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# Can parasites be indicators of free-living diversity? Relationships between species richness and the abundance of larval trematodes and of local benthos and fishes

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**Abstract** Measuring biodiversity is difficult. This has led to efforts to seek taxa whose species richness correlates with the species richness of other taxa. Such indicator taxa could then reduce the time and cost of assessing the biodiversity of the more extensive community. The search for species richness correlations has yielded mixed results, however. This may be primarily because of the lack of functional relationships between the taxa studied. Trematode parasites are highly promising bioindicators. Diverse assemblages of larval trematode parasites are easily sampled in intermediate host snails. Through their life cycles these

parasites are functionally coupled with the surrounding free-living diversity of vertebrate and invertebrate animals. It has been shown that larval trematodes in snails correlate positively with bird diversity and abundance. Here, we explore whether trematodes also correlate with standard measures of fishes, and large and small benthos, for 32 sites in three wetlands. We found associations between trematodes and benthic communities that were not consistent across wetlands. The associations were, however, consistently positive for large benthic species richness and density. Some of the contrasting associations between trematode and benthos may be explained by negative associations between large and small benthos. We found no associations with fish communities (probably because of the inadequacy of standard “snapshot” sampling methods for highly mobile fishes). The results support further exploration of trematodes as bioindicators of diversity and abundance of animal communities.

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## Introduction

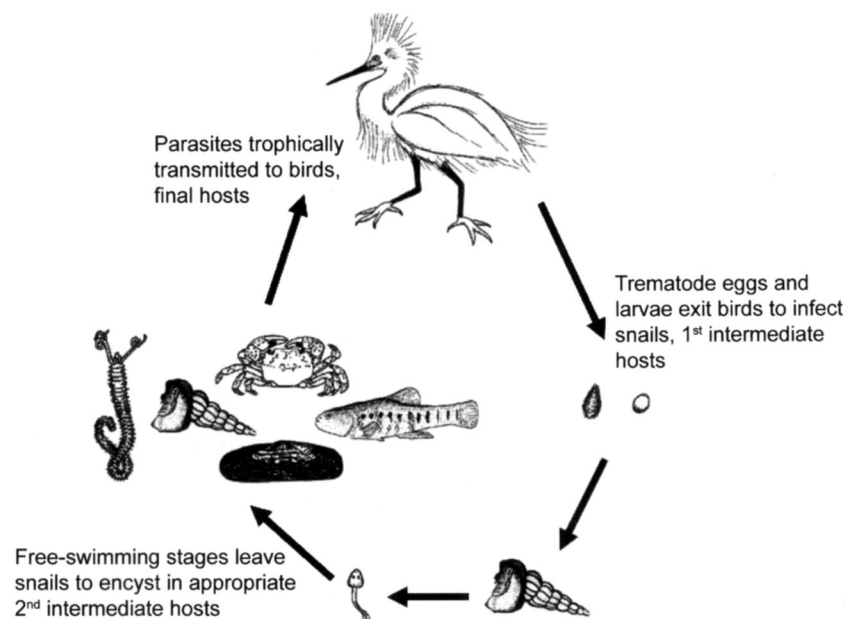
People love shortcuts. Scientists and habitat managers are not immune to this, particularly given the limited time and resources available to accomplish difficult tasks, for example assessment of biodiversity. In such assessments we often want information about multiple taxa from several replicated sites. Yet, measuring the biodiversity of entire communities is extremely difficult or impossible. This difficulty has led to a search for indicator taxa whose species richness is consistently corre-

lated with the species richness of other taxa (Lawton et al. 1998; Vessby et al. 2002; Olsgard et al. 2003; Kati et al. 2004). Varied results from this search led Gunnarsson et al. (2004) to suggest focusing on groups of organisms that provide habitat or resources for other groups of organisms. Because these organisms are *functionally* coupled, correlations between the condition (e.g., diversity and abundance) of these groups would tend to be more consistent than those between taxa without such direct connections. But, the problem here is that the presence of the indicator group (the providers of habitat or resources) does not necessitate the presence of the groups to be indicated (the users of the habitat or resources). The converse situation does not suffer from this weakness, however. Organisms that obligatorily use other organisms as habitat or resources should be excellent indicators. The indicator groups directly depend on the condition of the groups to be indicated. Many parasites have multiple-host life cycles that necessarily link them to several different taxa of surrounding animal communities. These sorts of parasite may therefore be excellent indicators of other components of community structure and function (Gardner and Campbell 1992; Marcogliese and Cone 1998). Here, we explore how an easily sampled community of trematode parasites in snails is associated with more difficult to sample communities of fishes and benthic invertebrates. The discovery of relationships between these parasites and surrounding free-living community components would strongly support further exploration of these parasites as bioindicators.

