Effects of Invasional Meltdown on Community Structure in Marine Ecosystems in the Damariscotta Estuary of Maine

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Introduction

Basibionts are organisms that provide a habitable surface for other organisms referred to as epibionts (Wahl *et al.* 1989). When invasive species establish themselves in given habitats, this can lead to a positive feedback loop of recruitment of other invasive species through facilitative interaction; this is referred to as invasional meltdown (Simberloff and Von Holle 1999, Ricciardi 2001). The purpose of this study was to analyze the impact of invasive species in marine ecosystems by looking at invasion status and frequency of associated epibionts on basibiont specimens. Through these factors, this study aimed to determine if invasional meltdown is impacting community structure in a marine ecosystem in the Gulf of Maine. The research questions proposed are as follows: 1) does the invasion status of the basibiont alter the frequency of invasive epibiont settling compared to native epibiont; 2) are there any differences in epibiont diversity on native and invasive basibionts? The hypothesis of this study is that **there will be no significant difference in the frequency of invasive epibiont settlement or in the diversity of epibionts on invasive and native basibionts.**

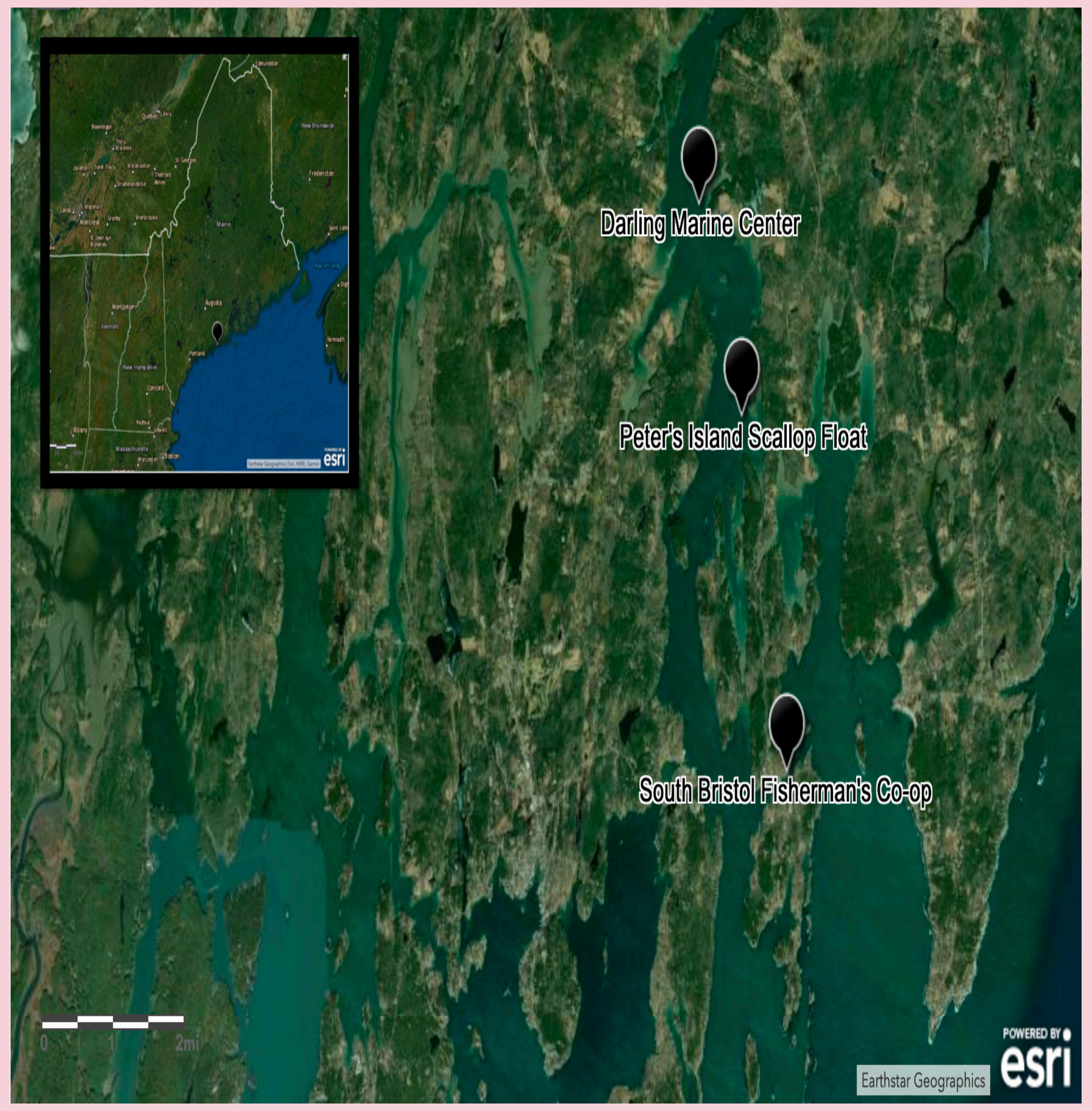

Figure 1. Map showing the location sites of the samples, which were taken from three sites in Maine. (Map courtesy of Dr. Auker)

