**Spatial dynamics of animal-mediated nutrients** **in temperate waters**

Em G Lim1,2\*, Claire M Attridge1, Jasmin M Schuster3,4, Kieran D Cox1, Kiara R Kattler1,5, Emily J Leedham1, Bridget Maher3, Andrew L Bickell3, Francis Juanes3, Isabelle M Côté1

1Department of Biological Sciences, Simon Fraser University, Burnaby, British Columbia, Canada

2Bamfield Marine Sciences Center, Bamfield, British Columbia, Canada

3Department of Biology, University of Victoria, Victoria, British Columbia, Canada

4Hakai Institute, Campbell River, British Columbia, Canada

5University of Alberta, Edmonton, Canada  
\*Corresponding author: Em Lim, em.g.lim13@gmail.com

**Abstract**

Consumer-mediated nutrient dynamics (CND), through which animals’ metabolic waste products fertilize primary producers, drives variability in nutrient availability and thus primary productivity and community functioning in tropical waters. Yet, examinations of CND as a driver of variation in nutrient availability in temperate marine ecosystems are limited. To assess the scale and drivers of spatial variation in CND within temperate marine ecosystems, we quantified the occurrence of 48 fish and 92 macroinvertebrate taxa and estimated their contributions to the ammonium budget at 27 northeast Pacific rocky reefs for three years and 17 kelp forests of varying density for one year. Ammonium concentrations ranged from 0.01 to 2.5 uM across rocky reefs separated by tens of km. The relationship between animal biomass and ammonium among sites was mediated by water flow, whereby flood tides seemed to “wash away” the effect of animals, but enrichment may be possible on ebb tides. Ammonium was significantly higher within than at the edge of kelp forests, ~ 5 m away, a difference that increased with tide exchange, kelp biomass, and to a lesser degree animal biomass. Using caging experiments, we found that fine-scale ammonium variability and nutrient enrichment on a scale of meters was only possible under low-flow conditions. Our results suggest CND-driven variability acts on scales ranging from one meter to over 20 km, contributing to finer-scale variation in nutrient availability than allochthonous nutrient sources such as upwelling. Therefore, consumer-mediated nutrient dynamics could drive spatial variation in primary productivity at a range of scales in a way previously thought possible only in tropical marine environments.

**Introduction**

Variation in resource availability across spatial and temporal scales can drive substantial heterogeneity in the growth, biomass and composition of primary producers (Dayton et al., 1999; Leibold, 1991; McInturf et al., 2019; Tilman, 1984). In many marine ecosystems, community structure is under bottom-up control, i.e., it depends on factors that generate variability in the resources available to lower trophic levels (Gruner et al., 2008). Although marine ecologists have historically focused on external, abiotic sources of nutrients (e.g. upwelling) as drivers of variability in nutrient availability, there is now substantial evidence that consumers also contribute to bottom-up effects (Allgeier et al., 2017). The metabolic waste products (i.e., excretion and egestion) of animals fertilize primary producers via a process termed consumer-mediated nutrient dynamics (CND, Vanni, 2002). Consumers excrete metabolic waste in the form of ammonium (NH₄⁺), which is preferentially taken up by primary producers over other forms of nitrogen like nitrate and nitrite (Lobban and Harrison, 1994; Phillips and Hurd, 2004). However, the ecological importance of consumer-regenerated nutrients across scales remains unclear. Therefore, identifying the scales at which biologically relevant variation in nutrient availability contributes to heterogeneity in primary productivity remains an active area of research (Allgeier et al., 2017).

Heterogeneity in consumer habitat use contributes substantially to spatial and temporal variation in nutrients supplied by animal waste (Benkwitt et al., 2019; Roman and McCarthy, 2010; Uthicke, 2001a). For example, tropical coral reefs provide habitat, shelter, and food sources that attract dense aggregations of vertebrate and invertebrate consumers, which regenerate nutrients (Archer et al., 2015; Meyer et al., 1983; Shantz et al., 2015). On a broad scale, productivity increases with proximity to reefs with high densities of fishes (Layman et al., 2016), while on a finer scale, sheltering schools of fish increase nitrogen concentrations around individual heads of corals relative to neighboring uninhabited corals (Holbrook et al., 2008). Diurnal migrations are another source of temporal and spatial variation as some fishes travel away from reefs to forage at night, then return to excrete waste around their hiding spots during the day (Francis and Côté, 2018; Meyer and Schultz, 1985). Even larger-scale variation can arise from the migration of megafauna; for instance, whales transport and deposit nutrients across thousands of kilometers as they travel from their feeding to breeding grounds (Doughty et al., 2016). However, the current understanding of animal-driven spatio-temporal variability of nitrogen is drawn substantially from tropical ecosystems (Allgeier et al., 2013; Holbrook et al., 2008; Meyer et al., 1983), often overlooking productive temperate marine ecosystems.

In temperate oceans, external sources of nutrients, such as upwelling and freshwater runoff, are generally considered the dominant drivers of nitrogen variability (Dayton et al., 1999; Mann, 1973). Due to the open nature of nearshore environments, high water flow due to currents, tides, and wave action are believed to limit small-scale nutrient variation (Probyn and Chapman, 1983). Therefore, research on intertidal and shallow subtidal ecosystems has traditionally focused on top-down trophic interactions as drivers of community composition at small scales (1 to 100 m2), and considered resource limitation mainly at large, regional or continental scales (Menge, 1992; Paine, 1986). However, evidence suggests meso-scale (10 to 100 km, Broitman et al., 2001) variation in allochthonous nitrogen via upwelling may contribute to bottom-up control of marine communities (Menge et al., 1997; Nielsen and Navarrete, 2004) and even weaken top-down control (Sellers et al., 2020). For example, the amount of nitrogen regenerated by intertidal mussel beds varies with mussel cover along an entire coastline (Pfister et al., 2014). In wave-exposed shorelines, mussel beds also contribute to nutrient regeneration on small, local scales by increasing the concentration of nitrogen in the water column directly over the beds (Aquilino et al., 2009). Vertical gradients in nitrogen concentration in the water column can also arise from microbial remineralization in marine sediments (Lowman et al., 2023). Therefore, regenerated nitrogen may contribute substantially to large-, meso-, and small-scale variation in nutrient availability, even in high-flow, upwelling-dominated nearshore coastal ecosystems.

Shallow subtidal rocky reefs and kelp forests are two temperate nearshore communities that attract dense aggregations of fishes and invertebrates, many of which are economically, ecologically, and culturally important (Steneck et al., 2002). Elevated NH₄⁺ excretion from the high biomass and biodiversity of these animals may also contribute to nutrient hotspots on small to meso scales. Fast-growing canopy kelps, which form expansive underwater forests, may benefit from these excretions directly as a source of nitrogen (in the form of NH₄⁺), especially during low upwelling periods (Brzezinksi et al., 2013; Lees et al., 2024). These kelps, which comprise giant kelp (*Macrocystis pyrifera*) and bull kelp (*Nereocystis leutkeana*) in the northeast Pacific region, also affect seawater hydrodynamics and physical composition, both slowing water flow within forests and creating gradients of carbon content, pH, alkalinity, and oxygen (Gaylord et al., 2007; Jackson and Winant, 1983; Pfister et al., 2019). These modifications to the physical environment could affect the productivity and community composition of other primary producers and contribute to small-scale spatial nutrient heterogeneity.

We aimed to quantify the contribution of animal-regenerated nitrogen to spatial variability of nutrients in a temperate, wave-swept upwelling region: Barkley Sound in British Columbia (BC), Canada. This region is located on the traditional territories of the Huu-ay-aht First Nations and comprises an archipelago of islands dotted with rocky reefs and kelp forests. We hypothesized that animal-regenerated nutrients could contribute to variability in resource availability across multiple scales. Specifically, we predicted that NH₄⁺ variation might be detectable at the largest scale studied due to variation in animal abundance among sites. We also expected to find some variation in NH₄⁺ concentrations at the smaller scales studied (i.e., within natural sites and between experimental cages), but only under conditions that allow local enrichment (e.g., low tidal exchange). To test these predictions, we measured variation in NH₄⁺ concentrations among rocky reef sites (meso scale of ~10s of km), in and out of kelp forest sites (small scale of 5 m), and near experimentally caged consumers (smaller scale of < 2 m, Fig. 1a, b, c). We quantified the abundance and diversity of fishes and invertebrates at each rocky reef and kelp forest site and measured kelp forest metrics and other abiotic variables to explore drivers of potential variation in NH₄⁺ concentrations. By characterizing the scale at which animal-driven nutrients vary, we hope to elucidate the potential for consumers in temperate regions to structure communities not only from the top down, but also from the bottom up.