Trematode flatworm parasites are a particularly promising indicator group (Kuris and Lafferty 1994; Huspeni and Lafferty 2004; Huspeni et al. 2005), because it is common for many trematode species to specialize on the same snail species as first intermediate host (where they can be efficiently sampled) but to diverge in the other hosts they use to complete their life cycles (where they are associated with many species at higher trophic levels) (Fig. 1). In these circumstances high species richness of parasites in snail hosts *requires*, and thus indicates, the presence of numerous other taxa (i.e. the hosts required for other parts of the life cycles). Further, most trematodes are trophically transmitted to final hosts in their life cycles. Thus, not only do such parasites reflect the presence of surrounding taxa, they are also directly indicative of functioning trophic linkages (Gardner and Campbell 1992; Marcogliese and Cone 1998).

In many aquatic and marine systems birds act as important hosts for adult trematodes and are the sources of the trematode stages that infect snails (Fig. 1). Hechinger and Lafferty (2005) demonstrated positive correlations between the diversity of birds and diversity of trematodes infecting snail populations. This pattern probably exists because different trematode species use different bird species as final hosts. Smith (2001), Hechinger and Lafferty (2005), and Fredensborg et al. (2006) also found positive associations between the abundance of birds and the prevalence of trematode parasites in snails. This was expected, because birds should transmit more trematodes to

**Fig. 1** A generalized representation of the trematode life cycles in our system



snails in areas where birds are more common. Trematodes are good indicators of birds, because accurately quantifying bird communities on small spatial scales and long-term scales is difficult (Hechinger and Lafferty 2005; Huspeni et al. 2005).

In this study we investigate whether, like birds, local fish and benthic invertebrate communities are positively associated with local trematode communities in snails. This prediction has two general bases (Huspeni et al. 2005). First, fishes and benthic invertebrates attract birds (Colwell and Landrum 1993; Gawlik 2002), which are the sources of the trematode stages that infect snails. Thus, sites with greater species richness and abundance of fishes and benthos should have greater richness and abundance of birds. Consequently, this brings a greater richness and abundance of trematodes to infect snails. Second, as mentioned above, different trematode species use different fishes and benthic invertebrates as second intermediate hosts. A diverse and abundant trematode community in snails does not, therefore, merely reflect, but on some scale requires, the presence of diverse and abundant fishes and benthic invertebrates. We also predicted, because we assessed benthic invertebrates and fishes using standard “snapshot” techniques, that trematodes would most strongly associate with the more stationary component of the community—that is, the benthos—rather than the vagile fishes. Determining whether ecological relationships exist between trematodes and free-living communities is a critical step in assessing their value as bioindicators (McGeoch 1998). Here we find associations that suggest we should further investigate the use of larval trematodes as indicators of surrounding free-living species richness and abundance.

## Materials and methods

### Study system

We studied a community of 20 trematode species that complete their life cycles (Fig. 1) in Pacific tidal wetlands of California and Mexico. These trematodes parasitize populations of the California horn snail (*Cerithidea californica* (Haldeman 1840)), as first intermediate host (Martin 1972 and references therein; Sousa 1983, 1990; Kuris 1990). Infections in snails are usually long-lived (Sousa 1983, 1990; Kuris 1990). The parasites continually asexually produce swimming stages (cercariae) which leave their host snail to encyst in, or on, second intermediate hosts. Different species of trematodes infect different types of second intermediate hosts, for example fishes, clams, polychaetes, and

crabs. The parasites are tropically transmitted to final host wetland birds when the birds eat second intermediate hosts (except for one of the trematode species, which lacks a second intermediate host and the cercariae infect birds directly). The trematodes mature in the birds, usually in the digestive tract. Trematode eggs or larvae pass with the birds' excreta and subsequently infect snails. Thus, although the 20 species of these trematodes diverge with regard to which hosts they require to complete their life cycles, they all converge in populations of the horn snail. Information on which second intermediate and bird final hosts are used by the different trematode species is available elsewhere (Huspeni and Lafferty 2004; Lafferty et al. 2006).

### Field sampling

We sampled fish, benthic invertebrate, and snail trematode assemblages in three California coastal wetlands (Morro Bay (35.34°N, 120.83°W), Carpinteria Salt Marsh (34.40°N, 119.53°W), and Mugu Lagoon (34.10°N, 119.10°W)) in the summers of 2001 and 2002. We sampled 20 sites in 2001 (four at Morro, eight at Carpinteria, and eight at Mugu) and 12 different sites in 2002 (four at Morro, three at Carpinteria, and five at Mugu). Each site was a 20-m stretch of tidal creek running through pickleweed (*Salicornia virginica*) salt marsh. Tidal creeks ranged from 2.8 to 29.5 m in width (mean 10.5 m, median 7.9 m). The sites with horn snails were selected as part of other extensive ecological projects (details are available on the website for the Pacific Estuarine Ecosystem Indicator Research Consortium at <http://www.bml.ucdavis.edu/peeir/>). In 2001, the sites were selected to ensure interspersed throughout each wetland. In 2002, in each wetland, sites were chosen along one or more tidal creeks to ensure interspersed throughout the reach of each creek. Although sites were in different tidal creeks or separated by at least 150 m, spatial autocorrelation could still have resulted in non-independence of the data. To assess whether this was a problem for measures of trematode abundance and species richness, we calculated the exact probability of each site being more similar to its nearest neighbor than expected by chance (on the basis of the frequency of being equally or more similar to non-nearest neighbors). Only 3/32 sites (for trematode abundance) and 1/30 sites (for trematode species richness) had nearest neighbor similarities with  $P \leq 0.05$ . Because the probability of observing this many or fewer  $P \leq 0.05$  by chance alone is respectively 0.73 and 0.34 (calculated using the binomial probability function; Sokal and Rohlf 1981), we did not regard spatial autocorrelation as a problem.



