# Host taxonomy constrains the properties of trophic transmission routes for parasites in lake food webs: Appendix S1

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# Section S1: Detailed methods for data collection

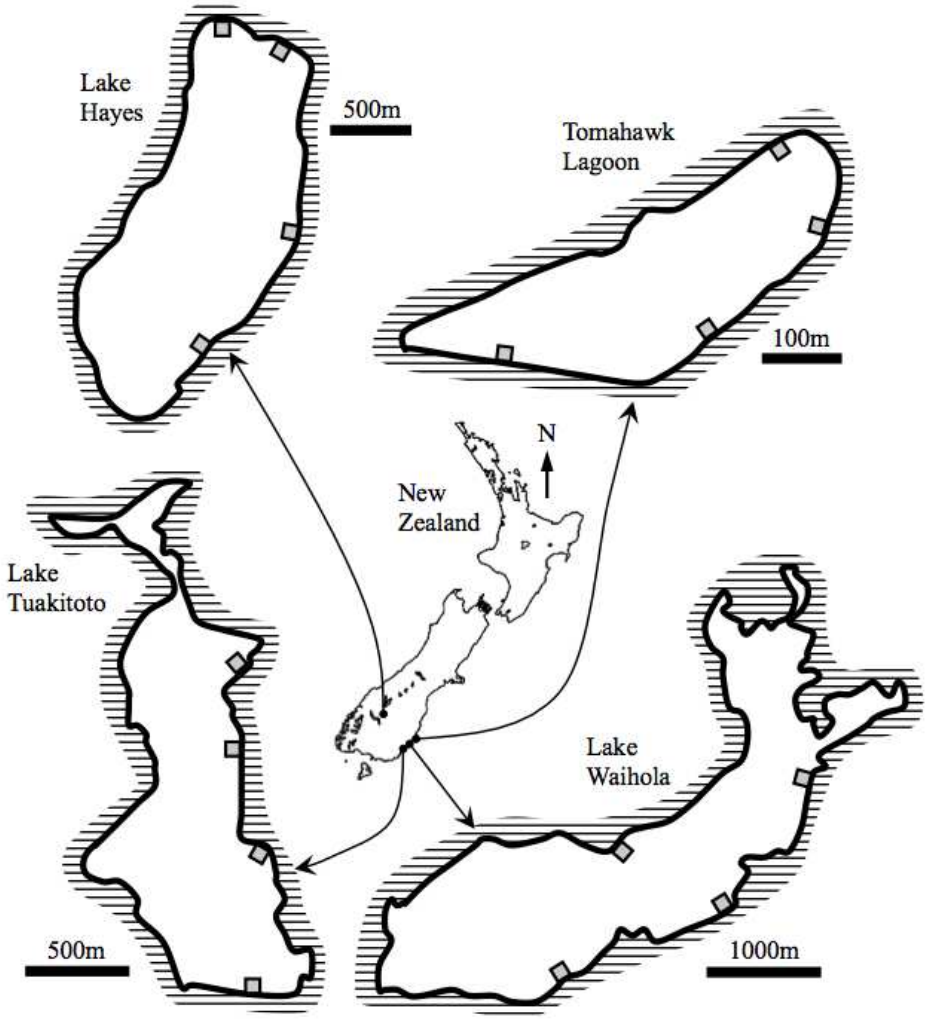
## Study lakes and sampling sites

Detailed field data on food web composition and structure, including parasites, was obtained from four lake ecosystems. Based on existing knowledge and accessibility, Lake Hayes, Lake Tuakitoto, Lake Waihola, and Tomahawk Lagoon (South Island, New Zealand) were selected to provide a variety of lake types (size, depth, altitude; Table S1) and freshwater communities (coastal versus alpine, oligotrophic versus eutrophic, tidal or not, etc.). Within each lake, 4 sampling sites were selected along the littoral zone. Site selection was partly restricted by accessibility and sampling permit specification (New Zealand Department of Conservation permit OT-34204-RES and Fish and Game New Zealand permit to capture fish for research purposes), but was ultimately made to represent all habitat types (substrate, macrophytes, riparian vegetation, etc.) present within each lake. Sampling sites consisted of $225m^2$ square areas (15m $\times$ 15m) with one side of the square following the lake shore line (Figure S1). Distances between sampling sites varied within and among lakes according to lake size and shape as well as sampling site distribution (Table S1; Figure S1). The four lakes were sampled in early spring, mid-summer, and late autumn (austral seasons: September 2012, January and May 2013). In each lake and in each season (4 lakes $\times$ 3 seasons = 12 full sets of samples), fish, benthic and demersal invertebrates, plankton, periphyton, and macrophytes were sampled in each sampling site (4 sites per lake-season combination) to determine their local species composition, density and/or biomass as well as that of their parasites, and potential temporal and spatial variability within and among lakes. In all cases, we averaged values across the four sites within a lake and sampling period— giving 12 food webs —prior to any analysis.

