**Invertebrate beta diversity varies among eelgrass meadows**

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**Running head:** Variation in epifaunal eelgrass diversity

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ABSTRACT: Seagrass habitats form spatially heterogeneous landscapes that support high secondary productivity and biodiversity. The spatial structure of seagrass landscapes could support high biodiversity through metacommunity dynamics of seagrass-associated animals. Here, we tested whether spatial patterns of eelgrass-associated invertebrate biodiversity are consistent with metacommunity processes across meadows. For 9 meadows in Barkley Sound, British Columbia, we quantified epifaunal biodiversity on eelgrass *Zostera marina*, and tested the following hypotheses: after controlling for depth and edge effects, epifaunal diversity and composition i) vary randomly within meadows but ii) vary systematically among meadows reflecting abiotic factors and metacommunity dynamics. Finally, we hypothesized that differences among meadows reflect their position in the landscape, and therefore persist throughout the season such that iii) variation among meadows is consistent through time over a single summer. We found that within meadows, invertebrates were non-randomly distributed, showing signals of greater intra-specific aggregation than expected by chance. Non-random distributions of epifauna are consistent with checkerboard patterns, but we did not detect a clear signal of other predictors (*but maybe of fetch…grazer abundance increased with exposure).* *Grazer / fetch pattern was stable over time, though signals of recruitment events by mussels are strong.*

Faunal assemblages are temporally dynamic and vary substantially within meadows, and we have shown here that meadows can be similar to each other in patterns that suggest that wave energy and dispersal may be important controls on biodiversity.

**INTRODUCTION**

Understanding the distribution and abundance of species is a central goal of ecological research. Achieving this goal for spatially structured habitats is essential to not only understanding ecological communities but also to making informed decisions about landscape management and biodiversity conservation. In coastal marine habitats, rich in biodiversity, knowledge of how biodiversity is structured across spatial scales is limited by a lack of basic information about where and when species occur, and how species are distributed across habitat patches (Bostrom et al 2006, Guichard or Baskett papers?, Gaston 2000). While a spatially discrete habitat patch such as a seagrass meadow or a kelp bed may appear to represent the local community, the habitat or resources provided by that foundation species is one of several processes that influence biodiversity of a local patch. In addition, population dynamics and species interactions structure species assemblages at finer (within meadow) and broader (landscape) spatial scales (Leibold et al 2004, Bostrom et al 2006, Pillai et al 2011).

The purpose of this study is to quantify faunal biodiversity across scales in a seagrass meadow seascape to determine whether individual seagrass meadows, or a set of meadows in a landscape, represent meaningful spatial units for associated faunal biodiversity. Spatial variation in biodiversity is related to the spatial scales of ecological processes that influence the relative abundance and presence or absence of species (Ricklefs 2004, Liebold et al 2004, Bostrom et al 2006). Over broad spatial scales evolutionary and dispersal processes (immigration) influence the regional species pool, while at finer scales local species diversity reflects biotic interactions (predation, competition, facilitation, resource provision) and abiotic conditions (gradients, disturbance, stochastic variation). Between local and regional scales, dispersal and colonization dynamics connect species populations among habitat patches, leading to mesoscale diversity patterns that reflect local processes and dispersal (Shurin). These mesoscale patterns have been described by metacommunity dynamics (Leibold and Mikkelson, Liebold et al).

Diversity at fine scales ('alpha' diversity, often described for a sample of a habitat) can reflect the regional availability of species, the quality of the habitat, species interactions, and the propensity for like individuals to aggregate in space (). Fine scale diversity is often the easiest to sample, and therefore is often reported, yet this measure does not fully describe diversity patterns in a spatially structured community. Comparison of alpha diversity estimates among sites or studies can make inference or comparisons across spatial scales challenging (Azaele et al. 2015, Chase and Knight 2013). Missing from alpha diversity estimates is the variation of diversity present in the region, but not captured in a particular patch or sample, known as ‘beta’ diversity. For example, dispersal and connectivity among patches promote biodiversity at the landscape scale if patches host different species assemblages so that in total lead to a greater regional species pool (gamma diversity) than observed in any habitat patch (Crist & Veech 2006).

