

# Ecosystem energetic implications of parasite and free-living biomass in three estuaries

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Parasites can have strong impacts but are thought to contribute little biomass to ecosystems<sup>1–3</sup>. We quantified the biomass of free-living and parasitic species in three estuaries on the Pacific coast of California and Baja California. Here we show that parasites have substantial biomass in these ecosystems. We found that parasite biomass exceeded that of top predators. The biomass of trematodes was particularly high, being comparable to that of the abundant birds, fishes, burrowing shrimps and polychaetes. Trophically transmitted parasites and parasitic castrators subsumed more biomass than did other parasitic functional groups. The extended phenotype biomass controlled by parasitic castrators sometimes exceeded that of their uninfected hosts. The annual production of free-swimming trematode transmission stages was greater than the combined biomass of all quantified parasites and was also greater than bird biomass. This biomass and productivity of parasites implies a profound role for infectious processes in these estuaries.

Standing stock biomass and biomass production are traditional measures of the energetics of ecosystems (see, for example, refs 4–6). Infectious agents are perceived to contribute negligible biomass to ecosystems<sup>1–3</sup>. If so, it may be appropriate to set them aside from investigations of energetics, ecosystems or food webs. However, some parasites markedly influence host individuals (notably humans), wildlife populations and sometimes host communities. These effects

imply a general role for infectious processes in the dynamics of ecosystems. Here we quantify the biomass of free-living organisms and their parasites in three estuaries.

Over the course of five years we performed an extensive quantification of the free-living and infectious biomass in three estuaries in Baja California (Bahia Falsa in Bahia San Quintín (BSQ) and Estero de Punta Banda (EPB)) and California (Carpinteria Salt Marsh (CSM)). Cumulatively, the study included 199 species of free-living animals, 15 species of free-living vascular plants and 138 species (including 1 plant species) of infectious agents (see Table 1). Unless specifically mentioned, biomass refers to wet weight, including hard parts.

Here we consider the biomass of free-living and parasitic species grouped by taxonomic categories and, for parasites, by life-history strategy<sup>7,8</sup>. We also determined the proportion of the mass in each host category that was parasite tissue. Additionally—because several parasites in our study were parasitic castrators, usurping the phenotype of their hosts—we noted the biomass in each estuary of castrated hosts (parasite extended phenotypes<sup>9</sup>). Trematode castrators in snail intermediate hosts contributed the most substantial parasitic standing crop biomass in these estuaries, so we further estimated the rates of annual productivity for this infectious component of the system (asexual production of cercariae). To illustrate more sharply the importance of parasite biomass, we compare it directly with the biomass of free-living groups, particularly with that of the bird

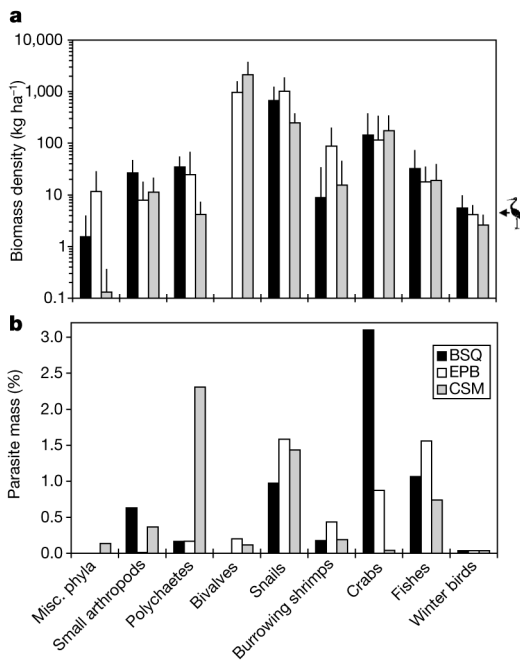
**Table 1 | Summary of free-living groups and animal parasite functional groups in this study, and number of hosts dissected**

Free-living group	No. of species	No. of individuals dissected	No. of parasite species				Sum
			Macroparasites	Trophically transmitted	Castrators	Pathogens	
Miscellaneous phyla	10	55	–	1	–	–	1
Small arthropods	33	258	–	2	–	–	2
Polychaetes	38	533	1	7	–	2	10
Bivalves	15	267	2	15	1	1	19
Snails	11	14,158	–	9	24	1	34
Burrowing shrimps	2	87	1	7	2	–	10
Crabs	3	949	1	19	2	6	28
Fishes	17	965	6	19	–	1	26
Birds	70	162	30	–	–	–	30
Total host–parasite combinations	–	–	41	79	29	11	160
Total species, life stages or individuals	199	17,434	40	72	29	9	150

Totals for numbers of parasite species may be less than the sum of the rows because some parasite species use more than one host group. Italic numbers indicate species for which we did not quantify biomass.