**Methods**

*Site description*

Barkley Sound is located in an upwelling region on the west coast of Vancouver Island, Canada. Upwelling supplies nitrates in the spring and early summer, while storms flush riverine inputs into the nearshore in the winter and spring (Pawlowicz, 2017). Due to the proximity of the Bamfield Marine Sciences Centre (BMSC), this region has been a long-term focal area for studies seeking to document large-scale patterns of kelp response to heatwaves, establish ecological baselines, and unravel ecosystem dynamics (Attridge et al., 2024; Howard et al., 2019; Starko et al., 2024, 2022; Tanasichuk, 1998). Subtidal fish communities comprise at least 18 families including gobies, surfperches, rockfishes, greenlings, and sculpins (E.G. Lim, unpubl.). Invertebrate assemblages, which comprise over 49 families, are dominated by urchins, turban snails, sea stars, abalone, and sea cucumbers (E.G. Lim, unpubl.).

*Surveys of among-site (meso-scale) variation*

To explore meso-scale variation in animal-regenerated nutrients among rocky reefs, we measured ammonium (NH₄⁺) concentrations and surveyed fish and invertebrate communities at 27 subtidal sites ranging from 0.06 – 24 km apart in Barkley Sound (Fig. 1d). We used a globally standardized method (i.e., Reef Life Survey, RLS) at each site to estimate fish and invertebrate abundance and collected subtidal NH4+ samples during each survey. We conducted our surveys between the end of April and mid-May for three years (2021-2023), with all annual surveys occurring within two weeks of each other (Supplemental Table 1). A full explanation of the Reef Life Survey method is available online (http://www.reeflifesurvey.com/methods) and provided by Edgar and Stuart-Smith (2009) and Edgar et al. (2020). Briefly, at each rocky reef site, a pair of RLS trained SCUBA divers assessed fish and invertebrate abundance and diversity along each side of a 50 m transect line. First, fishes in the water column were counted and sized (total length, in various size class categories) within 5 m on either side of the transect line (500 m2), and then benthic cryptic fishes (also sized) and large mobile invertebrates (> 2.5 cm) were counted within 1 m on either side of the transect line (100 m2).

Immediately following each RLS survey, we collected three 60 mL subtidal seawater samples at 0, 25, and 50 m along the transect 0 – 2 m from the substrate and stored the syringes in sealed plastic bags upon collection to prevent contamination. Seawater samples were filtered into opaque amber bottles in the field and frozen for a maximum of two weeks before NH4+ analysis. We confirmed that freezing samples for this duration did not affect NH4+ concentration (E. G. Lim unpubl.). In 2021 and 2022, we followed the fluorometric method using 40 mL seawater samples (Holmes et al., 1999), and in 2023, we followed the fluorometric standard-additions protocol II (Taylor et al., 2007). These methods produce similar results, although the Holmes single spike method is associated with higher variability in measurements (Taylor et al., 2007). The three NH₄⁺ samples collected during each survey were averaged to determine the mean NH₄⁺ concentration for each site.

*Surveys of within-site (small-scale) variation*

To investigate within-site variation in animal-regenerated nutrients, we measured NH4+ concentrations in and around kelp forests and surveyed the neighbouring biological communities as potential moderators of this variation. Our 16 sites comprised forests of varying densities dominated by giant kelp or bull kelp and two no-kelp control sites. We conducted our surveys from July to September 2022 (Supplemental Table 2). First, to quantify the abundance and biodiversity of animal communities associated with each kelp forest, divers surveyed fish and invertebrate communities along 50 m transect lines parallel to the edge of the kelp forest following the RLS protocol as above. Next, we ran four 5 m-long transects perpendicular to the RLS transect (5 m apart) into the kelp forest to assess kelp density, canopy height, and biomass (Supplemental Fig. 1). Divers then counted the number of canopy kelp individuals (bull or giant kelp) within 0.5 m on either side of each kelp transect to measure kelp density. To estimate canopy height, we measured the length of five randomly chosen kelp individuals per kelp transect; for bull kelp we measured the total length from holdfast to pneumatocyst *in situ*, but for giant kelp, we collected five random individuals to measure the length from holdfast to apical meristem on dry land. To quantify bull kelp biomass, we measured the sub-bulb circumference (15 cm below the bottom of the bulb) of the same five bull kelps per transect *in situ* and calculated individual biomass using a quadratic diameter to biomass formula (C. M. Attridge unpubl.). For giant kelp biomass, we weighed to the nearest X g the same five individuals per transect that were collected for total length measurements. We multiplied the mean biomass estimate for each kelp species by the species density to calculate a biomass/m2 estimate for each kelp transect, which we then averaged over the four transects per forest to estimate overall mean forest biomass/m2. We estimated total forest area by swimming around the perimeter of the forest on the surface with a Garmin GPS, (model number?), which we used to calculate total forest biomass (kg).

Finally, to compare NH₄⁺ concentrations inside vs outside each kelp forest, we collected paired 60 mL syringes of seawater immediately outside the kelp forest within 0 – 2 m from the substrate, and 5 m into the kelp forest at the same depth. We collected three paired NH₄⁺ samples from each site, which were spaced 5 m apart by matching them with the first three kelp transects. Outside each kelp forest, we also filled a Whirl-PakTM sample bag with seawater for creating standards. Samples and standards were filtered into amber bottles in the field and stored on ice for transportation back to the laboratory, at which point we measured NH4+ concentration in each sample bottle following the fluorometric standard-additions protocol II for 40 mL samples (Taylor et al., 2007). For each paired inside and outside kelp forest NH₄⁺ sample, we calculated ∆NH₄⁺ = inside NH₄⁺ - outside NH₄⁺.

*Surveys of within-meters (smaller-scale) variation*

To quantify the ability of animals to affect the NH₄⁺ concentration in their immediate vicinity we conducted two caging experiments *in situ* near Bamfield. We used California sea cucumbers (*Apostichopus californicus*) in the first caging experiment because they’re a large, abundant invertebrate with a high excretion rate (Bray et al., 1988). The first experiment took place at Scott’s Bay (48°50'05.2"N, 125°08'49.3"W), a wide, exposed bay that opens into Trevor Channel (Fig. 1d), on May 27 – 28, 2021. We constructed 18 wire cages (26 x 26 x 26 cm), which we covered in 2 mm plastic mesh. These cages were spaced 3 m apart along two weighted lines and deployed at 3 to 5.8 m depth (9 cages per line). We collected adult California sea cucumbers from the site via SCUBA, measured contracted sea cucumber length and girth, and immediately placed them into the cages in randomly assigned densities of 0, 1, or 2 sea cucumbers (n = 6 replicates per density). After 24 h, we returned to collect water samples from each cage *in situ*. While underwater, we minimized water movement by reducing our fin and hand movements while opening the mesh lids, which were secured with wire, just wide enough to collect a 60 mL syringe of seawater. Once at the surface, we filtered 40 mL of each sample into amber bottles and transported them on ice to the lab, where we measured NH4+ using the fluorometric method (Holmes et al., 1999).

