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3 **Trematode parasites exceed aquatic insect biomass in Oregon stream food webs**

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8 *Estimating catch efficiencies* – We conducted mark-recapture surveys and three-pass  
9 electrofishing at one reach in each stream (Oak, Soap, Berry) to estimate the catch efficiencies of  
10 reticulate sculpin, cutthroat trout, Pacific giant salamanders, brook lamprey, and signal crayfish.  
11 We set up block nets at the upstream and downstream ends of the reach (~ 45 m in reach length).  
12 On the first day of each mark-recapture survey, we used three-pass electrofishing to capture all  
13 five species with a four-person crew. We used a backpack electroshocker (Smith-Root LR20B),  
14 a block net (1.0 x 1.0 m) and two dip nets (0.30 x 0.25 m) to collect fish, salamanders, and  
15 crayfish. Each captured vertebrate was anesthetized with Aqui-S and then marked with a clip on  
16 the tail fin or toe (for salamanders) using sterilized scissors. Crayfish were marked with a clip on  
17 the telson. Lamprey were not marked. After a recovery period in aerated stream water, all  
18 organisms were released. Twenty-four hours after the initial surveys, we re-surveyed each site  
19 with single-pass electroshocking. For sculpin and trout, we followed Krebs (1989) to estimate  
20 abundances within each habitat unit based on the number of fish marked on the first visit, the  
21 total caught on the second visit, and the number marked on the second visit. For salamanders,  
22 lamprey, and crayfish, the total captures were too low to generate mark-recapture estimates. For  
23 these three taxa, we estimated abundances based on three-pass depletion estimates (Hauer and

24 Lamberti 2007). We used the 'FSA' package in R (Ogle 2017) to conduct the mark-recapture and  
25 three-pass depletion analyses. The estimated catch efficiencies of single-pass electrofishing  
26 based on these methods were 36% for sculpin; 44% for trout; 27.5% for salamanders; 47.6% for  
27 crayfish; and 26.6% for lamprey. These capture efficiency estimates were then used to estimate  
28 abundances of the five taxa in our field surveys based on the numbers captured.

29 *Trematode identifications* – All observed trematodes were grouped into cercarial  
30 morphotypes and compared to local species from *Juga* snails described in the literature (Burns  
31 and Pratt 1953, Bennington and Pratt 1960, Burns 1961, McCauley and Pratt 1961, Pratt and  
32 McCauley 1961, Meade and Pratt 1965). For future studies, representative *Juga* snails and all the  
33 trematodes sequenced were deposited as vouchers in the Museum of Southwestern Biology  
34 (Hoberg et al., 2009; Holmes et al., 2016) and sequences were submitted to GenBank  
35 (accession MW000373-MW000456). In addition to our morphological assessment, we  
36 sequenced trematodes from two to five infected snails per observed morphotype. We used a  
37 region of the nuclear rDNA 28S gene as a yardstick to determine trematode genetic diversity as a  
38 proxy for species diversity. This region was chosen because a) the primers used work across a  
39 wide range of digenean families and b) most of the digenean genetic diversity in the NCBI  
40 GenBank sequence database has at least some stretch of 28S represented. To obtain genetic data  
41 from the samples, DNA was extracted from 1-2 cercariae with the QIAamp DNA Micro Kit  
42 (Qiagen, Valencia, California) according to manufacturer's guidelines, except samples were  
43 eluted with 30ul of buffer. DNA was amplified by PCR (TaKara Ex Taq kit, Takara  
44 Biomedicals, Otsu, Japan) and sequenced (about 900 bases of the 5' end of 28S) with previously  
45 published primers (28S nDNA region primers U178 and L1642 Lockyer et al., 2003). PCR  
46 products were purified with QIAQuick PCR Purification Kit (Qiagen, Valencia, USA) and

47 sequenced using the Applied Biosystems BigDye direct sequencing kit, version 3.1 (Applied  
48 Biosystems, Foster City, CA, USA). Chromatograms were edited in Sequencher v 5.0 (Gene  
49 Codes Corporation, Ann Arbor, MI, USA). All sequences were BLASTED to those taxa  
50 available in the GenBank sequence database to assemble putative identifications.

51         The most common trematodes were members of the superfamily Microphalloidea, at least  
52 some of which grouped with the family Lecithodendriidae based on the molecular data.  
53 Morphologically, some of these cercariae were consistent with a species described as  
54 *Acanthatrium oregonense* (Burns 1961), although the presence of at least three cryptic species  
55 with similar cercarial morphology is indicated by the molecular data. The cercariae that grouped  
56 within the Hemiuroidea were morphologically consistent with the species *Deropegus aspina*,  
57 which has been reported locally from *Juga* snails (McCauley and Pratt 1961, Law 1975).  
58 Samples of trematodes in the genus *Plagioporus* were closely aligned with the recently described  
59 *P. hageli* (99% similarity), although *P. siliculus* has also been recorded from *Juga* in our study  
60 region and may also be present (Fayton and Andres 2016). Lastly, the Aporocotylid was very  
61 consistent morphologically with the species *Sanguinicola* (= *Cardicola*) *alseae*, and probably  
62 represents this taxon (Meade and Pratt 1965). Additional work describing the diversity of  
63 trematodes from *Juga* snails would be useful to further clarify identities of the species observed  
64 in our study.