In coastal marine systems, faunal biodiversity is distributed among patchy seascapes comprised of foundation species such as seagrass or kelp. Despite the apparent similarity of these habitats from patch to patch, the biodiversity of animals living among the shoots or stipes can vary substantially from place to place (seagrass diversity refs). For invertebrates and small vertebrates, seagrasses provide a physically complex and resource rich habitat, often in the form of disjunct meadows creating a heterogenous landscape of meadow and non-meadow areas (Bostrom et al 2006, etc). Within meadows, alpha diversity at 0.5 – 1 m2 is typically relatively constant and much lower than meadow-scale species diversity (Barnes 2013, Barnes and Elwood 2012, etc). The processes responsible for low and consistent sample-scale alpha diversity are not known, and leading theoretical explanations of competition have been not strongly supported (Nelson, Barnes 2013). This pattern suggests that beta diversity should be high and a relatively important component of seagrass associated biodiversity within meadows, yet there are few reports of beta diversity from seagrass systems. Among meadows, variation in species composition and diversity has been reported, though it is not readily explained by abiotic attributes (Carr et al, etc), though a few studies report effects of fetch or some measure of energy (Bostrom et al JEMBE 2006, Robinson et al 2011 for fish in this region), or salinity (Baden).

Here, we test the hypotheses that i) alpha diversity does not vary systematically among meadows, but beta diversity does vary among eelgrass meadows, and ii) spatial variation in species composition is consistent with metacommunity-scale processes structuring biodiversity. To test these hypotheses, we quantified spatial structure in eelgrass-associated epifaunal biodiversity across nine meadows to answer the following questions for a system of discontinuous eelgrass (*Zostera marina*; eelgrasses are seagrasses in the genus *Zostera*) meadows in British Columbia, Canada. When possible, we attempted to test possible biotic and abiotic drivers of biodiversity patterns within and among meadows.

**MATERIALS AND METHODS**

**Study system**

We sampled epifaunal biodiversity in eelgrass *Zostera marina* meadows in Trevor Channel, Barkley Sound, British Columbia, where *Z. marina* is the only meadow-forming seagrass species (Figure 1).  In this region, *Z. marina* forms primarily subtidal, perennial meadows that range in size from < 10 m2 to > 25,000 m2 (Mason et al 2015). *Zostera*, like other seagrasses, hosts a rich faunal assemblage of gastropods, crustaceans and annelids that live on and among the eelgrass blades. These epifauna consume epiphytic algae growing on seagrass, detritus and each other, forming the base of a highly productive food web.

We quantified biotic attributes of eelgrass meadows that could explain variation in eelgrass associated invertebrate biodiversity. We estimated shoot density, leaf area index (LAI), and meadow area. Shoot density and LAI were estimated from four 0.28 m2 quadrats collected outside each corner of a 4 x 4 m grid demarcated for community sampling (described below) in May and August at each of our main sites (i.e., the five sites that we sampled three times; Figure 1, Table 1) concurrently with epifaunal sampling. We removed, dried and weighed eelgrass and its associated epiphytes, and standardized epiphyte mass to eelgrass mass. To estimate LAI, we counted the number of blades per eelgrass shoot and measured the longest blade for length (from top of sheath to tip of blade) and width (at the midpoint). We then multiplied the width and length of the longest blade by the number of blades for each shoot (after Borg et al. 2010).

To quantify meadow-scale abiotic conditions, we monitored temperature and salinity using a hand held temperature/salinity probe (YSI Inc., OH USA). Measurements were taken throughout the tidal cycle on biodiversity sampling days, and opportunistically on other days. Three stations were established at each site representing approximately the center and furthest edges of the largest contiguous meadow. At each station we recorded temperature and salinity at the surface, 2 m below the surface, and directly above the bottom. If the bottom was at 2 m, we only recorded surface and 2 m depth. If the bottom was shallower than 2 m, we recorded the bottom depth and took surface and bottom measurements. No measurements were taken below 5 m or taken in the intertidal zone. We used position in the watershed to represent the estuarine gradient of salinity and temperature. Position was estimated as linear distance in kilometers from the nearest freshwater source (Sarita or Alberni inlet). We estimated fetch by calculating the distance to nearest land from the eelgrass meadow (is there a Gregr ref for this?)

**Biodiversity sampling**

To estimate epifaunal biodiversity and characterize variation within meadows, we used a 4 x 4 m grid of 16 standard plots (0.28 m2), each separated by 1 m, in each meadow (after Sanders 2007). This sampling design allowed for comparison of diversity among plots and meadows while standardizing for total area sampled and the spatial arrangement of samples. We placed sampling grids within contiguous meadows at least 2 m from any meadow edge.  In each plot, we cut away eelgrass at the sediment-water interface and placed it into a 250 µm mesh bag, collecting all eelgrass and epifauna. All sampled areas were at least 1 m below lower low water large tide (LLWLT), and did not vary in depth by more than a meter at any given site. We collected samples using SCUBA, then transported to the lab in seawater, where all invertebrates were removed and preserved in 70% EtOH within 24 hours of collection.

