts negative	731	789 − 58
Helminth individuals	75	Pooled worm recovery
Prevalence	7.35%	95% Wilson CI 5.73–9.39%
Mean intensity	1.29	75 / 58 infected hosts
Mean abundance	0.095	75 / 789 examined hosts
Working taxa or morphotypes	13	Eight cestodes, three nematodes, two trematodes

Major helminth groups

Cestodes accounted for eight of the 13 working units (61.5%), followed by nematodes (three; 23.1%) and trematodes (two; 15.4%). Worm recovery showed the same ordering: 50 cestodes (66.7%), 16 nematodes (21.3%) and nine trematodes (12.0%). Figure 2 distinguishes richness composition from individual-worm distribution. Neither panel represents the percentage of fish infected by each class.

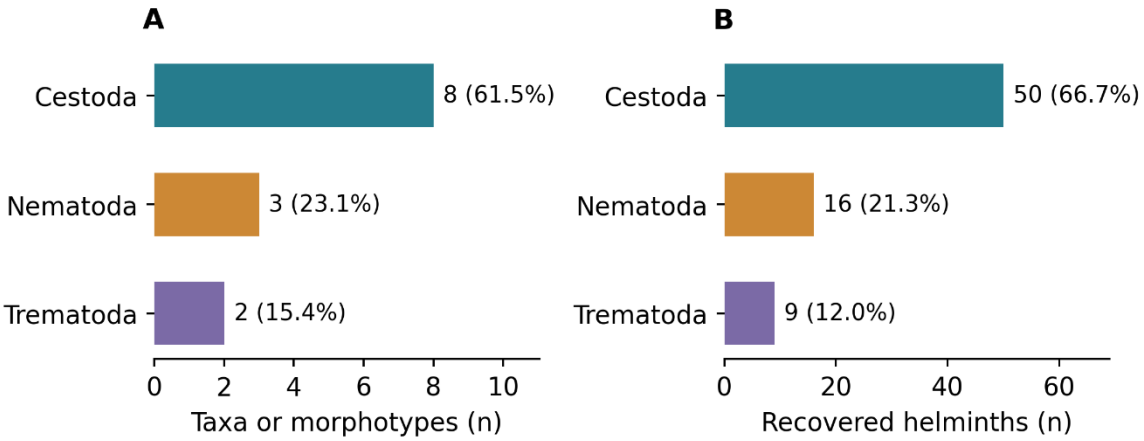


Figure 2. Higher-group composition of the reported helminth assemblage. A, number and share of 13 working taxa or morphotypes. B, number and share of 75 helminth individuals. The denominators differ between panels.

At least 41 of the 58 infected fish carried a single worm, because 75 worms allowed only 17 worms above one per positive host. This arithmetic bound does not identify each host's burden or quantify tissue damage.

Taxonomic inventory and organ associations

The reported inventory comprised eight cestode forms, three nematode forms and two trematodes (Table 2). Four cestode units were retained within *Gangesia*, two within or close to *Senga*, and two at family or subfamily level. The nematode record included larval *Contracaecum* and adult camallanid forms. Trematodes included *Isoparorchis* in the swim bladder and a clinostomid metacercaria associated with cysts or viscera.

Table 2. Conservative working inventory of helminths reported from the Nashik Wallago attu survey.

Code	Working identification	Stage	Reported organ or site
C1	*Gangesia* sp. morphotype C1	Adult	Anterior–mid intestine
C2	*Gangesia* sp. morphotype C2	Adult	Mid intestine
C3	*Gangesia* sp. morphotype C3	Adult	Posterior intestine
C4	*Gangesia* sp. morphotype C4	Adult	Mid intestine
C5	*Senga* cf. *lucknowensis*	Adult	Mid intestine
C6	*Senga* sp.	Adult	Posterior intestine
C7	Proteocephalidae gen. sp.	Adult	Anterior intestine
C8	Gangesiinae gen. sp.	Adult	Posterior intestine
N1	*Contracaecum* sp.	L3 larva	Mesentery or serosa
N2	*Camallanus* cf. *anabanti*	Adult	Posterior intestine
N3	*Procamallanus* sp.	Adult	Mid intestine
T1	*Isoparorchis hypselobagri*	Adult	Swim bladder
T2	*Clinostomum* cf. *complanatum*	Metacercaria	Cyst or viscera

Codes retain the 13-unit reporting structure. "cf." indicates tentative resemblance; "gen. sp." indicates an unresolved genus and species within the stated higher group. L3 denotes a third-stage larva. The four *Gangesia* units are morphological records, not four confirmed species.