**Table S1:** Geographical locations and characteristics of the four study lakes (South Island of New Zealand), and distance between sampling sites (straight lines).

| Lake | GPS coordinates | Surface area ($km^2$) | Depth (m) | | Altitude (m) | Dist. between sites (m) | | |
|---|---|---|---|---|---|---|---|---|
| | | | Mean | Max | | Min | Mean | Max |
| Hayes | 44°58'59.4"S 168°48'19.8"E | 2.76 | 3.1 | 33 | 329 | 314 | 1190 | 2250 |
| Tuakitoto | 46°13'42.5"S 169°49'29.2"E | 1.32 | 1.0 | 3 | 15 | 417 | 794 | 1590 |
| Waihola | 46°01'14.1"S 170°05'05.8"E | 6.35 | 1.3 | 2 | 4 | 1330 | 1620 | 2020 |
| Tomahawk Lagoon | 45°54'06.0"S 170°33'02.2"E | 0.10 | 1.0 | 1 | 15 | 124 | 253 | 438 |

**Figure S1:** Location, size (see scale bars) and shape of the four study lakes on the South Island of New Zealand. The position of the 4 sampling sites per lake is indicated by shaded squares (not drawn to scale).




## Field sampling

### Fish

Fish were sampled once per season at each sampling site in each lake (1 sample  4 sites  3 seasons = 12 replicates per lake). We used a combination of fish-catching gear types following a standardized protocol so that samples represented accurately fish diversity and density (Hayes, 1989). First, two fyke nets and ten minnow traps were set in the evening. Fyke nets were positioned perpendicularly to the shore at either edge of the sampling site (i.e., 15m apart) to stop and capture fish swimming in and out of the focal 225m$^2$ area.

Fyke nets consist of a cylinder of netting (2m length, 15mm mesh size) wrapped around a series of hoops to create a trap. Fish enter through the mouth of the trap and are retained by a series of funnel-shaped constrictions. One leader (or wing) is attached to the mouth and used to direct fish into the fyke net. The leader (3m length, 50cm height, 15mm mesh size) has a float-line at the top and lead-line at the bottom to keep it upright in the water and in close contact with the substrate. To prevent fish from swimming around it, the end of the leader was securely anchored to the lake shore. Along with the two fyke nets, 10 minnow traps were set overnight in each sampling site. Traps were set diagonally across the sampling area at regular intervals (i.e., ≈1.7m apart). Minnow traps are small fish traps that typically consist of two funnel-shaped entrances (25mm entrance diameter) at either end of a mesh box (40 × 25 × 25cm, 2mm mesh size). Fyke nets and minnow traps were set during the night, when fish are more active, as they are passive sampling methods relying on fish to willingly encounter and enter traps (Hubert, 1996). The next day, all trapped fish were recovered from the nets and a subsample of fish from each species was set aside for later dissection. Remaining individuals were identified to species, counted and measured to the nearest mm (fork length). These fish were then released at least a hundred meters away from the sampling site.

Fish sampling was then complemented using two 15m long multi-mesh gillnets. Gillnets were benthic weighted sets with top floats, 1.5m high and comprised 3 panels of 25, 38 and 56mm meshes, each 5m long. Nets were set 15m apart similarly to fyke nets, perpendicularly to the shore line and anchored to the lake shore on the edge of the 225m$^2$ sampled area with the finer mesh panel closer to shore on one side and further from shore on the other. Gillnets covered the whole water column in all cases and were checked every 15 min for an hour. Fish caught in the nets were removed immediately to avoid excessive accumulation and potential visual deterrence to incoming fish (Lagrue et al., 2011). Fish caught in fyke nets and gillnets were either entering or exiting the sampling site and thus considered as site "users/occupants". All fish were identified, counted, and measured. Again, a subsample was kept for later dissection and the remaining fish released away from the sampling site.

Finally, fish sampling was completed using a standard, fine-mesh purse seine net. As an active sampling method, seine netting captures small and/or sedentary (i.e., resident) fish that are not captured by passive gear like fyke nets or gillnets (Thorogood, 1986). The seine net was 20m long and 1.5m high (5mm mesh size), thus covering the whole water column, and dragged by two people across the whole sampling area, catching virtually all small, sedentary fish remaining in the 225m$^2$ area. A final subsample of fish was kept for dissections and all other fish captured in the seine net were identified, counted, measured, and immediately released. All fish set aside for later dissection were killed immediately following University of Otago Animal Ethics Committee guidelines (permit ET 10/12) to inhibit the digestion process and stored on ice to preserve internal tissues, stomach contents, and parasites for future identification, counts, and other measures.

### Plankton

Four plankton samples were taken per site and per season in each lake (4 samples $\times$ 4 sites $\times$ 3 seasons = 48 replicates per lake). Sampling was done at night when planktonic organisms migrate up from the shelter of the substrate to the open water (Iwasa, 1982; Haney, 1988; Rhode et al., 2001). Samples were taken using plankton net tows. The net used was a conical device (25cm mouth diameter) made of fine nylon mesh (90$\mu$m mesh size) pulled through the water for a set distance. Since we sampled the littoral zone of shallow lakes, water depth was always less than a meter. We thus used a three meter horizontal pull repeated four times within each sampling area (i.e., four samples per site). Samples were distributed haphazardly across the 225m$^2$ area. Animals captured at the bottom of the net were rinsed into a storage jar and fixed in 70% ethanol for later identification and count. The amount of water from which zooplankton are removed was estimated as length of tow (3m) times mouth diameter of the net (25cm). Plankton density and biomass could thus be later determined using the sample count, volume of water filtered, and water depth at the sampling site.