To estimate variation in diversity among meadows, we sampled nine meadows spanning a watershed gradient beginning near the open coast and moving inland towards Alberni Inlet (Figure 1; Table 1).  We chose these meadows among the subset of known meadows in Trevor channel (n ~ 20) because they are evenly distributed along Trevor Channel (Figure 1), they are large meadows (i.e., min 0.25 ha, not fringing), and they capture many of the shallow areas where eelgrass might occur. To determine whether spatial biodiversity patterns varied through time, we sampled five of these meadows three times, in May (early summer, time A), June/July (midsummer, time B) and August (late summer, time C) of 2012 (Table 1).

We sorted invertebrate collections by size into the following fractions: 1-2 mm, 2-4 mm, 4-8 mm, and > 8 mm. We identified every invertebrate > 1mm in each sample to the lowest taxonomic resolution possible using light microscopy. Though many of our identifications are to species level, many other taxa are identified to higher levels (family or order). Each of these groups possibly includes numerous species; consequently our reference to taxa below reflects varying resolution, and our taxonomic diversity estimates should be considered minimum estimates. We did not include egg masses or colony-forming species (e.g., bryozoans) in our analyses. We classified invertebrate species to broad trophic groups (grazer, predator, filter feeder, detritivore) based on our observations and published information (MacDonald et al. 2010, Light and Smith). The grazer functional group includes organisms that consume micro- or macro-algae, including biofilms, growing on eelgrass.

**Biodiversity estimation**

To estimate diversity within and among meadows, we created species-plot and species-site matrices with abundance data for each taxon, using information on every individual collected from each plot (no subsampling; Gotelli and Colwell 2010). We estimated multiple biodiversity metrics: species richness (number of species observed), their relative abundance, and the likelihood that additional taxa were present but unobserved in estimating and comparing biodiversity among samples and meadows. We estimated alpha diversity by rarifying (ENS) and using raw richness values (R), Shannon diversity (H’), and Simpson evenness (S). The effective number of species (ENS) is derived from the probability of an interspecific encounter (PIE), to characterize diversity at the plot scale (Dauby & Hardy 2012). ENS can be interpreted as the number of equally-abundant species that would exist in a sample of a given diversity value (Jost 2006). We used the R package vegan (Oksanen et al. 2013) for biodiversity analyses.

We quantified beta diversity in two ways. First, beta diversity can defined as the difference between alpha and gamma (regional) diversity (Veech oikos). We estimated beta diversity for each meadow by subtracting the mean alpha (R) from the estimated meadow-scale gamma (*chao2? Or just observed?*). Other definitions of beta diversity capture the magnitude of compositional turnover among samples or habitat patches (Anderson et al. 2006, 2010). We estimated variation in species composition and turnover with a Bray-Curtis dissimilarity matrix by measuring multivariate homogeneity of group dispersions (Anderson et al. 2006, 2010). We compared differences among meadows at each sampling period with a permutational test for homogeneity of multivariate dispersions that generated pairwise comparisons based on 999 permutations. This method excludes joint absences and focuses on relative abundance among data sets, and is well suited to zero-rich community data. [*is this accurately capturing the approach for the comparison with the null model?*]

Spatial patterns in beta diversity can be used to infer the possible role of underlying ecological processes that could structure communities in space, or alternatively, can indicate random distributions of species not clearly explained by a particular ecological model (Liebold and Mikkelson 2002). We used a null model to test whether observed patterns of species turnover whether different from an expectation based on random distributions. To generate null models of beta diversity for each meadow, we created a statistical function in the program R (R Core Team 2013) that permutes observed community composition using the *permat* function from the vegan package (Oksanen 2013).  Beta diversity was calculated within each meadow with a Bray-Curtis dissimilarity matrix, and resampled 999 times to generate null expectations based on observed compositions. The resulting mean value of the median was used to represent the expected null value for multivariate dispersion, correcting for underestimation bias (Stier et al. 2013).

EMS: to test for classicly defined metacommunity structure, we conducted an analysis of the Elements of Metacommunity Structure (EMS). We compared species presence/absence distributions among meadows against a null model with fixed site richness and species occurrences assigned to sites based on their marginal probabilities. 1000 random matrices were generated, and the observed species absences per meadow were compared against the distribution of absences to determine sifnicance, following Preston et al (2012) and using the R package Metacomm. (Presley et al 2012, Henriques da Silva)

**Statistical analyses**

To test our first hypothesis that faunal beta diversity (turnover among samples) varies among meadows but alpha diversity (sample-level species diversity) does not, we used one-way anova on univariate diversity metrics among nine meadows sampled in July (midsummer, time B). To explore possible explanations for variation in diversity within and among meadows, we tested whether spatial patterns in grazer diversity varied with season, distance, biotic and abiotic meadow attributes. We conducted linear regression analyses using sampling date, distance among plots, meadow area, fetch and position in the watershed as predictors. We explored correlations among predictors (*and found that density and LAI also varied along this gradient?).* Abundance and ENS were log-transformed to meet the assumption of homoscedasticity.

