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Bottom-up and Top-down Controls on Sedimentary Ecosystem Functioning in a Seagrass

Habitat.

A Dissertation

Presented to

The Faculty of the School of Marine Science

The College of William and Mary in Virginia

In Partial Fulfillment

Of the Requirements for the Degree of

Doctor of Philosophy

by

Amanda C. Spivak

APPROVAL SHEET

This dissertation is submitted in partial fulfillment of

the requirements for the degree of

Doctor of Philosophy

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ABSTRACT

Coastal seagrass ecosystems are complex habitats that are increasingly influenced by human perturbations. Disturbances that affect the strength of bottom-up (i.e. resource availability) and top-down (i.e. consumer) controls may also influence biomass distribution between trophic levels, sediment biogeochemistry, and seagrass ecosystem metabolism. Here, I experimentally tested how top-down and bottom-up perturbations interact with community structure (diversity, food chain length of epibenthic consumers) to alter sediment biogeochemistry and ecosystem metabolism in an experimental eelgrass (Zostera marina) system. My data indicated that resource availability influenced SOM composition and ecosystem metabolism. Light availability tended to be a stronger determinant of SOM composition while nutrient enrichment affected secondary production of invertebrate grazers more strongly than primary producers or SOM. Topdown predator effects on SOM composition and ecosystem flux rates tended to be weak. However, the strength of the trophic cascade may partly be a function of grazer community composition and grazer susceptibility to predation. Finally, my results indicated that grazer species identity and community composition strongly influenced SOM composition. In addition to the main effects of light, nutrients, predators, and grazers there were a variety of interactive effects between resources and food web composition. Consequently, the effects of resource availability and food web composition on seagrass ecosystem functioning should not be considered in isolation.

Top-down and bottom-up controls on seagrass ecosystem functioning.

Chapter 1. Introduction

Project Summary

Coastal seagrass ecosystems are complex habitats that are increasingly influenced by human perturbations. Disturbances that affect the strength of bottom-up (i.e. resource availability) and top-down (i.e. community structure) controls may also influence biomass distribution between trophic levels, sediment biogeochemistry, and seagrass ecosystem metabolism. Utilizing two mesocosm experiments and one field manipulation, I tested how top-down (food chain length) and bottom-up (light and nutrient) perturbations interact with benthic community structure (diversity, food chain length) to alter sediment biogeochemistry and ecosystem metabolism in an experimental eelgrass (*Zostera marina*) system. I estimated changes in sediment biogeochemistry by analyzing sediment organic carbon and nitrogen content as well as fatty acid biomarkers, which are functional proxies for organic matter. Ecosystem metabolism was estimated by measuring flux rates of dissolved oxygen and dissolved inorganic nitrogen and phosphate. Results from this study demonstrate that environmental perturbations are interactive and that results from single variable experiments cannot be used to predict the outcome of experiments with multiple variables and/or diverse species assemblages.

Introduction

Seagrass ecosystems provide habitat for economically and ecologically important organisms, transform nutrients through biogeochemical processes, and buffer anthropogenic sediment and nutrient inputs (Kemp et al. 2005; Orth et al. 2006). Despite their importance to human economies and populations, seagrass ecosystems are increasingly threatened by perturbations such as nutrient runoff, erosion due to land development, and over-fishing (Cloern 2001; Kemp et al. 2004; Orth et al. 2006). Alone and in combination, such anthropogenic disturbances can affect top-down (i.e. food chain length) and bottom-up (i.e. resource availability) controls in seagrass beds. Further, interactions between food web structure and abiotic processes have substantial consequences for ecosystem dynamics and function (McGrady-Steed et al. 1997; Tilman et al. 1997; Heck et al. 2000; Duffy et al. 2003; Hughes et al. 2004; Canuel et al. 2007). Thus, a goal of this project was to determine how top-down and bottom-up controls affect sediment biogeochemistry and ecosystem metabolism.

Perturbations that reduce predator abundance in seagrass ecosystems may precipitate changes in the biomass and diversity of neighboring trophic levels (Heck et al. 2000; Duffy et al. 2005; Heck and Valentine 2006; 2007). Eventually, such changes in food web structure and composition may cascade to affect ecosystem productivity and sediment biogeochemistry (Duffy et al. 2003; Canuel et al. 2007). For instance, predators such as fish and crabs consume grazing invertebrates, which feed on a variety of primary producers including epiphytes, macroalgae, benthic microalgae, and eelgrass blades (Valentine and Heck 1999; Duffy et al. 2001; Heck and Valentine 2006; Valentine and Duffy 2006). By altering primary producer community composition and biomass, grazers can affect primary productivity and organic matter (OM) cycling. Shifts in trophic structure and biodiversity that affect OM deposition may also influence nutrient cycling since OM quality is a partial determinant of sediment microbial activity and remineralization processes (Boschker and Cappenberg 1998) (Fig. 1). While the strength of this cascade is unknown, it has potentially important implications for carbon transfer to higher trophic levels, organic matter decomposition, nutrient recycling, and carbon sequestration in the sediments.

In addition to fluctuations in top-down controls (i.e. predator presence vs. absence), seagrass beds may be subjected to variations in bottom-up forcings (i.e. light and nutrient availability). For instance, the availability of excess nutrients in coastal waters is linked to increased surface water chlorophyll and seagrass loss (Cloern 2001; Kemp et al. 2005; Orth et al. 2006). While studies evaluating the effects of nutrient enrichment have focused on changes in water quality, dramatic alterations in sediment geochemistry can also occur. For example, in systems that have experienced prolonged eutrophication, such as the Chesapeake Bay, sediment organic matter accumulation has increased and its composition has been altered (Zimmerman and Canuel 2000; 2002). Fatty acids indicative of plankton (polyunsaturated fatty acids) and microbes (branched fatty acids) have increased since the early 1900's suggesting changes in microbial responses in the water column and sediments (Zimmerman and Canuel 2000; 2002). Thus, nutrient-mediated shifts in bottom-up forcings hold significant implications for ecosystem productivity, OM cycling, and sediment microbial activity.

Despite the importance of seagrass beds to human economies, health, and sustenance, carbon transformations are still ambiguous. A large body of research has examined the influence of allochthonous nutrients on water quality and seagrass

production and density (Neckles et al. 1993; Moore et al. 1996; Orth et al. 2006; McGlathery et al. 2007). Other studies have described the characteristic species and their trophic interactions (Jernakoff et al. 1996; Duffy et al. 2001; Alfaro et al. 2006; Heck and Valentine 2006). Research emphasis has also been placed on microbial processes and decomposition of plant material (Cebrian and Duarte 2001; Holmer et al. 2004; Bouillon and Boschker 2006). Despite intensive research in these separate areas, little is understood about how biology and geochemistry interact to shape dynamic seagrass systems and the services they provide to society.

Experimental objectives.

The goal of this dissertation project was to experimentally test the interactive effects of eelgrass bed community structure (invertebrate grazer diversity and food chain length) and bottom up forcings (nutrient concentrations and light availability) on sediment organic matter (SOM) composition and whole ecosystem metabolism. This was accomplished using a suite of complementary studies, including two mesocosm experiments and one field experiment. The experiments were designed to test the effects of common anthropogenic disturbances: fishing-induced food web alteration, nutrient loading, and subsequent shading. Food web structure and composition were manipulated by varying predator presence and grazer biodiversity (species richness and identity), respectively. Bottom-up perturbations were simulated by varying light availability, an indirect effect of sediment loading and algal growth due to increased nutrient concentrations.

Experimental Hypotheses.