The cestode distinctions in the survey summaries involved scolex form, apical armature, neck length and proglottid structure. Nematode separation relied on larval form and buccal-capsule characters. We distinguished adult Isoparorchis from the encysted clinostomid form by stage, body organisation, and organ association. This combination described the material at a practical morphological level. The 13-unit count is therefore an operational measure of recorded diversity. It may change after voucher re-examination, synonymy assessment or molecular matching. Species-specific worm burdens were not assigned from the higher-group totals, and no claim of a novel species or first regional record was made.

Temporal distribution of infection

The annual sample sizes were similar: 392 fish in Year I and 397 in Year II. Each year contained 29 infected fish, yielding prevalences of 7.40% and 7.30%, respectively. Worm recovery was 37 in Year I and 38 in Year II. The between-year comparison gave $\chi^2 = 0.0025$ with one degree of freedom (unadjusted p = 0.9600), indicating no detectable annual separation in these summaries. Seasonal prevalence was 4.01% in monsoon (11/274), 7.62% in winter (23/302) and 11.27% in summer (24/213). Recovery increased from 13 worms in monsoon to 28 in winter and 34 in summer. The summer-to-monsoon prevalence difference was 7.25 percentage points. The corresponding unadjusted odds ratio was 3.04 (95% CI 1.45–6.35). The omnibus seasonal association remained significant after Holm adjustment, although its effect size was modest (V = 0.109; Table 3).

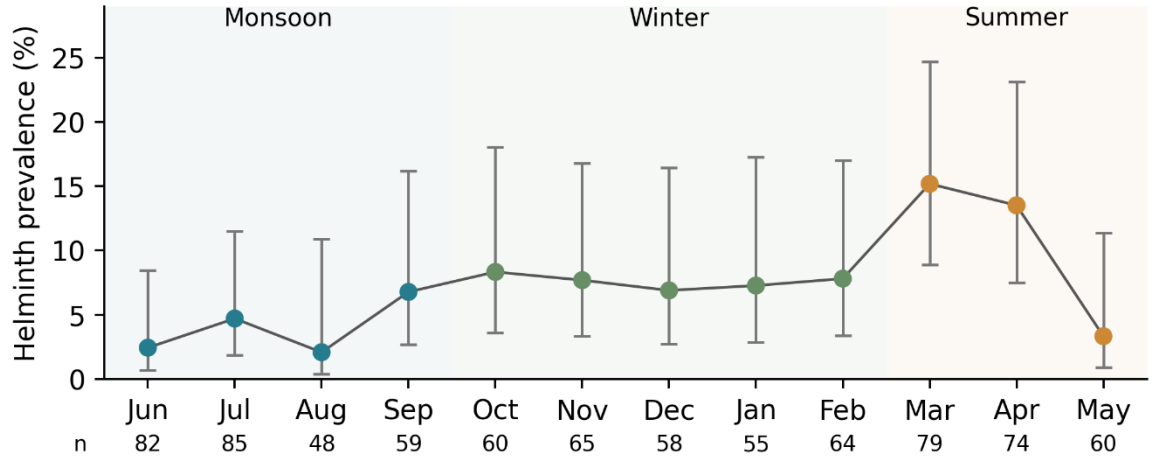


Figure 3. Monthly helminth prevalence pooled across the two survey years. Points show infected/examined proportions and error bars show nominal 95% Wilson intervals. Numbers below month labels are examined hosts. Seasonal bands follow the definitions in Methods; the connecting line only guides the eye.

Monthly estimates were highest in March (12/79, 15.19%) and April (10/74, 13.51%). August had the lowest pooled estimate (1/48, 2.08%). March and April together accounted for 22 of 58 positive hosts and 32 of 75 recovered worms, while contributing 153 of 789 examinations. The concentration of positive examinations in these months reflects the timing of detection, not the date each infection was acquired. The late-summer course was not a continuous increase. May prevalence fell to 3.33% (2/60), despite its inclusion in the same seasonal group as March and April.