Beta and alpha diversity patterns can differ if species are aggregated within meadows (as opposed to randomly distributed throughout the meadow), or if aggregation varies among species and dominance varies among meadows. We estimated aggregation within meadows using standardized Morisita’s index (I), and then compared aggregation scores for species in each meadow with their rank. We specifically asked, *a)* is there aggregation within meadows, is it driven by the most abundant species, and are the most abundant species the same across meadows? (*do species I scores vary among meadows? b) do morisita scores vary with species rank?*.)

To determine whether spatial patterns of biodiversity are consistent with metacommunity processes, we applied the elements of metacommunity (EMS) framework (Leibold and Mikkelson) using the implementation in the R package Metacom (Presley et al). This analysis first tests for coherence in species distributions, random distributions or… If coherence is identified, subsequent tests allow determination of whether patterns are consistent with nested community structures, clementsian or gleasonian (refs). We analyzed metacommunity structure for the 9 meadows sampled in July 2012.

We ranked models using AICc, and compared them using likelihood ratio tests, δaic and Akaike weights (*w*).Models with a δaic < 2 can be considered equivalent to the best model (Burnham & Anderson 2002). In the case of multiple highly ranked models, we selected the set of models that produced a cumulative *w* > 0.95, representing our confidence (95%) that the set includes the best model, and we averaged these models to produce coefficients of effects (Burnham & Anderson 2002).  We examined residual plots for deviations from the assumptions of linearity or homoscedasticity, (*with the exception of parallel lines in a plot of the models’ fitted values vs. residuals*).  This phenomenon resulted from including repeated values of position in the estuary in the model (Searle 1988). We tested hypotheses on a subset of our full dataset - the meadows sampled at all three time points - to conservatively test for an effect of temporal variation. We then repeated the analysis with the full dataset (including the four sites sampled only once).

**RESULTS**

*Biodiversity summary and meadow attributes*

We collected 304 eelgrass samples, and identified of approximately 81,500 epifaunal invertebrates, representing at least 47 epifaunal taxa in 42 families, across the nine eelgrass meadows, five of which were sampled three times (Table 1). We observed between 0 and 1200 individual epifauna per 0.28 m2. The position in watershed predictor captured correlations with other variables: temperature, salinity, shoot density (appendix, table?). Moving from Alberni Inlet to the ocean, meadows increased in shoot densities (0.27 shoots/km) and associated LAI (240.73 cm2/km) (Tables 1, 2; Appendix 2). Shoot density and LAI increased between May and August at the fresher sites but remained relatively high all summer at the seaward meadows (Appendix 2; Tables 1, 2). Epiphyte load was highly variable between meadows, and did not change predictably with position in the estuary (Appendix 2; Tables 1, 2). Epiphyte abundances and the type of epiphytes present (periphyton vs. bladed algae) varied both spatially and temporally (Appendix 3). The bladed brown epiphyte *Punctaria* *sp.* was abundant at two of the marine sites (Dodger Channel and Wizard Islet), and absent from the fresher Numukamis Bay.

Mean total abundance of all taxa at the plot scale did not vary among meadows in May, but did increase over the summer such that by August abundance was 2-3 times higher in seaward meadows (DC, WI, RP) compared to meadows nearer Alberni Inlet in which abundance was stable over time (CB, NB; Tables 2, 3; Figure 2). Abundance (logged) differed among meadows… The seasonal increase in seaward meadows is clear in both the small (1-2 mm) and large (>2 mm) size fractions.

[*Summary of general composition*]Of the 27 taxonomic groups identified, 24 are herbivorous or omnivorous consumers of epiphytic algae, and therefore belong to the functional group “grazers” (Table 2). These comprised approximately 72% of all individuals; and 6.0 (± 0.15) grazer taxa (isopods, harpacticoid copepods, amphipods, and gastropods) were detected on average in each meadow. Grazers include (Appendix 1). Other functional groups include predators (polychaetes, crabs, free-living mites, two species of amphipod), filter feeders (bivalves), and deposit feeders/detritivores (shrimp). Across all samples, epifaunal assemblages were dominated by small (1-2 mm) invertebrates, which made up ~83% of individuals, whereas large invertebrates (> 8 mm) such as crabs, sea stars and urchins made up less than 3% of individuals.