65         *Juga* prey identification times – Detailed methods on estimating prey identification times  
66 are provided in Preston et al. 2017. Methods and results on *Juga* prey identification times in  
67 reticulate sculpin are provided in Preston et al. 2018. Here, we focus on feeding trials involving  
68 Pacific giant salamanders, which were not previously published. We did not derive a specific  
69 prey identification time function for trout. *Juga* snails were extremely rare in trout diets (5 snails

70 recovered from 479 trout) and we did not attempt to feed *Juga* snails to trout in the laboratory.  
71 For this reason, we applied the mean prey identification time of snails in sculpin and salamanders  
72 to the five *Juga* snails consumed by trout. Relative to variation driven by predator densities, prey  
73 masses, and the number of prey consumed, applying this mean prey identification time to trout  
74 prey should not have strongly affected the estimated biomass flows.

75 A total of 21 salamanders ranging from 51 to 157 mm in total body length (mean = 105  
76 mm) were fed 109 *Juga* snails over multiple feeding trials. Each salamander was locally  
77 collected from Berry, Oak, or Soap creeks and housed individually in a temperature controlled  
78 room. For separate trials, the temperature was varied between 10.5°C and 18°C and the size of  
79 *Juga* snails varied from 3 mm to 18.5 mm. The co-variables were varied in a continuous and  
80 randomized manner across trials. The salamanders were lavaged between 20 and 100 hours post-  
81 feeding. We then fit Weibull survival curves to the observed prey status (identifiable or not) as a  
82 function of the covariates (Klein and Moeschberger 2005, Kleinbaum and Klein 2006). We used  
83 the *Survival* package in R (Therneau 2015). The estimated laboratory coefficients from the  
84 Weibull survival functions were used with observed covariate information from our field surveys  
85 (i.e. salamander and snail sizes and water temperatures) to estimate prey identification times for  
86 each snail recovered from the salamander's stomach. For each snail, the identification time was  
87 estimated as the mean of the probability density function that corresponded to the Weibull  
88 survival function under the observed covariate values (Preston et al. 2017). We then used the  
89 average *Juga* snail prey identification times within each survey to calculate the feeding rates  
90 using eqn. 1.

91 The mean prey identification time of *Juga* snails in salamanders (i.e. the time at which  
92 snails could no longer be recovered from stomach contents) was 63 hours. As expected, increases

93 in water temperature, increases in predator size, and decreases in prey body size all decreased  
94 prey identification times. The survival and density functions for prey identification times of *Juga*  
95 snails in salamanders under average co-variate values are shown in Fig. S7.

96 *Juga growth rates* – To quantify *Juga* snail growth rates, we deployed them into Oak  
97 Creek for a period of 76 days (July 19 to Oct 3, 2018). The snails were marked using a numbered  
98 label (3.2 x 1.6 mm) that was printed on weatherproof paper and then affixed to the shell of the  
99 snail using Super Glue brand adhesive. Glue was applied beneath and above the label, forming a  
100 protective coating. After marking, snails were provided a recovery period in stream water and  
101 then deployed into the cages. Stream cages were 0.5 m<sup>2</sup> in area and were constructed of a  
102 rectangular PVC plastic frame that was covered in plastic mesh (2 mm openings). We deployed  
103 40 snails in each of 5 cages, which is on the low end of the observed snail densities in Berry,  
104 Oak, and Soap Creeks. Snails were measured for total shell length, operculum diameter, and wet  
105 mass before and after being deployed in the stream cages. At the beginning of the deployment  
106 period, snails ranged in total length from 7 to 27 mm.

107 All of the marked snails survived the duration of the caging study. We found that the  
108 labelling method resulted in ~60% of the labels remaining attached and legible after the  
109 deployment period. Growth rate estimates were therefore based on 126 of the 200 snails. We  
110 adjusted the estimated snail ages from the growth rate function to account for a lack of growth  
111 over four winter months each year, which is observed in natural *Juga* populations (Furnish  
112 1989). The oldest individuals in the populations were estimated to be ~7 years in age,  
113 corresponding with previous estimates of the maximum lifespan for *Juga* snails (Diamond 1982).  
114 Growth rates decreased with increasing snail size. On average, snails increased by 3.18 mg day<sup>-1</sup>  
115 g<sup>-1</sup> wet mass and 9.4 x 10<sup>-4</sup> mm day<sup>-1</sup> mm<sup>-1</sup> shell length. We also compared the *in situ* snail

116 growth rate estimates from cages with previously published values, which were similar (Earnest  
117 1967, Diamond 1982, Furnish 1989).

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**Table S1.** Stream organisms observed in field surveys in Oak, Soap, and Berry Creeks. The 'Regression Applied' and 'Source' columns indicate where the equations to estimate dry mass originated for each taxon. In some cases, equations from closely related taxa or higher taxonomic levels (i.e. Order) were applied. The 'Equation' column provides the estimated dry mass based on either body size in mm (L) or wet mass in grams (WM). Estimated dry masses from the equations are in milligrams for benthic invertebrates and grams for salamanders, sculpin, and trout. This table was modified from Preston et al. 2018.