Research for this dissertation was structured around two overarching hypotheses: **Hypothesis 1:** Above-ground benthic community composition (i.e. mesograzer identity and composition) and food chain length (i.e. predator presence) will alter the primary producer community resulting in changes in gross ecosystem production and sediment organic matter (SOM) composition.

Hypothesis 2: Bottom-up forcings (light availability and nutrient concentrations) will increase primary and secondary productivity thereby influencing SOM composition and quality.

Experimental Approach.

Experiment 1. The first mesocosm experiment examined top-down and bottom-up controls on SOM composition in an experimental seagrass ecosystem (Chapter 2). This experiment, conducted over 6 weeks in Summer 2003, was a factorial manipulation of grazer diversity (df = 2), predator presence (df = 1), and light intensity (df = 1). Grazer diversity treatments contained 0, 2, or 4 grazer species; grazers were chosen from a pool of six species, including three amphipods (*Gammarus mucronatus, Ampithoe longimana*, and *Caprella penantis*) two isopods (*Idotea balthica* and *Erichsonella attenuate*) and a gastropod (*Bittium varium*). Trophic structure was manipulated by exposing half of the grazer treatments to the generalist predator *Callinectes sapidus*. Light intensity was manipulated by shrouding half of the tanks with shade cloths, reducing natural light by 69%. There were 12 treatments replicated 5 times each. The experiment tested the following hypotheses:

H-1a: High light availability will increase biomass accumulation of above-ground and benthic algae, SOM lability, and sediment microbial activity.

H-1b: More species_rich grazer communities will reduce algal biomass but increase seagrass and benthic algal biomass, leading to changes in the composition and quality of algal material incorporated in the sediments.

H-1c: Predators will increase accumulation of algal biomass through a trophic cascade, thereby increasing SOM quantity, quality, and microbial activity.

Experiment 2. The second experiment was a field manipulation where I tested how community composition and nutrient availability alter SOM composition in a seagrass bed_(Chapter 3). The field experiment, conducted over 4 weeks in Summer 2005, was a factorial manipulation of grazer presence (df = 1), predator presence (df = 1), and nutrient concentrations (df = 1). Because field cages were more likely to be contaminated by nontarget grazer species than the mesocosm tanks, I manipulated grazers through the presence or absence of a multi-species community. Food chain length was manipulated through the presence or absence of blue crabs. Nutrient concentrations were varied over two levels: ambient and enriched (approximately 5x's ambient). There were eight treatments, replicated five times for a total of forty caged treatments. In addition to the caged treatments there were two uncaged treatments (with versus without nutrients). Grazer and predator presence were not manipulated in the uncaged treatments since it was impractical to maintain those treatments without cages. The two uncaged treatments were replicated five times each for a total of ten uncaged plots. The field experiment was conducted in the York River Estuary, VA and tested the following hypotheses:

H-2a: Nutrient enrichment will increase algal biomass and the deposition of algal-derived OM to the sediments. The increased lability of SOM will, in turn, stimulate sediment heterotrophic bacterial activity and the deposition of bacterial FA. Algae will indirectly decrease eelgrass abundance by increasing competition for light and nutrients.

H-2b: Grazers will reduce algae, as well as the abundance of the fatty acids characteristic of algae in the sediment, but will increase eelgrass.

H-2c: Predators will produce a trophic cascade in which grazer abundance is reduced and algal biomass and OM contributions to the sediment are increased.

Experiment 3. The third experiment was a mesocosm experiment where I tested how nutrient availability and food web composition affect ecosystem metabolism and SOM composition in an experimental seagrass habitat. (Chapters 4, 5). This experiment, conducted over five weeks in Summer 2006, was a factorial manipulation of grazer richness (df = 3), predator presence (df = 1), and nutrient enrichment (df = 1). Grazer richness was varied over four levels as treatments contained 0, 1, 3, or 5 species. The 1 species treatment was a monoculture of *G. mucronatus*, a perennially abundant amphipod. The 5 species treatment contained amphipod grazer species present in the York River at the time of the experiment: *G. mucronatus, Ampithoe valida, Elasmopus levis, Melita nitida*, and *Sympleustes* spp. The 3 species treatment contained grazers randomly drawn from the 5 grazer pool. Trophic structure was varied over two levels through the presence or absence of blue crabs. Water column nutrient availability was manipulated by adding fertilizer (5-30 x's ambient concentrations) to half of the tanks.

Thus, there were 16 treatments, each replicated 3 times for a total of 48 tanks. The goal of this experiment was to test the following hypotheses:

H-3a: Nutrient additions will increase algal biomass and, consequently, ecosystem productivity. Accumulation of algal biomass will, in turn, increase SOM quality, sediment microbial activity, and dissolved inorganic nitrogen (DIN) flux rates. H-3b: Grazers will reduce algal biomass and algal contributions to SOM but will increase inorganic nitrogen flux by recycling consumed material back into the water column via excretion.

H-3c: Predator presence will initiate a trophic cascade whereby grazing activities are reduced but algal biomass, gross ecosystem productivity, and SOM quality are increased. DIN flux will be lower due to uptake by above-ground algae.

The results from the three experiments will be compared in detail in Chapter 6. This synthesis chapter will allow for a direct comparison of the effects of resource availability and top-down controls on SOM composition and ecosystem metabolism. In addition, this chapter will include an assessment of the relative importance of resource identity (i.e. nutrients vs. light) to ecosystem properties and functioning.

Significance.

A recent report by the National Academy of Sciences identified the first and second "grand challenges in environmental science" as understanding biogeochemical cycles and biological diversity and ecosystem functioning (NAS, 2000). While there are

clear challenges in both of these areas, an even greater challenge is to address the linkages between them. This challenge was further highlighted in a recent NSF report noting the importance of studies identifying the role of functional diversity in geochemical transformations (Jumars and Hay 1999). This dissertation addresses gaps in our understanding of linkages between ecological and biogeochemical responses to human perturbations to coastal ecosystems. It is amongst the first studies to investigate the importance of food web composition and resource availability to both sediment biogeochemistry and seagrass ecosystem metabolism. Literature cited.

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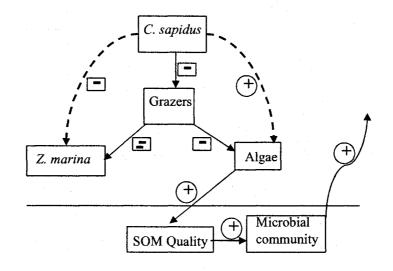
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Chapter 2:

Top-down and bottom-up controls on sediment organic matter composition in an experimental seagrass ecosystem

Amanda C. Spivak¹, Elizabeth A. Canuel, J. Emmett Duffy, and J. Paul Richardson

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Abstract

Using an experimental mesocosm system, we tested the singular and interactive effects of resource availability (light) and community composition (food chain length and herbivore species richness) on eelgrass (Zostera marina) ecosystem properties and functioning. Food chain length was manipulated through the presence or absence of blue crab (*Callinectes sapidus*) predators, while grazer species richness varied across three levels (0, 2, or 4 crustacean species). We found important and interacting effects of bottom-up and top-down forcings on sediment organic matter (SOM) composition. Light increased eelgrass and algal biomass and sediment organic carbon and nitrogen content. Increasing grazer diversity generally decreased algal biomass and ecosystem production but interacted with food chain length (i.e., presence of predatory crabs) and light. Predators generally increased algal biomass and ecosystem production through a trophic cascade, which was stronger at high grazer diversity and under ambient light. SOM composition, determined using fatty acid biomarkers, was sensitive to all manipulated variables. Increasing grazer species richness often decreased the contributions of fatty acids derived from plant and algal sources, while increasing light had the opposite effect. Food chain length was generally a less important determinant of SOM composition than light, although predators did increase fatty acids representative of heterotrophic bacteria. Resource availability and epibenthic community composition strongly influence organic matter cycling, SOM composition, and the bacterial community in seagrass-bed sediments.