*Hypothesis 1: alpha diversity does not vary systematically among meadows, but beta diversity does vary among eelgrass meadow.* We found that raw plot-level alpha diversity [R] differed as much within meadows as among meadows, with the exception of high alpha diversity at Robbers Passage and Boyson Islands (F = 8.9, df = 8, 136, P < 0.001). We observed similar patterns in Shannon diversity (F = 4.6, df = 8, 136, P < 0.001) and Simpson diversity (F = 3.8, df = 8, 136, P < 0.001). Rarified diversity estimates are more variable among meadows (Figure 2C; F = 3.62, df = 8, 120, P = 0.002). We did not have plot-level data on other biotic and abiotic attributes (shoot density, temperature, salinity, etc) to test for drivers of variation in alpha diversity among plots. The higher diversity of Robbers Passage, lower S of Dodger Channel, and differences in ENS were not explained by meadow-scale predictors such as position in the watershed, shoot density, meadow area or fetch (Appendix Table 1).

In contrast to the apparent spatial stability of alpha diversity, beta diversity did vary among meadows. *Beta diversity patterns. Then can get into aggregation as one explanation of this.* Aggregation and species rank results (Table 3): Within meadows, there is evidence of spatial aggregation of taxa consistent with clumping of species in space more than expected based on a random spatial distribution of species within the meadow (Figure 3). When the composition of each of the 16 plots is compared with the median composition, the average distance to the median serves as a metric of meadow-scale beta diversity. Average distance to median ranged from 0.20 to 0.49 across all sites and times (Appendix 5). In all cases, observed beta diversity exceeded the null expectation from <1% to >19%, with an average difference of 9.7% (Figure 3, Appendix 5).

We observed slightly higher beta-diversity among plots, suggesting greater spatial aggregation within meadows, in meadows nearer Alberni Inlet (Figure 3). Further, comparing within-meadow estimates of beta diversity across time suggested that beta diversity declined slightly toward the end of the summer (May - 0.33, June/July - 0.34, August - 0.29). However, these trends were not statistically significant. Although beta diversity did not vary predictably along the watershed gradient, a permutation test of multivariate homogeneity of group dispersions showed that meadows did have significantly different values of beta diversity (Appendix 6).

*Hypothesis ii: spatial variation in species composition is consistent with metacommunity-scale processes structuring biodiversity*

*Composition: NMDS results, include temporal dimension.*

Extending the comparisons to across meadows, we found that samples collected within meadows were typically more similar to samples from the same meadow than to samples from other meadows, suggesting meadow-scale aggregation and similarity in faunal assemblages (Figure 4). This species turnover among meadows was driven by both shifts in relative abundance, and by species turnover (Figure 4). Although many species were rare but present at most sites and times, no species was common everywhere at all times. Five taxa were detected at every site and sampling time (the grazers *Pentidotea resecata*, *Caprella* spp., and *Aoroides* *columbiae*; the predator *Eogammarus confervicolus*; and the filter-feeding *Mytilus trossulus*), and eight additional taxa were detected at all sites but one. Conversely, four species were only detected at one time and place (*Alia carinata* at BI, *Strongylocentrotus* sp.at WI, *Solaster* sp.at CB, and *Dinophilus* sp. at DC; Appendix 1), and eight taxa were observed only twice. Whether a species was present at a site was fairly consistent through time. For example, *Photis brevipes*, *Pontogeneia* sp., *Platynereis bicanaliculata* and *Lacuna* sp. were not observed at Crow Cove at any of the three sampling times (48 samples in total).

Across all meadows, five taxa accounted for > 80% of invertebrates collected: the caprellid amphipods *Caprella* spp. (*C. laeviuscula* and *C. californica*), the sea hare *Phyllaplysia taylori* (primarily juveniles), the mussel *Mytilus trossulus* (primarily juveniles), the polychaete worm *P*. *bicanaliculata*, and the sea spider *Pycnogonum* sp.  However, the abundances of these species were not consistently high across all meadows and all sampling periods.  For example, in the midsummer sampling period the number of caprellids ranged from 488 individuals/plot in Numukamis Bay to less than 0.1 individual/plot at Ellis Island.

NMDS visualization reveals a community dominated by epiphyte grazers (*Caprella spp*., amphipods *A. columbiae, P*. *brevipes*, the isopod *Pentidotea resecata,* the sea hare *P. taylori*) in meadows toward the ocean end of Trevor Channel, and a community dominated by filter feeders (primarily mussels), *Pycnogonum* sp. and nematodes at meadows toward the Inlet (Figure 4). These differences are conserved through time, except at Wizard Islet (which resembled marine sites until a major recruitment of mussels in July; Figure 4).

The identity of dominant taxa varied through time. We observed large temporal changes in the abundance of many common species: for example, *Caprella* spp. abundance increased more than ten-fold (from an average of 16 individuals/plot to 237 individuals/plot) from early to mid-summer, but by late summer a recruitment event of *P. taylori* let this species to outnumber *Caprella* spp*.* at Robbers Bank and Dodger Channel (at the marine end of the estuary).  However, these changes in abundance were not consistently observed across sites. For example, the *P. taylori* recruitment event occurred at two sites, while a major mussel recruitment event occurred at other sites including Numukamis Bay and Crickitt Bay later during the same period.