Order	Family	Life Stage	Regression Applied	Equation	Source
Achatinoidea	Semisulcospiridae	Juvenile	Species ( <i>Juga plicifera</i> )	$0.00002 * L^{2.6534}$	Preston et al. 2018
Amphipoda			Order (Amphipoda)	$0.0058 * L^{3.015}$	Benke et al. 1999
Annelida			Family (Lumbriculidae)	$\exp(-9.19 + 3.25 * \log(L))$	Miserendino 2001
Araneae			Family (Elmidae)	$0.0074 * L^{2.879}$	Benke et al. 1999
Bivalve			Species ( <i>Juga plicifera</i> )	$0.00002 * L^{2.6534}$	Preston et al. 2018
Coleoptera		Adult	Order (Coleoptera)	$\exp(-2.0076 + 3.2271 * \log(L))$	Towers et al. 1994
Coleoptera	Elmidae	Adult	Family (Elmidae)	$\exp(-2.0076 + 3.2271 * \log(L))$	Towers et al. 1994
Coleoptera	Elmidae	Larvae	Family (Elmidae)	$0.0074 * L^{2.879}$	Benke et al. 1999
Collembola			Order (Collembola)	$\exp(-1.8749 + 2.3002 * \log(L))$	Ganihar 1997
Copepod			Order (Amphipoda)	$0.0058 * L^{3.015}$	Benke et al. 1999
Decapoda	Astacidae		Species ( <i>Pacifastacus leniusculus</i> )	$WM * 0.28$	This study
Diptera		Adult	Order (Diptera)	$0.0025 * L^{2.692}$	Benke et al. 1999
Diptera	Athericidae	Larvae	Family (Athericidae)	$0.004 * L^{2.586}$	Benke et al. 1999
Diptera	Cecidomyiidae	Larvae	Order (Diptera)	$0.0025 * L^{2.692}$	Benke et al. 1999
Diptera	Ceratopogonidae	Larvae	Family (Ceratopogonidae)	$0.0025 * L^{2.469}$	Benke et al. 1999
Diptera	Chironomidae	Larvae	Family (Chironomidae)	$0.0018 * L^{2.617}$	Benke et al. 1999
Diptera	D023	Adult	Order (Diptera)	$0.0025 * L^{2.692}$	Benke et al. 1999
Diptera	Dixidae	Larvae	Family (Dixidae)	$0.0025 * L^{2.692}$	Benke et al. 1999
Diptera	Empididae	Larvae	Family (Empididae)	$0.0054 * L^{2.546}$	Benke et al. 1999
Diptera		Larvae	Order (Diptera)	$0.0025 * L^{2.692}$	Benke et al. 1999
Diptera	Pelecorhynchidae	Larvae	Family (Pelecorhynchidae)	$0.0025 * L^{2.692}$	Benke et al. 1999
Diptera	Psychodidae	Larvae	Family (Psychodidae)	$0.0025 * L^{2.692}$	Benke et al. 1999

Diptera	Ptychopteridae	Larvae	Family (Ptychopteridae)	$0.0025 * L^{2.692}$	Benke et al. 1999
Diptera		Pupae	Order (Diptera)	$0.0025 * L^{2.692}$	Benke et al. 1999
Diptera	Simuliidae	Larvae	Family (Simuliidae)	$0.002 * L^{3.011}$	Benke et al. 1999
Diptera	Stratiomyidae	Larvae	Order (Diptera)	$0.0025 * L^{2.692}$	Benke et al. 1999
Diptera	Tanyderidae	Larvae	Order (Diptera)	$0.0025 * L^{2.692}$	Benke et al. 1999
Diptera	Tipulidae	Larvae	Family (Tipulidae)	$0.0029 * L^{2.681}$	Benke et al. 1999
Ephemeroptera		Adult	Order (Ephemeroptera)	$0.0071 * L^{2.832}$	Benke et al. 1999
Ephemeroptera	Ameletidae	Larvae	Family (Ameletidae)	$0.0077 * L^{2.588}$	Benke et al. 1999
Ephemeroptera	Baetidae	Larvae	Family (Baetidae)	$0.0053 * L^{2.875}$	Benke et al. 1999
Ephemeroptera	Ephemerellidae	Larvae	Family (Ephemerellidae)	$0.0103 * L^{2.676}$	Benke et al. 1999
Ephemeroptera	Heptageniidae	Larvae	Family (Heptageniidae)	$0.0108 * L^{2.754}$	Benke et al. 1999
Ephemeroptera	Leptophlebiidae	Larvae	Family (Leptophlebiidae)	$0.0047 * L^{2.686}$	Benke et al. 1999
Ephemeroptera	Potamanthidae	Larvae	Family (Potamanthidae)	$0.0056 * L^{2.839}$	Benke et al. 1999
Hemiptera			Order (Hemiptera)	$0.0108 * L^{2.734}$	Benke et al. 1999
Hemiptera	Gerridae		Family (Gerridae)	$0.015 * L^{2.596}$	Benke et al. 1999
Hemiptera	Mesoveliidae		Family (Mesoveliidae)	$0.0108 * L^{2.734}$	Benke et al. 1999
Hemiptera	Saldidae		Order (Hemiptera)	$0.0108 * L^{2.734}$	Benke et al. 1999
Hemiptera	Veliidae		Family (Veliidae)	$0.0126 * L^{2.719}$	Benke et al. 1999
Hydracharina			Order (Hydracharina)	$\exp(-2.02 + 1.66 * \log(L))$	Baumgartner and Rothhaup 2003
Isopoda			Order (Amphipoda)	$0.0058 * L^{3.015}$	Benke et al. 1999
Lepidoptera			Order (Diptera)	$0.0025 * L^{2.692}$	Benke et al. 1999
Megaloptera	Sialidae	Larvae	Order (Megaloptera)	$0.0037 * L^{2.838}$	Benke et al. 1999
Neuroptera			Order (Megaloptera)	$0.0037 * L^{2.838}$	Benke et al. 1999
Odonata	Gomphidae	Larvae	Family (Gomphidae)	$0.0088 * L^{2.787}$	Benke et al. 1999
Ostracoda			Order (Amphipoda)	$0.0058 * L^{3.015}$	Benke et al. 1999
Plecoptera		Adult	Order (Plecoptera)	$0.0094 * L^{2.754}$	Benke et al. 1999
Plecoptera	Capnidae	Larvae	Order (Plecoptera)	$0.0094 * L^{2.754}$	Benke et al. 1999
Plecoptera	Chloroperlidae	Larvae	Family (Chloroperlidae)	$0.0065 * L^{2.724}$	Benke et al. 1999