To assess the fish community at each site, we employed a standard technique widely used to monitor coastal wetlands in southern California (PERL 1990). During mid-tidal levels we isolated a 20-m stretch of channel by rapidly deploying two blocking nets. We then sequentially made five passes between the blocking nets with a 10 m two-pole seine. All nets had a mesh size of 3.2 mm. All captured fish were identified to species (in accordance with Miller and Lea 1972) and counted on-site. For each site, we calculated the species richness and density of the total fish community.

At each site, we separately characterized large and small benthic animals. We sampled the large benthos (e.g. crabs and bivalves) using large cores, and the small benthos (e.g. amphipods and polychaetes) using small cores. Large cores were 78.5 cm<sup>2</sup> in area, 50 cm deep and were sieved on-site through a 3-mm mesh screen. We identified to species the specimens retained on the sieves (primarily in accordance with Smith and Carlton 1975; McLean 1978; Morris et al. 1980; Coan et al. 2000). We released most animals at the site of capture but some were returned to the laboratory for identification and to provide voucher specimens. We excluded taxa from the large core analysis that were primary targets of small cores (mainly polychaetes). Small cores were 19.6 cm<sup>2</sup> in area and 5 cm deep. These were fixed in 10% formalin after collection and sieved later in the laboratory through a 0.5-mm mesh. Animals remaining on the sieve were then stained with Rose Bengal, sorted, and the specimens were identified to lowest possible taxonomic category, primarily by use of the identification guides cited above. To position replicate cores at each site, we adopted an elevationally stratified sampling layout widely used to monitor coastal wetlands in southern California (PERL 1990). We sampled three elevations at each site:

- 1 high (just below the lower limit of the pickleweed);
- 2 low (the deepest part of the channel); and
- 3 mid (the elevational mid-point).

At each elevation, we took three replicates of both core types (large and small), spaced 10 m apart (in 2002, we took five replicates of each core type at the low elevation, 5 m apart). For each site, for large and small benthos, we calculated species richness (“taxonomic richness” for small cores) and total density. To control for sampling effort when calculating species richness we ignored the two additional large cores taken at the low elevation in 2002 (but the additional cores were still used to provide improved density estimates). Some small cores from three Morro Bay sites

were lost before processing. Two of these sites were excluded from all analyses; one (for which most cores were not lost) was still used for small benthos density estimates.

To assess larval trematode communities we haphazardly collected 100 20–25 mm *Cerithidea californica* snails from within 10 m of each site (from within 50 m, occasionally, because of low-snail density). Snails were dissected in the laboratory and their infection status was determined. We identified all trematodes to species, in accordance with Martin (1972) and Huspeni and Hechinger (unpublished manuscript). For each site, we described the trematode community by calculating species richness and the summed prevalence of all trematode species ( $\times 100$ ). Because we encountered multiple-species infection in some snails, the summed prevalence of trematode species better described trematode numbers than did simple prevalence of infected snails. Also, trematode assemblages in snail populations often have high levels of interspecific competition and competitive loss (because dominant trematode species infect snails and kill subordinate trematode species) (Kuris and Lafferty 1994). Thus, observed trematode prevalence may significantly underestimate actual numbers (because many of the subordinates have been killed; Kuris and Lafferty 1994; Lafferty et al. 1994). We therefore also calculated summed “pre-interactive” prevalence using the techniques outlined in Lafferty et al. (1994). The formulas, using knowledge of the trematode dominance hierarchy (Kuris 1990; Huspeni 2000), simply apply the prevalence of each trematode species in “competitor-free” snails to the portion of the snail population infected with dominant trematode species. This provides an estimate of how many subordinate infections have been killed. Pre-interactive prevalence for each trematode species is then, simply, the number of killed infections plus the number of observed infections divided by the total number of sampled snails. To determine whether pre-interactive prevalence offered additional insight, we used these values in analyses parallel to those using observed trematode prevalences (detailed below). We excluded two sites from species-richness analyses because we were unable to sample 100 first intermediate host snails, because of low-snail abundance.

#### Data analysis

Our primary goal was to discover any associations between the trematode community in snails at a site and common measures of the free-living fish and benthic invertebrate communities at the same site. We

therefore separately analyzed relationships between species richness and the prevalence of trematodes and the three free-living assemblages measured (fishes, small benthos, and large benthos). We used general linear models (GLMs) with trematode measures as predictor variables and the free-living measures as response variables.