Confidence intervals were wider for individual months than for the pooled survey because monthly denominators and positive counts were smaller. We interpreted these month-level estimates descriptively, without asserting independent monthly differences.

Spatial and host-related comparisons

Reach-specific prevalence was 5.07% at S1 (11/217), 8.61% at S2 (26/302) and 7.78% at S3 (21/270). The upstream estimate was numerically lower, but the overall reach comparison was not significant (unadjusted p = 0.2962; V = 0.056). Figure 4 displays the seasonal and reach estimates on the same percentage scale. It supports a descriptive spatial ordering rather than designation of a confirmed infection hotspot.

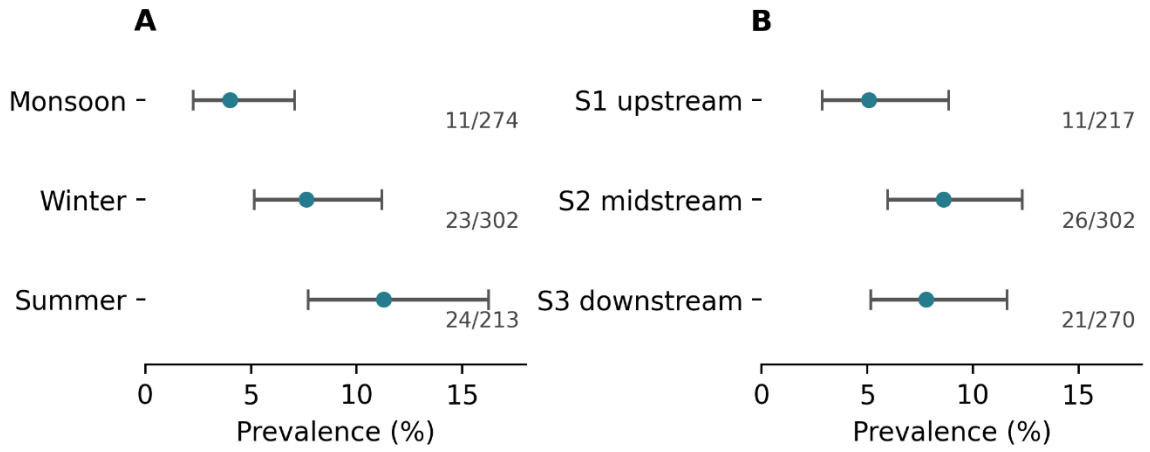


Figure 4. Prevalence estimates with nominal 95% Wilson confidence intervals by season (A) and sampling reach (B). Fractions give infected/examined hosts. Omnibus statistical tests, rather than interval overlap alone, were used for group comparisons.

Table 3. Tests of infection status across five sampling or host factors (N = 789).

Factor	χ^2	df	p value	Holm p	V
Study year	0.003	1	0.9600	1.0000	0.002
Season	9.307	2	0.0095	0.0381	0.109
Sampling reach	2.433	2	0.2962	0.8887	0.056
Length class	9.881	1	0.0017	0.0083	0.112
Sex	0.173	1	0.6779	1.0000	0.015

Pearson tests used infected and negative counts without continuity correction. Holm correction was applied to the five p values together. V = Cramér's V (absolute phi for two-category factors). These are unadjusted factor associations, not independent effects from a multivariable model.

Larger fish had a prevalence of 9.65% (47/487), compared with 3.64% (11/302) in fish <45 cm. The size association remained significant after correction (Holm p = 0.0083); the unadjusted odds ratio was 2.83 (95% CI 1.44–5.54). Male prevalence was 7.73% (31/401) and female prevalence was 6.96% (27/388). Their difference was small and not significant. The available summaries did not permit simultaneous adjustment of size, season, reach and sex.

DISCUSSION

Low pooled burden with cestode-dominated recorded diversity

The main result was the coexistence of low pooled prevalence and a relatively varied morphological inventory. The sample included 13 working units, yet fewer than 1 in 10 examined fish were positive, and mean intensity remained close to 1. These findings are compatible because richness counts distinct forms, whereas prevalence measures

affected hosts and intensity measures worms within positive hosts. A large denominator can reveal uncommon forms without implying that most hosts experience heavy infection. Cestodes dominated both working-unit richness and individual recovery. This parallel ordering suggests that their prominence was not solely a consequence of how the inventory was labelled. It is consistent with trophic exposure in a predatory fish, particularly given the fish prey recorded in earlier Godavari-basin feeding studies.[1] However, the present aggregate results did not identify infected intermediate hosts, reconstruct the actual diet of positive fish or establish a complete transmission cycle. Cestode dominance therefore reflects assemblage composition, with trophic transmission as a biologically supported interpretation.