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**Figure 1 | Biomass of animals and proportional contribution of parasites in three estuaries.** **a**, Ecosystem-level biomass density of free-living animal groups. **b**, Parasite tissue as a percentage of total biomasses. The arrow at the bird icon in **a** marks the mean biomass of winter birds ( $4.1 \text{ kg ha}^{-1}$ ) across the three estuaries. Error bars in **a** indicate upper 95% confidence limit. The Supplementary Information contains the standard errors and degrees of freedom for the stratified means, and confidence limits for this and all other figures.

assemblage (an obvious and important component of the estuarine ecosystem that includes most of the top predators<sup>10</sup>).

Vascular plants composed the greatest fraction of the biomass in all three estuaries: a mean of  $136,166 \pm 33,848$  (95% confidence limits)  $\text{kg ha}^{-1}$  at BSQ,  $61,754 \pm 14,512 \text{ kg ha}^{-1}$  at EPB, and  $169,035 \pm 26,606 \text{ kg ha}^{-1}$  at CSM. At CSM, the parasitic dodder, *Cuscuta salina*, infecting leaves and stems, was 0.27% of the plant biomass. Dodder was less common at EPB and scarce at BSQ. We recognized 199 species of free-living animals and 150 species (or life stages) of metazoan parasites (Table 1).

Faunal composition was similar across these estuaries. As regards the species that contribute the top 95% of all biomass, 28% of free-living and 71% of parasite species were common to all three estuaries, and 67% of free-living species and 74% of parasite species were common to at least two estuaries. The biomasses of all free-living

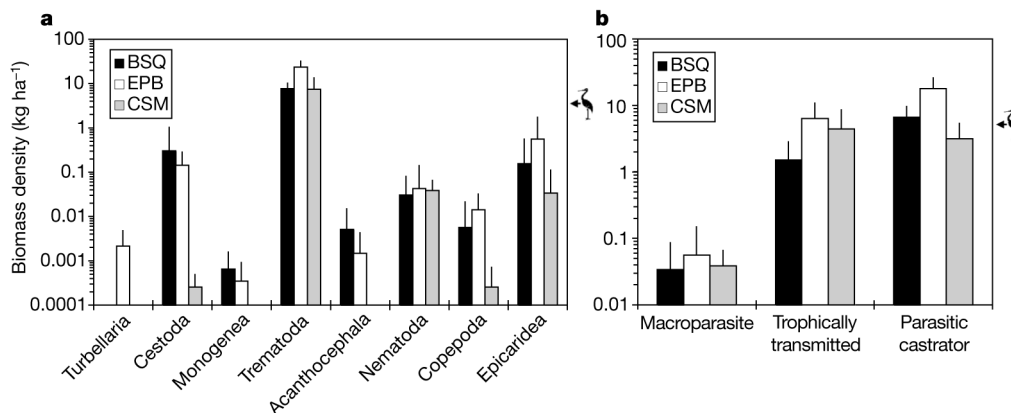
animals (including their infectious agents) were  $925 \text{ kg ha}^{-1}$  at BSQ,  $2,240 \text{ kg ha}^{-1}$  at EPB, and  $2,594 \text{ kg ha}^{-1}$  at CSM. In the three estuaries, parasites composed 1.2%, 0.9% and 0.2% of the total animal biomass, respectively. Additionally, parasite biomasses were 6.3%, 13.2% and 3.2% of the combined biomass of their free-living trophic counterparts—that is, the main free-living groups that also feed on multiple trophic levels, namely crabs, fishes, miscellaneous phyla and birds.

For visual presentation, we combined free-living species into broad taxonomic categories (Fig. 1a and Table 1). Our estimates for free-living biomass compare with those from other estuaries (see, for example, refs 11–13). The most substantial contributors to animal biomass were the snails, bivalves and crabs. Across estuaries, the biomasses of the broad categories were generally consistent, the striking exception being the lack of bivalves at BSQ. Other biomass differences between estuaries were driven to a large extent by differences in relative habitat areas (for example marsh habitat, which was relatively extensive at CSM, supported fewer fishes and invertebrates). When all parasites were combined within the free-living groups, the total mass of parasites was generally less than 2% of the biomass of their host categories (Fig. 1b). However, the percentage of parasite biomass varied between estuaries and sometimes reached more than 3% of the mass of their free-living host groups.