We were also interested in determining whether relationships were consistent between wetlands. Thus, each initial full model included, as predictor variables, the trematode measure (species richness or prevalence), wetland (Mugu Lagoon, Carpinteria Salt Marsh, and Morro Bay), and the trematode  $\times$  wetland interaction (i.e., the initial full model fitted separate regression lines, for each wetland, between trematodes and the free-living assemblages). In accordance with Neter et al. (1996) and Quinn and Keough (2002), when interactions were included, we used centered trematode predictor variables to eliminate problems of collinearity. We sequentially deleted interaction terms and wetland when their contributions to the model were not significant ( $P > 0.10$ ). When there was an indication that the relationship between trematodes and a free-living assemblage differed between wetlands (i.e. when the trematode  $\times$  wetland interaction was significant), we investigated whether the two most similar wetlands should be combined. This was done primarily to determine whether trematodes consistently indicated the free-living assemblage in those two wetlands. To do this we performed partial  $F$ -tests, comparing the full model (with all three wetlands and their interaction with trematodes) to the reduced model (combining the two most similar wetlands and maintaining a wetland  $\times$  trematode interaction term) (Neter et al. 1996; Quinn and Keough 2002). Because we sampled each of the three wetlands over 2 years, we also determined whether the effect of wetland was affected by year. The effect of wetland on all of the fish or benthic invertebrate measures was consistent across years (i.e. there were no wetland  $\times$  year interactions; all  $P > 0.20$ ). Thus, we did not consider year further and focused on wetland as the potential cofactor with the trematode measures.

Some of the free-living benthic species do not usually serve as hosts for any of the horn snail trematodes (but all of the fish species are potential hosts). This is particularly true for the small benthos (e.g. nematodes and insects are not trematode hosts in our system). We would expect relationships between trematodes and free-living assemblages to be strongest for those taxa that are potential hosts for trematodes. We therefore performed parallel analyses for the large and small benthic assemblages, one set using only potential host

species and another using all encountered species. We determined which species or taxa were potential hosts using the best available knowledge (published data and our unpublished data on trematode host use; Martin 1972; Lafferty et al. 2006 and references therein).

To gain insight into potential mechanisms explaining the relationships with trematodes we occasionally examined relationships between different measures of the free-living assemblages. These associations were analyzed using GLMs, again by following the general procedure described above.

We ensured assumptions regarding homogeneity of variance and approximate normality of residuals were met by inspecting plots of residuals against model-predicted values, and normal quantile plots with Lilliefors' curves (Neter et al. 1996; Quinn and Keough 2002). All  $P$ -values are conservatively two-tailed (even though our hypotheses were one-tailed). Also, we focus on nominal  $P$ -values (with a critical value of 0.05 for each test) but also considered the effect of multiple comparisons on the family wide error rate for the final tests in each taxon. All significant  $P$ -values remained significant after controlling the family wide error rate by using the sharper sequentially rejective Bonferroni procedure (Hochberg 1988). We performed all analyses using the software platform JMP Version 5.1.2 (2003 SAS Institute).

## Results

We sampled 39,930 fish of 18 species, 894 individual large benthic animals of 20 species, and 60,345 individual small benthic animals of 92 taxa (electronic supplementary material (ESM) Table S1). We also dissected 3,079 snails and discovered 926 individual trematode infections belonging to 16 species (Table 1). We estimated the total pre-interactive trematode prevalence to be 1,003 individuals (Table 1).

There were always positive associations between benthic species richness and density measures using potential hosts and measures including all species (Fig. S1). These correlations were extremely (and necessarily) strong for the large benthos (Figs. S1a, b), because there were only a few rare species of large benthos that are not potential hosts for trematodes (Table S1). The positive relationships were also very strong for small benthos densities, but less so for species richness (Figs. S1c, d).

Fish species richness was not associated with trematode species richness (Fig. 2a,  $R^2=0.069$ ,  $F_{1,28}=2.09$ ,  $P=0.16$ ,  $n=30$ ). Neither wetland nor its interaction with trematode richness were significant factors ( $F_{2,26}=0.085$ ,  $P=0.92$ , and  $F_{2,24}=0.21$ ,  $P=0.81$ , respectively).

**Table 1** Trematode species sampled from first intermediate host California horn snails (*Cerithidea californica*), their total abundances, and second intermediate host use

Species	Total abundance	Total pre-interactive abundance	Primary second intermediate host used <sup>a</sup>
<i>Euhaplorchis californiensis</i> <sup>b</sup>	324	348	Fish
<i>Himastha rhigedana</i>	137	138	Crabs
Small cyathocotylid	100	104	Fishes
<i>Probolocoryphe uca</i>	78	87	Crabs, amphipods <sup>c</sup>
<i>Himastha</i> sp. B	49	52	Snails, annelids
<i>Renicola buchmanii</i>	45	51	Fishes
<i>Acanthoparyphium spinulosum</i>	42	47	Clams, snails, annelids <sup>d</sup>
Large xiphidiocercaria (renicolid)	39	46	Annelids <sup>e</sup>
<i>Catatropis johnstoni</i>	36	46	Snails
<i>Austrobilharzia</i> sp.	15	15	None
<i>Parorchis acanthus</i>	15	15	Clams, shrimp
<i>Phocitrema ovale</i>	12	14	Fishes
<i>Cloacitrema michiganensis</i>	11	12	Clams, shrimp
<i>Pygidiopsisoides spindalis</i>	11	13	Fishes
<i>Mesostephanus appendiculatus</i>	9	11	Fishes
<i>Renicola cerithidicola</i>	3	4	Fishes