### Demersal and benthic invertebrates

Six demersal and six benthic invertebrate samples were taken per site and per season in each lake (6 samples $\times$ 4 sites $\times$ 3 seasons = 72 replicates per lake for each sample type). Benthic sampling was done using a standard Surber sampler net with a 0.1m$^2$ horizontal metal frame (0.33 $\times$ 0.3m) fitted with a 250$\mu$m mesh collecting net. Samples were taken by embedding the Surber's metal frame into the lake bottom. Substrate and macrophytes enclosed within the frame were manually scooped up into the net to a depth of 5cm so that animals living on or within (hyporheic habitat) the substrate were captured into the net. Demersal invertebrates living on or near the substrate but either too fast or too rare to be captured in Surber nets were sampled using a rectangular dip net (i.e., a 30cm wide and 22cm high frame fitted with a 250$\mu$m mesh net and attached to a long pole). Each demersal sample consisted of a fast, two meter long sweep of the net along the lake bottom without dredging the substrate. Again, the 12 samples (6 benthic and 6 demersal) were distributed haphazardly across the 225m$^2$ sampling area so that none overlapped. Substrate, wood debris, and macrophytes contained in the net (Surber or dip net) were placed into a bucket of water and stirred, shaken, and/or scrubbed to dislodge attached invertebrates, and then transferred into another bucket. Animals and substrate remaining in the first bucket were transferred onto a sieve (250$\mu$m mesh size) so fine sediment could be rinsed off. Samples were then stored individually in jars filled with 70% ethanol for later sorting, identification, count, and measurement of invertebrates. Benthic and demersal invertebrate density and biomass were then determined using sample counts and sampling surface area.

### Periphyton

Periphyton growing on hard substrate (rocks, gravels) was brushed off rocks with a toothbrush and rinsed with lake water into a container. We used a 3.9cm diameter PVC pipe as a template to standardize sampling surface (11.9cm$^2$; Hughes et al., 2012). Periphyton from soft sediment bottom (sand or mud) was sampled from the top 5mm layer of sediments. The top half of a Petri dish (9cm in diameter, 63.6cm$^2$ sampling surface) was pushed into the lake bottom sediment and a small spatula was slipped under, sealing the sample inside the Petri dish. Then the sample was lifted and rinsed with lake water into a container. Five samples of periphyton, distributed haphazardly across the 225m$^2$ area, were taken per sampling site. The number of periphyton samples from soft and hard substrate parts of each sampling site was representative of the relative proportion of each substrate type within each sampling area. Samples were preserved in Lugol's solution and stored in the dark for later identification and count (Wood et al., 2012).

### Macrophytes

Macrophytes recovered in benthic invertebrate samples were used to examine macrophyte diversity and abundance within sampling sites. During benthic sampling, macrophytes transferred into Surber nets with substrate and invertebrates were recovered, rinsed to dislodge invertebrates and wash off all sediment, and bagged into zip-lock bags. Macrophyte samples were frozen for later sorting, identification and biomass assessment.

### Birds

Birds could not be sampled for dissections (permission was not granted by the New Zealand Department of Conservation). However, species composition and relative species abundances of the bird communities foraging at each sampling site of each lake and during each season were assessed by visual counts carried out from shore with binoculars. Once per site and per season, birds present around each sampling area were identified to species (Heather and Robertson, 1996). Birds were observed over a one hour period and every bird present or passing through a 200m radius zone centered on the sampling site was counted. Given the small size of Tomahawk Lagoon, all birds present on the lake were identified and counted. Note that bird counts were done during the day and did not account for highly secretive and/or nocturnal bird species like the Australasian bittern (*Botaurus poiciloptilus*) or marsh crake (*Porzana pusilla*). However, these birds are rare and represent a negligible fraction of the bird populations in our study lakes.

## Laboratory analyses

### Fish

In the laboratory, fish were identified to species, measured to the nearest mm (fork length), weighed to the nearest 0.01g and then dissected. Their gastrointestinal tract, from esophagus to anus, and all internal organs (heart, liver, gall bladder, gonads, swim bladder, etc.) were removed and preserved in 70% ethanol for later diet and parasite analyses. Fish bodies were frozen individually.

All fish bodies were later examined for parasites. The head, gills, eyes, brain, and spine of each fish were examined under a dissecting microscope using fine forceps to pull apart fish tissues to obtain an accurate overall parasite count for each fish. Soft tissues (muscle and skin) were removed from the spine, crushed between two glass plates, and examined by transparency under a dissecting microscope to identify and count parasites. Internal organs and gastrointestinal tract were first rinsed in water to wash off the ethanol. The digestive tract was then separated from other organs. Liver, swim bladder, gall bladder, gonads, and other organs and tissues from the body cavity (fat, mesentery, kidneys, heart, etc.) were all screened for parasites. Finally, the digestive tract was dissected and stomach contents were removed and examined. Prey items were counted and identified to genus or species when possible to assess diet composition and the dietary importance of each prey taxon. Esophagus, stomach, pyloric ceca (when present), intestine, and rectum were then examined for gastrointestinal parasites. All parasites were identified, counted, and a subsample of 20 individuals per genus/species (or all individuals when less than 20 were found in a fish) were measured to the nearest 0.01mm (diameter for spherical parasites; length, width, and thickness for flattened ellipsoids; length and width for cylinder-shaped parasites).