The average parasite group had a biomass three orders of magnitude lower than that of the average free-living group (Fig. 2a). Certain parasitic groups dominated the parasite biomass, reaching levels similar to those of common free-living groups. For instance, the biomass of trematode worms was comparable to that of the fishes, burrowing shrimps, polychaetes or small arthropods. In all estuaries, trematode biomass exceeded bird biomass by threefold to ninefold. The epicaridean isopods were the second biggest biomass component of the parasite groups (along with tapeworms at BSQ and EPB). As with the free-living groups, biomass estimates for parasite groups were similar for all estuaries, with exceptions being the small contribution of cestodes and parasitic copepods at CSM.

Parasitic castrators and trophically transmitted parasite stages dominated parasite biomass, attaining  $1\text{--}10 \text{ kg ha}^{-1}$  (Fig. 2b). This mass density was comparable to—or exceeded—that of the vertebrate groups in these estuaries. Macroparasites contributed much less to estuary biomass. This was partly due to the relatively low biomass of their principal hosts (birds and fishes). The total biomasses of the functional groups of parasites were also similar across estuaries.

A host infected with a parasitic castrator has the effective genotype of the parasite<sup>14</sup>. Hence, the entire mass of each castrated host constitutes the extended phenotype<sup>9</sup> of its parasitic castrator. For a host group, the biomass of parasitically castrated hosts approached and sometimes exceeded the biomass of their uninfected hosts (Fig. 3).



**Figure 2 | Ecosystem-level biomass density of animal parasites in three estuaries.** **a**, Parasites grouped by major taxon. **b**, Parasites grouped by functional group. The reference arrow at the bird icon marks the mean

winter bird mass density across the three estuaries ( $4.1 \text{ kg ha}^{-1}$ ). Error bars indicate upper 95% confidence limit.

For example, across the three estuaries, parasitically castrated *Cerithidea californica* commandeered 37–130% of the soft-tissue biomass compared to the uninfected snail populations (Fig. 4). Thus, parasites effectively controlled much of the host biomass of some free-living groups. This probably applies to the many other marine and aquatic systems in which hosts for parasitic castrators (for example crabs, shrimps and snails) are common.

The snail *C. californica* and its larval trematode parasitic castrators were considerable components of animal biomass. *C. californica* had the greatest biomass of any invertebrate in the two southern estuaries (569 kg ha<sup>-1</sup> at BSQ, 854 kg ha<sup>-1</sup> at EPB) and ranked eighth among the invertebrates at CSM (144 kg ha<sup>-1</sup>). The larval parthenitae of 18 recognized trematode species parasitically castrated many of these snails, including almost all of the largest individuals. The trematodes average 22% of the total soft-tissue weight of individual infected snails<sup>15</sup>. In total, the trematode biomass in *C. californica* matched or exceeded the high winter biomass of birds and substantially exceeded their summer biomass (Fig. 4).

We quantified the combined cercarial production of the 18 trematode species infecting *C. californica* snails. Because their snail hosts were large and abundant, these cercariae comprised a substantial component of parasite productivity. Cercariae are released from snails in a daily pulse<sup>16</sup> and have ephemeral life spans of about 24 h. The annual cercarial biomass produced by all *C. californica* trematodes could therefore be compared with the standing crop biomass of other (long-lived) animals. Annual production of cercariae was about threefold that of trematode parthenitae standing-stock biomass and threefold to tenfold that of winter bird biomass (Fig. 4). Further the annual production of cercariae exceeded 1.3–2.2-fold the standing stock of all parasites combined. Reproductive effort—the biomass of offspring (cercariae) produced in a year divided by the biomass of parents (infected snail soft-tissue mass)—was 0.53–0.86. This reproductive effort lies outside the range of values (0.065–0.29) reported for 13 iteroparous marine mollusc species<sup>17,18</sup>. Both parthenitae in *C. californica* and cercariae produced by trematodes infecting *C. californica* had greater densities in the two southern estuaries, primarily as a result of the abundance of *C. californica* throughout the vegetated marsh at BSQ and EPB, whereas at CSM snails were rare in this extensive habitat (50–53% of all habitat area at BSQ and EPB, and 77% of that at CSM).