Taxonomic caution materially affects that interpretation. Revisionary studies show that nominal Gangesia diversity can be inflated when inadequate specimens or incomplete characters are used to define species. [2,6] Later molecular analyses further refined relationships among catfish tapeworms.[7] Retaining C1–C4 as morphotypes preserves distinctions in the survey record without asserting four validated species. The same principle applies to tentative *Senga*, camallanid and clinostomid assignments. Morphotype richness is a useful descriptive result, but it should not be presented as a final species census.

Season and host size as exposure signals

The omnibus analysis supported the seasonal association, and it remained detectable after correction for five comparisons. Summer prevalence was higher than monsoon prevalence, but the small V value indicates considerable overlap between seasons at the individual-host level. Most summer fish were still negative. The appropriate interpretation is seasonal concentration of detected infection within this sample, rather than a seasonal outbreak or a reliable forecast for any particular fish. Hydrological concentration of prey, changing host movements and temperature-dependent development could contribute to the seasonal ordering. These processes may operate together, and parasite groups can respond differently. The May decline also shows that a single warm-season explanation is incomplete. Sahreen and Saifullah documented temporal variation in *Isoparorchis* infection in *Wallago attu* elsewhere, reinforcing the need for local, parasite-specific timing rather than direct transfer of a seasonal peak from another region.[4] The larger-fish association is compatible with accumulated exposure, a changing prey spectrum, or longer parasite persistence. It does not establish any of these mechanisms individually because length also covaries with age, habitat and capture selectivity. The non-significant sex contrast likewise cannot establish equal susceptibility: its precision and the lack of joint adjustment limit that conclusion. Ecological work linking host diversity to parasite diversity illustrates how several host and food-web components can structure parasite records, but it does not identify the intermediate hosts responsible for this Nashik assemblage.[16]

Spatial interpretation and limits of environmental attribution

The highest observed prevalence occurred at S2, while the omnibus reach comparison was not significant. This finding does not support a firm upstream-to-downstream gradient in infection. Mobile fish can acquire persistent parasites away from their capture reach, and catch composition can differ among locations. Published Godavari water-quality results provide a reason to investigate environmental effects, but they cannot be substituted for paired fish and water observations in this survey.[5] Pollution, oxygen stress and habitat change remain hypotheses rather than demonstrated causes.

Study limitations and implications

The analysis used aggregate survey tables rather than a fish-by-fish matrix. This restricted joint adjustment, repeat-capture

checks, assessment of clustering and modelling of worm-count variation. Wilson intervals and chi-square tests treated examinations as independent; unmeasured clustering by catch or month could reduce their effective precision. Without a documented probability-sampling frame, the estimates characterise the examined fish and should not be treated as an unbiased census of all *Wallago attu* in Nashik. The analysed record lacked voucher-linked molecular confirmation for morphological assignments. Sampling completeness and definitive species richness could not be assessed from three higher-group totals. Mean intensity also does not measure tissue damage, host condition or mortality. Future surveillance should retain unique fish identifiers, capture provenance, parasite counts by taxon and organ, calibrated specimen images and accessible voucher numbers. Larval records may have food-safety relevance, but genus-level or tentative identification does not quantify human risk. Clinical reports establish that some clinostomid infections can follow consumption of infected raw freshwater fish; they do not demonstrate zoonotic transmission from the Nashik specimens.[17] This survey did not estimate edible-tissue infection, larval viability, or human exposure, so its prevalence estimate does not support any declaration of food safety or human disease burden.

CONCLUSION

In the reported June 2022-May 2024 Nashik dataset, 58 of 789 *Wallago attu* were infected, and 75 helminths were recovered. Prevalence was 7.35%, mean intensity 1.29 and mean abundance 0.095. Cestodes dominated the 13-unit morphological inventory and individual recovery. Seasonal and length-class associations remained significant after Holm correction, whereas reach, sex and year comparisons did not. The results provide a descriptive baseline and identify temporal and host-size patterns to test with audited fish-level and voucher-linked records.

Declaration by Authors

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