Plecoptera		Larvae	Order (Plecoptera)	$0.0094 * L^{2.754}$	Benke et al. 1999
Plecoptera	Leuctridae	Larvae	Order (Plecoptera)	$0.0094 * L^{2.754}$	Benke et al. 1999
Plecoptera	Nemouridae	Larvae	Family (Nemouridae)	$0.0056 * L^{2.762}$	Benke et al. 1999
Plecoptera	Peltoperlidae	Larvae	Family (Peltoperlidae)	$0.0170 * L^{2.737}$	Benke et al. 1999
Plecoptera	Perlidae	Larvae	Family (Perlidae)	$0.0099 * L^{2.879}$	Benke et al. 1999
Plecoptera	Perlodidae	Larvae	Family (Perlodidae)	$0.0196 * L^{2.742}$	Benke et al. 1999
Plecoptera	Pteronarcyidae	Larvae	Family (Pteronarcyidae)	$0.0324 * L^{2.573}$	Benke et al. 1999
Salmoniformes	Salmonidae		Family (Salmonidae)	WM*0.21	Lantry and O'Gorman 2007
Scorpaeniformes	Cottidae		Species ( <i>Cottus perplexus</i> )	WM*0.24	Lantry and O'Gorman 2007
Thysanoptera		Adult	Order (Diptera)	$0.0025 * L^{2.692}$	Benke et al. 1999
Trichoptera	Calamoceratidae	Larvae	Family (Calamoceratidae)	$0.0056 * L^{2.839}$	Benke et al. 1999
Trichoptera	Glossosomatidae	Larvae	Family (Glossosomatidae)	$0.0082 * L^{2.958}$	Benke et al. 1999
Trichoptera	Hydropsychidae	Larvae	Family (Hydropsychidae)	$0.0046 * L^{2.926}$	Benke et al. 1999
Trichoptera		Larvae	Order (Trichoptera) Family	$0.0056 * L^{2.839}$	Benke et al. 1999
Trichoptera	Lepidostomatidae	Larvae	(Lepidostomatidae)	$0.0079 * L^{2.649}$	Benke et al. 1999
Trichoptera	Philopotamidae	Larvae	Order (Trichoptera) Family	$0.0056 * L^{2.839}$	Benke et al. 1999
Trichoptera	Polycentropodidae	Larvae	(Polycentropodidae)	$0.0047 * L^{2.705}$	Benke et al. 1999
Trichoptera	Rhyacophilidae	Larvae	Family (Rhyacophilidae)	$0.0099 * L^{2.48}$	Benke et al. 1999
Urodela	Ambystomatidae	Larvae	Family (Salamandridae)	WM*0.14	Preston et al. 2012

**Table S2.** *Juga* dissected in each stream reach from Berry, Oak, and Soap creeks. The number of snails dissected per reach, trematode infection prevalence, and the minimum, maximum, mean, and standard deviation of the shell sizes of dissected individuals are provided in the table.

Stream	Reach	<i>Juga</i> Dissected	Infection Prevalence (%)	<i>Juga</i> Shell Length (mm)			
				Mean	St. Dev.	Min.	Max.
Berry	1	245	6.1	12.5	4.1	4	24
Berry	2	194	7.2	13.7	3.9	4	25
Berry	3	106	17.0	13.7	4.6	4	30
Oak	1	126	25.4	14.8	5.7	5	31
Oak	2	119	17.6	15.8	5.1	5	29
Oak	3	132	22.7	15.9	5.0	1	25
Soap	1	112	25.9	16.2	5.1	5	30
Soap	2	133	32.3	14.2	5.4	4	26
Soap	3	195	45.1	16.3	5.3	4	26

**Table S3.** Trematode voucher numbers in the Museum of Southwestern Biology and GenBank accession numbers for samples that were sequenced. The samples sequenced were collected in the focal study streams (Oak, Soap or Berry Creeks) for five of the morphotypes observed in the current study. One of the trematodes was very rare at the study streams and the sequence data came from samples collected at other streams within the Willamette Valley (Aporocotylidae).