### Plankton

Plankton samples were examined under a dissecting microscope. All individuals were counted, identified to genus, and a subsample of 20 individuals per genus per sample (or all individuals when less than 20 were found in a sample) was measured to the nearest 0.01mm (body length) to assess potential within genus variations in body size across sites, seasons, and/or lakes. Planktonic crustaceans were examined for parasites by crushing subsamples of individuals from each genus between two glass plates, but no metazoan parasite could be detected in any sample.

### Demersal and benthic invertebrates

Demersal and benthic samples were sorted under a dissecting microscope. All invertebrates were separated from debris and sediment, identified to genus or species when possible (using

identification keys; see Winterbourn et al., 1989; Moore, 1997; Chapman et al., 2011), and counted. Again, a subsample of 20 individuals per taxon (genus or species) and per sample (or all individuals when less than 20 were found in a sample) were measured to the nearest 0.01mm (body length) to assess potential within-taxon variations in body size across sites, seasons, and/or lakes. Invertebrates were then dissected under a dissecting microscope using fine forceps and examined for parasites. For abundant invertebrate taxa (chironomid larvae, gastropods, amphipods, etc.), subsamples of 20 to 80 individuals per sample were dissected. All parasites were identified, counted, and a subsample of 20 individual parasites per genus/species (or all individuals when less than 20 were found in a sample) were measured to the nearest 0.01mm (diameter for spherical parasites; length, width, and thickness for flattened ellipsoids; length and width for cylinder shaped parasites). Stomach contents of carnivorous invertebrates (odonate larvae, leeches, Trichoptera larvae, etc.) were also examined. Prey items were counted and identified to genus or species when possible to assess diet composition and the dietary importance of particular prey taxa.

### Periphyton

Periphyton samples were topped up with distilled water to standardize sample volume to 50ml and stored in the dark until analysis. Samples were then homogenized and, using a compound microscope and a Palmer-Maloney counting chamber, algae, diatoms, and cyanobacteria cells were identified and counted. An aliquot of the homogenized sample was first transferred into the counting chamber and cells were allowed to settle at the bottom. Cells were then counted and identified following standard protocols for quantitative periphyton analysis (Biggs and Kilroy, 2000). Because of their small size, periphyton cells were not measured. Mean body sizes of the different taxa recorded were obtained from the literature and used to calculate body volumes for each taxon and for later biomass estimation (Biggs and Kilroy, 2000).

### Macrophytes

Macrophytes from each sample were sorted by species and identified (Clayton and Edwards, 2006). Plants were patted dry to eliminate excess moisture and weighed to determine the fresh weight of each species (all individuals combined) within each sample.

## Body mass

Body mass was calculated/measured differently for different types of organisms. Parasites were too small to be individually weighed and body measurements indicated that they varied little in size within each life stage of each taxonomic species. We thus calculated body volume for the subsamples of parasite individuals measured during host dissection

based on the most appropriate formula for each species shape (e.g. adult nematodes and acanthocephalans, trematode rediae and sporocysts = cylinder, adult trematodes = flattened ellipsoid, encysted juvenile trematodes [metacercariae] = spheres). Body volume was then calculated for each life stage of each species and their volume was converted to mass assuming their density equaled that of water. We could thus calculate a mean (± SE) individual body mass for each life stage of each parasite species. In the case of trematodes in their snail first intermediate host, since rediae or sporocysts are the product of clonal multiplication, all rediae or sporocysts have the same genotype (with infrequent exceptions) and are issued from the same larva hatched from a single egg. Individual parasite body mass was thus considered as the sum of all rediae/sporocysts present in a snail host. Although rediae and sporocysts size (length and width) and volume (cylinder) were measured or calculated for each redia/sporocyst for convenience, individual parasite body mass for that life stage was reported as the total body mass of all rediae/sporocysts present in a snail host.

Most free-living invertebrates were large enough to be weighed individually (isopods, chironomids, odonates, large Trichoptera larvae, adult hemiptera, mollusks, leeches, etc.). Invertebrates varied little in size within taxonomic species or genus and by weighing a subsample of individuals for each taxon (to the nearest 0.01mg) we could calculate the mean body mass of an individual for all invertebrate taxa. For small free-living invertebrates, which varied little in size intraspecifically (amphipods, small Trichoptera larvae, oligochaetes, planktonic crustaceans, etc.), we pooled 5, 10, or 20 conspecific individuals (depending on individual body size) from random subsamples, weighed them as a group, and from the total mass calculated the average body mass of one individual.

For fish, each individual was weighed individually and fish body mass could be directly inferred from the data. Consequently fish body mass data for a given species varied across lakes and seasons, while the body mass of smaller organisms was treated as constant for each genus/species (or life stage of parasites within a taxonomic genus/species).

Similarly to parasites, periphyton cells were too small to be weighed. Taxon-specific sizes and shapes were obtained from the literature and used to calculate body volume (Biggs and Kilroy, 2000). Body volume was then converted to body mass assuming their density equaled that of water.