<sup>a</sup> Information on second intermediate host use is based primarily on our familiarity with the system (but see Martin 1972 and references therein; Huspeni and Lafferty 2004; Lafferty et al. 2006)

<sup>b</sup> Approximately 7% of these were *Stictodora hancocki*, which was unrecognized in 2001. For consistency across years we combined the 23 *S. hancocki* encountered in 2002 with *Euhaplorchis californiensis*

<sup>c</sup> We have recently discovered that our “*Probolocoryphe uca*” were actually two microphallid trematode species, one of which uses crabs and one which uses gammaridean amphipods (Hechinger and Smith, unpublished data)

<sup>d</sup> On the basis of preliminary data (Hechinger and Smith, unpublished data) and a note in Martin (1972), *Acanthoparyphium spinulosum* may be two cryptic *Acanthoparyphium* species with different second intermediate host specificities

<sup>e</sup> Hechinger and Smith (unpublished data)

The species richness of potential host large benthos was positively associated with trematode species richness for all three wetlands (Fig. 2c,  $R^2=0.43$ ,  $F_{1,28}=21.2$ ,  $P<0.0001$ ,  $n=30$ ). Here, neither wetland nor its interaction with trematode richness were significant factors ( $P=0.60$  and  $0.45$ , respectively). We obtained similar results when we included non-host large benthic invertebrate species (Fig. S2a).

Our final model for potential host small benthos species richness indicated that trematode species richness was positively related to potential host small benthos richness for two wetlands and negatively in the other wetland (Fig. 2e; effect of trematode richness and its interaction: partial  $R^2=0.41$ ,  $F_{2,23}=8.13$ ,  $P=0.0021$ ; full model  $R^2=0.41$ ,  $P=0.0060$ ,  $n=27$ ). The initial complete model suggested there was an interaction between wetland and trematode species richness (interaction effect,  $F_{2,21}=3.76$ ,  $P=0.070$ ; full model  $R^2=0.51$ ,  $P=0.0075$ ,  $n=27$ ). The regression line for Morro Bay had a negative slope whereas those for Carpinteria Salt Marsh and Mugu Lagoon were positive. This model (allowing separate effects and regressions for all three wetlands) was not significantly better than the final model, combining Carpinteria Salt Marsh and

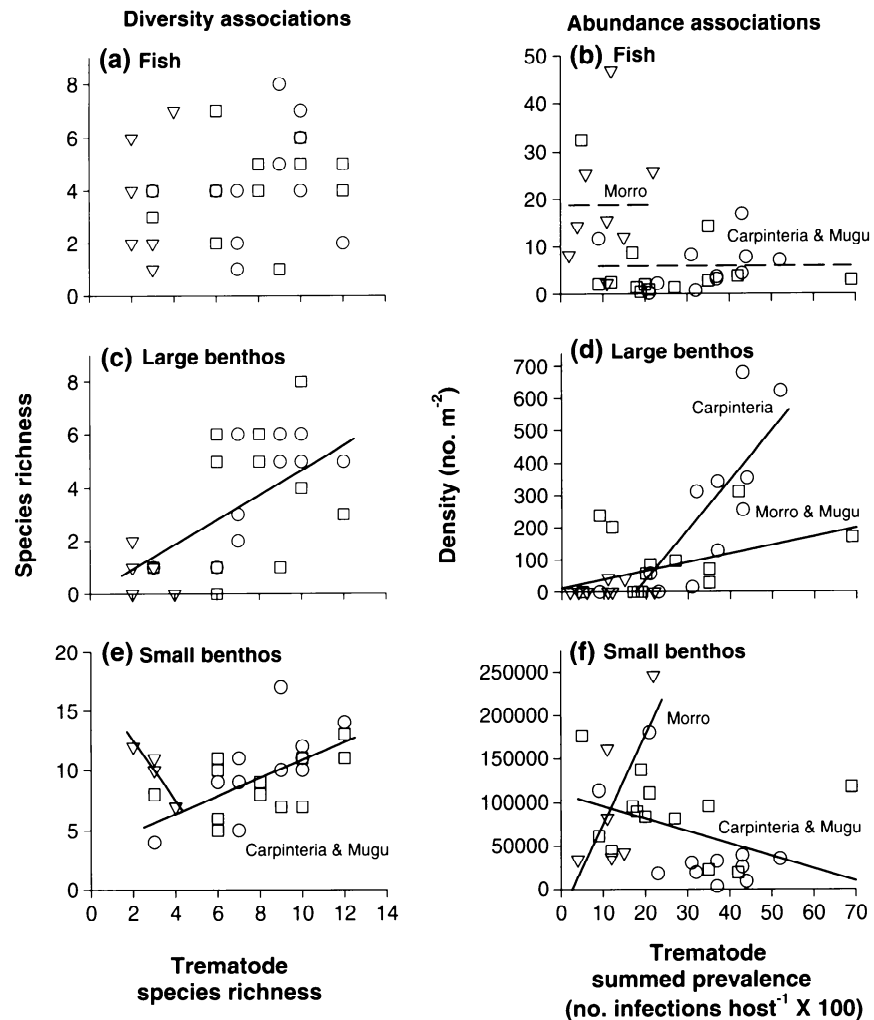
Mugu Lagoon ( $F_{2,21}=2.00$ ,  $P=0.16$ ). We obtained similar results when we included non-host species in the analysis (ESM S2c).