Introduction

Coastal ecosystems are often affected by multiple disturbances that alter both resource availability and community composition simultaneously. In the Chesapeake Bay, for example, seagrass beds are affected by commercial harvesting of the blue crab, *Callinectes sapidus* (Stephan et al. 2000), and by suspended sediment and nutrient loading that can lead to reduced light availability (Kemp et al. 2004). Changes in abundance of important predators, like striped bass or the blue crab, may precipitate changes in biomass of lower trophic levels (Hairston et al. 1960; Strong 1992; Pace et. al 1999). These shifting trophic interactions, along with reduced light availability, can affect primary producer abundance and productivity (Heck et al. 2000; Hughes et al. 2004; Borer et al. 2006) and, in turn, sediment organic matter (SOM) content (Canuel et al. 2007). Consequently, cascading changes in animal and plant biomass may alter the rates and pathways by which organic matter (OM) is cycled in an ecosystem (Schindler et al. 1997; Dangles and Malmqvist 2004).

Predicting how changing trophic structure affects OM cycling is complicated by the fact that predators induce shifts not only in prey biomass but also in prey community structure. In seagrass systems, for example, grazing invertebrates can consume epiphytic algae, macroalgae, benthic microalgae, and/or vascular plants (Valentine and Duffy 2006). Thus, shifts in grazer community composition may affect the abundance of different primary producers. Since seagrasses, macroalgae, and epiphytes differ in their biochemical composition and proportion of structural components, the food preferences of grazing invertebrates may, in turn, affect the quantity and lability of organic carbon delivered to the sediments and thus, the quantity and quality of sediment organic carbon

(Canuel et al. 2007). Such compositional changes need not be dramatic to affect ecosystem properties: small shifts in grazer richness and species composition can significantly affect plant and algal biomass and influence total sediment organic carbon (e.g., Duffy et al. 2003; Canuel et al. 2007).

Because sediment microbial communities are important mediators of carbon and other elemental cycles in coastal environments (Boschker et al. 1999; Holmer et al. 2001, 2004), changes in above-ground trophic structure and diversity that alter OM delivery to seagrass sediments may have important consequences for carbon cycling and storage. In terrestrial soils, by analogy, microbial community composition and activity are sensitive to changes in above-ground community structure (Setälä et al. 1998; Wardle et al. 2005). Though studies from marine habitats are fewer, microbial activity in sediments is strongly related to OM deposition (Canuel and Martens 1993; Boschker and Cappenberg 1998; Boschker et al. 2000). The potential cascade from consumer control of aboveground production to delivery and accumulation of below-ground OM may thus be important to carbon remineralization, recycling, and sequestration in the sediments.

Effective conservation and management of seagrass ecosystems requires a clear understanding of relationships between community ecology and biogeochemical cycling. A variety of studies have investigated coastal eutrophication (Cloern 2001; Duarte 2002 and references therein), trophic interactions in seagrass beds (Valentine and Duffy 2006; Heck and Valentine 2006 and references therein), and interactions between nutrient enrichment and food web ecology (McClelland and Valiela 1998; Deegan et al. 2002; Tewfik et al. 2005). Others have examined sediment nutrient and bacterial processes in seagrass beds (Holmer et al. 2001, 2004). Yet few studies have examined the

relationships and feed-backs between above-ground ecology and below-ground geochemical cycling. Geochemical tools provide a way to detect and quantify such linkages between community structure and organic matter cycling. Specifically, lipid biomarkers are compounds reliably produced by a specific group of organisms that are sufficiently resistant to degradation to be preserved in sediments (Killops and Killops 1993). Diagnostic biomarkers often have site-specific methyl groups, double bonds, or cyclic side chains useful in tracing the sources of organic matter (Killops and Killops 1993). Bacteria, for example, synthesize iso- and anteiso- branched fatty acids while microalgae contain highly unsaturated long chain fatty acids (or alkanoic acids) (Volkman et al. 1998). One class of lipids, the fatty acids, is particularly useful because they have high source fidelity and exhibit a range of chemical reactivity (Canuel et al. 1995; Canuel and Martens 1996). Additionally, a sub-class of the fatty acids, the phospholipid-linked fatty acids (PLFA), are good indicators of recently viable cells since they are mainly derived from membrane lipids, which are rapidly hydrolyzed after cell death (White et al. 1979; Killops and Killops 1993). By quantifying both the total fatty acids and the PLFAs it is possible to compare OM contributions from detrital and viable or recently viable sources. Thus lipid biomarkers, and fatty acids in particular, provide a quantifiable link between the above-ground community and sediment geochemistry.

To assess the effects of changing community structure on carbon fate and storage in seagrass beds, we conducted an experimental manipulation of bottom-up forcing (light availability), community composition (grazer diversity), and food chain length (predator presence) and measured their interacting effects on ecosystem productivity, SOM quality, and sediment microbial activity. Specifically, we built on previous studies examining top-

down effects on the above-ground community (Duffy et al. 2003) and on SOM (Canuel et al. 2007) to test several hypotheses. First, higher diversity of epibenthic grazers will reduce algal biomass but increase seagrass and benthic algal biomass, leading to changes in the composition and quality of algal material incorporated in sediments. Secondly, predators will increase accumulation of algal biomass through a trophic cascade, thereby increasing SOM quantity, quality, and sediment microbial activity. Finally, high light availability will increase biomass accumulation of above-ground and benthic algae, SOM lability, and sediment microbial activity.

Methods

Experimental design

We conducted a mesocosm experiment to examine the main and interactive effects of grazer species richness, food chain length, and light intensity on ecosystem properties including production, algal biomass accumulation, and sediment organic matter (SOM) content and composition. We established three grazer richness treatments containing no grazer species, random combinations of two grazer species, or four grazer species. Grazers were chosen from a pool of six species, including three amphipod crustacean species (*Ampithoe longimana, Gammarus mucronatus*, and *Caprella penantis*), two isopods (*Idotea baltica* and *Erichsonella attenuata*), and a gastropod (*Bittium varium*). These invertebrate grazers are common in the York River estuary during the spring and summer (Duffy et al. 2001, 2003). Food chain length was manipulated by exposing a parallel set of grazer treatments to a generalist predator common in the Chesapeake Bay, the blue crab, *Callinectes sapidus*. Light intensity was

manipulated by covering half of the tanks with shade cloths (69% attenuation). There were a total of twelve treatments, each replicated five times. Due to extinctions and contaminations, however, six replicates were removed from the final analyses. Consequently, 54 replicates were used in statistical analyses; the zero grazer treatments had five replicates in ambient light and four replicates in low light, the two grazer treatments had four replicates, and the four grazer treatments had five replicates.