We used red rock crabs (*Cancer productus*) in the second caging experiment to see if a species with an even higher individual-level excretion rate could produce small-scale nutrient variation. The second experiment took place in Bamfield Inlet (48°49'53"N 125°08'11"W), a narrow, sheltered inlet (Fig. 1d), from June 10 – 19, 2023, and we replicated it again from June 19 – 28, 2023 following the same methodology. For these experiments, we used red rock crabs. We collected crabs from the site using crab traps and kept them at BMSC in flow-through sea tables for 2 – 10 days. Crabs were fed salmon every 2 – 4 days, and all crabs were fed the night before each experiment started. We constructed 12 cages from clear plastic (40 x 28 x 17 cm), with two 15 x 9 cm windows covered in a dual layer of 10 mm plastic mesh and 1 mm mesh to allow for water flow. The cages were randomly distributed every 2 m along a lead line anchored with cement blocks 0.8 m below chart datum. Each cage contained either one large crab (carapace 15.0 – 15.9 cm), one medium size crab (11.6 – 14.4 cm), or a control (i.e., a small rock, scraped clean, so weight was similar across all cages) (n = 4 replicates per experiment). During both experiments, we replaced the crabs after 4 days with freshly fed, similar-sized crabs, at this point, we re-randomized the order of the cages along the line. We measured seawater NH₄⁺ concentration via snorkel at low tide at the beginning, middle, and end of each nine-day experiment by drawing water samples using a 60 mL syringe and a fixed narrow rubber tube that began in the centre of the cage and extended several inches outside the mesh window. We filtered 40 mL of each sample into amber bottles, which were stored on ice before NH₄⁺ analysis via fluorometric standard-additions protocol II (Taylor et al., 2007).

*Statistical analyses*

All statistical analysis were conducted in R (v4.1.2, R Core Team, 2019) using RStudio (v1.3.1093, RStudio Team, 2016). We used tidyverse packages for data manipulation and visualization (Wickham et al., 2019), ‘glmmTMB’ for all modelling (Brooks et al., 2017), and DHARMa to check model fit (Hartig, 2022). We ensured all models met assumptions by inspecting residuals using DHARMa::simulateResiduals, and checked for collinearity between variables using car::vif with a cutoff value of 2. All data and code are available at <https://github.com/em-lim13/Ch2_Spatial_pee>.

For each Reef Life Survey conducted, we calculated fish biomass from fish length following the formula:

W is fish weight, L is the fish length, a and b are species-specific constants from FishBase (Froese et al., 2014). All mobile invertebrates were counted, but only sunflower sea stars (*Pycnopodia helianthoides*) and economically important species (abalone [*Haliotis kamtschatkana*] and scallops [*Crassadoma gigantea*]) were sized, so we used published length–weight relationships to calculate wet weight from length for these three species. For all other invertebrates, we used published wet weights to estimate biomass for each taxon. We used shell-free wet weight for species with large shells such as hermit crabs and snails. When biomass information was unavailable for a species, we used estimates from the closest relative or most similarly sized species available (Supplemental Table 3). Animal abundance per m2 was calculated as the total number of fishes and invertebrates counted on each survey (divided by 500 m2 for pelagic fishes and by 100 m2 for cryptic fishes and macroinvertebrates), and we used the ‘vegan’ package to calculate Shannon and Simpson diversity indices (Oksanen et al., 2022). We calculated the tide exchange by computing the percent change of the tide height every minute, averaged over the hour-long survey.

Among-site (meso-scale) variation

To explore variation in NH₄⁺ among sites, we constructed generalized linear mixed-effect models (GLMMs) with NH₄⁺ concentration as the response variable, and animal abundance, tide exchange, an interaction between abundance and tide, Shannon diversity, and survey depth as predictors, and random effects of site (1|site) and year (1|year). All predictors were scaled and centered around the mean using the scale function. We used a gamma distribution (link = ‘log’). To test the robustness of our modelling approach, we considered animal biomass as a predictor instead of abundance, and Simpson’s diversity instead of Shannon diversity; alternative models including these predictors were not better supported by AIC (Supplemental Table 4). We ran additional models considering the effect of only the most abundant families of fishes and invertebrates, which are fully described in Electronic Supplement 2.

Within-site (small-scale) variation

To determine whether NH₄⁺ concentration differed inside and outside of kelp forests, we used a linear mixed-effects model (LMM) with ∆NH₄⁺ as the response variable (n = 3 estimates per site), and kelp species, mean forest kelp biomass (per m2), tide exchange, animal biomass, survey depth, Shannon diversity, and interactions between kelp biomass and tide exchange, kelp biomass and animal biomass, and animal biomass and tide exchange as fixed effects. All continuous predictors were scaled and centered around the mean as above. We included site as a random effect (1|site) as each site contributed 3 estimates to the analysis and used a Gaussian distribution. As above, we chose our final set of predictors upon comparing AIC values of models with alternate predictors (Supplemental Table 5). We then ran additional models considering the effect of only the most abundant families of fishes and invertebrates (Electronic Supplement 2).

Within-meters (smaller-scale) variation

We constructed separate linear models for each caging experiment to quantify the impact of caged animals on adjacent NH₄⁺ concentration. For the sea cucumber experiment, we regressed cage NH₄⁺ concentration against the treatment (i.e., sea cucumber density: 0, 1, or 2 sea cucumbers) and cage depth (centered) using a Gaussian distribution. We calculated the NH₄⁺ excretion rate for each sea cucumber using a previously generated size-to-excretion relationship (E. G. Lim unpubl.). For the red rock crab experiment, we constructed a generalized linear mixed-effects model (GLMM) with cage NH₄⁺ concentration as the response variable and treatment (no crab, medium crab, or large crab) as the predictor variable. We included a random effect of sampling day because we measured NH₄⁺ three times per experiment, and a random effect of experimental week, because we replicated the whole experiment twice, and used a gamma distribution (link = ‘log’). We used a previously developed carapace-to-excretion relationship to calculate NH₄⁺ excretion rates for each crab (E. G. Lim unpubl.).

**Results**

We found evidence of meso-scale variation in ammonium (NH₄⁺) concentrations, which ranged from 0.07 μM – 2.06 μM among rocky reefs in Barkley Sound (Fig. 1d). Overall, we found no evidence that NH₄⁺ concentration was correlated with animal abundance (GLMM, p = 0.57), tide exchange (p = 0.99), Shannon diversity (p = 0.41), or survey depth (p = 0.61, Fig. 2a). However, we did find a significantly negative interaction between animal abundance and tide exchange (p = 0.01, Fig. 2b), revealing a weakly positive effect of total animal abundance per m2 on NH₄⁺ concentration, but only at ebb tide.

We also found evidence of significant small-scale, within-site variation (Fig. 3); NH₄⁺ concentrations were 1.3x higher inside giant kelp forests and 1.6x higher inside bull kelp forests than outside (LMM, p < 0.001; Fig. 3b). The ‘excess’ NH₄⁺ concentration inside kelp forests increased with kelp biomass (p < 0.001; Fig. 3c), and tide exchange (p = 0.007; Fig. 3a). We found limited evidence for an effect of animal biomass (p = 0.07; Fig. 3a), survey depth (p = 0.07; Fig. 3a), and Shannon diversity on ∆NH₄⁺ (p = 0.09; Fig. 3a). There was a positive interaction between kelp forest biomass and tide exchange, whereby the positive effect of kelp biomass on ∆NH₄⁺ increased with tide exchange (p < 0.001, Fig. 3a,c). We also found a negative interaction between kelp biomass and animal biomass (p = 0.006; Fig. 3a & d), and a negative interaction between tide exchange and animal biomass (p = 0.004, Fig. 3a,e). The change in NH₄⁺ was negative between samples taken 5 m apart at the no-kelp control sites (p = 0.003, Fig. 3b).

We found mixed evidence for animal-related variability in NH₄⁺ concentration at the smallest scale studied. For sea cucumbers, we found no effect of sea cucumber density on cage NH₄⁺ concentration despite a supply rate of 14 μM/h and 28 μM/h for the low and high treatments, respectively. Overall, the mean NH₄⁺ concentration was 0.92 ± 0.04 μM across all cages (LM, p > 0.75 for both treatments, Fig. 4a). However, we did find a positive effect of cage depth, whereby NH₄⁺ increased by 0.38 ± 0.05 μM per m increase in depth (p < 0.001). For red rock crabs, both medium and large crabs significantly increased the cage NH₄⁺ concentration relative to control cages, by 8.7x and 12.1x respectively (GLMM, p < 0.001 for all, Fig. 4b). Medium crabs excreted on average 88 μM/h while large crabs excreted 150 μM/h.