There was a positive association between large and small benthos species richness (which we examined because both were positively related to trematode richness). We found this positive relationship whether we analyzed host species only, or all large and small benthos species (Fig. S3). In the analysis using all benthic species (Fig. S3b), there was a significant effect of wetland, with Morro Bay having more small benthic species than either Carpinteria Salt Marsh or Mugu Lagoon (~3–13 more species, 95% confidence intervals, Tukey HSD).

Fish density was not associated with trematode prevalence (Fig. 2b; partial  $R^2=0.0033$ ,  $F_{1,28}=0.092$ ,  $P=0.76$ ,  $n=32$ ). Here, wetland was a significant factor affecting fish density ( $F_{2,28}=3.60$ ,  $P=0.041$ ), but the wetland × trematode prevalence interaction was not significant ( $F_{2,26}=0.89$ ,  $P=0.42$ ).

Our final model for density of potential host large benthos indicated that trematode prevalence was positively related to density of potential host large benthos, strongly in one wetland and weakly over the other two

**Fig. 2** Trematode species richness and abundance associations with potential host fishes (a, b), small benthos (c, d), and large benthos (e, f) in three coastal wetlands, Morro Bay (open triangles), Carpinteria Salt Marsh (open circles), and Mugu Lagoon (open squares). Trend lines are shown for when trematodes were significantly associated with the free-living community component. The dashed lines in b indicate the significant effect of wetland ( $P=0.041$ ). The names of the appropriate wetlands are placed near the lines when separate regressions for different wetlands best described associations.  $R^2$  and  $P$ -values for the effect of trematodes (including their interactions for d, e, and f) are  $R^2=0.069$ ,  $P=0.16$  for a;  $R^2=0.0033$ ,  $P=0.76$  for b;  $R^2=0.43$ ,  $P<0.0001$  for c;  $R^2=0.54$ ,  $P<0.0001$  for d;  $R^2=0.41$ ,  $P=0.0021$  for e; and  $R^2=0.30$ ,  $P=0.011$  for f



wetlands (Fig. 2d; effect of trematode prevalence and its interactions, partial  $R^2=0.54$ , partial  $F_{2,28}=16.3$ ,  $P<0.0001$ ; full model  $R^2=0.66$ ,  $P<0.0001$ ,  $n=32$ ). The initial complete model showed that the relationship between large benthos density and trematode prevalence varied across wetlands (interaction effect:  $F_{2,26}=8.0$ ,  $P=0.0020$ ; full model  $R^2=0.67$ ,  $P<0.0001$ ,  $n=32$ ). The regression slope for Carpinteria Salt Marsh was strongly positive whereas the slopes for Morro Bay and Mugu Lagoon were less so (that for Morro Bay being almost flat). Further model comparison revealed that Morro Bay and Mugu Lagoon could be combined. That is, keeping all three wetlands separate did not significantly provide further explanatory power than did combining the two similar wetlands ( $F_{2,26}=0.55$ ,  $P=0.59$ ). Inclusion of non-host large benthos species yielded similar results (Fig. S2b).

Our final model for potential host small benthos density showed that trematode prevalence associated with host small benthos density, positively at one

wetland and negatively at the other two wetlands (Fig. 2f; effect of trematode prevalence and interactions, partial  $R^2=0.30$ ,  $F_{2,26}=5.44$ ,  $P=0.011$ ; full model  $R^2=0.33$ ,  $P=0.015$ ,  $n=30$ ). The initial complete model indicated there was significant variation across wetlands with regard to the relationship between trematode prevalence and the density of small benthos (interaction effect:  $F_{2,24}=5.32$ ,  $P=0.012$ ; full model  $R^2=0.43$ ,  $P=0.015$ ,  $n=30$ ). Further analysis revealed that this model (keeping each wetland separate) was not significantly better than the model combining the two most similar wetlands, Carpinteria Salt Marsh and Mugu Lagoon ( $F_{2,24}=2.08$ ,  $P=0.15$ ). Inclusion of non-host small benthos species yielded similar results (Fig. S2d).

Because there were inconsistent associations of trematode abundance with large and small benthos density, we examined the relationship between these two components of the benthos. There was a negative association between the density of large and small



benthos for all three wetlands, whether we used potential host species, or all benthic species (Fig. S4).

Similar results were obtained when we used pre-interactive trematode prevalence to examine associations with free-living assemblage densities (see ESM S5).