Outdoor mesocosm experiments were conducted over six weeks during the summer of 2003 in an array of 113-liter, translucent fiberglass tanks that were continuously supplied with flowing estuarine water from the York River, Virginia (Duffy et al. 2003). Water passed first through a sand filter and then through 150 μ m mesh. This eliminated larger invertebrates and minimized invasion by non-target animals while permitting passage of invertebrate larvae and algal spores, which often colonized the tanks. Water was supplied through "dump buckets" which regularly spilled the filtered water into the tanks, providing both turbulence and aeration. Tanks were stocked with clean sand to a depth of 10 cm; the percent total organic carbon (TOC) was below detection. Low OM content sand was used as a substrate in order to reduce initial heterogeneity between the tanks and to increase our ability to detect newly-deposited SOM (Canuel et al. 2007). Seventy-five pre-weighed eelgrass (Zostera marina) shoots, cleaned of grazers and epiphytes, were planted in the sand in each tank. This eelgrass density is within the range found in the York River estuary system (Orth and Moore 1986). One week after the grass was planted, invertebrate grazers were added to each grazer mesocosm (45 each for two-species treatments, 15 of each for four-species); these densities were near the low end of those found in the York River. Blue crabs (C. sapidus)

were added two days after the grazers had acclimated. The six week experimental incubation time was chosen to minimize the risks of invasion by non-target grazer species and of complete consumption of the eelgrass, which increase at longer time intervals. This time period allows for major changes in animal (one to two grazer generations) and plant community development and in surface sediment characteristics (see Duffy et al. 2003, 2005; Canuel et al. 2007). Despite limitations, this experimental infrastructure simulates several aspects of the biotic and abiotic field situation well (Duffy et al. 2001). Results of the experiment for above-ground biomass and composition of seagrass and the associated community are reported elsewhere (Duffy et al. unpubl.). Here, we focus on patterns of SOM accumulation and composition.

Gross ecosystem production

As an estimate of whole-ecosystem metabolism, we measured gross ecosystem production (GEP; mmol L⁻¹ O₂ d⁻¹ m⁻²) one week before the experiment was terminated. Due to time constraints and instrument availability these measurements were conducted only in ambient light treatments. Clear plastic wrap was placed on the water's surface of each tank to minimize oxygen exchange with the atmosphere and the water supply was shut off. Dissolved oxygen (DO) measurements were taken three to four times during each of two 4-hour incubations (10:00 – 14:00 h and 22:00 – 02:00 h) using a YSI Data Sonde to capture net daytime production and total respiration respectively (assuming that little to no production occurs at night). Tank water was stirred prior to each reading to disrupt any temperature or DO stratification that may have formed, while maintaining a closed system. If DO fell to hypoxic levels (2 mg L⁻¹) measurements ceased on that tank

and the plastic cover was removed. We calculated the slope of changes in DO concentration versus the time elapsed and divided this by the area of the tank to obtain flux in O_2 mmol $L^{-1} d^{-1} m^{-2}$. Hourly light and dark rates were scaled to 14 hours of daylight and 10 hours of darkness to estimate net daily summer time GEP.

Bulk sediment organic matter

At the end of the experiment, three sediment cores (2.6 cm diameter) were collected from each mesocosm; and the upper 1 cm from each core was removed. Sub-samples from each core were combined into a composite sample in a pre-combusted (450 °C) jar. The sediment sample was homogenized and aliquots were removed to pre-combusted glass scintillation vials for analyses of benthic chlorophyll *a* (Chl *a*; a measure of microalgal biomass) and sediment TOC and total nitrogen (TN). All samples were stored at -20°C until analysis. Samples of benthic Chl *a* were analyzed within 6 weeks of collection according to Neubauer et al. (2000). Concentrations of TOC and TN were analyzed by standard methods using a Fisons CHN analyzer (Model EA1108) after removing inorganic carbon (Hedges and Stern 1984); acetanilide was used as the standard.

Lipid biomarker analyses

Lipid biomarker compounds were analyzed using a modified Bligh and Dyer (1959) method (Canuel and Martens 1993; Canuel et al. 2007). Briefly, sediment samples were extracted with methylene chloride:methanol (2:1, v:v) using an accelerated solvent extraction system (Dionex ASE 200). Following extraction, the samples were partitioned

and the organic phase removed. Hexane was added to the aqueous phase and the samples were partitioned a second time; after which the hexane layer was added to the original organic phase. The combined organic phases sat over anhydrous Na₂SO₄ overnight to remove traces of water and were concentrated to 1 mL using turbo-evaporation (Zymark Turbo Vap 500). The total lipid extracts were separated into non-polar (F1/2) and polar (F3) fractions by eluting solvents of increasing polarity through silica gel columns (Guckert et al. 1985). F1/2 (neutral and glyco-lipids) and F3 (phospholipids) were each saponified, using procedures described in Canuel et al. (2007). Following saponification, the residue was extracted under basic (saponified-neutral; SAP-N) and acidic pH (saponified-acids; SAP-A). The SAP-A fractions were methylated using BF₃-CH₃OH and purified using silica gel chromatography. Just before GC injection, samples were evaporated to dryness under N_2 and a small volume of hexane (30 μ L for the polar fraction and 100 μ L for the non-polar) was added. The fatty acids (as methyl esters) were analyzed by gas chromatography following previously-published procedures (Canuel et al. 2007 and references therein). Peaks were quantified relative to an internal standard, methyl heneicosanoate, added just prior to GC analysis. Peak identities were verified using reference standards and by combined gas chromatography-mass spectrometry (GC-MS) using a Hewlett-Packard 6890 GC interfaced with a mass selective detector (MSD) operated in electron impact (EI) mode. Fatty acids are designated as A:B ω C, where A is the total number of carbon atoms, B is the number of double bonds, and C is the position of the first double bond from the aliphatic " ω " end of the molecule. The prefixes "i" and "a" refer to iso and anteiso methyl branched fatty acids (see Canuel et al. 1995 and references therein). Results for two classes of fatty acids are presented: phospholipid-

linked fatty acids (PLFA) which represent viable or recently viable biomass and total fatty acids which represent neutral, glyco-, and phospholipids and include the sum of the viable and detrital contributions.

Statistical analyses

The experiment was analyzed as a fully factorial 3-way analysis of variance (ANOVA), with grazer treatment (df=2), food chain length (i.e., predator presence or absence, df=1, and light availability (df=1) as fixed variables, using SAS version 9.0 for Windows. Analyses of fatty acid data were conducted on percent abundance. GEP data were subjected to a 2-way ANOVA since data were only available for ambient light treatments. From the ANOVAs we calculated the magnitude of main and interactive effects (ω^2 , percentage of the variance explained). Due to contaminations and extinctions, two control and four 2-species mesocosms were removed from all statistical analyses; results presented here use the type III sum of squares (SS) from the ANOVA model. Included in the statistical analyses were five replicates in ambient light and four in low light of the zero grazer treatments, four replicates of the two grazer treatments, and five replicates of the four grazer treatments. There were two criteria for elimination: (1) grazer contamination totaled more than 500 mg AFDM and (2) failure of two grazer species (Caprella and Bittium) to establish necessitated elimination of mesocosms where this pair of species was initially stocked. To separate effects of grazer presence versus grazer species richness, we conducted a priori contrasts that partitioned the grazer SS from the ANOVA into two orthogonal components (see Duffy et al. 2005). The first contrast compared the two- and four-species treatments against the zero-species treatment (species

presence contrast) and the second compared the two- vs. four-species treatments (species richness contrast).

To aid in interpreting the fatty acid data, we performed multiple regression analyses modeling the fatty acid groups as a function of biomass of the major primary producers, eelgrass, total algae, and benthic Chl *a*. The partial r^2 was calculated by dividing the type III SS for each response variable by the total SS. The analyses were performed on %TOC, individual fatty acids, and groups of fatty acids normalized to the sum of all fatty acids (% total FA or %PLFA). Additionally, we conducted principal components analysis (PCA; using Minitab 14) to better elucidate relationships between manipulated and response variables. We only performed PCA on SOM variables as these responded to primary producer abundance determined by grazers and crab predators. PCA loadings describe the relationships between the SOM response variables and the dominant principal components. PCA scores illustrate relationships between the observations and the dominant principal components. PCA loadings were also regressed against the major primary producer groups (*Z. marina*, total algal biomass, and benthic Chl *a*) to help interpret the non-dimensional results.