## Density

Density of organisms (number of individuals per $m^2$ and its variance) was calculated for all taxa except macrophytes for which only biomass (mg per $m^2$) was estimated. For fish, we obtained a single estimate of abundance (number of fish per species) per sampling site per season. Since we used a combination of passive and active gear types and virtually captured all fish individuals present in (sedentary individuals) or passing through (user/occupant) each sampling area, we considered the number of fish captured as representative of the fish community present at and/or using the site. Fish density was

thus calculated as the total number of fish captured divided by the surface of the entire sampling area ($225m^2$). One value of fish density was thus obtained per sampling site per season per lake and for each species present.

Densities of benthic and demersal invertebrates were simply calculated as the number of individuals of each taxon captured in a sample divided by the surface of the lake bottom sampled, regardless of water depth since these organisms live in, on and/or close to the substrate. Sample surface was $0.1m^2$ for benthic and $0.6m^2$ (0.3m net width $\times$ 2m sweep of the net) for demersal invertebrates. Invertebrate densities were calculated for all samples and could then be used to estimate mean densities per site, season and/or lakes.

Plankton density in each sample was first expressed as the number of individuals per $m^3$ of water filtered by dividing the number of individuals captured in a sample by the volume of the sample ($0.15m^3$; 0.25m net diameter and 3m net tow). Density per $m^3$ was then converted to density per $m^2$ by projection of the number of individuals per plankton taxon contained in $1m^3$ of lake water onto the flat surface necessary to contain that $1m^3$ of water according to water depth at each sampling site.

Parasite populations are usually quantified as individuals per host rather than per surface area. Here, we calculated parasite densities (individuals per $m^2$) to provide a common metric for all free-living and parasite taxa. Also, because distinct life stages of parasites with complex life cycles exploit completely different host species, we estimated parasite densities separately for each life stage of these parasites (trematodes, nematodes, acanthocephalans, etc.). Parasite abundance (mean number of parasites per individual host) was first calculated for each parasite taxon in each host species from dissection data. Parasite abundance was then multiplied by host density (number of hosts per $m^2$) to obtain parasite density. Parasite densities were also estimated in all individual samples. In the case of trematode parasites in their snail host, we did not count each individual redia or sporocyst as separate individual parasites, since these are the product of clonal multiplication. All rediae or sporocysts are issued from the same larva hatched from a single egg and were considered as a single individual. Density of these life stages was thus estimated as the number of infected snail hosts per $m^2$.

Density of periphyton was calculated from the number of cells counted in the volume of the subsample contained in a Palmer-Maloney counting chamber (0.05ml). By multiplying the number of periphyton cells found in the subsample by 1000 we obtained an estimation of the number of cells in a whole sample. That number was then divided by sampling surface ($11.9cm^2$ for hard substrate and $63.6cm^2$ for soft sediments) to obtain periphyton density (cells per $m^2$) in each sample. Mean density per site, season and/or lake could then be estimated.

Density of birds was estimated per species from the number of individuals identified during bird counting. Density (number of individuals per $m^2$) was thus calculated as the number of birds counted per species divided by the area sampled. Area sampled corresponded to the whole lake for Tomahawk Lagoon or circular sector centered on each sampling site and

delimited by two 150m shoreline radii and an arc within which birds were counted.

## Biomass

Biomass of organisms (mg fresh weight per $m^2$) was calculated for all taxa. For fish, only one biomass estimate could be calculated per site in each season (4 biomass estimates per season in each lake) because only one density estimate was obtained per site. First we calculated a mean body mass for each fish species in each sampling site. Mean body mass of each species was then multiplied by the species density (number of individuals per $m^2$) in the same sampling site, giving the biomass of each species in each sampling site for all seasons and lakes.

For invertebrates and parasites, biomass was simply the product of the mean individual body mass of each taxon by the density (number of individuals per $m^2$) of that particular taxon in each sample. We thus obtained biomass estimates for all individual samples.

Biomass of macrophytes was calculated as the mass of each species (mg of fresh weight per sample) recovered in Surber nets during benthic samples divided by the surface sampled ($0.1m^2$ with Surber nets). Since 6 replicates were taken in each site, a mean macrophyte biomass per site could be calculated.

Biomass of birds was calculated for each species as the product of the density (number of individuals per $m^2$) of each species observed at each sampling site by the mean individual body mass obtained from the literature.

## Weighted trophic links

Because we recorded diet of predatory taxa both qualitatively and quantitatively, we could calculate weighted trophic links. While the diets of primary consumers were estimated from the literature and the actual food sources available in each sampling site, stomach contents recorded during dissections of predator taxa were used to calculate the proportion of each prey taxon in the diet of predators, both numerically and in terms of biomass/energy transfer. First, we calculated the proportional contribution of each resource taxon, in terms of biomass, to the total diet of a consumer taxon, and assigned a fraction (between 0 and 1) to each resource-consumer link such that the sum of all trophic links toward any consumer species equaled 1. This was done for all consumers.

The diet of grazers and detritivores could not be quantified from stomach contents. Instead, we assumed that the diet of grazers consisted of a mixture of periphyton taxa proportional to their local abundance at the site and season of sampling. The diet of detritivores was assumed to consist entirely of detritus (not measured in the present study).