<b>Taxon</b>	<b>MSB Catalog No.</b>	<b>GenBank Accession</b>	<b>Stream</b>	<b>Lat</b>	<b>Long</b>
Hemiuroidea	MSB:Para:30782	MW000382	Oak Creek	44.6069752	-123.33222
Hemiuroidea	MSB:Para:25351	MW000454	Soap Creek	44.642105	-123.31421
Hemiuroidea	MSB:Para:25355	MW000448	Soap Creek	44.642105	-123.31421
<i>Metagonimoides</i>	MSB:Para:30734	MW000402	Oak Creek	44.5596773	-123.28926
<i>Metagonimoides</i>	MSB:Para:25352	MW000455	Soap Creek	44.642105	-123.31421
<i>Metagonimoides</i>	MSB:Para:25353	MW000456	Soap Creek	44.642105	-123.31421
<i>Metagonimoides</i>	MSB:Para:25354	MW000447	Soap Creek	44.642105	-123.31421
Microphalloidea	MSB:Para:25350	MW000453	Oak Creek	44.601473	-123.33466
Microphalloidea	MSB:Para:30756	MW000411	Oak Creek	44.6069752	-123.33222
Microphalloidea	MSB:Para:30757	MW000412	Oak Creek	44.6069752	-123.33222
Microphalloidea	MSB:Para:30820	MW000415	Soap Creek	44.64244	-123.33031
<i>Nanophyetus</i>	MSB:Para:25349	MW000452	Oak Creek	44.601473	-123.33466
<i>Nanophyetus</i>	MSB:Para:30755	MW000374	Oak Creek	44.5596773	-123.28926
<i>Nanophyetus</i>	MSB:Para:25356	MW000449	Soap Creek	44.642105	-123.31421
<i>Nanophyetus</i>	MSB:Para:30766	MW000375	Soap Creek	44.64244	-123.33031
<i>Plagioporus</i>	MSB:Para:25357	MW000450	Soap Creek	44.642105	-123.31421
<i>Plagioporus</i>	MSB:Para:25358	MW000451	Berry Creek	44.707344	-123.29873
Aporocotylidae	MSB:Para:30742	MW000445	King Creek	44.1617371	-122.16854
Aporocotylidae	MSB:Para:30749	MW000441	Hills Creek	43.9878153	-122.8233
Aporocotylidae	MSB:Para:30751	MW000446	Dell Creek	43.7860451	-122.54838
Aporocotylidae	MSB:Para:30792	MW000444	Hills Creek	43.9878153	-122.8233
Aporocotylidae	MSB:Para:30799	MW000442	Taylor Creek	44.0718429	-122.75116
Aporocotylidae	MSB:Para:30800	MW000443	McKenzie River	44.0558698	-122.82871

**Table S4.** Sample sizes of *Juga* snails dissected for biomass quantification of five trematode taxa. The mean snail size and the percentage of trematode tissue per taxon are shown. A sixth trematode taxon (Aporocotylidae) was extremely rare and was not quantified for trematode biomass.

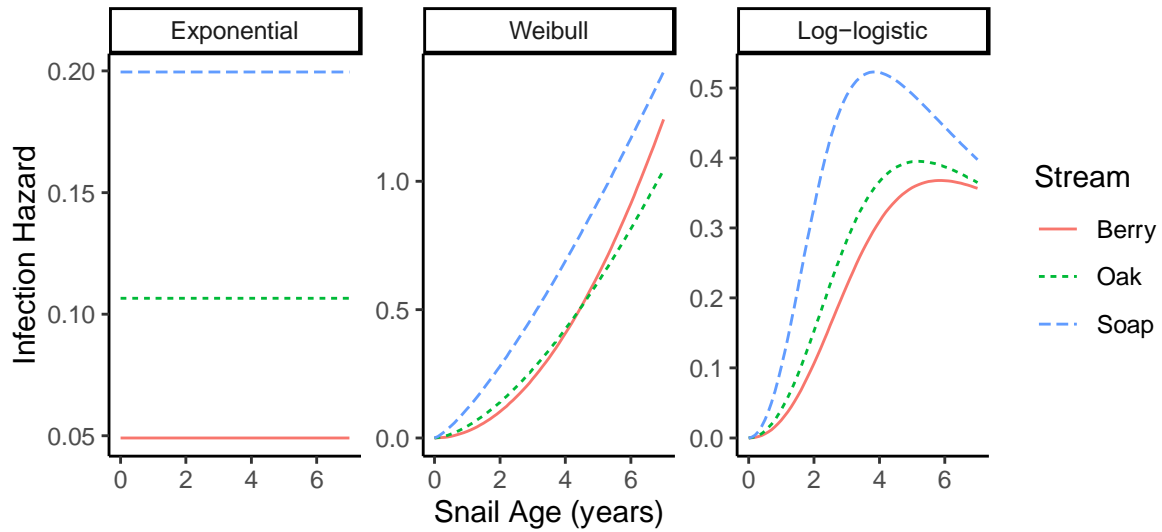
Taxon	<i>Juga</i> Dissected	Mean Snail Size (mm) (+/- SE)	Mean % Trematode Tissue (+/- SE)
<i>Plagioporus</i>	2	18.5 (+/- 0.50)	17.8 (+/- 0.14)
Hemiuroidea	16	20.4 (+/- 0.41)	28.1 (+/- 2.1)
Microphalloidea	21	22.6 (+/- 0.61)	31.0 (+/- 1.7)
<i>Nanophyetus</i>	19	22.4 (+/- 0.65)	33.7 (+/- 2.4)
<i>Metagonimoides</i>	17	23.7 (+/- 1.00)	45.0 (+/- 2.9)