Results

Primary producer biomass and gross ecosystem production (GEP)

In general, primary producer biomass was enhanced by light and predator presence and decreased by grazers. Above-ground, light increased biomass of both *Z. marina* and algae (Table 1, Fig. 1A, B). Cascading predator effects resulted in grazers reducing primary producer biomass only in the absence of predators (grazer x predator interaction, Table 1). For example, grazer presence and richness decreased *Z. marina* biomass in the absence of predators (p=0.002, $\omega^2=0.28$). Further, total algal biomass was reduced by grazer presence and richness, but increased when predators were present. Several other interactions between grazers, predators, and light were also significant (Table 1). In the sediments, benthic Chl *a* was increased by ambient light (p=0.023, $\omega^2=0.06$, Fig. 1C), decreased by grazer presence (p=0.004, $\omega^2=0.01$), and unaffected by crab predators.

Gross ecosystem production (GEP) in the ambient-light mesocosms was influenced by the interaction of predators and grazers (p=0.002, $\omega^2=0.19$, Table 1, Fig. 2). Overall, blue crab predators increased GEP (p<0.001, $\omega^2=0.29$), but only in the presence of grazers, reflecting a trophic cascade. Increasing grazer species richness reduced GEP, but only in the absence of predators (p=0.001, $\omega^2=0.39$). Thus, grazer presence, richness, and predator presence are all important interacting determinants of GEP (Table 1).

Bulk sediment organic matter (SOM)

Over the course of the six-week experiment, measurable levels of TOC and TN accumulated in surface sediments (Table 1, Fig. 3). Sediment %TOC and %TN content were higher in ambient light than in shaded treatments (p=0.004, $\omega^2=0.12$ and p<0.001, $\omega^2=0.18$ respectively). Neither grazers nor predators significantly affected %TOC or %TN. Thus, bottom-up forcing had a stronger effect on TOC and TN accumulation than top-down processes.

Total fatty acids (total FA)

While bulk indicators of SOM were sensitive only to light availability, fatty acid composition was strongly influenced by both bottom-up and top-down forcing. On average, total fatty acid (total FA) abundance normalized to TOC (μ g mg⁻¹) was significantly reduced by light but was unaffected by predators and grazers (Fig. 4A). For further analysis, both the total and phospholipid-linked fatty acids were categorized into sub-classes based on chain length, number of double bonds, and carbon branching patterns representing different sources of OM (Fig. 5).

Total FA composition was dominated (29 - 47% total FA) by even-numbered saturated compounds ($C_{12:0}$ - $C_{18:0}$), representing algal and bacterial sources. The relative abundance of short-chain fatty acids (SCFA; %($C_{12:0}+C_{14:0}$)) was highest in ambient light in the presence of predators (Table 1, Fig. 5A). Grazer presence, however, decreased SCFA. SCFA were also positively related to benthic Chl *a* (Table 2). The contributions of %C_{16:0} and %C_{18:0} fatty acids were unaffected by any of the treatments and were unrelated to either eelgrass or benthic Chl *a* abundance (Table 1). The long-chain fatty acid C_{24:0}, comprising 3-16% of total FA, was increased by ambient light on average (Table 1, Fig. 5B), and decreased by grazers, but more so in ambient light and predator treatments. C_{24:0} was also positively related to benthic Chl *a* (Table 2). Overall, light increased fatty acids that were positively associated with benthic microalgae (Chl *a*) while grazers, the dominant top-down control, generally, had the opposite effect.

Relative abundance of polyunsaturated fatty acids ($C_{18:4}$, $C_{20:4}$, $C_{20:5}$, $C_{22:5}$, $C_{22:6}$; grouped as polyunsaturated fatty acids, PUFA) was reduced by predators, but only in shaded treatments, reflecting an interaction between predators and light (Table 1, Fig. 5C). %PUFA abundance was not related to either eelgrass biomass or benthic Chl *a*

(Table 2). Linoleic (C_{18:206}) and linolenic (C_{18:303}) acids, were decreased when grazers were present (p=0.035, $\omega^2=0.07$; Table 1, Fig. 5D) but only in ambient light treatments (grazer by light interaction, p=0.007, $\omega^2=0.12$). *Z. marina* was positively related to $%(C_{18:206} + %C_{18:303})$ (Table 2). Overall top-down controls were important determinants of PUFA abundance, with predators decreasing %PUFA and grazers decreasing linoleic and linolenic acids.

Branched fatty acids (iso- and anteiso- $C_{13:0}$, $C_{15:0}$, $C_{17:0}$, $C_{19:0}$), representative of sediment heterotrophic bacteria, were sensitive to all three manipulated variables (Fig. 5E). Light generally decreased the relative abundance of branched fatty acids, though this effect was driven mainly by the two-grazer species treatment and translated into a grazer by light interaction effect (Table 1). Relative abundance of branched fatty acids was consistently higher in predator treatments (p=0.013, $\omega^2=0.07$). Branched fatty acids were positively related to benthic Chl *a* (Table 2). These results suggest that sediment heterotrophic bacteria are sensitive to both bottom-up and top-down controls.

Principal component analysis provided a summary of these changes in SOM with manipulation of light and epibenthic community composition. Principal components 1 (PC1) and 2 (PC2) explained 31.7% and 25.9% of the variance in total fatty acid composition, respectively (Fig. 6A, B). Percent TOC, $%C_{24:0}$, and $%(C_{12:0} + C_{14:0})$ had the most positive loadings on PC1 (Table 3) and also responded positively to ambient light (Figs. 3, 5). The association between PC1 and light is also supported by the positive relationship between benthic Chl *a* and PC1 loadings ($r^2=0.33$; p<0.001). In contrast, PC2 separated SOM variables according to crab predator or grazer effects. Variables with negative PC2 loadings (%PUFA and %BrFA) were affected by crab predators, albeit in

opposite directions, while those with positive PC2 loadings (%($C_{12:0} + C_{14:0}$), %($C_{18:2} + C_{18:3}$), and % $C_{24:0}$ (ambient light only)) were decreased by grazers (Table 3). Bottom-up forcing interacted with top-down forcing of SOM composition as PC scores were influenced by crab predators and grazers differently depending on light availability (Fig. 6A, B). In ambient light (Fig. 6A), grazer-free treatments had positive PC1 and PC2 scores while the two- and four-grazer treatments were near zero or negative on PC2. In contrast, under low light (Fig. 6B), treatments with crabs had more positive PC2 scores while no-crab treatments were negative. Under both light regimes, the pattern is most evident for the zero- and four-grazer treatments (Fig. 6A, B). Thus, PCA results suggested that the dominant top-down control (grazers vs. crab predators) influenced total FA composition differently with light availability.

Phospholipid-linked fatty acids (PLFA)

Like total fatty acids, PLFA (μ g PLFA mg⁻¹ TOC; Fig. 4B), indicative of viable or recently viable OM sources, were also sensitive to top-down and bottom-up influences. None of the manipulated treatments affected total PLFA, %(C_{12:0}+C_{14:0}), %C_{16:0}, or %C_{18:0} PLFA (Table 1). The relative abundance of C_{24:0} PLFA and linoleic and linolenic PLFA (%C_{18:2\omega6} and %C_{18:3\omega3}) were higher under ambient light but only in the absence of grazers, which reduced linoleic and linolenic acid contributions (Fig. 5G, I). Predators increased linoleic and linolenic (C_{18:2\omega6} and C_{18:3\omega3}) PLFA only under ambient light; this translated into a predator by light interaction (Table 1). Branched PLFA were lower in ambient light treatments (*p*=0.006, ω^2 =0.08). In addition to main effects, there were a variety of interactive effects on PLFA composition and abundance (Table 1). Overall, the

PLFA results echo those for total FA, showing that community structure and light availability alter SOM deposition and probably sediment microbial response.