Our conservative estimates (see Methods) indicate that parasite biomass is comparable to that of several major groups of free-living animals and greater than that of the principal top predators in these estuaries. Parasite biomass was not equally distributed among host or parasite groups; the parasitic castrator functional group comprised most of the parasitic biomass. Consideration of the influence of their

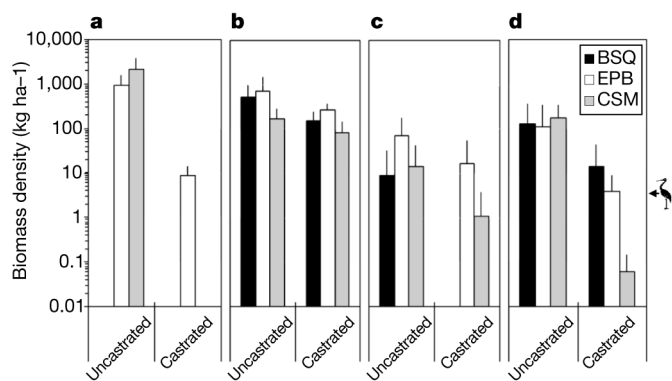
extended phenotypes indicates a large ecological role for such parasites. Further, parasite biomass relative to the free-living biomass was up to 6–12-fold the 0.1–0.2% ‘best guess’ used for an ecosystem model of coral reefs that predicted a significant increase in trophic efficiency when parasites were included in the model<sup>19</sup>.

Large standing-stock biomass is not the only indication of energetic importance to ecosystems: productivity is also fundamental<sup>4,5,20</sup>. Parasites efficiently convert food to growth and reproduction, perhaps because they are released from the homeostatic, food gathering and mobility tasks conducted by their hosts<sup>21</sup>. Thus, parasites—such as larval trematodes in snails—may generally have substantial biomass (like many macroorganisms) and high productivity (like microbial organisms).

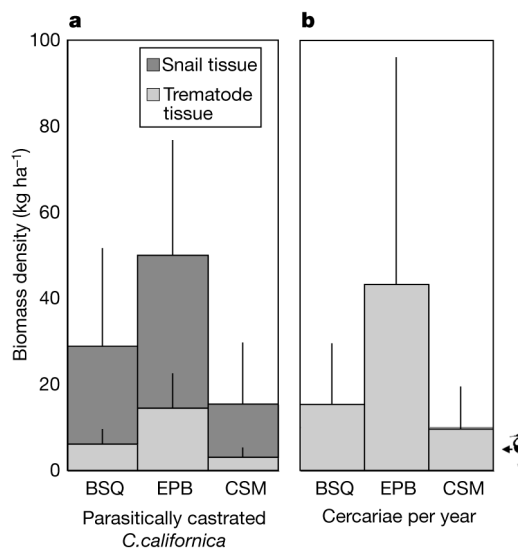
Additionally, parasites drain host energy beyond that which they consume. Resistance to parasites can be energetically costly (as a result of physiological and behavioural traits to detect, prevent and respond to infection)<sup>22</sup>. In particular, immune systems require substantial standing investment and incur inductive energetic costs<sup>23</sup>, and added to that are costs of repairing tissue damaged or consumed by parasites. If parasites have relatively high productivity compared with free-living consumers, and non-consumptive effects on their resources, their effects at the ecosystem level could be disproportionately greater than suggested by their biomass.

This investigation of the biomass of parasites at the ecosystem level fits with emerging interest in the role of parasites in food webs. Parasites can significantly affect food-web topology (for example, increasing chain length and connectance) and are commonly consumed<sup>24,25</sup>. Further, by modifying the behaviour of intermediate hosts, parasites can selectively strengthen links between predator and prey<sup>26</sup>. A quantification of biomass allows the assignment of mass to these potentially important parasitic nodes and therefore represents a step towards fully dynamic food-web models that incorporate infectious processes.

The substantial biomass and productivity attributed to parasites in these estuaries calls for the full integration of parasite ecology into the general body of ecological theory. Food-web analyses and ecosystem



**Figure 3 | Ecosystem-level biomass density of parasitically castrated (extended phenotypes) and uninfected phenotypes of hosts supporting parasitic castrators in three estuaries. a, Bivalves. b, Snails. c, Burrowing shrimps. d, Crabs.** The reference arrow at the bird icon marks the mean winter bird mass density across the three estuaries (4.1 kg ha<sup>-1</sup>). Error bars indicate upper 95% confidence limit.