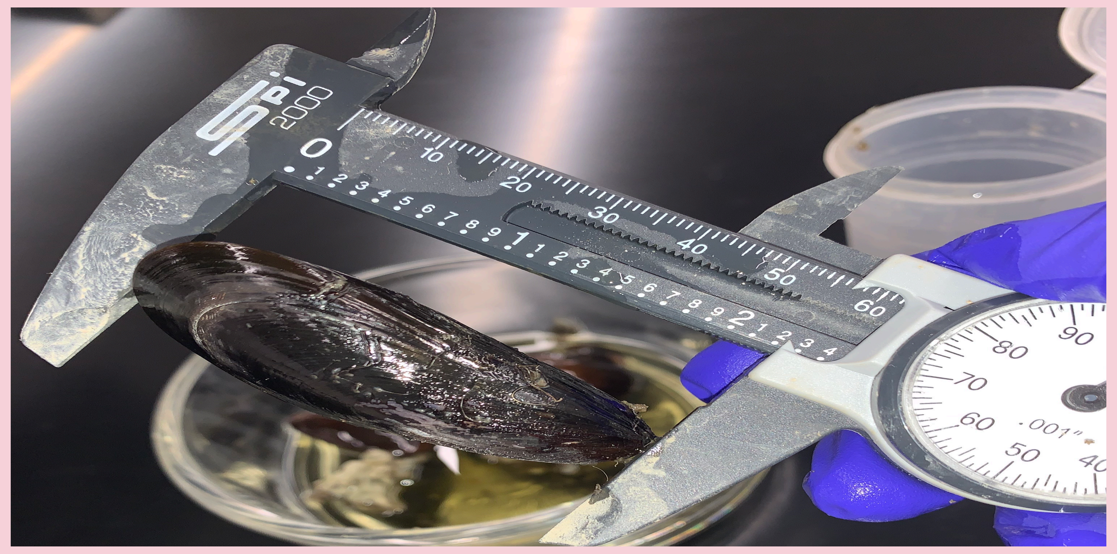

Figure 2. Measuring the length in millimeters of a blue mussel (*Mytilus edulis*) using a vernier caliper.

Methods and Materials

The samples used in this study were collected from floating docks at 3 sites in the Damariscotta estuary in Maine on October 11, 2019, by mechanism of hand and net. The samples came from the 3 following sites: a scallop float at Peter's Island (49°54'32.68" N, 69°34'05.05" W), South Bristol Fishermen's co-op (43°51'50.07" N, 69°33'16.67" W), and Darling Marine Center (43°56'3.16" N, 69°34'46.41" W) (Figure 1). There were 15-20 samples taken from each of the three sites and each sample consisted of one basibiont organism and attached epibionts. The samples were placed in numbered vials and preserved in alcohol (initially preserved in 99% isopropyl alcohol, and once received in the lab, 70% ethanol). For each sample, all specimens were identified by species using dichotomous keys and classified by invasion status (which was either native, invasive or cryptogenic/unknown). For basibiont organisms, the species name, size (measured in mm using a vernier caliper, see Figure 2) and mass were determined. For epibiont organisms, species name and mass were determined, along with the number of epibiont organisms present in each sample . For data analysis, a t-test was conducted using basibiont invasion status and Shannon Diversity Index. A chi-square analysis was conducted using basibiont and epibiont invasion status along with the proportion of invasive organisms in each sample.