PC1 and PC2 explained 25.3% and 19.5% of the variance, respectively, in PLFA composition (Fig. 6C, D). Similar to the results for total FA, PC1 separated PLFA variables according to light availability. Percent TOC, $%C_{24:0}$, and $%(C_{18:2} + C_{18:3})$, which were increased by light (Figs. 3, 5) and correlated with primary producer biomass (Table 2), had more positive PC1 loadings (Table 3). PC1 was also positively related to total algal biomass, which increased in ambient light (r^2 =0.10; p=0.018). In ambient light, PC2 separated response treatments by grazer presence (near zero) and absence (more negative) (Fig. 6C). The association of PC2 with grazers is supported by the negative relationship between PC2 and benthic Chl *a* (r^2 =0.10; p= 0.017). In shaded treatments, neither PC1 nor PC2 clearly separated grazer and crab treatments (Fig. 6D).

Discussion

A realistic assessment of ecosystem functioning under changing conditions requires simultaneous consideration of top-down and bottom-up effects (Strong 1992; Hughes et al. 2004; Borer et al. 2006). In benthic, sedimentary systems, this should include effects on biomass and composition of above-ground primary producers and animals (Heck et al. 2000; Hughes et al. 2004; Borer et al. 2006), the below-ground community (Wardle et al. 2005), and organic matter composition in sediments (Holmer et al. 2004; Canuel et al. 2007). In this study, we showed experimentally that epibenthic food web structure and resource (light) availability strongly influenced the abundance and composition of SOM. Specifically, light increased and grazers decreased most

measures of primary producer biomass and sediment organic matter. Grazer effects on primary producers and SOM composition were generally stronger in ambient light treatments, showing that animal communities and resource availability together shaped properties of this seagrass ecosystem. Perhaps surprisingly, given the strong effects of predators on above-ground algal biomass in this system (Duffy et al. 2005), effects of predators (food chain length) on SOM were less pervasive than those of light availability or grazers. Nevertheless, predators increased OM contributions from microbial sources generally (%SCFA, total FA), and from sediment heterotrophic bacteria specifically (%BrFA, total FA). This suggests that the previously demonstrated cascading effects of crab predators on primary producer biomass (Duffy et al. 2005; Canuel et al. 2007) also affect the accumulation of labile OM, eliciting a bacterial community response.

Bottom-up forcing

Many seagrass ecosystems suffer from suspended sediment and nutrient loading, both of which can reduce light availability (Duarte 2002; Kemp et al. 2004). Decreased water clarity negatively effects seagrass performance and has cascading effects on associated fauna, water quality, and sediment erosion (Orth and Moore 1983; Duarte 2002). With such wide-ranging effects it is likely that decreased water transparency would also affect SOM accumulation and biogeochemical processes in seagrass sediments (McGlathery et al. 1998; Holmer et al. 2004). Thus, a primary goal of our study was to elucidate how light availability, alone and in concert with changing food web structure, influences OM composition.

In our experimental system, light strongly increased above-ground plant and algal biomass (Table 1, Fig. 1), confirming that the level of shading we used limited primary production and accumulation of producer biomass. In the sediments, light increased benthic microalgal biomass and, presumably as a result, TN and TOC as well. These light effects translated into changing SOM composition by increasing the abundance of algal and microbial fatty acids (%($C_{12:0} + C_{14:0}$); total FA), % $C_{24:0}$ (total FA, PLFA), and linoleic and linolenic acids (PLFA), and by decreasing heterotrophic bacterial fatty acids (%BrFA; total FA, PLFA) (Fig. 5). When expressed as a fraction of total FA, linoleic and linolenic acids were positively correlated with eelgrass biomass while $%(C_{12:0} + C_{14:0})$ (total FA), %C_{24:0} (total FA), and branched fatty acids (total FA) were positively correlated with benthic microalgal biomass (Chl a). The positive relationship between benthic Chl a and heterotrophic bacterial fatty acids suggests that, in our system, microalgae served as a primary organic matter source for sediment bacteria. This is consistent with recent work showing that microalgae are often a major source of SOM and drive microbial degradation processes in seagrass beds (Boschker et al. 2000; Bouillon and Boschker 2006).

Although it is generally accepted that $C_{12:0} + C_{14:0}$ derive from aquatic algal and microbial sources, the origin of $C_{24:0}$ is less clear. Vascular plants are typically considered the source of long chain fatty acids; however, diatoms have been reported to contribute as much as 30% of $C_{24:0}$ in some sediments (Volkman et al. 1980). Other studies have reported $C_{24:0}$ fatty acid in cyanobacterial mats (Edmunds and Eglinton 1984), diatoms (Viso and Marty 1993), and microalgae (Volkman et al. 1998 and references therein). These organisms are often associated with the community of organisms composing the

microphytobenthos. In addition, $%(C_{12:0} + C_{14:0})$ (aquatic algal and microbial OM) and $%C_{24:0}$ had similar PC1 and PC2 scores (Table 3). These FA classes responded similarly to light and food-web treatments, suggesting that they may share an organic matter source in our system.

Overall, light availability increased the abundance of above-ground primary producers, sediment TN and TOC content, and the relative contributions of FA typically considered to derive from aquatic sources such as algae and microbes. These results demonstrate that resource availability affects below-ground organic matter storage and cycling in this seagrass system in addition to the more obvious accumulation of plant biomass above-ground. Consequently, changes in water quality that result in reduced light availability may alter carbon cycling and storage in seagrass ecosystem sediments.

Community structure and top-down forcing

The community structure of seagrass ecosystems is rapidly changing as a result of reduced water quality, fishing pressure, and other human influences (Duarte 2002; Orth et al. 2006). The resulting shifts in community composition at multiple trophic levels may precipitate changes in ecosystem functioning (Heck et al. 2000; Duffy 2002). For example, loss of a top predator can indirectly reduce primary producer biomass via a trophic cascade (Hairston et al. 1960; Pace et al. 1999; Shurin et al. 2002). In seagrass systems specifically, shifts in species composition at intermediate trophic levels may also alter ecosystem properties and/or OM accumulation (Duffy et al. 2003; Canuel et al. 2007). A goal of this experiment was to determine how simultaneous changes in food

web composition and resource availability influence ecosystem properties and functioning.

Food chain length (predator presence or absence) strongly influenced GEP, total algal biomass, and SOM composition (Table 1). This effect of crab predators was evidently mediated indirectly, as crabs inhibited or consumed grazing invertebrates, increasing algal biomass and, consequently, GEP. In the sediments, these effects of predators increased algal and microbial organic matter ($(C_{12:0} + C_{14:0})$ total FA; Fig. 5A), presumably through the same trophic cascade mechanism. Interestingly, predators decreased the relative contribution of even-numbered polyunsaturated fatty acids (%PUFA Total FA; Fig. 5C), which are considered proxies for "fresh" algal material (Canuel and Martens 1993). This effect was strongest in shaded treatments where primary producer biomass was lower. Importantly, predators also increased OM contributions from sediment heterotrophic bacteria (%BrFA total FA; Fig. 5E), suggesting that trophic cascades can extend beyond animals and plants to OM and biogeochemical cycling. Consequently the removal of top predators may alter not only biomass and production of herbivores and plants, but also ecosystem processes mediated by sediment or soil communities (Setälä et al. 1998; Wardle et al. 2005). This has implications for seagrass ecosystems in Chesapeake Bay and elsewhere where blue crabs and predatory fishes are commercially harvested.