**Table S5.** Effects of varying the estimates of snail age on the transfer of biomass from snails to trematodes. The top row presents the estimated mean across all three streams based on the original function to estimate snail age. The rows below show estimates when snails ages are adjusted by +/- 1 standard deviation, +/- 2 standard deviations, and +/- 3 standard deviations. The standard deviation is based on the mean estimated snail ages in each of the nine stream reaches.

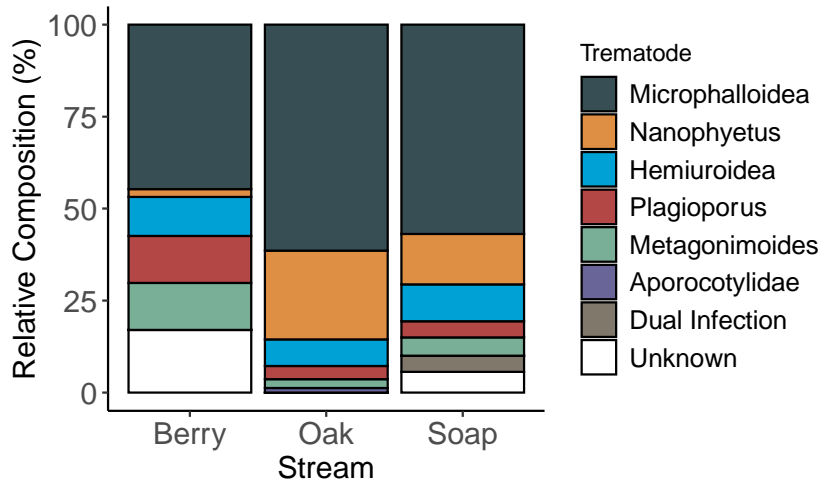
Snail Age Variation	Snail Transfer to Trematodes (g m <sup>-2</sup> yr <sup>-1</sup> )
None	0.384
1 SD	0.277 to 0.514
2 SD	0.192 to 0.664
3 SD	0.131 to 0.834

**Table S6.** Force of infection models, AIC values, and model parameters that were estimated from functions fit to the *Juga* snail age-prevalence data in each stream. The Weibull model provided the best relative performance of the candidate models for all streams.

Model	Stream	AIC	Alpha (hazard)	Beta
Exponential	Soap	453.6	0.20	na
Weibul	Soap	412.6	0.27	2.30
Loglogistic	Soap	415.9	0.33	3.01
Exponential	Oak	328.2	0.11	na
Weibul	Oak	295.1	0.21	2.61
Loglogistic	Oak	300.2	0.24	3.05
Exponential	Berry	284.1	0.05	na
Weibul	Berry	261.7	0.20	2.99
Loglogistic	Berry	263.5	0.22	3.16

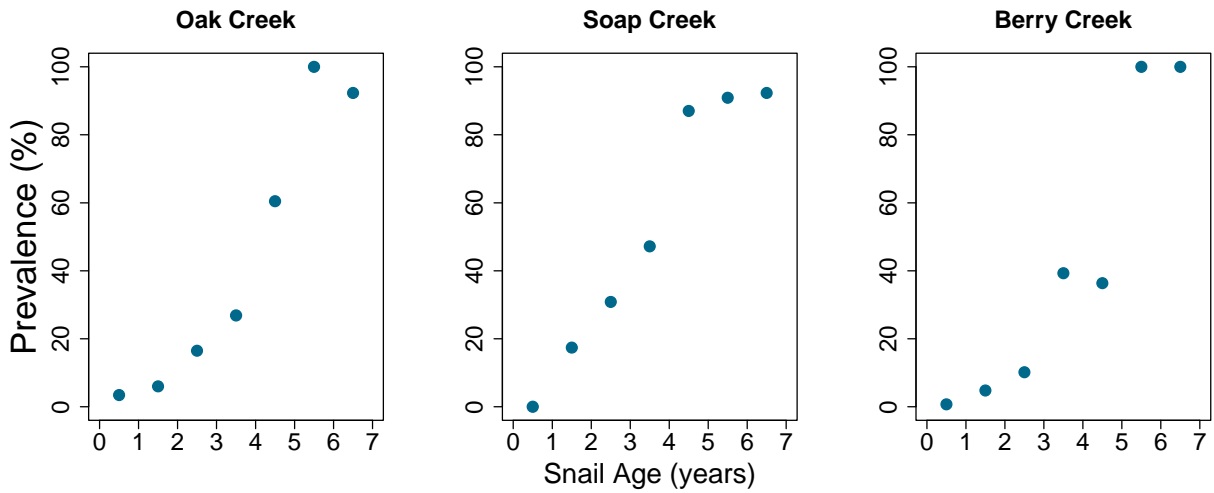


**Figure S1.** Infection hazards from exponential, Weibull, and log-logistic models that were fit to the age-prevalence data. The Weibull model (center) provided the best relative fit (lowest AIC) and indicated that infection risk increased with snail age at all streams.