## Discussion

Previous work has identified consistent positive relationships between the diversity and abundance of trematode communities in snails and final host bird communities (Smith 2001; Hechinger and Lafferty 2005; Fredensborg et al. 2006). In this work we have found evidence suggesting the existence of associations between free-living benthic communities and communities of trematode parasites in snails. Our results also indicate, however, that these relationships may not be consistent in all wetlands. Overall, the clearest findings were for species richness and for large benthos. Trematode species richness was positively associated with species richness of large and small benthic invertebrates (although, for small benthos, only in the two wetlands for which we have the most data). With regard to measures of abundance, we found no consistent relationships between trematode prevalence and benthos or fish densities. Trematode prevalence was, however, positively associated with the density of large benthic invertebrates in all wetlands.

Why did we find no associations between larval trematode communities and measures of the fish community? We had expected this outcome because we used a standard “snap-shot” sampling of the vagile (and thus highly temporally variable) fish community. Seining with blocking nets is not likely to accurately characterize the fish community’s temporally integrated use of a site. An example of this may be seen in Fig. 2b—the four data points with the highest fish densities (and for which trematode prevalence is low) are sites where, by chance, we captured large groups of mobile schooling fishes (*Fundulus parvipinnis* or *Atherinops affinis*), which may have simply been “passing through”. Trematode infections in snails should, on the other hand, integrate the temporal variation in fish use of a site (because trematodes are long-lived in snails). This suggests that the lack of an association between fishes and trematodes might reflect the inadequacies of standard seining methods for counting fishes, rather than inadequacies of trematodes to act as indicators of fish communities. This question must probably be examined on the scale of a drainage system within wetlands, rather than on the small scale evaluated here

(see below), or fishes must be sampled in a more time-integrative fashion.

Even when trematodes are significantly associated with the benthos, there is much variation about the regression lines for these relationships (Fig. 2). In particular, there are sites with relatively large numbers of trematode species but with few species of large benthic invertebrates (Fig. 2b). Can insufficient sampling of benthos also explain much of the unexplained variation in their relationships with trematodes? We know from personal experience that standard coring can miss benthic species present at a site. Of course, predatory birds (which bring the trematodes to snails) would not be as likely to miss the presence of benthic prey.

The associations we observed between trematodes and the benthos were not strongly affected by whether we included non-host species in the analyses. This was expected for large benthos, because non-host taxa are few and rare (necessitating the observed tight correlations between measures using or excluding non-host taxa (Figs. S1a, b). The similar results are, however, particularly interesting for small benthos, because a relatively large number of taxa and individuals (e.g. nematodes and insects; Table S1) are non-hosts. Here too, however, the similar results are explained because measures of small benthic hosts strongly covary with measures of small benthos that include non-hosts (Figs. S1c, d), although the species richness relationship has more unexplained variation.

Associations among the free-living taxa could confound interpretations of the associations between free-living taxa and trematodes. For example, we suggest that the unexpected negative association in two wetlands between trematode prevalence and small benthos density (Fig. 2f) can be explained by the negative correlation between the densities of large and small benthos in those wetlands (Fig. S4). Large benthic animals (e.g. brachyuran crabs) may directly reduce the density of small benthos (e.g. polychaetes) by predation (Quammen 1984) and, logically, via asymmetric competition for space. This negative association could also arise indirectly, as a result of the different components of the benthos responding differently to environmental conditions. For example, some small benthic animals (e.g. the polychaete *Capitella capitata*) can dominate the benthos under conditions unfavorable for most animals (Nordby and Zedler 1991). The negative association between large and small benthos densities contrasts with the positive correlation between the species richness of the same communities in the same two wetlands (Fig. S3). This positive association for species richness may also be both causal and because of covariance with additional factors. For example, some

large benthic animals modify the environment (e.g. by burrowing) and this increased heterogeneity may provide microhabitats for a greater diversity of small benthic animals. Conditions favorable to the development of a rich community of large benthos (e.g. high-tidal flushing; Nordby and Zedler 1991) may also be conducive to the development of a rich community of small benthos. Whatever the mechanism that affects the relationship between large and small benthos, the species richness of both components was positively associated with trematode species richness in snails (with the apparent exception of small benthos species richness at Morro Bay). We expect this relationship to be proximally driven, because more species of birds would be expected to visit sites with more species of benthic prey, and these birds will consequently bring more species of trematodes to infect snails at those sites.

We investigated relationships between communities on very local scales (e.g. 20 m reaches of tidal creeks). We expect, however, that associations between trematode communities in snails and surrounding animal communities will also occur on scales of entire wetlands or regions. Although our study was not designed to thoroughly assess patterns among wetlands, there is some evidence for this in our data. There were average differences among wetlands in species richness and abundance. For example, Morro Bay had the lowest values for trematode species richness and prevalence (Fig. 2). Morro Bay also had low values for large benthos species richness and density (Figs. 2c, d). Surveys of birds in these wetlands indicate that the densities of wetland birds in tidal creeks at Morro Bay are lower than at either Carpinteria Salt Marsh or Mugu Lagoon (Lafferty, unpublished data). This is consistent with previously demonstrated positive associations between abundance (Smith 2001; Hechinger and Lafferty 2005; Fredensborg et al. 2006) and species richness (Hechinger and Lafferty 2005) of birds and trematodes in snails on local scales. Thus, we speculate that fewer birds use tidal creeks at Morro Bay. This lack of habitat use results from the lower abundance of benthic invertebrates in these creeks. As a consequence of lower bird use, fewer trematodes are present in these snail populations. It is worth noting, however, that the Morro Bay sites did not have relatively low values for species richness and density of small benthos or fishes. More extensive sampling of Morro Bay would be worthwhile to clarify any associations there.