**Discussion**

We found evidence of variability of animal-regenerated nutrients from the largest to the smallest scale examined, albeit the signal strength varied across scales. Ammonium (NH₄⁺) varied by up to 16x between rocky reef sites within a year, 1.9x inside vs outside kelp forests, and 40x between cages with crabs vs cages without crabs. Water flow mediated the capacity for animals to saturate the water column with nutrients; among sites a flooding tide seemed to “wash away” the impact of animals on NH₄⁺ concentrations, but within sites moving water made kelps’ ability to slow flow and trap animal-regenerated nutrients more pronounced. In the very-small scale caging experiments we only detected an effect when the nutrient providers were crabs – an effect that we attribute mainly to the low water flow in the protected inlet rather than to a taxonomic effect. Nevertheless, across all three scales, there was animal-mediated spatial heterogeneity in nutrient availability, which may contribute to bottom-up effects.

*Meso-scale variation*

Among rocky reef sites, we detected a 16-fold difference in NH₄⁺ among sites with the lowest and highest concentrations. This difference is substantially larger than previous measurements of among-site variation in nitrate (3.7x and 6.5x) and (0.4x and 0.8x) from the same region (Druehl et al., 1989; Hurd et al., 2000), and larger than among-site NH₄⁺ differences measured in nearby Washington State (1.1x, Pfister et al., 2014). We had predicted that variation in NH₄⁺ concentration among sites would be driven primarily by animal abundance. We were partly correct since the only predictor of among-site differences in NH₄⁺ that emerged from our analyses was a negative interaction between tide exchange and animal abundance, whereby animal excretions may enrich the seawater when the tide is ebbing and standing still, but the effect of animal abundance is washed away when the tide comes in. We did not quantify intertidal animals or microbial regeneration, which are additional sources of NH₄⁺ (Aquilino et al., 2009; Lowman et al., 2023), but these might be more important in shallower waters and in soft-sediment areas than on the subtidal rocky reefs we studied. We conclude that CND likely contribute to meso-scale variation in NH₄⁺ in an unexpected, dynamic, tide-associated manner, which could drive among-site variation in primary productivity and thus bottom-up control.

*Small-scale variation*

We found evidence of kelp-mediated nutrient variation on a smaller scale (5 m) than previously established. Previous studies have found that nitrate from external sources (e.g. upwelling and run-off) becomes depleted or unchanged as it flows through a kelp forest (Pfister et al., 2019; Stewart et al., 2009) in contrast to NH4+ which is regenerated by animals within and around the forest and seemingly retained there. Higher NH₄⁺ inside high-density kelp forests has been documented (e.g., Pfister et al., 2019), but these studies compared nutrient samples taken from the middle of very large kelp forests to sites more than 50 m away from the forest edges (Pfister et al., 2019; Stewart et al., 2009; Traiger et al., 2022). By sampling across a gradient of kelp densities we further demonstrate a positive relationship between kelp biomass and NH₄⁺ retention. The retention of NH₄⁺ observed is likely due to the dampening of flow within the kelp forest bed and subsequent acceleration of flow around the edges (Gaylord et al., 2007; Rosman et al., 2007). Indeed, as predicted, we found the effect of kelp biomass on NH₄⁺ retention was more pronounced when the tide was rising (flood tide). Unfortunately, we never sampled on ebbing tides, and did not quantify water motion due to waves or currents, so we could only contrast slack and flooding tides. Nevertheless, it seems that water flow due to tidal exchange enhances NH₄⁺ variability within kelp forests instead of masking it.

We uncovered additional drivers of differences in NH₄⁺ concentration in and out of kelp forests, namely kelp species and animal biomass. We found higher ∆NH₄⁺ in bull kelpforests compared to giant kelp forests, which may be due to their different allocations of biomass in the water column and thus different alterations of water flow. Indeed, Traiger et al., (2022) found the effect of giant kelp forests on water chemistry was smaller than that of bull kelp forests, previously described by Murie and Bourdeau (2020). The surprising negative ∆NH₄⁺ at our no-kelp control sites may result from “outside” samples at control sites being slightly deeper than the “inside” samples due to the slope of the substrate. The fact that NH₄⁺ tends to *increase* with depth (Brzezinksi et al., 2013), a trend that our no-kelp sites seem to confirm, strengthens our finding of higher NH₄⁺ concentrations within kelp forests than at their slightly deeper edges.

Even though kelp forests attract dense aggregations of fishes and invertebrates, the positive effect of animal biomass on ∆NH₄⁺ was weak and mediated by water flow and kelp biomass. The negative interactions between animal biomass and both tide and kelp biomass suggest a potentially saturating relationship among these variables. When animal biomass was low, increased kelp biomass or tidal exchange increased ∆NH₄⁺ but at high animal biomass, increasing kelp or flow had no effect. There may therefore be a threshold for how much animals can saturate and therefore increase ∆NH₄⁺. Beyond this point, increased water motion or kelp biomass no longer enhances NH₄⁺ inside kelp forests relative to the forest edge.

*Even smaller-scale variation*

When we zoom into the smallest scale of variability tested, we found evidence of smaller-scale variation in NH₄⁺ only in our cage experiments in the sheltered inlet, which may suggest that water motion mediates variation at this scale as well. Alternative or complementary explanations include a taxonomic effect and/or an experimental effect. The crabs in the sheltered cages excreted NH₄⁺ at a rate roughly 6x higher than the sea cucumbers caged in the more exposed location. This difference in NH₄⁺ production could have given us more scope to detect differences among treatments in the protected inlet. In addition, the crab cages were constructed with only two mesh windows, in contrast to the fully meshed cages of sea cucumbers, which could have promoted nutrient retention in the former.

Ammonium enrichment by animals is nevertheless possible in wave-exposed conditions; for example, seawater above mussel beds had ~16x higher NH₄⁺ compared to neighbouring rock without mussels on the northern California coast (Aquilino et al., 2009). Our cage experiments were not designed to test why variation was found in one experiment and not the other, but rather to see whether small-scale variation might arise at all. Therefore, we simply conclude that at least in sheltered conditions, variation on the scale of tens of centimetres driven by animal biomass is possible.

*A role for species diversity*

It was difficult to predict the effect of biodiversity on variation in NH₄⁺, either among or within sites. Marine species diversity sometimes covaries with animal abundance or biomass (Müller et al., 2018; Yee and Juliano, 2007), in which case we might have expected both to have a similar, positive effect on NH₄⁺. This was not the case. Shannon diversity had a neutral effect on NH₄⁺ concentrations among sites and a weakly negative effect on ∆NH₄⁺ within sites. Abundance and species richness are sometimes decoupled (Kerr and Alroy, 2023), because they have different drivers (Mellin et al., 2010). The scale of variation in species richness might also be much larger than the largest scale studied here. For instance, Archambault and Bourget (1996) found that scale of variation in richness for intertidal species was km while scale for variation in abundance was cm. Nevertheless, we did find more species at our kelp sites compared to the rocky reef sites, supporting extensive research on the positive effect of kelp forests on biodiversity (Graham, 2004; Miller et al., 2018; Smale et al., 2013).

*Conclusion*

Despite the mixing forces of currents and tides, spatial heterogeneity in NH₄⁺ concentration is detectable at a broad range of scales. This finding has two main implications. The first relates to our understanding of variation in local primary productivity. Heterogeneity in primary productivity arises from variation in resource supply. Increased primary productivity has been seen with orders of variation in NH₄⁺ from 1.3 – 9x in NH₄⁺ (Allgeier et al., 2020; Arzul, 2001; Meyer et al., 1983; Sandoval-Gil et al., 2016; Savage, 2019; Shantz et al., 2015; Uthicke, 2001b; Uthicke and Klumpp, 1998; Vinther and Holmer, 2008; West et al., 2009), which is within the range of variation we saw at all three spatial scales. Even in nutrient-replete upwelling ecosystems, an increase in NH₄⁺ from 0.08 uM to 1.26 uM (15.8x difference) was linked to increased tissue nitrogen and coverage of an intertidal seaweed (Aquilino et al., 2009), and a 1.8x increase in NH₄⁺ increased growth in subtidal seaweeds in Barkley Sound (Druehl et al., 1989). Given the annual depletion of nitrates each summer (Druehl et al., 1989), primary producers’ preference for NH₄⁺ over nitrate (Phillips and Hurd, 2004), and capacity for surge uptake of NH₄⁺ (Cedeno et al., 2021), it seems likely the animal-driven variation in NH₄⁺ we observed could contribute to heterogeneity in primary productivity.