**Figure 4 | Standing crop biomass and cercarial productivity of trematodes in *Cerithidea californica* snails. a, Ecosystem-level biomass density of host and parasite tissues of parasitically castrated *C. californica*. b, Biomass density of the free-swimming stages (cercariae) produced annually by infected snails.** Uninfected *C. californica* tissue biomass was 78.8 ± 73.4 (95% confidence limits) kg ha<sup>-1</sup> at BSQ, 110.5 ± 119.4 kg ha<sup>-1</sup> at EPB, and 11.8 ± 9.0 kg ha<sup>-1</sup> at CSM. For clarity we do not include the snail shell mass, which is about 80% of the total mass. The reference arrow at the bird icon marks the mean winter bird-mass density across the three estuaries (4.1 kg ha<sup>-1</sup>). Summer bird biomass is 0.89 kg ha<sup>-1</sup> across the three estuaries. Error bars indicate upper 95% confidence limit.

modelling that include parasites<sup>19,24,25,27,28</sup> provide a starting point for this theoretical expansion.

## METHODS SUMMARY

We quantified animal and plant wet biomass by sampling 23 random sites in each estuary, stratified over the four major habitats (vegetated marsh, pans, channels, and mudflats and sandflats). At each site we sampled the density and sizes of most free-living organisms more than 1 mm in body size: birds with visual surveys, fishes with nets, benthos with quadrats and cores, and plants with clip quadrats and cores. We estimated free-living animal biomass by applying weight–length curves to the sampled individuals (for birds we used average adult weight).

From each sample site we examined fishes and invertebrates for a wide range of infectious agents, focusing on metazoans. We examined all soft-tissue types in squash preparations. Ethical and pragmatic issues prevented extensive sampling of most bird species for parasites, so we performed a partial estimation of parasite communities of birds by using our own dissections and published information. In general, our methodology probably underestimated the presence of infectious disease (for example, by excluding many pathogens).

We estimated parasite biomass in our samples by multiplying species-specific estimates of individual parasite mass by their abundance<sup>29</sup> in individual hosts. We obtained the masses of most metazoan parasites by directly weighing individuals, or by estimating their mass by multiplying an estimate of their volume by a tissue density of 1.1 g ml<sup>-1</sup> (ref. 30). To generate estimates for the abundance of parasites in hosts (other than birds), we used statistical models based on data from our dissected hosts.

We estimated the annual productivity of trematode cercariae by multiplying species-specific estimates of individual cercaria mass by species-specific estimates of mean number of cercariae shed daily multiplied by infection density multiplied by 365 days.

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Supplementary Information is linked to the online version of the paper at [www.nature.com/nature](http://www.nature.com/nature).

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## METHODS

The three estuaries were spread over 600 km of coastline and total areas were 144 ha for BSQ, 707 ha for EPB, and 61 ha for CSM (these areas exclude lagoonal portions of BSQ and EPB). We delineated habitats and calculated their areas using satellite imagery and ArcGIS software (ESRI 1996). We used IKONOS satellite imagery with 1:4,800 map accuracy and 8-bits per pixel (1 meter color product) for BSQ, and (1 meter + 4 meter multispectral product) for EPB, purchased from GeoEye (formerly Space Imaging). The image area for both wetlands was 100 km<sup>2</sup>. Satellite imagery was projected in UTM with WGS84 datum. To georeference the satellite imagery of BSQ, we collected ground control points using Garmin handheld GPS units and ArcPad, and ERDAS Imagine software. We georectified the image of CSM from State plane projection in NAD27 datum to UTM projection in WGS84 datum using ERDAS Imagine software.

At each of the 69 randomly selected sites, we sampled the density and sizes of most organisms over 1 mm in body size. We sampled birds using multiple, timed (15 min), visual daytime surveys within a 200 m diameter area, walking a 50 meter-radius circular transect at each sampling site. To capture daily, tidal, and seasonal variation in bird abundance, we sampled each site six times in winter (December-January) and four times in summer (June-July). We quantified fishes at mid-tide levels using 3 mm mesh blocking nets to enclose an area followed by five sweeps with seines (the last performed with the blocking nets). We used the blocking nets to enclose a 10 meter stretch of channel, on flats we enclosed a similarly sized area. We seined the entire area of pans. Also, we sampled the benthos at each site over a plot with the maximum dimensions of 10 x 10 m (sometimes limited by channel or pan size). We randomly sampled epibenthic invertebrates during low tidal levels with ~20 10 x 50 cm quadrats, and infaunal

invertebrates with 5-20 large cores (10 cm diameter x 50 cm deep) sieved through a 5 mm mesh and 5 or more composited small cores (5 cm diameter x 5 cm deep) sieved through a 1 mm mesh. Within a site, for some large benthic animals, we sometimes employed a stratified random sampling scheme<sup>31</sup> to reduce variance in our estimates when we could readily identify habitat from “non-habitat”. We sampled crabs by using five random ‘cores’ (each being three adjacent 0.24m diameter cores), randomly placed within the crab burrow habitat.