The patterns we observed using trematode prevalence were not altered when we analyzed data that accounted for competitive loss of trematode infections. This is worth noting, because calculation of “pre-interactive” prevalence requires knowledge or

postulation of the dominance hierarchy among trematode species (Kuris 1990; Kuris and Lafferty 1994; Lafferty et al. 1994). Although determining pre-interactive prevalence is not difficult, it does add an additional step to the analysis of trematode communities. With regard to using trematodes as a tool, it would be simpler if it were possible for wetland assessors to use observed prevalences only. Although our results suggest it may be possible to use observed prevalences, we infrequently found more than 50 infections per 100 snails. In situations where observed prevalences are higher, and thus trematode interspecific competition is more intense, pre-interactive prevalences will be more important (Kuris and Lafferty 1994). Trematode competitive displacement also places a ceiling on observed prevalence (by driving the number of infections toward one per snail). Pre-interactive prevalence removes this asymptote on observed abundance, because it provides an estimate of trematode numbers that can exceed one per snail. This should increase its value as an indicator in areas where prevalence is high.

Because we found evidence of some positive associations, these results support continued exploration of larval trematode communities as bioindicators of other community components (particularly large benthic invertebrates). These parasites occur throughout the world (Yamaguti 1975; Kuris and Lafferty 1994; Poulin and Mouritsen 2003) and, logically, should provide comprehensive, temporally integrative, environmentally safe, and cost-effective information about community structure and trophic linkages (Huspeni et al. 2005). It is important to emphasize that, unlike previously proposed indicators, trematodes may also reflect abundance of individuals within the different assemblages, not only species richness. Huspeni and Lafferty (2004) evaluated the ecological effects of a wetland restoration using trematode communities. They found that trematode species richness and prevalence increased after restoration. Unfortunately, they did not survey the free-living communities (it was too costly). It seems, nonetheless, likely that the trematode community became enriched in the restored wetland because birds were attracted to a newly established community of fishes and benthic invertebrates. Similarly, two other recent studies emphasize the promise of trematodes as indicators in other types of ecosystem. Loot et al. (2005) recently documented higher levels of trematode parasitism in Chilean rocky intertidal reserves compared with exploited areas and McIntyre et al. (2005) found greater levels of trematodes in snails in non-disturbed sites than in disturbed sites in an east African Rift Lake.

Can trematodes be used as indicators only in systems for which trematode life cycles are well-studied? As pointed out by Huspeni et al. (2005), it is straightforward to identify the taxonomic family of unknown larval trematodes from snail hosts, and this knowledge is usually sufficient to identify both the general type of second intermediate host (e.g. mollusc, copepod, fish, etc.) and the type of final host (e.g. fish, amphibian, reptile, bird, or mammal). Thus, although detailed knowledge of second intermediate host use certainly increases the resolution offered by trematodes as indicators, we suspect that trematodes may be usefully employed as ecological indicators even in little-studied systems.

What steps should we take to further the development of trematode communities as indicators? First, we should more thoroughly explore the ecological relationships between larval trematodes and surrounding communities of free-living organisms. For example, are the different trematode populations in snails directly affected by the abundance of their particular second intermediate hosts? Are crab-using trematodes in snails more common in areas with greater abundances of crabs? Second, it is also necessary to explore associations on the scale of whole habitats and entire wetlands, particularly because this is the scale on which management frequently operates. Finally, when any further ecological relationships between larval trematode and free-living communities have been established, evaluation of larval trematode communities as bioindicators must quantitatively analyze the most efficient way of combining use of trematodes with traditional methods of assessing biodiversity. Such cost-benefit analyses must account for the strength of the relationship between trematodes and measures of free-living communities, and the effort and cost required to obtain a sample of the target variable with comparable predictive accuracy.

To conclude and summarize, although previous work has revealed that trematodes may serve as good indicators of bird communities, it is still not clear to what extent they may serve as indicators of benthos and fishes. Although we found some positive associations between the species richness and abundance of trematodes in snail populations and surrounding benthic communities, the results were inconsistent. Our results indicate trematodes in snails can potentially be developed as indicators of large benthic invertebrates. Future work should more extensively explore within-wetland associations, examine larger-scale patterns, and then carefully quantify the costs and benefits of different sampling techniques. Diverse communities of trematodes are common throughout the world in both

fresh water and marine habitats (Kuris and Lafferty 1994; Poulin and Mouritsen 2003; Huspeni et al. 2005). Because it is important, yet costly, to monitor biodiversity in these habitats, we should seriously explore the relatively inexpensive use of trematodes as bioindicators of species diversity, abundance, and trophic function in these ecosystems.

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