The grazer species composition varied among meadows. *Pentidotea resecata*, amphipods *A. columbiae* and *Caprella* spp.*,* were observed in every meadow (Appendix 1), but tended to be less abundant in the meadows nearer Alberni Inlet. The eelgrass specialist *P. taylori* was not observed in every meadow (e.g., never at CC, and only 2 individuals observed at NB), but numerically dominated the fauna in some meadows (DC, RP and EI).

*EMS results*

Across all nine sites in midsummer, species composition patterns are consistent with a checkerboard pattern of species distribution among meadows (Table 3). We observed more species absences in meadows than would be expected from a null model, which indicates that there are pairs of taxa that do not co-occur.

**DISCUSSION**

We found that invertebrate biodiversity and abundance observed associated with foundation species can vary substantially between habitat patches and over the course of a season. A watershed gradient of salinity and eelgrass shoot density did not explain variation in alpha (meadow-scale) diversity or species turnover among meadows. However, differences in species composition suggest that meadows nearer the ocean in Trevor Channel host grazer-dominated assemblages, while meadows nearer Alberni Inlet are dominated by filter feeders and other non-grazer taxa. This pattern suggests oceanographic circulation and dispersal among meadows might play a role in influencing species composition, even in the absence of clear trends in total diversity and a continuous effect of salinity, temperature or shoot density on total diversity.

Estimated species richness at the meadow scale varied by a factor of four from 13 to 53 species, and plot-level invertebrate abundance ranged over three orders of magnitude. However, we emphasize again that because we did not identify every individual to species, our estimates of diversity are minimums and the true diversity in these meadows is likely higher.

**Spatial variation in biodiversity**

Contrary to our expectations, we did not observe a clear signal of continuous variation in biodiversity along the biotic and abiotic gradients associated with the watershed. The lack of a clear signal of salinity in the epifaunal community contrasts with previous findings in other seagrass systems. Barnes (2013) found that invertebrate assemblages in an extensive seagrass meadow in Knysna Bay (South Africa) respond strongly to estuarine gradients, with significant reductions in species diversity and richness at the fresh end of the estuary.  Yamada et al (2007) also found a positive relationship between salinity and invertebrate diversity. In contrast, we observed only weak, temporally inconsistent trends in invertebrate abundance and diversity with estuarine position (correlated with salinity and eelgrass structure).  However, the sites sampled by Barnes (2013) and Yamada et al. (2007) spanned a greater range in salinity (< 5 - 35 ppt and 6.2 – 32.2 ppt, respectively) than did ours (~14 - 28 ppt), and may have captured physiologically stressful, low-salinity conditions with a stronger influence on invertebrate assemblages.

Variation in species diversity at the plot- or meadow-scale could also be explained by meadow area. Larger meadows would be expected to host more species per area than smaller meadows. We only have area estimates for five of the meadows we sampled, and the low sample size (n = 5) and low variation in meadow area prevent robust statistical analysis of area as a predictor. Numukamis Bay (NB) was by far the largest meadow (72 ha), while the others were on the order of <1 to several hectares (Table 1). However, species diversity patterns do not suggest vastly greater species richness in NB than other sites, nor are there fewer species at the smallest (< 1 ha) meadows (Figure 2). Further, average plot scale diversity (7-20 species, Figure 3) and meadow-scale alpha diversity (Chao2 index estimate: 28 species per meadow) was in all cases much lower than regional species diversity (gamma diversity = 47 observed taxa), suggesting that some processes limit the presence of all regionally-present taxa in all meadows.

Despite the absence of a clear signal of an abiotic gradient or meadow area effect, we were able to distinguish between the composition of invertebrate assemblages at the marine and fresh ends of the estuary (Figure 4). Invertebrate assemblages in meadows including and to the southwest of Robber’s Passage (at the marine end of the estuary) tended to clump together in the NMDS similarity plot (Figure 4), and were dominated by grazers (amphipods, caprellids, the sea hare *Phyllaplysia taylori*). At the northeast (fresh) end of the estuary, invertebrate assemblages were dominated by juvenile mussels and nematodes. The one exception to this pattern was the invertebrate assemblage at WI, which showed a composition intermediate to those of the more marine and freshwater meadows despite its position at the marine end of the estuary (Figure 4). The emergence of two invertebrate assemblages associated with spatial areas in Trevor Channel could be explained by differences in connectivity, or meadow-to-meadow colonization and movement, within the two regions of Trevor Channel. The position of the break in species composition corresponds to a large sill in the bottom of Trevor Channel, at which the bottom depth rises to only 30 m from approximately 200 m. This sill could restrict mixing between the seaward and upstream ends of the Channel. Restricted exchange of water could be associated with distinct abiotic properties that influence species’ ability to persist or dominate in these environments. An alternate explanation is that population connectivity could be reduced between these two regions, such that meadows within one of the regions are more demographically connected and therefore more similar in composition than meadows in the other region.