Many of the top predators in the 4 lake food webs considered here are birds. Because we

were not allowed to sample birds, we used published information on their diet (O'Donnell, 1982; Sagar, P.M., Schwarz, A.-M., Howard-Williams, 1995; Wakelin, 2004) to establish the relative composition of their diet in terms of the main groups of fish or invertebrates or macrophytes. We assumed the diet of the birds at out study site matched that of the same bird species studied elsewhere, and used (where necessary) the species available locally to reconstruct the most likely diet of each bird species.

The 'diet' of each parasite taxon consists of the range of host species they use. For host-specific parasites, i.e., those occurring in only one host species at a given stage of their life cycle, the diet consists only of that host (a single trophic link of value 1 going to the parasite). For parasite species or life stages using more than one host species, we calculated the proportional contribution of each host taxon, in terms of the proportion of the parasite population harbored by each host, to the total diet of the parasite. Each link from a particular host was then assigned a fraction (between 0 and 1) such that the sum of all trophic links toward any parasite equaled 1.

Finally, many parasites are consumed by non-host predators that capture and eat their current host, a phenomenon known as concomitant predation on parasites. This creates trophic links in which these parasites become resources for the non-host predators. From stomach content analysis of all predator taxa, we estimated the contribution of concomitant predation on parasites to each predators diet. Furthermore, we determined whether parasites consumed by non-host predators were digested and thus assimilated to the predators diet or simply lost in the feces without being digested; trematode metacercariae protected by thick cysts are often passed through the feces intact and should not be included in the predators diet. For each parasite life stage of each species, the mean number of parasites per prey item was multiplied by the mean number of individual prey consumed by unsuitable hosts for that parasite. For parasites actually digested by the predator, after converting this number of parasites eaten into biomass, these new links were added to the more traditional prey-predator links going to a consumer, and as above assigned a fraction (always very small) representing their contribution to the total diet of the consumer.

## Potential host taxa for parasite life stages

**Table S2:** Potential host taxa for the parasite life stages observed in this dataset. For each life stage, we identify the host taxa for both the focal life stage and the next life stage in the parasite life cycle. If the next life stage is free-living or the current life stage is the adult (final) stage in the parasite's life cycle, there are no future hosts (indicated by a '-'). In our null model which accounted for parasites' host specificity, only those links where the prey was a potential current host and the predator was a potential future host were included as possible "transmission" links; links where the prey was a potential current host but the predator was not a potential future host were considered possible "loss" links; and all other links were categorized as "unused" (see *Material and Methods, Main Text* for details).

| Parasite | Life stage | Host for focal stage | Host for next stage |
|---|---|---|---|
| *Acanthocephalus galaxii* | Cystacanth | Amphipod | Fish |
| *Acanthocephalus galaxii* | Adult | Fish | - |
| *Anisakidae sp.* | Larva | Unknown | Fish |
| *Apatemon sp.* | Metacercaria | Fish | Bird |
| *Apatemon sp.* | Sporocyst | Gastropod | - |
| *Aporocotylid sp. I* | Sporocyst | Gastropod | - |
| *Coitocaecum parvum* | Metacercaria | Amphipod or Mysid | Fish |
| *Coitocaecum parvum* | Sporocyst | Gastropod | - |
| *Coitocaecum parvum* | Adult | Fish | - |
| *Deretrema sp.* | Adult | Fish | - |
| *Eustrongylides sp.* | Larva | Fish | Bird |
| *Gymnocephalous sp. I* | Redia | Gastropod | - |
| *Gymnocephalous sp. II* | Redia | Gastropod | - |
| *Hedruris spinigera* | Larva | Amphipod | Fish |
| *Hedruris spinigera* | Adult | Fish | - |
| *Hydracarina sp.* | Larva | Insects (aquatic) | - |
| *Lepocreadiidae sp.* | Metacercaria | Leech | Bird |
| *Maritrema poulini* | Metacercaria | Amphipod or Isopod | Bird |
| *Maritrema poulini* | Sporocyst | Gastropod | - |
| *Microphalloidea sp.* | Metacercaria | Trichoptera | Bird |
| *Microphallus livelyi* | Metacercaria | Gastropod | Bird |
| *Microphallus sp.* | Metacercaria | Amphipod or Isopod | Bird |
| *Microphallus sp.* | Sporocyst | Gastropod | - |
| *Neoechinorhynchus sp.* | Adult | Fish | - |
| *Notocotylus sp.* | Metacercaria | Mollusk | Bird |
| *Notocotylus sp.* | Redia | Gastropod | - |
| *Plagiorchioid sp.* | Sporocyst | Gastropod | - |
| *Pronocephaloid sp. I* | Metacercaria | Mollusk | Bird |
| *Pronocephaloid sp. I* | Redia | Mollusk | - |
| *Pronocephaloid sp. IV* | Metacercaria | Mollusk | Bird |
| *Pronocephaloid sp. IV* | Redia | Mollusk | - |
| *Stegodexamene anguillae* | Metacercaria | Fish | Fish |
| *Stegodexamene anguillae* | Redia | Mollusk | - |
| *Stegodexamene anguillae* | Adult | Fish | - |
| *Telogaster opisthorchis* | Metacercaria | Fish | Fish |
| *Telogaster opisthorchis* | Redia | Mollusk | - |
| *Telogaster opisthorchis* | Adult | Fish | - |
| *Tylodelphys sp.* | Metacercaria | Fish | Bird |
| *Virgulate sp. I* | Sporocyst | Mollusk | - |
| *Virgulate sp. II* | Sporocyst | Mollusk | - |
| Acaudate *Xiphidocercaria sp.* | Sporocyst | Gastropod | - |
| Unidentified "*Apatemon sp.*" | Metacercaria | Odonate | Bird |
| Unidentified cestode *sp.* | Larva | Fish | Bird |
| Unidentified nematode *sp.* | Adult | Fish | - |
| Unidentified trematode *sp.* | Metacercaria | Mollusk | Bird |
| Unidentified trematode *sp. A* | Adult | Fish | - |
| Unidentified trematode *sp. B* | Adult | Fish | - |