Overall, grazers strongly decreased ecosystem production, plant and algal biomass, and the contributions to the sediments of FA deriving from these sources (Table 1, Figs. 1, 2, 5). Above-ground, grazer presence decreased total algal and *Z. marina* biomass, resulting in reduced GEP; but only in the absence of predators, reflecting the

strong trophic cascade demonstrated previously in the above-ground portion of this system (Duffy et al. 2005). Both grazer presence and richness were strong determinants of GEP, confirming that invertebrate species composition and diversity can influence ecosystem-level rate processes (Jonsson and Malmqvist 2003; Dangles and Malmqvist 2004). In the sediments, grazer presence decreased benthic microalgal biomass (Chl *a*), microbial fatty acids ($%(C_{12:0} + C_{14:0})$ total FA), linoleic and linolenic acids (total FA and PLFA), and $%C_{24}$ (ambient light and with predators, total FA) (Fig. 5). Thus, grazing reduced the contribution of fatty acids characteristic of eelgrass and algae to SOM. Grazer richness only influenced heterotrophic bacterial fatty acid abundance (%BrFA total FA and PLFA; Fig. 5E), though this effect was mainly driven by the two species treatment. Overall, our results indicate that the presence of grazers is more important than the number of species in determining SOM composition and quality.

Overall, food chain length and grazers strongly affected GEP, primary producer biomass, and SOM composition. Predators mediated carbon flow and accumulation between lower trophic levels while grazers altered the composition of OM delivered to the sediment. Further, our results suggest that above-ground communities may influence sediment heterotrophic bacteria. Consequently, human-induced shifts in the abundance or composition of above-ground communities can indirectly affect sediment biogeochemistry by influencing the pathways (invertebrate grazers vs. bacteria) through which OM is cycled.

Interactions between bottom-up and top-down forcings

Since seagrass habitats are perturbed by multiple stressors, developing a comprehensive understanding of ecosystem responses is imperative for conservation and restoration (Duarte 2002; Orth et al. 2006). However, most studies have investigated the effects of human stressors, such as eutrophication (see Cloern 2001) or changing biodiversity (see Duffy 2006), on seagrass systems singularly (but see Heck et al. 2000 and Hughes et al. 2004). Thus a major goal of this work was to investigate how interactions between decreased resource (light) availability and altered food web structure (grazer community and predator presence) affect ecosystem properties. Interactions between the three manipulated variables had pervasive effects on the abundances of above-ground eelgrass and algal biomass and SOM composition. While the majority of interactions were between grazers and light or predators, there were also several three-way interactions.

Overall, most interactive effects of the treatments on SOM largely stemmed from light or predators mediating grazer effects on primary producer biomass and organic matter. Generally, grazer effects were stronger in ambient light while predator controls were more prevalent in shaded treatments (Table 1), suggesting that the strength of trophic cascades may depend on the availability of light or other resources, as in some freshwater systems (Chase 2003). The results of the PCA analyses best summarize the interactive effects of light, grazers, and predators on SOM (Table 3, Fig. 6), suggesting that grazers can strongly determine SOM composition, that their effects are damped by predators, and that changing light intensity affects the relative strength of this trophic cascade.

Our results largely confirm our original hypotheses. Grazers decreased total algal biomass and altered SOM composition. Predator inclusion resulted in a trophic cascade whereby total algal biomass, algal and microbial organic matter ($(C_{12:0}+C_{14:0})$) Total FA), and bacterial fatty acid abundance (%BrFA of Total FA) in the sediments were increased. Ambient light increased above-ground and sediment primary producer abundance, sediment total nitrogen and organic carbon, and algal and microbial organic matter (%($C_{12:0}+C_{14:0}$) total FA, % $C_{24:0}$ total FA and PLFA). Contrary to our predictions, grazers decreased Z. marina biomass, benthic Chl a, and fatty acids derived from algal and microbial organic matter (% $(C_{12:0}+C_{14:0})$ total FA) while reduced light availability increased bacterial organic matter (%BrFA total FA). This latter result was largely driven by the treatment with two grazer species. The complex interactive effects among resources, predators, and grazers suggest that above-ground and sediment properties are unlikely to respond in simple, predictive ways to multiple disturbances. Further, our results demonstrated that resource availability and food web structure strongly influence ecosystem properties and that synergism between bottom-up and top-down controls may affect sediment carbon composition and storage in natural seagrass beds. This underscores the need for additional multi-factorial experimental and field approaches to understanding the cycling of organic matter in estuarine systems. Realistic mesocosm experiments are initially helpful in identifying subtle changes in SOM and focusing research questions and methods. However, field experiments will clearly be necessary to explore how linkages between above-ground processes and SOM are related in the more complex natural environment. Combined, results from both approaches should be useful

in designing more effective management strategies for the preservation of productive seagrass ecosystems.

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Table 1. Tests of significance, estimated magnitudes of effect (0²), and contrasts of grazer richness vs. presence for light availability, food chain length, grazer species richness, and their

interactions on ecosystem production, plant biomass, sediment total nitrogen, sediment organic carbon, and sediment fatty acid abundance. When an interaction between grazers and light or

predators was significant, the data set was divided according to the interaction (i.e., low light vs. ambient light or no predators vs. predators) and an ANOVA was performed again. For interactive

effects, G refers to grazers, C to crab predators, and L to light. For contrast analyses, P indicates where grazer presence affected the response variable and R refers to a richness effect. Significant

p values are in bold.

Response	Light				Crab predators			Grazers			Interactions			Error		Contras
	MS	Р	ω²	MS	р	ω²	MS	p	ω ²		MS	P	ω ²	MS	ω²	
Gross ecosystem production	NA			23.38	<0.001	0.29	5.42	0.014	0.12	GxC	8.33	0.002	0.19	1.03	0.40	PR
No predators							13.26	0.001	0.39					0.59	0.61	PR
Predators							0.49	0.661	0.00					1.14	1.03	
. marina (AFDW)	80.95	0.027	0.06	28.50	0.180	0.01	37.11	0.101	0.04	GxC	61.94	0.025	0.09	15.31	0.61	Р
No predators	78.71	0.005	0.17				67.22	0.002	0.28					7.87	0.57	PR
Predators	14.84	0.428	0.00				31.82	0.269	0.03					22.75	1.04	
otal algae (log AFDW + 0.001)	6.79	0.005	0.04	35.46	<0.001	0.25	16.69	<0.001	0.23	GxC	12.52	<0.001		0.76	0.33	PR
No predators	0.65	0.473	0.00				56.83	<0.001	0.77						0.25	PR
Predators		0.019	0.15				0.35	0.230	0.03						0.87	
Benthic Chl a (µg cm ⁻²)	352.73	0.023	0.06	100.12	0.217	0.00	408.49	0.004	0.01					63.60	0.8	Р
%TOC	0.06	0.004	0.12	0.01	0.669	0.00	0.01	0.398	0.00					0.01	0.90	
%TN	0.01	<0.001	0.18	0.00	0.955	0.00	0.00	0.294	0.00					0.00	0.89	
Total fatty acids (TFA)*																
FA:OC (ug mg _{Toc} ⁻¹)	193.25	0.016	0.08	1.18	0.846	0.00	32.46	0.359	0.00					30.87	0.89	
SCFA (C12+C14) of TFA	95.18	<0.001	0.30	20.06	0.014	0.06	15.70	0.010	0.08					3.02	0.59	Р
C1650 of TFA	3.43	0.851	0.00	61.69	0.427	0.00	206,40	0.129	0.04					95.84	1.00	
CI8:1 of TFA	0.44	0.826	0.00	9.25	0.319	0.00	1.01	0.895	0.00							
C ₂₄ of TFA		0.003	0.11	0.00	0.983	0.00	1.85	0.277	0.01	GxL	6.98	0.011	0.10	1.40	0.72	
		01000		0.00	0.50.	0.00	1100	01-01		GxC	6.58	0.014	0.09			
Low light				0.15	0.636	0.00	0.88	0.290	0.02	GxC	2.37	0,047	0.15	0.67	0.86	
Ambient light				0.14	0.799	0.00	8.48	0.030	0.16						0.76	Р
No predators	4.97	0.045	0.09		01777		0.75	0.516	0.00						0.80	-
Predators	8.95	0.032	0.10				7.67	0.023	0.16					1.70	0.67	Р
PUFA of TFA	0.20	0.927	0.00	104.82	0.042	0.05	9.18	0.682	0.00	GxL	100.43	0.021	0.10	23.77	0.89	
										LxC	100.01	0.047	0.05			
Low light				197.48	0.002	0.27	23,42	0.259	0.02					16.21	0.73	
Ambient light				0.03	0.976	0.00	91.26	0.072	0.13					30.63	0.97	Р
(C18:2 + C18:3) of TFA	44.80	0.061	0.04	4.75	0.534	0.00	43.86	0.035	0.07	GxL	67.44	0.007	0.12	12.10	0.77	Р
Low light				5.33	0.398	0.00	2.34	0.725	0.00					7.16	1.09	
Ambient light				30.67	0.188	0.02			0.28					16.59		Р
BrFA (i,a C13-C19) of TFA	47.83	0.023	0.06	57.81	0.013	0.02	46.15	0.008	0.11	GxL	47.37	0.007	0.11		0.72	R