Like alpha diversity metrics, beta diversity did not vary predictably along the watershed gradient. However, our results show that non-directional beta diversity is significantly greater than expected by chance (Figure 3), suggesting aggregation of species within meadows is greater than expected at random. Spatial aggregation within meadows can indicate micro-habitat variation, species interactions such as competition, predation or facilitation, or historical effects such as recovery from disturbance. Despite this signal of aggregation, suggesting species turnover within meadows over fine scale, we observed greater turnover in composition among meadows than within meadows. Greater turnover among meadows could, again, reflect either spatial distance among samples, variation in meadow-scale properties (properties not measured in this study), connectivity, asynchronous community trajectories, or historical events such as disturbance and associated recovery.

To date, there are only a few other beta diversity estimates for seagrass-associated epifauna with which to compare our findings. These studies have typically focused on directional beta diversity, i.e., beta diversity along some gradient.  Previous research has shown that beta diversity in seagrass beds can be driven by variation in salinity, seagrass species, tidal height, and sub-habitat type (e.g., seagrass shoots or sediment; Barnes and Ellwood 2012, De Troch et al. 2001, De Troch et al. 2003, Knight et al. 2015). However, we know very little about non-directional beta diversity within seagrass meadows, and (to our knowledge) no study has attempted to distinguish observed patterns in beta diversity from null expectations (Kraft et al. 2011).  The comparison of null expectations to empirical datasets allows us to infer whether random processes such as chance colonization and extinction, or deterministic processes like environmental filtering or competition are generating observed patterns in community composition (Chase and Myers 2011).

Eelgrass meadows are known for their ability to support a high diversity of fish species (Robinson et al. 2011, Robinson & Yakimishyn 2008). In British Columbia, over 80 fish species occur in eelgrass meadows (Robinson & Yakimishyn 2008). However, not all eelgrass meadows support the same fish assemblages (Robinson et al. 2011), and salinity is one abiotic driver of differences in fish assemblage composition. Though we did observe differences in species assemblages of fish across the meadows, there was no clear correlation between fish composition or diversity and invertebrate abundance or diversity. One limitation to this test in our study is the limited sampling effort for fish diversity and thus low sample sizes. Based on other reports from the region, there likely were many more fish species in these meadows that we missed, and we consequently limit our inferences on fish as a driver of invertebrate composition at this time.

**Temporal trends**

Temporal variation in abundance and diversity within meadows balanced in magnitude the variation we observed over 30 km and nine distinct meadows. Rather than a directional seasonal in abundance or diversity within meadows, these metrics tended to peak in mid-summer (July) and decline again in August. Despite the observed variation, there was no clear overall directional trend through time (Table 3). Dominant species did shift through time, within meadows. These shifts through time reflected recruitment events of several species, notably *Phyllaplysia taylori* and *Mytilus trossulus*. Local reproductive events by the non-dispersing offspring of *P. taylori* dominated the marine sites RP and DC in August. At other sites, planktonic dispersing larvae of mussels colonized and dominated eelgrass assemblages. These trends suggest that reproductive events, regardless of dispersal type, characterize seasonal trends in epifauna diversity and abundance between May and August in this system. Other taxa shifted in abundance substantially, including an increase in nematode abundance at NB between May and July. Grazer taxa such as amphipods and isopods with continuous population dynamics and overlapping generations increased between May and July at all sites except NB. This latter pattern suggests some site-level factors such as food availability, seasonal warming, or reduction in predation between May and July that was then reversed in DC, CB and NB by August. Despite this variation in univariate metrics and the identities of dominant species, multivariate metrics suggested composition overall was relatively stable through time, suggesting that the differences in abundance and richness are reflecting changes in dominance (Figure 4).

The temporal patterns we observed are different from patterns reported epifauna in eelgrass meadows in the east coast of North America. In those systems, grazer and invertebrate abundance and diversity peaks in winter, and from May declines substantially until grazers are virtually absent in late summer (Nelson 1979). This trend has been attributed to seasonal fish predation that intensifies in June each year. In Chesapeake Bay eelgrass systems, epifaunal grazers remain relatively stable in abundance between May and August, though their relative abundance shifts from *Caprella* and *Gammarus* dominated assemblages to the amphipod *Erichsonella attenuata* (Douglass et al. 2010). Our observations are consistent with other reports of seasonal variation in epifaunal assemblages from Puget Sound, WA, showing increasing abundance of grazers (*P. resecata*, *Lacuna* sp., and *Caprella* sp.) between May and late summer (Thom et al. 1995). Best and Stachowicz (2014) also report peak abundance of epifaunal taxa in August, and that peak abundance can vary among habitat patches. These patterns are not clearly consistent with a major seasonal change in predation pressure in this system, despite fish assemblages that include seasonal juveniles (Robinson et al 2011).