# Section S2: List of models considered

**Table S3:** The properties included in each model are indicated by 'X'. The full model included terms for each property, and the null model included only an intercept. No interactions among fixed effects were considered. All models also included random effects for lake, season, and parasite life stage. We also give the DIC score for each model when host specificity was ignored ('naive' models) or included as a random effect ('taxonomically-informed' or 'taxon.' models).

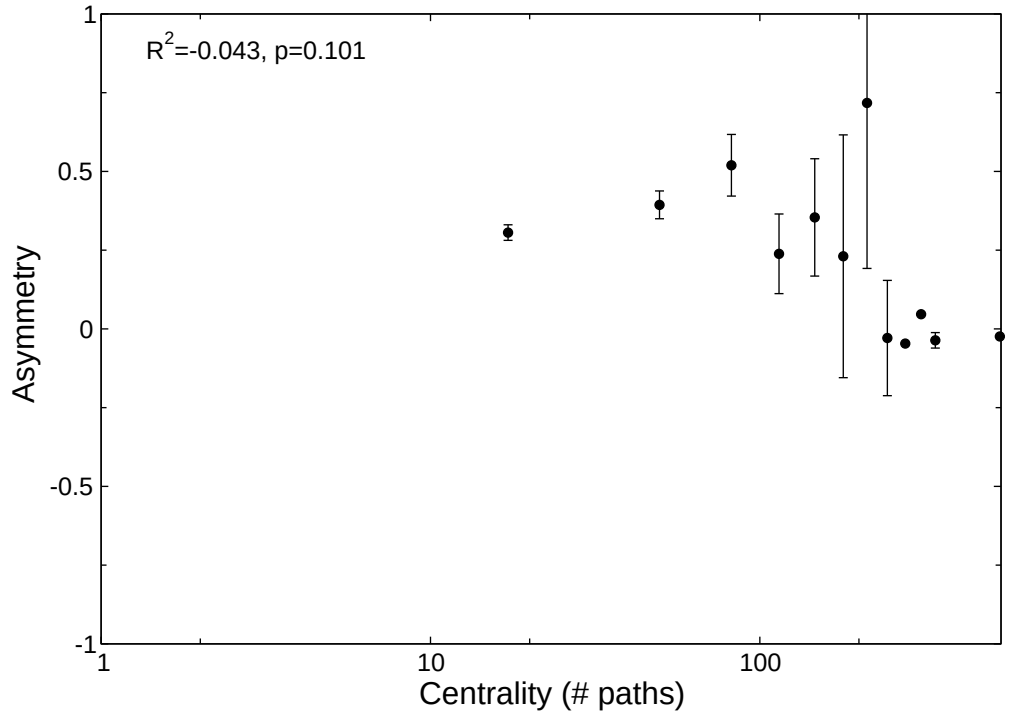
| Model | Contribution to predator's diet | Prey abundance | Prey biomass | Biomass transfer | Centrality | Asymmetry | DIC (naive) | DIC (taxon.) |
|---|---|---|---|---|---|---|---|---|
| 1 (full) | X | X | X | X | X | X | 9103 | 699 |
| 2 | X | X | X | X | X | | 8916 | 709 |
| 3 | X | X | X | X | | X | 9652 | 683 |
| 4 | X | X | X | | X | X | 9057 | 722 |
| 5 | X | X | | X | X | X | 11623 | 682 |
| 6 | X | | X | X | X | X | 9120 | 683 |
| 7 | | X | X | X | X | X | 8725 | 716 |
| 8 | X | X | X | X | | | 9649 | 661 |
| 9 | X | X | X | | X | | 9118 | 702 |
| 10 | X | X | | X | X | | 11584 | 655 |
| 11 | X | | X | X | X | | 8968 | 678 |
| 12 | | X | X | X | X | | 8933 | 734 |
| 13 | X | X | X | | | X | 9946 | 717 |
| 14 | X | X | | X | | X | 12833 | 670 |
| 15 | X | | X | X | | X | 9831 | 649 |
| 16 | | X | X | X | | X | 9930 | 712 |
| 17 | X | X | | | X | X | 11540 | 648 |
| 18 | X | | X | | X | X | 9259 | 732 |
| 19 | | X | X | | X | X | 9054 | 691 |
| 20 | X | | | X | X | X | 11698 | 722 |
| 21 | | X | | X | X | X | 11612 | 716 |
| 22 | | | X | X | X | X | 9013 | 693 |
| 23 | X | X | X | | | | 9771 | 690 |
| 24 | X | X | | X | | | 12890 | 635 |
| 25 | X | X | | | X | | 11825 | 655 |
| 26 | X | X | | | | X | 13071 | 620 |
| 27 | X | | X | X | | | 9644 | 705 |
| 28 | X | | X | | X | | 9143 | 708 |
| 29 | X | | X | | | X | 9893 | 690 |
| 30 | X | | | X | X | | 12023 | 626 |