The second implication relates to our general understanding of the importance of CND, especially in temperate areas. Our results disrupt the dominant paradigm that bottom-up effects are primarily driven by external sources of nutrients acting primarily on large scales, and animals contribute to smaller-scale variation mainly through top-down, consumptive effects. Animal-driven spatio-temporal variability of nitrogen is known to drive bottom-up effects in the tropics, but our results suggest animal-regenerated nutrients may play a previously unappreciated role in shaping nutrient availability in temperate regions too.

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**Figures**

**A screenshot of a map

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**Figure 1.** Scales of study and site locations in Barkley Sound, BC.(a) Among-site, (b) within-site, and (c) within-meters schematics of the three spatial scales of variability investigated. (d) Rocky reefs (circles) surveyed for meso-scale (among-site) ammonium variation, and kelp forests surveyed (triangles) for small-scale (within-site) ammonium variation. Site colour indicates mean ammonium concentration found at each site across all three years, with darker points having higher concentrations of ammonium. (★) Indicates the location of the sea cucumber caging experiment and (\*) denotes location of the crab caging experiment.

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**Figure 2.** Ecological drivers of seawater ammonium concentration observed across 27 rocky reef sites in Barkley Sound, British Columbia, Canada. (a)Model coefficients surrounded by 95% confidence intervals, and (b) model-generated predictions with shaded 95% confidence intervals of the effect of the interaction between animal abundance and tide exchange on among-site variation in ammonium concentration. The coefficients were generated from a generalized linear mixed-effects model, which used a gamma distribution (link = ‘log’) so coefficients are presented in log space. Continuous predictors were centred and scaled for comparison of effect sizes between predictors with varying units.

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**Figure 3.** Drivers of variation in ammonium concentration inside vs outside kelp forests across 16 sites in Barkley Sound, British Columbia, Canada. (a) Model coefficients surrounded by 95% confidence intervals and (b-e) model-generated predictions with shaded 95% confidence intervals of the effects of significant drivers of within-site variation in ammonium concentration. Continuous variables were scaled and centered to facilitate comparisons between variables measured in different units.

****

**Figure 4.** Smaller-scale effect of animals on ammonium concentration. Mean ammonium concentration in experimental cages containing (a) zero (control), one, or two California sea cucumbers (n = 6), and (b) zero (control), one medium-size, or one large red rock crab (n = 8 for control and medium, n = 7 for large). Error bars indicate 95% confidence intervals.

**Electronic Supplement 1.** Supplementary tables and figures.

**A green hill with yellow dots

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**Supplemental Figure 1.** Schematic of methods used to survey biological communities adjacent to a kelp forest, kelp forest density, and NH₄⁺ inside vs outside the forest. We first ran a 50 m Reef Life Survey transect parallel to the kelp forest (green shaded area) and surveyed fishes in the water column 5 m on either side of the transect (light blue shaded areas), and cryptic fishes and macroinvertebrates 1 m on either side of the transect (darker blue shaded area). Next, we ran four 5 m long transects into the kelp forest 5 meters apart from each other to assess kelp density and biomass 0.5 m on either side of the transect (four perpendicular black lines). We took NH₄⁺ samples at the beginning and end of the first three kelp transects (yellow circles) to compare NH₄⁺ inside vs outside kelp forests.

**Supplemental Table 1.** List of rocky reef sites sampled using Reef Life Survey methods, and the years each site was surveyed.

|  |  |  |  |
| --- | --- | --- | --- |
| **Site code** | **Site name** | **Coordinates** | **Years sampled** |
| BMSC1 | Dodger Channel | 48.82894897, -125.1975708 | 2021, 2022, 2023 |
| BMSC2 | Kirby | 48.85039902, -125.1987686 | 2021, 2023 |
| BMSC3 | Ohiat | 48.85558319, -125.1837997 | 2021, 2022, 2023 |
| BMSC4 | Kii xin | 48.81511688, -125.1753311 | 2021, 2023 |
| BMSC5 | Taylor Rock | 48.82733154, -125.1966019 | 2021, 2022, 2023 |
| BMSC6 | Baeria Rocks South Island | 48.95023346, -125.1555481 | 2021, 2022, 2023 |
| BMSC7 | Baeria Rocks N Island Southside | 48.95464325, -125.1539917 | 2021 |
| BMSC8 | Baeria Rocks N Island Northside | 48.95508194, -125.1533737 | 2021, 2022, 2023 |
| BMSC9 | Eagle Bay | 48.83478928, -125.1470261 | 2021, 2022, 2023 |
| BMSC10 | Ross Islets Slug Island | 48.87051773, -125.160347 | 2021, 2022, 2023 |
| BMSC11 | Wizard Island South | 48.85746765, -125.1582336 | 2021, 2022, 2023 |
| BMSC12 | Wizard Island North | 48.858284, -125.1609192 | 2021, 2022, 2023 |
| BMSC13 | Effingham West | 48.8650322, -125.3137207 | 2021, 2022 |
| BMSC14 | Effingham Archipelago | 48.87908173, -125.2974014 | 2021, 2022 |
| BMSC15 | Raymond Kelp Rock | 48.88028336, -125.3128815 | 2021, 2022 |
| BMSC16 | Faber Islets | 48.89070129, -125.300499 | 2021, 2022 |
| BMSC17 | Wouwer Channel | 48.86548233, -125.3614807 | 2021, 2022 |
| BMSC18 | Eussen Rock | 48.91161728, -125.2670364 | 2021, 2022 |
| BMSC19 | Ed King SW Pyramid | 48.82860184, -125.2212982 | 2021, 2022, 2023 |
| BMSC20 | Ed King East | 48.83566666, -125.214798 | 2021, 2022, 2023 |
| BMSC21 | Dixon SW | 48.85205078, -125.1235657 | 2021, 2022, 2023 |
| BMSC22 | Dixon Inside | 48.85426712, -125.1170349 | 2021, 2022, 2023 |
| BMSC23 | Aguilar Point | 48.837589, -125.144145 | 2022, 2023 |
| BMSC24 | Swiss Boy | 48.916073, -125.131174 | 2023 |
| BMSC25 | Goby Town | 48.838595, -125.135015 | 2023 |
| BMSC26 | Hosie South | 48.9071, -125.037017 | 2023 |
| BMSC27 | San Jose North Island | 48.901183, -125.060433 | 2023 |

**Supplemental Table 2.** List of kelp forest site names, coordinates, survey dates and dominant kelp forest species. Macro = giant kelp (*Macrocystis pyrifera*), Nereo = bull kelp (*Nereocystis luetkeana*).

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Site code** | **Site name** | **Coordinates** | **Date** | **Kelp** |
| KCCA1 | Ross Islet Slug Island | 48.87039, -125.1599 | 2022-07-04 | Macro |
| KCCA2 | Between Scott & Brady | 48.83287, -125.1493 | 2022-07-05 | Macro |
| KCCA3 | Dodger Channel 1 | 48.83072, -125.19439 | 2022-07-06 | Macro |
| KCCA4 | Flemming 112 | 48.87868, -125.1434 | 2022-07-07 | Macro |
| KCCA6 | Less Dangerous Bay | 48.87535, -125.0915 | 2022-07-24 | None |
| KCCA7 | Ed King East Inside | 48.83608, -125.2131 | 2022-07-25 | Macro |
| KCCA9 | Wizard Islet South | 48.85728, -125.1595 | 2022-07-27 | Macro |
| KCCA12 | North Helby Rock | 48.85831, -125.1649 | 2022-08-03 | Macro |
| KCCA14 | Danvers Danger Rock | 48.877, -125.0923 | 2022-08-06 | Macro |
| KCCA15 | Cable Beach | 48.82484, -125.16067 | 2022-08-07 | Nereo |
| KCCA16 | Tzartus 116 | 48.90084, -125.0811 | 2022-08-18 | Macro |
| KCCA17 | Turf Island 2 | 48.884864, -125.146937 | 2022-08-20 | Macro |
| KCCA18 | Second Beach | 48.815969, -125.174 | 2022-08-21 | Nereo |
| KCCA19 | Wizard Islet North | 48.85916, -125.15908 | 2022-08-22 | None |
| KCCA21 | Bordelais Island | 48.81822, -125.2294516 | 2022-09-01 | Nereo |
| KCCA22 | Taylor Rock | 48.82721, -125.19717 | 2022-09-05 | Macro |