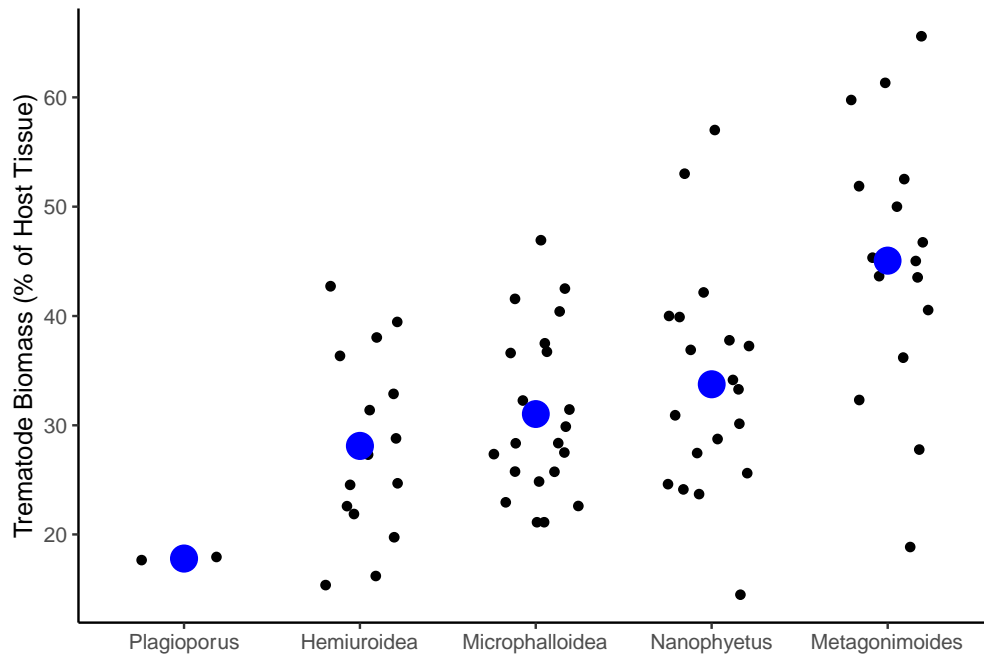


**Figure S2.** Trematode community composition across the three streams. Total numbers of infected snails were 47 of 545 (Berry), 83 of 377 (Oak), and 160 of 440 (Soap).