Table S3, cont.

| Model | Contribution to predator's diet | Prey abundance | Prey biomass | Biomass transfer | Centrality | Asymmetry | DIC (naive) | DIC (taxon.) |
|---|---|---|---|---|---|---|---|---|
| 31 | X | | | X | | X | 12528 | 677 |
| 32 | X | | | | X | X | 11926 | 669 |
| 33 | | X | X | X | | | 9441 | 691 |
| 34 | | X | X | | X | | 9048 | 723 |
| 35 | | X | X | | | X | 10001 | 678 |
| 36 | | X | | X | X | | 11620 | 652 |
| 37 | | X | | X | | X | 12794 | 654 |
| 38 | | X | | | X | X | 11777 | 667 |
| 39 | | | X | X | X | | 9099 | 712 |
| 40 | | | X | X | | X | 9689 | 674 |
| 41 | | | X | | X | X | 9061 | 685 |
| 42 | | | | X | X | X | 11684 | 687 |
| 43 | X | X | | | | | 13146 | 664 |
| 44 | X | | X | | | | 9794 | 642 |
| 45 | X | | | X | | | 12916 | 644 |
| 46 | X | | | | X | | 12134 | 674 |
| 47 | X | | | | | X | 12871 | 661 |
| 48 | | X | X | | | | 9524 | 719 |
| 49 | | X | | X | | | 13118 | 639 |
| 50 | | X | | | X | | 11931 | 696 |
| 51 | | X | | | | X | 13177 | 654 |
| 52 | | | X | X | | | 9631 | 663 |
| 53 | | | X | | X | | 8983 | 716 |
| 54 | | | X | | | X | 9613 | 678 |
| 55 | | | | X | X | | 12012 | 670 |
| 56 | | | | X | | X | 12542 | 642 |
| 57 | | | | | X | X | 12058 | 686 |
| 58 | X | | | | | | 13285 | 632 |
| 59 | | X | | | | | 13269 | 664 |
| 60 | | | X | | | | 9800 | 629 |
| 61 | | | | X | | | 13157 | 633 |
| 62 | | | | | X | | 12317 | 659 |
| 63 | | | | | | X | 12879 | 641 |
| Null | | | | | | | 13296 | 617 |

# Section S3: Correlation between asymmetry and centrality

**Figure S2:** Asymmetry and centrality were not significantly correlated. We show the best-fit loess regression (red line) with a 95% confidence interval (shaded area) together with the means (±2 SE) of the observed property for 10 bins.



# Section S4: Supplemental model summaries

**Table S4:** Posterior means and 95% confidence intervals of parameter estimates in the second-best model which incorporated parasite host-specificity (DIC=620 compared to DIC=617 for the best-fitting model). Note that this model also contained random effects for lake, season, parasite life stage, and the set of potential outcomes for each link.

| | Loss | | | Transmission | | |
|---|---|---|---|---|---|---|
| Parameter | Mean | 95% CI | pMCMC | Mean | 95% CI | pMCMC |
| Intercept | -8.30 | (-9.96, -6.46) | <0.001 | -9.07 | (-10.9, -6.95) | <0.001 |
| Contribution to predator's diet | 0.046 | (-0.053, 0.130) | 0.550 | -0.034 | (-0.116, 0.032) | 0.433 |
| log(Prey abundance) | -0.437 | (-1.757, 1.172) | 0.600 | 0.176 | (-0.829, 1.425) | 0.842 |
| Asymmetry | 0.177 | (0.016, 0.279) | 0.028 | -0.058 | (-0.233, 0.144) | 0.562 |

**Table S5:** Posterior means and 95% confidence intervals of parameter estimates in the third-best model which incorporated parasite host-specificity (DIC=626 compared to DIC=617 for the best-fitting model). Note that this model also contained random effects for lake, season, parasite life stage, and the set of potential outcomes for each link.

| | Loss | | | Transmission | | |
|---|---|---|---|---|---|---|
| Parameter | Mean | 95% CI | pMCMC | Mean | 95% CI | pMCMC |
| Intercept | -8.50 | (-10.2, -6.53) | <0.001 | -9.54 | (-11.7, -7.18) | <0.001 |
| Contribution to predator's diet | 0.049 | (-0.010, 0.110) | 0.143 | -0.007 | (-0.097, 0.122) | 0.831 |
| log(Biomass transfer) | 1.042 | (-0.660, 2.174) | 0.126 | -0.656 | (-3.044, 1.075) | 0.898 |
| log(Centrality) | 1.247 | (0.229, 2.038) | <0.001 | 1.204 | (-0.020, 1.782) | 0.068 |

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