**Supplemental Table 3**. Wet weight estimates for each invertebrate species used to calculate total biomass for Reef Life Survey data. We used shell-free wet weight for species with large shells (e.g. hermit crabs, snails). When weight information was unavailable for a species, we used estimates from the closest relative or most similarly sized species available. For the three species we measured *in situ*; *Pycnopodia helianthoides*, *Crassadoma gigantea*, and *Haliotis kamtschatkana*, we used published length-weight relationships to calculate wet weight from size.

|  |  |  |
| --- | --- | --- |
| **Species** | **Weight (g)** | **Source, proxy species if applicable** |
| *Cancer productus* | 200 | E.G. Lim, unpubl. |
| *Glebocarcinus oregonensis* | 3 | Hines 1982, small crabs |
| *Romaleon antennarium* | 3 | Hines 1982, small crabs |
| *Chorilia longipes* | 1.235 | Hines 1982, *Pugettia richii* |
| *Pugettia foliata* | 1.235 | Hines 1982, *Pugettia richii* |
| *Pugettia gracilis* | 1.235 | Hines 1982, *Pugettia richii* |
| *Pugettia producta* | 46 | Hines 1982 |
| *Pugettia richii* | 1.235 | Hines 1982 |
| *Scyra acutifrons* | 2 | Hines 1982 |
| *Scyra spp.* | 1.235 | Hines 1982 |
| *Cryptolithodes sitchensis* | 3 | Hines 1982, small crabs |
| *Cryptolithodes typicus* | 3 | Hines 1982, small crabs |
| *Hapalogaster mertensii* | 65 | Stewart et al 2015, *Phyllolithodes papillosus* |
| *Lopholithodes mandtii* | 65 | Stewart et al 2015, *Phyllolithodes papillosus* |
| *Phyllolithodes papillosus* | 65 | Stewart et al 2015 |
| *Oregonia gracilis* | 3 | Hines 1982, small crabs |
| *Paguroidea spp.* | 0.43 | McKinney et al 2004, Paguroidea |
| *Pagurus beringanus* | 0.43 | McKinney et al 2004, Paguroidea |
| *Pagurus hemphilli* | 0.43 | McKinney et al 2004, Paguroidea |
| *Pandalus danae* | 0.11 | McKinney et al 2004, *Palaemonetes pugio* |
| *Pandalus gurneyi* | 0.11 | McKinney et al 2004, *Palaemonetes pugio* |
| *Pandalus spp.* | 0.11 | McKinney et al 2004, *Palaemonetes pugio* |
| *Pandulus spp.* | 0.11 | McKinney et al 2004, *Palaemonetes pugio* |
| *Lophopanopeus bellus* | 3 | Hines 1982, small crabs |
| *Pachycheles pubescens* | 4.25 | Stillman and Somero 1996, *Petrolisthes spp.* |
| *Petrolisthes eriomerus* | 4.25 | Stillman and Somero 1996, *Petrolisthes spp.* |
| *Heptacarpus stylus* | 0.11 | McKinney et al 2004, *Palaemonetes pugio* |
| Brachyura spp. | 3 | Hines 1982, small crabs |
| Unidentified shrimp | 0.11 | McKinney et al 2004, *Palaemonetes pugio* |
| *Polyorchis penicillatus* | 0.01 | Båmstedt 2015, *Bolinopsis infundibulum* |
| *Mitrocoma cellularia* | 0.01 | Båmstedt 2015, *Bolinopsis infundibulum* |
| *Pleurobrachia bachei* | 0.01 | Båmstedt 2015, *Bolinopsis infundibulum* |
| *Bolinopsis infundibulum* | 0.01 | Båmstedt 2015 |
| *Evasterias troschelii* | 66.5 | O'Clair 1985 |
| *Leptasterias hexactis* | 5.5 | Menge 1975, *Leptasterias spp.* |
| *Leptasterias spp.* | 5.5 | Menge 1975, *Leptasterias spp.* |
| *Orthasterias koehleri* | 66.5 | O'Clair 1985, *Evasterias troschelii* |
| *Pisaster brevispinus* | 146.18 | Peters et al 2019, Pisaster giganteus |
| *Pisaster ochraceus* | 128 | Sanford 2002 |
| *Pycnopodia helianthoides* | 0.018\*size^3.13 | Lee 2016 |
| *Stylasterias forreri* | 66.5 | O'Clair 1985, *Evasterias troschelii* |
| *Patiria miniata* | 26.97 | Peters et al 2019 |
| *Henricia pumila* | 10 | Menge 1975, *Henricia spp*. |
| *Henricia spp.* | 10 | Menge 1975 |
| *Dermasterias imbricata* | 92 | Montgomery 2014 |
| *Mediaster aequalis* | 10 | Menge 1975, *Henricia spp*. |
| *Solaster dawsoni* | 486 | Montgomery 2014, *Solaster stimpsoni* |
| *Solaster stimpsoni* | 486 | Montgomery 2014 |
| *Pteraster tesselatus* | 10 | Menge 1975, *Henricia spp.* |
| *Mesocentrotus franciscanus* | 29.51 | Schuster and Bates 2023 |
| *Strongylocentrotus droebachiensis* | 20 | Stewart et al 2015, *Strongylocentrotus polyacanthus* |
| *Strongylocentrotus purpuratus* | 20 | Stewart et al 2015, *Strongylocentrotus polyacanthus* |
| *Apostichopus californicus* | 319.31 | Peters et al 2019, *Apostichopus parvimensis* |
| *Chlamys hastata* | 2.5 | MacDonald 1991, *Chlamys spp.* |
| *Crassadoma gigantea* | 0.038\*size^2.39 | MacDonald 1991 |
| *Enteroctopus dofleini* | 137.5 | Osborn 1995, *Octopus rubescens* |
| *Octopus rubescens* | 80 | Osborn 1995 |
| *Opalia wroblewskyi* | 0.91 | Palmer 1982, *Nucella spp.* |
| *Diodora aspera* | 0.91 | Palmer 1982, *Nucella spp.* |
| *Megathura crenulata* | 0.91 | Palmer 1982, *Nucella spp.* |
| *Haliotis kamtschatkana* | 0.00058\*size^3.2 | Zhang 2007 |
| *Neverita lewisii* | 0.91 | Palmer 1982, *Nucella spp.* |
| *Ceratostoma foliatum* | 0.91 | Palmer 1982, *Nucella spp.* |
| *Nucella lamellosa* | 0.91 | Palmer 1982, *Nucella spp.* |
| *Armina californica* | 0.54 | McKinney et al 2004, gastropods |
| *Cadlina luteomarginata* | 0.54 | McKinney et al 2004, gastropods |
| *Cadlina modesta* | 0.54 | McKinney et al 2004, gastropods |
| *Cadlina sylviaearleae* | 0.54 | McKinney et al 2004, gastropods |
| *Coryphella verrucosa* | 0.54 | McKinney et al 2004, gastropods |
| *Dendronotus iris* | 0.54 | McKinney et al 2004, gastropods |
| *Dirona albolineata* | 0.54 | McKinney et al 2004, gastropods |
| *Dirona pellucida* | 0.54 | McKinney et al 2004, gastropods |
| *Diaulula odonoghuei* | 0.54 | McKinney et al 2004, gastropods |
| *Diaulula sandiegensis* | 0.54 | McKinney et al 2004, gastropods |
| *Peltodoris nobilis* | 0.54 | McKinney et al 2004, gastropods |
| *Doris montereyensis* | 0.54 | McKinney et al 2004, gastropods |
| *Doris odhneri* | 0.54 | McKinney et al 2004, gastropods |
| *Antiopella fusca* | 0.54 | McKinney et al 2004, gastropods |
| *Hermissenda crassicornis* | 0.54 | McKinney et al 2004, gastropods |
| *Acanthodoris hudsoni* | 0.54 | McKinney et al 2004, gastropods |
| *Acanthodoris nanaimoensis* | 0.54 | McKinney et al 2004, gastropods |
| *Onchidoris bilamellata* | 0.54 | McKinney et al 2004, gastropods |
| *Limacia cockerelli* | 0.54 | McKinney et al 2004, gastropods |
| *Polycera tricolor* | 0.54 | McKinney et al 2004, gastropods |
| *Triopha catalinae* | 0.54 | McKinney et al 2004, gastropods |
| *Triopha modesta* | 0.54 | McKinney et al 2004, gastropods |
| *Triopha spp.* | 0.54 | McKinney et al 2004, gastropods |
| *Melibe leonina* | 0.54 | McKinney et al 2004, gastropods |
| *Tritonia festiva* | 0.54 | McKinney et al 2004, gastropods |
| *Acmaea mitra* | 0.91 | Palmer 1982, *Nucella spp.* |
| *Lottia scutum* | 0.91 | Palmer 1982, *Nucella spp.* |
| *Berthella chacei* | 0.91 | Palmer 1982, *Nucella spp.* |
| *Calliostoma ligatum* | 0.91 | Palmer 1982, *Nucella spp.* |
| *Tegula funebralis* | 0.91 | Palmer 1982, *Nucella spp.* |
| *Pomaulax gibberosus* | 31 | Schuster and Bates 2023 |
| *Eurylepta leoparda* | 0.54 | McKinney et al 2004, gastropods |