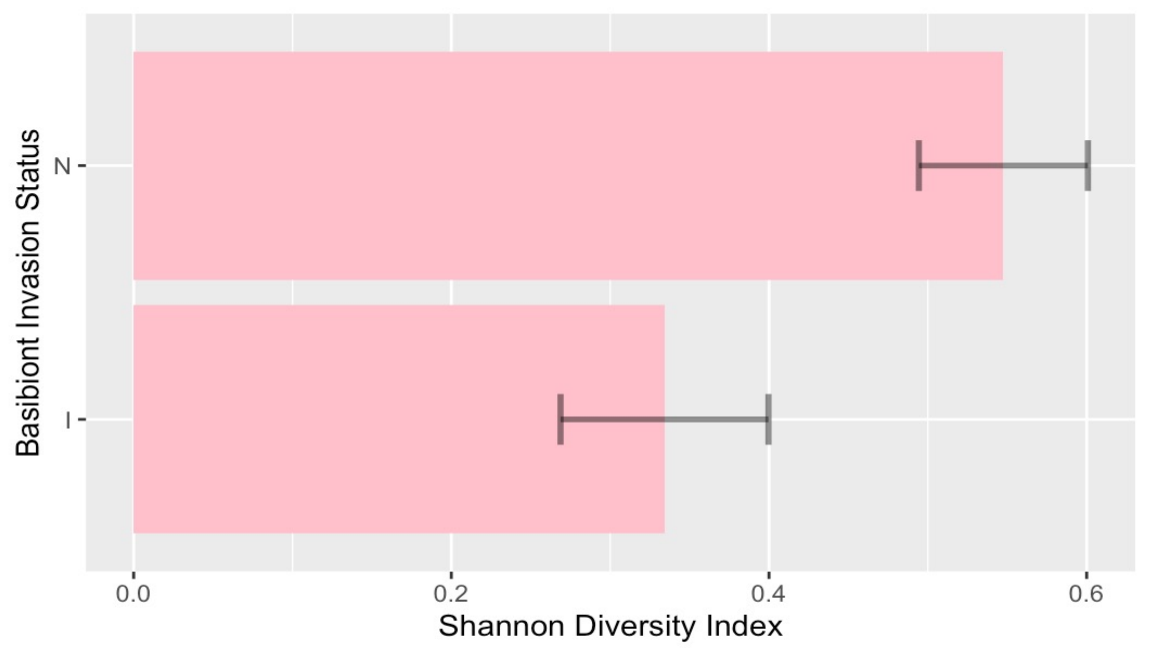

Figure 3. Shannon Diversity Index value given per invasion status (where N is native, and I is invasive) of the basibiont organism. Statistical analysis was carried out using the ggplot package in R studio & a t-test.