We generated the weight-length curves for the most common species, and applied curves of related or similarly-shaped animals for others (for birds, we used published records of average weight<sup>32,33</sup>).

For parasitological examinations, if a host species was numerous, we took a random or haphazard sample, stratified across host body sizes as necessary. If species of benthic invertebrates appeared to be important hosts, we usually haphazardly collected additional individuals to increase sample sizes for dissections. For birds, we dissected 49 individuals of 20 species to estimate trematode, cestodes, and acanthocephalan biomass. We improved our estimates for trematodes using data on 113 dissected individuals of 22 bird species from Russell<sup>34</sup>.

We used generalized linear models<sup>35</sup>, based on data from our dissected hosts, to generate estimates for the abundance of parasites in the individual hosts in our density samples. We used Poisson regression (with a log-link and an over-dispersion term) for most cases, and logistic regression for parasites where presence-absence was the pertinent datum (e.g., for larval trematode infections in molluscs). These models were applied to every host-parasite combination in each estuary (except for birds, described below), and the initial full model typically included host size, habitat (nested in estuary), site of collection (nested within habitat), and, for crabs, sex (since this was apparent during field

sampling of densities). We employed backwards elimination to remove main effects and interactions that did not significantly contribute explanatory power (at  $p < 0.10$ ). For bird parasites, we estimated the mean proportional biomass across bird species (weighted by sample size) of acanthocephalans, cestodes, and trematodes in individual birds, by multiplying the mean no. worms per individual bird by individual worm mass. We then multiplied this proportion by the total bird biomass in each estuary.

We estimated mean mass for most metazoan parasites either by directly weighing individuals, or by conservatively estimating their mass by multiplying an estimate of their volume by a tissue density of  $1.1 \text{ g/mL}^{30}$ . Because parasitic castrators of crustaceans grow in close proportion to host growth (e.g.,  $r = 0.84^7$ ), we estimated parasite to host weight ratios for these groups and then multiplied this ratio by the mass of infected hosts. It was difficult to separate larval trematode parthenitae from snail tissues, so we determined the proportion of infected snails that was trematode tissue using serial cross-sections<sup>15</sup>.

For the final estimate of parasite biomass density at the ecosystem level, we calculated the same type of mean (stratified by habitat) that we employed for free-living organisms.

For our estimate of annual productivity of trematode cercariae originating from infected *C. californica*, species-specific cercarial mass was conservatively estimated by multiplying estimates of their biovolumes (based on published and direct measurements of their bodies and approximations to simple geometric shapes) by  $1.1 \text{ g/cm}^2$ . Species-specific mean daily cercariae shed rates were based on measurements taken approximately every two months over two years from individual snails placed in enclosed vials during a tidal cycle in a CSM channel.

For vascular plant biomass, 30, 0.05 m<sup>2</sup> plots were randomly selected from the vegetated marsh habitat of each estuary. Above ground vegetation was removed with shears. At each plot, we took a core 0.008 m diameter by 0.5 m depth to sample the below ground vegetation. Samples were rinsed, blotted dry and weighed. From these samples, we calculated the summed wet weight of vascular plants (above plus below ground). We present data on the parasitic plant, *Cuscuta salina*, separately.

We will make the dataset containing information at the sampling site level available upon request.

<sup>31</sup>Thompson, S.K., *Sampling*, 2nd ed. (Wiley, New York, 2002).

<sup>32</sup>Poole, A. and Gill, F. eds., *The birds of North America: life histories for the 21st century*. (American Ornithologists' Union/Academy of Natural Sciences of Philadelphia, 1992-2003).

<sup>33</sup>Sibley, D.A., *The Sibley field guide to birds of western North America*. (Knopf, New York, 2003).

<sup>34</sup>Russell, H.T., Ph. D. thesis, University of California, 1960.

<sup>35</sup>Myers, R.H., Montgomery, D.C., and Vining, G.G., *Generalized linear models: with applications in engineering and the sciences*. (Wiley, New York, 2002).