**Supplemental Table 4**. Akaike’s Information Criterion (AIC) values calculated for each model of ammonium concentration in relation to animal abundance (AA) or animal biomass (AB), Shannon diversity (SHD) or Simpson diversity (SID), tide exchange rate (T), depth (D), and an interaction term. RE = random effect of both site and year. df is the degrees of freedom in the model. The model with the lowest AIC score is the “best” model; ΔAIC is the difference in AIC score between a given model and the “best” model; AIC weight represents the probability that a model is the best model, given the data and the set of candidate models.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Predictors** | **k** | **AIC** | **ΔAIC** | **AIC weight** |
| AA + SHD + T + D + AA:T + RE | 9 | 45.60 | 0.00 | 0.50 |
| AA + SID + T + D + AA:T + RE | 9 | 46.09 | 0.50 | 0.39 |
| AB + SHD + T + D + AB:T + RE | 9 | 49.70 | 4.10 | 0.06 |
| AB + SID + T + D + AB:T + RE | 9 | 49.98 | 4.38 | 0.06 |

**Supplemental Table 5**. Akaike’s Information Criterion (AIC) values calculated for each model of delta ammonium concentration in vs outside kelp forests in relation to animal abundance (AA) or animal biomass (AB), Shannon diversity (SHD) or Simpson diversity (SID), kelp species (KS), kelp biomass (KB), tide exchange rate (T), depth (D), and three interaction terms. RE = random effect of site. df is the degrees of freedom in the model. The model with the lowest AIC score is the “best” model; ΔAIC is the difference in AIC score between a given model and the “best” model; AIC weight represents the probability that a model is the best model, given the data and the set of candidate models.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Predictors** | **k** | **AIC** | **ΔAIC** | **AIC weight** |
| AB + SHD + KS + KB + T + D + AB:T + AB:KB + KB:T + RE | 13 | -34.76 | 0.00 | 0.33 |
| AA + SHD + KS + KB + T + D + AA:T + AA:KB + KB:T + RE | 13 | -34.56 | 0.2 | 0.30 |
| AA + SID + KS + KB + T + D + AA:T + AA:KB + KB:T + RE | 13 | -34.12 | 0.64 | 0.24 |
| AB + SID + KS + KB + T + D + AB:T + AB:KB + KB:T + RE | 13 | -33.01 | 1.75 | 0.14 |

**Electronic Supplement 2.** Effect of individual families of fishes and invertebrates on among- and within-site variation in ammonium.

**Among-site (meso-scale) variation**

We further explored the effect of animals on variation in NH₄⁺ concentration among rocky reef sites by considering only the abundance of one animal family at a time. For each of the top 15 most abundant families observed on our surveys, we constructed an GLMM identical to the top model shown in Table S4, using only the abundance of that family (NH₄⁺ regressed against family abundance, tide exchange, an interaction between family abundance and tide, Shannon diversity, survey depth, with a random effect of site and year and a gamma distribution). Here, we present the three fish families (Hexagrammidae, Gobiidae, and Sebastidae) and three invertebrate families (Muricidae, Asteriidae, and Acmaeidae) with the highest R2 values. These six families constitute 17% of the total abundance.

We found evidence of a positive relationship between NH₄⁺ concentration and the abundance of greenlings (Hexagrammidae, GLMM, p = 0.03, Supplemental Fig. 1), weak evidence of an interaction between greenling abundance and tide (p = 0.09), but no evidence for an effect of any other predictors (p > 0.10). We also found evidence of a positive relationship between NH₄⁺ concentration and the abundance of whitecap limpets (Acmaeidae, GLMM, p = 0.03), but no evidence of an effect of any other predictors (p > 0.40). We found no evidence of an effect of any predictors on NH₄⁺ concentration in the models for the families Sebastidae, Gobiidae, Asteriidae, or Muricidae (p > 0.10). Full model outputs are available in Supplemental Table 1.

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Description automatically generated with medium confidence**

**Supplemental Figure 1.** Model-generated predictions of ammonium concentrations in relation to abundance across rocky reef sites for the 6 animal families with the highest R2.

**Supplemental Table 1.** Model summaries from the among-site, meso-scale models including only the biomass of one family (indicated in the top left cell) for each model.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Sebastidae** | **Estimate** | **Std. error** | **z-value** | **p-value** |
| Intercept | 0.13 | 1.23 | 0.11 | 0.91 |
| Abundance | 1.98 | 3.22 | 0.61 | 0.54 |
| Tide exchange | -0.53 | 1.00 | -0.53 | 0.60 |
| Biodiversity | -0.10 | 0.13 | -0.75 | 0.45 |
| Depth | -0.02 | 0.13 | -0.18 | 0.86 |
| Abundance:Tide | -1.79 | 2.82 | -0.63 | 0.53 |

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Muricidae** | **Estimate** | **Std. error** | **z value** | **p value** |
| Intercept | -0.43 | 0.33 | -1.30 | 0.19 |
| Abundance | 0.79 | 0.51 | 1.55 | 0.12 |
| Tide exchange | 0.05 | 0.12 | 0.44 | 0.66 |
| Biodiversity | 0.00 | 0.10 | -0.04 | 0.97 |
| Depth | 0.04 | 0.09 | 0.43 | 0.67 |
| Abundance:Tide | 0.12 | 0.55 | 0.22 | 0.83 |

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Asterinidae** | **Estimate** | **Std. error** | **z value** | **p value** |
| Intercept | -0.58 | 0.26 | -2.28 | 0.02 |
| Abundance | 0.21 | 0.26 | 0.80 | 0.42 |
| Tide exchange | 0.12 | 0.07 | 1.80 | 0.07 |
| Biodiversity | -0.12 | 0.09 | -1.29 | 0.20 |
| Depth | 0.06 | 0.09 | 0.62 | 0.54 |
| Abundance:Tide | 0.07 | 0.27 | 0.26 | 0.80 |

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Hexagrammidae** | **Estimate** | **Std. error** | **z value** | **p value** |
| Intercept | 4.96 | 2.54 | 1.95 | 0.05 |
| Abundance | 14.67 | 6.69 | 2.19 | 0.03 |
| Tide exchange | -3.35 | 2.01 | -1.67 | 0.10 |
| Biodiversity | 0.01 | 0.09 | 0.11 | 0.91 |
| Depth | 0.02 | 0.09 | 0.25 | 0.81 |
| Abundance:Tide | -9.01 | 5.35 | -1.68 | 0.09 |

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Acmaeidae** | **Estimate** | **Std. error** | **z value** | **p value** |
| Intercept | -0.19 | 0.33 | -0.59 | 0.56 |
| Abundance | 1.42 | 0.67 | 2.13 | 0.03 |
| Tide exchange | 0.03 | 0.16 | 0.21 | 0.84 |
| Biodiversity | -0.01 | 0.09 | -0.09 | 0.93 |
| Depth | 0.00 | 0.09 | 0.05 | 0.96 |
| Abundance:Tide | -0.16 | 0.58 | -0.28 | 0.78 |

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Gobiidae** | **Estimate** | **Std. error** | **z value** | **p value** |
| Intercept | -0.64 | 0.29 | -2.19 | 0.03 |
| Abundance | 0.17 | 0.23 | 0.75 | 0.45 |
| Tide exchange | 0.04 | 0.07 | 0.52 | 0.61 |
| Biodiversity | -0.01 | 0.10 | -0.11 | 0.91 |
| Depth | -0.06 | 0.11 | -0.55 | 0.58 |
| Abundance:Tide | 0.13 | 0.17 | 0.80 | 0.43 |

**Within-site (small-scale) variation**

As above, we further explored the effect of animals on ∆NH₄⁺ – the difference in NH₄⁺ concentration between inside and outside kelp forests – by rerunning our the top LMM in Table S5 with the biomass of only one animal family at a time. We ran models for the 15 most abundant families, but only present the three fish families (Gobiidae, Cottidae, and Embiotocidae) and three invertebrate families (Echinasteridae, Strongylocentrotidae, and Asteriidae) with the highest R2 values. These six families contribute almost half (48%) of the total biomass observed on the surveys.