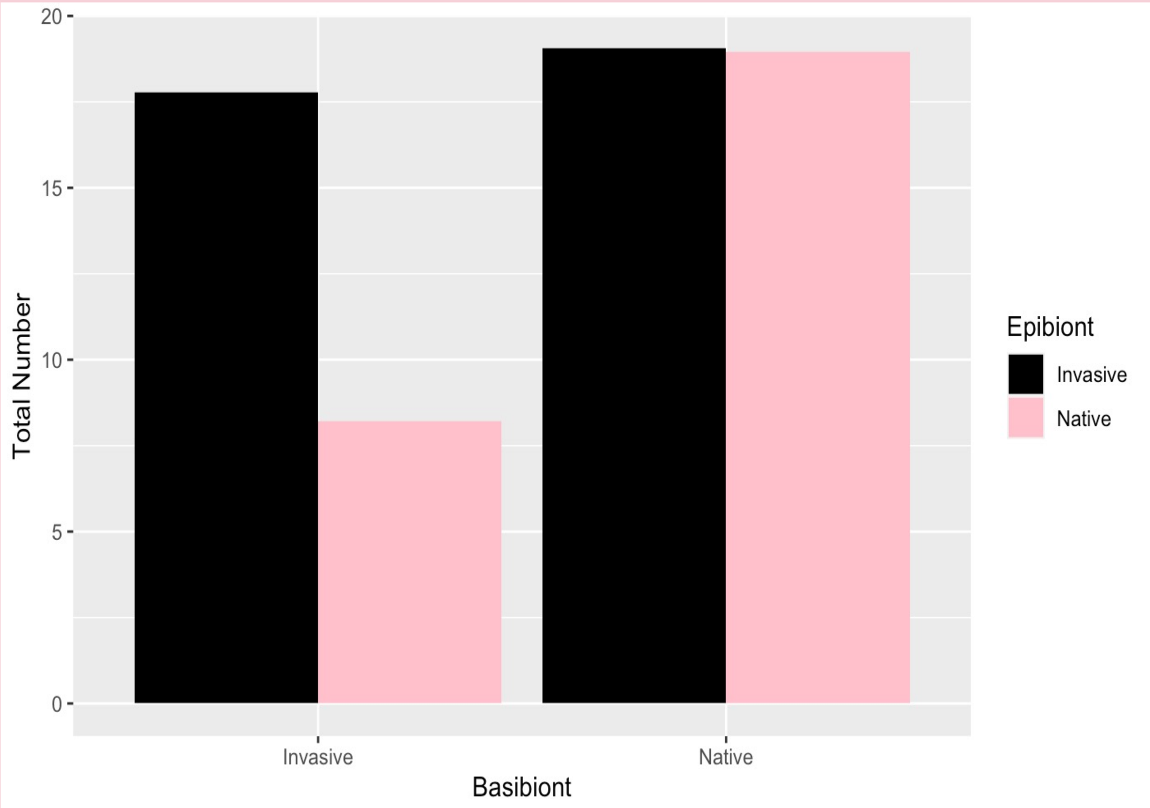

Figure 4. Total number of invasive and native epibiont organisms observed on sample basibionts of both native and invasive status.

Results

The most abundant basibiont species present in the samples was the native blue mussel (*Mytilus edulis)* (n= 20), and the most abundant epibiont species present was the invasive carpet sea squirt (*Didemnum vexillum)* (n= 32) . The results of the t-test showed that species diversity of epibionts on native basibiont species (Shannon index: 0.55 ± 0.33) was significantly higher than on invasive basibiont species (Shannon index: 0.33 ± 0.33) ($t = -2.5291$, $df = 53.254$, $P = 0.01443$) (Figure 3). Invasive basibionts had a total number of 17.79 invasive epibionts and 8.21 native epibionts, while native basibionts yielded 19.05 invasive epibionts and 18.95 native epibionts (Figure 4). The chi-square (X^2) analysis of epibiont type vs basibiont yielded no significant difference between observed and expected proportion of native and invasive epibionts on native and invasive basibionts ($X^2 = 1.4319$, $df = 1$, $P = 0.2315$) (Figure 4).

Figure 5. A sample containing a clump of *Mytilus edulis*, or blue mussels. These mussels were held together by byssal threads, which were cut for measurement and weight purposes.

Figure 6. Lab sample containing a red algal species with epibionts preserved in 70% ethanol.

Conclusions

The data gathered allow ***a rejection of the hypothesis*** **that there would be no difference in the diversity of epibionts on invasive and native species, but** ***failure to reject the hypothesis*** **that there would be no significant difference in the frequency of invasive epibiont settlement on invasive and native basibionts**. While there was no difference in proportion of epibionts that were invasive on the two types of basibionts, there was a significantly more diverse assemblage of epibionts on *native basibionts*. A study conducted by Munari (2008) in Mediterranean lagoons showed the opposite trend, this being that an invasive mussel basibiont *Musculista senhousia* ultimately led to higher biodiversity in areas that it invaded. The invasive basibionts had over double the number of invasive epibionts compared to native epibionts. Keeping this in mind, these data trends can lead to the suggestion that in this case the native basibionts are providing substrate for any epibiont regardless of invasion status, and that invasive basibiont species are not supporting as many epibiont species. This is important as we consider how the presence of invasive epibionts structure marine communities. Mussels, as ecosystem engineers, are a fundamental part of marine communities as they alter the substrate and facilitate interactions with many other species (Gutiérrez *et al.,* 2019; Auker *et al.,* 2014; O'Connor *et al.,* 2006, Buschbaum *et al.,* 2016). Data gathered may suggest the possibility that invasive basibiont organisms inhabiting an area can result in less biodiversity of accompanying epibionts (and the presence of more invasive epibionts observed here). Future research should investigate these epibiont and basibiont relationships and how they differ based on location to determine whether this is a universal trend, or location-based observation.

Literature Cited

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