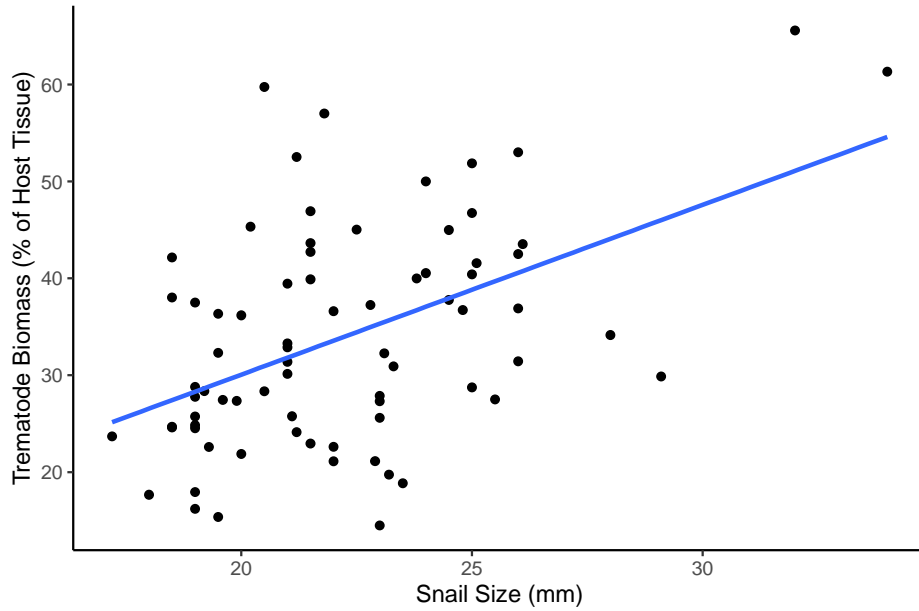




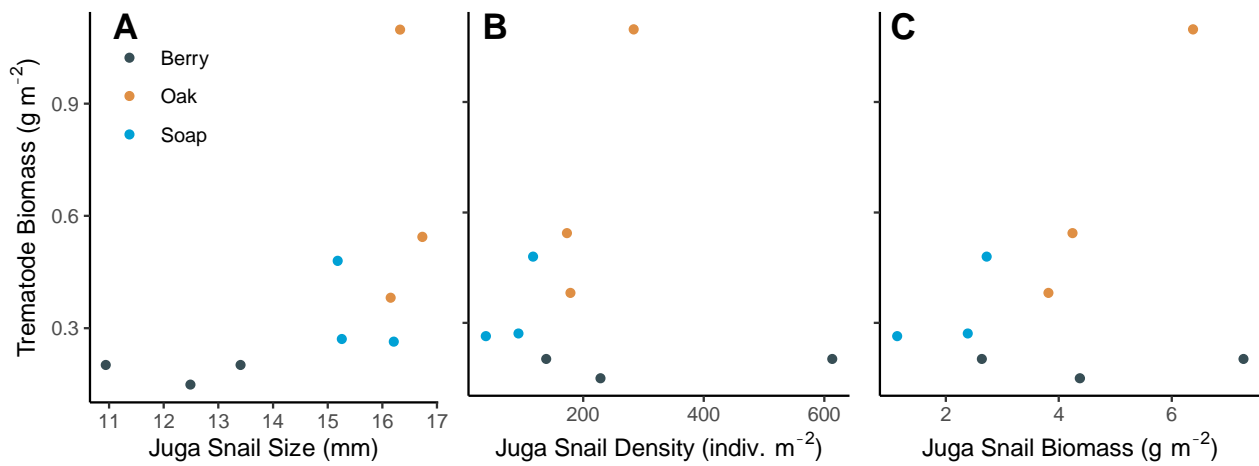
**Figure S3.** Age-prevalence curves for the snail dissected from each of the three streams.



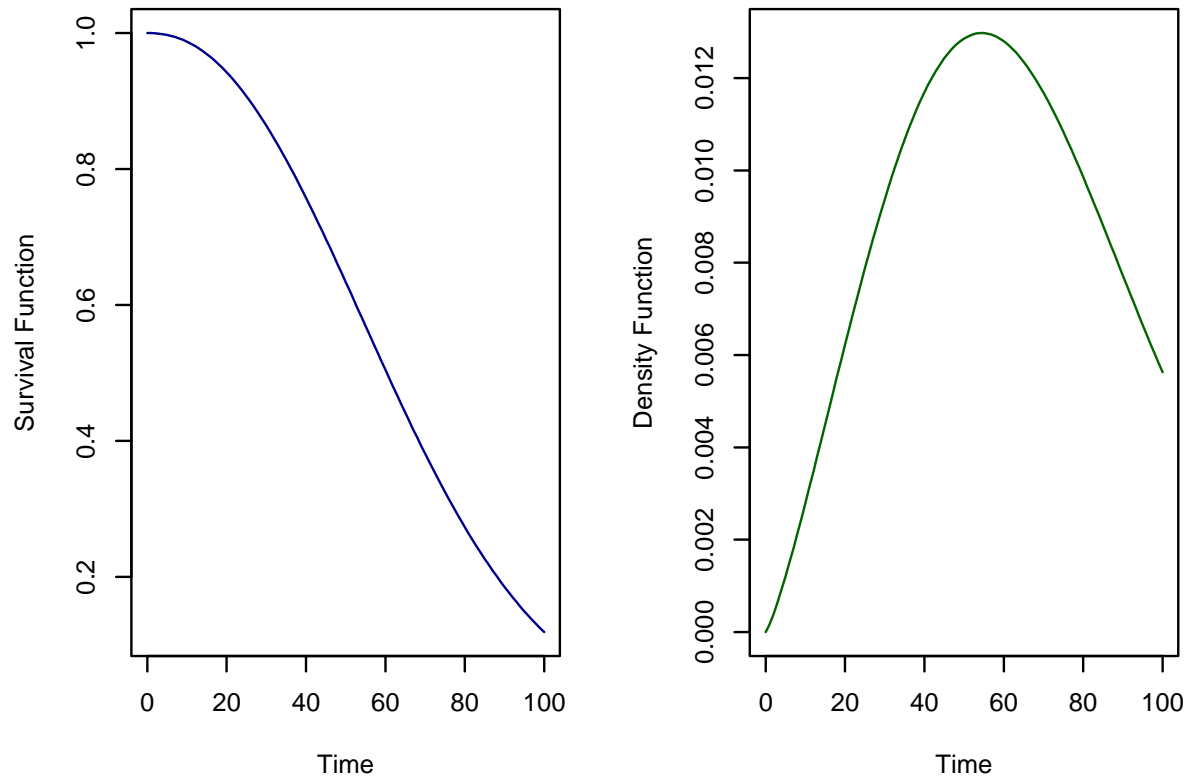
**Figure S4.** Trematode biomass as a proportion of individual *Juga* host snail tissue biomass. The blue points indicate the mean proportional trematode biomass and the points are individual biomasses from each snail dissected. Proportions exclude the mass of the snail shell. Sample sizes of infected snails that were dissected for trematode biomass quantification are as follows: *Plagioporus* (n = 2), *Hemiuroidea* (n = 16), *Microphalloidea* (n = 21), *Nanophyetus* (n = 19), *Metagonimoides* (n = 17).



**Figure S5.** Proportional trematode biomass per host as a function of host snail size ( $n = 75$  snail dissected from 5 trematode taxa).



**Figure S6.** Trematode biomass density per stream reach plotted against snail population characteristics, including mean snail shell size (A), mean snail density (B), and mean snail biomass (C).



**Fig. S7.** Survival and probability density functions for prey identification times of *Juga* snails consumed by Pacific giant salamanders (times in hours in shown on the x-axis). The functions shown include mean covariate values for water temperature, snail size and salamander size based on the laboratory feeding trials. The mean prey identification time was 63 hours