**Conclusions**

Understanding spatial and temporal variation is essential to linking the abiotic and biotic features of a marine seascape to the ecosystem functions that promote biodiversity as well as secondary productivity that emerges at higher trophic levels including fish, wading birds, and marine mammals.  Although biodiversity patterns in seagrass meadows have been to date quantified primarily within individual, discrete meadows, many of the processes that influence these patterns, including potentially damaging processes such as eutrophication, the introduction of non-native species, and severe weather, operate across much larger spatial scales (Duarte 2002).  This disconnect between sampling scale and the spatial extent of disturbance has been shown to lead to conflicting and misleading conclusions about the effects of disturbance on ecosystems, particularly with respect to changes in local population persistence and species richness (Powell et al. 2013).  As anthropogenic pressure on valuable coastal ecosystems continues to accelerate, it is more important than ever that we develop a baseline understanding of how biodiversity in seagrass meadows is maintained across ecologically relevant scales. This study represents one of the first comprehensive assessments of eelgrass-associated biodiversity in the Pacific Northwest, and is perhaps the most comprehensive assessment and analysis of eelgrass-associated biodiversity on Vancouver Island.

We have shown here that species diversity and abundance vary among seagrass meadows within a region, and that the variation is not clearly predictable based on an estuarine gradient and related predictors. Although *Z. marina* provides relatively homogenous habitat, *Z. marina* meadows host distinct communities, and each appears to host a subset of epifaunal species observed in the larger region. These patterns are indicative of a metacommunity system, and suggest that the processes that maintain diversity in eelgrass communities may reflect a seascape of many meadows connected through dispersal. If true, then conservation of eelgrass systems will require a network approach that preserves numerous meadows within the region. Examining biodiversity patterns across a seascape has expanded our view of seagrass biodiversity, and additional research is required to meet the challenges of understanding how spatial turnover in diversity is related to the function and resilience of these ecosystems.

**[outtakes from intro that might be useful here:** The diversity and composition of epifaunal grazers can influence ecosystem functions, including resilience to disturbance and control of algal epiphytes (Blake & Duffy 2012, Duffy et al. 2003, Duffy et al. 2015, Eklöf et al. 2012). Diversity of epifaunal grazers (algae-consumers) has been shown to stabilize trophic processes in seagrass meadows, with the additional effect of controlling epiphytic algal abundance and facilitating seagrass growth (Hughes et al. 2004). However, grazers are often analyzed as part of a larger pool of invertebrates that includes predators and detritivores, in large part because the natural history of many of these invertebrates is not well documented and consequently it is difficult to separate species into trophic groups. As a result, we have a limited understanding of how grazers vary in their distribution and abundance, and what proportion of invertebrates is actually contributing to algal consumption in seagrass meadows.

Seagrass habitat is considered an indicator of high biodiversity for assessments and prioritization schemes (Shokri & Gladstone 2013), yet seagrass-associated epifaunal diversity can vary substantially over relatively fine spatial and temporal scales (Boström et al. 2010, Carr et al. 2011, Robinson et al. 2011, Nelson 1979).  Seagrass meadows exist in discrete patches that range over several orders of magnitude in size (Mason et al. 2015), and are often separated by physical barriers such as deep water, fast currents, rocky substrates and human developments. Many factors can drive variation in diversity within meadows, including predation (Amundrud et al. 2015, Huang et al. 2015, Nelson 1979), productivity (De Troch et al. 2006), seagrass shoot density and phenotype (McCloskey & Unsworth 2015), and the regional species pool (Duffy et al. 2015, France & Duffy 2006). At the seascape scale, meadow size and abiotic factors including salinity (Yamada et al. 2007, Robinson et al. 2011), temperature (Barnes & Ellwood 2012), and connectivity (movement) among meadows (Boström et al. 2010, Tanner 2003) also influence biodiversity. ]

Patterns of species diversity and composition across scales reflect the distribution of individuals within species across space. A nearly-universal pattern in ecological communities is the rank-abundance distribution, or the pattern in which few species are common and most are rare. Another ubiquitous pattern is that of intraspecific aggregation in space. Together, these two attributes of how individuals are distributed in the environment mean that diversity at fine spatial scales – several orders of magnitude of the body size of individuals – can be decoupled from diversity at broader spatial scales over an environmental or spatial gradient.

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