We found a negative relationship between ∆NH₄⁺ and the biomass of gobies (Gobiidae) and evidence of positive kelp:goby biomass and tide:goby biomass interactions (GLM, p < 0.003, Supplemental Fig. 2). ∆NH₄⁺ was positively correlated with the biomass of sculpins (Cottidae; p = 0.046) and surfperches (Embiotocidae; p < 0.001), but no interactions with biomass were significant (p > 0.06). Sea stars in the family Echinasteridae displayed a positive relationship with ∆NH₄⁺, a negative kelp:sea star biomass interaction, and a positive tide:sea star biomass interaction (p < 0.001). We found evidence for a smaller but still positive relationship between the biomass of urchins in the family Strongylocentrotidae and sea stars in the family Asteropseidae and ∆NH₄⁺ (p < 0.005), but no interactions with biomass were significant (p > 0.17). Full model outputs are available in Supplemental Table 2.



**Supplemental Figure 2.** Model-generated predictions of difference in ammonium concentrations between inside and outside kelp forests in relation to animal biomass for the 6 animal families with the highest R2.

**Supplemental Table 2.** Model summaries from the within-site, small scale models including only the biomass of one family (indicated in the top left cell) for each model.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Echinasteridae** | **Estimate** | **Std. error** | **z value** | **p value** |
| Intercept | 3.22 | 0.71 | 4.56 | < 0.01 |
| Kelp nereo | 0.23 | 0.03 | 6.79 | < 0.01 |
| Kelp none | -0.09 | 0.07 | -1.33 | 0.18 |
| Kelp biomass | -2.82 | 0.89 | -3.17 | < 0.01 |
| Tide exchange | 3.02 | 0.76 | 3.99 | < 0.01 |
| Animal biomass | 7.36 | 1.68 | 4.39 | < 0.01 |
| Biodiversity | -0.13 | 0.02 | -5.96 | < 0.01 |
| Depth | 0.04 | 0.02 | 2.19 | 0.03 |
| Kelp:tide | 0.20 | 0.04 | 5.39 | < 0.01 |
| Kelp:animals | -7.66 | 2.14 | -3.58 | < 0.01 |
| Tide:animals | 6.87 | 1.78 | 3.86 | < 0.01 |

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Gobiidae** | **Estimate** | **Std. error** | **z value** | **p value** |
| Intercept | -0.56 | 0.24 | -2.35 | 0.02 |
| Kelp none | 0.89 | 0.34 | 2.61 | 0.01 |
| Kelp biomass | 1.06 | 0.38 | 2.81 | < 0.01 |
| Tide exchange | 4.79 | 0.98 | 4.89 | < 0.01 |
| Animal biomass | -1.71 | 0.57 | -3.01 | < 0.01 |
| Biodiversity | 0.14 | 0.04 | 3.55 | < 0.01 |
| Depth | 0.00 | 0.03 | -0.10 | 0.92 |
| Kelp:tide | 0.11 | 0.08 | 1.35 | 0.18 |
| Kelp:animals | 2.65 | 0.98 | 2.69 | 0.01 |
| Tide:animals | 12.22 | 2.48 | 4.93 | < 0.01 |

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Cottidae** | **Estimate** | **Std. error** | **z value** | **p value** |
| Intercept | 1.23 | 0.56 | 2.20 | 0.03 |
| Kelp nereo | 0.12 | 0.07 | 1.63 | 0.10 |
| Kelp none | -0.43 | 0.09 | -4.66 | < 0.01 |
| Kelp biomass | -0.35 | 0.37 | -0.96 | 0.34 |
| Tide exchange | -0.68 | 1.14 | -0.60 | 0.55 |
| Animal biomass | 2.56 | 1.28 | 2.00 | 0.05 |
| Biodiversity | -0.16 | 0.04 | -4.40 | < 0.01 |
| Depth | 0.11 | 0.03 | 3.82 | < 0.01 |
| Kelp:tide | 0.17 | 0.08 | 2.13 | 0.03 |
| Kelp:animals | -1.59 | 0.86 | -1.85 | 0.06 |
| Tide:animals | -1.88 | 2.68 | -0.70 | 0.48 |

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Strongylocentrotidae** | **Estimate** | **Std. error** | **z value** | **p value** |
| Intercept | 0.00 | 0.06 | 0.01 | 0.99 |
| Kelp nereo | 0.07 | 0.08 | 0.83 | 0.41 |
| Kelp none | -0.67 | 0.12 | -5.40 | < 0.01 |
| Kelp biomass | 0.20 | 0.06 | 3.42 | < 0.01 |
| Tide exchange | 0.07 | 0.07 | 0.99 | 0.32 |
| Animal biomass | 0.08 | 0.03 | 3.21 | < 0.01 |
| Biodiversity | 0.04 | 0.03 | 1.14 | 0.25 |
| Depth | 0.10 | 0.03 | 3.21 | < 0.01 |
| Kelp:tide | 0.15 | 0.06 | 2.43 | 0.01 |
| Kelp:animals | -0.02 | 0.02 | -1.12 | 0.26 |
| Tide:animals | -0.02 | 0.02 | -1.06 | 0.29 |

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Embiotocidae** | **Estimate** | **Std. error** | **z value** | **p value** |
| Intercept | 0.27 | 0.04 | 6.32 | < 0.01 |
| Kelp nereo | -0.03 | 0.08 | -0.45 | 0.66 |
| Kelp none | -0.28 | 0.13 | -2.11 | 0.03 |
| Kelp biomass | 0.25 | 0.05 | 5.31 | < 0.01 |
| Tide exchange | 0.15 | 0.04 | 3.74 | < 0.01 |
| Animal biomass | 0.55 | 0.12 | 4.60 | < 0.01 |
| Biodiversity | -0.09 | 0.03 | -2.85 | < 0.01 |
| Depth | 0.07 | 0.03 | 2.39 | 0.02 |
| Kelp:tide | 0.18 | 0.07 | 2.61 | 0.01 |
| Kelp:animals | -0.05 | 0.11 | -0.48 | 0.63 |
| Tide:animals | 0.31 | 0.20 | 1.59 | 0.11 |

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Asteriidae** | **Estimate** | **Std. error** | **z value** | **p value** |
| Intercept | 0.06 | 0.04 | 1.34 | 0.18 |
| Kelp nereo | 0.05 | 0.09 | 0.52 | 0.61 |
| Kelp none | -0.24 | 0.11 | -2.18 | 0.03 |
| Kelp biomass | 0.23 | 0.07 | 3.14 | < 0.01 |
| Tide exchange | -0.02 | 0.08 | -0.23 | 0.82 |
| Animal biomass | 0.13 | 0.05 | 2.76 | 0.01 |
| Biodiversity | -0.10 | 0.03 | -3.09 | < 0.01 |
| Depth | 0.05 | 0.03 | 1.56 | 0.12 |
| Kelp:tide | 0.12 | 0.08 | 1.52 | 0.13 |
| Kelp:animals | 0.00 | 0.03 | 0.16 | 0.87 |
| Tide:animals | 0.13 | 0.10 | 1.32 | 0.19 |

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**Data Availability Statement**

All data and code on github…