Low light		23.75 0.06	5 0.24	3.86 0.215	0.03		2.32 0.78	
Ambient light		34.81 0.13	2 0.04	89.57 0.007	0.26		14.25 0.74	R
Phospholipid linked fatty acids (PL	FA)*							
PLFA:OC (ug mg _{TOC} ")	0.35 0.399 0.00	0.39 0.32	5 0.00	0.45 0.407	0.00		0.485 1.04	
%SCFA (C12+C14) of PLFA	1.39 0.587 0.00	7.11 0.22	3 0.01	10.19 0.125	0.03	GxCxL 21.20 0.016 0.10	4.66 0.85	
%C16:0 of PLFA	38.88 0.536 0.00	36.72 0.54	8 0.00	246.27 0.097	0.04	GxCxL 469.76 0.014 0.10	99.90 0.84	
%C _{18:0} of PLFA	148.45 0.188 0.01	162.97 0.16	8 0.02	105.10 0.291	0.01		82.74 1.00	
%C _{24:0} of PLFA	9.98 <0.001 0.17	0.44 0.42	5 0.00	0.46 0.516	0.00		0.68 0.76	
%PUFA of PLFA	19.39 0.221 0.01	37.30 0.09	2 0.03	56.42 0.017	0.10		12.57 0.83	P
%(C18:2 + C18:3) of PLFA	587.83 0.005 0.08	223.76 0.07	4 0.02	377.71 0.007	0.09	LxC 303.22 0.039 0.03	66.52 0.57	Р
						GxL 499.44 0.002 0.12		
						GxCxL 253.48 0.030 0.05		
Low light		2.90 0.31	9 0.00	4.34 0.235	0.03	GxC 10.14 0.045 0.15	2.79 0.82	
Ambient light		544.12 0.04	8 0.07	940.86 0.003	0.25	GxC 463.56 0.04 0.11	124.46 0.58	Р
%BrFA (i,a C13-C19) of PLFA	60.24 0.006 0.08	1.68 0.62	9 0.00	60.19 <0.001	0.15	GxL 51.29 0.002 0.12	66.52 0.60	R
						GxCxL 27.38 0.029 0.06		
Low light		5.29 0.39	4 0.00	18.22 0.098	0.10		6.97 0.88	Р
Ambient light		18.09 0.12	6 0.03	91.99 <0.001	0.40		7.15 0.51	R

* Biomarker response variables are expressed either as % of total fatty acids or as % of phospholipid-linked fatty acids. Data were analyzed by 3-factor Model III ANOVA. p values <0.05 are in bold.

P and R indicate whether grazer presence or richness effects, respectively, were significant as determined through contrast analysis.

Table 2. Regression analyses of Z. marina biomass (AFDW, g) and benthic Chl a (μ g cm⁻²) against the major fatty acids groups.

Significant relationships (p < 0.05) are noted in bold.

Response	Z. marina				Total		
	Coefficie	ent Partial r	p	Coefficie	ent Partial r ²	* p	Model r^2
Total fatty acids (TFA)							
%SCFA (C _{12:0} + C _{14:0}) of TFA	0.09	0.03	0.171	0.12	0.22	<0.001	0.25
%C _{24:0} of TFA	0.00	0.00	0.968	0.07	0.22	<0.001	0.22
%PUFA of TFA	-0.13	0.01	0.428	0.03	0.00	0.718	
$(C_{18:2} + C_{18:3})$ of TFA	0.26	0.08	0.041	0.05	0.01	0.439	0.09
%BrFA (i,a C_{13} - C_{19}) of TFA	-0.20	0.06	0.066	0.11	0.08	0.034	0.14
Phospholipid linked fatty acids (PLFA)							
%SCFA (C _{12:0} + C _{14:0}) of PLFA	0.06	0.02	0.285	0.00	0.00	0.897	
%C _{24:0} of PLFA	0.05	0.07	0.052	0.00	0.00	0.813	_
%PUFA of PLFA	-0.07	0.01	0.588	-0.05	0.01	0.449	
$(C_{18:2} + C_{18:3})$ of PLFA	0.32	0.04	0.121	0.20	0.08	0.037	0.12
%BrFA (i,a C ₁₃ -C ₁₉) of PLFA	-0.16	0.04	0.137	-0.03	0.00	0.509	·

*Partial r^2 were calculated by dividing the Type III SS by the Total SS.

Table 3. Loadings from principal components analysis of sediment organic matter composition and content for total fatty acids (total FA) and phospholipid linked fatty acids (PLFA). Polyunsaturated fatty acids (PUFA) are comprised of: $C_{18:4}$, $C_{20:4}$, $C_{20:5}$, $C_{22:5}$, $C_{22:6}$.

	To	otal FA	PLFA			
Variable	PC1	PC2	PC1	PC2		
TOC (mg g^{-1})	0.494	-0.221	0.324	-0.148		
$(C_{12:0} + C_{14:0})$	0.512	0.169	0.526	0.140		
%C _{16:0}	-0.229	0.527	-0.536	-0.168		
$(C_{18:2} + C_{18:3})$	0.222	0.453	0.137	-0.662		
%C _{24:0}	0.583	0.118	0.216	-0.557		
%PUFA	-0.018	-0.632	0.492	0.290		
%BrFA (i,a C _{13:0} -C _{19:0})	0.228	-0.160	-0.152	0.312		

Figure Captions.

Fig. 1. Effects of grazers, predators, and light availability on above ground primary producers (*Z. marina* and total algae) and benthic Chl *a*. Light, generally, increased primary producer biomass. Grazers decreased *Z. marina* biomass (in the absence of predators) and total algal biomass. Predators decreased both *Z. marina* and total algal biomass but the magnitude of this effect varied with grazer richness, resulting in grazer by predator interactive effects. Error bars represent standard error. There were four replicates of each zero grazer treatment in low light and five in high light; four replicates of each two grazer treatment and five replicates of each four grazer treatment. Statistical results are reported in Table 1.

Fig. 2. Effects of grazers and predatory crabs on summer gross ecosystem production, measured as dissolved oxygen (DO) flux. Predators (crabs) mediated a negative grazer effect on gross ecosystem production through a trophic mechanism. The magnitude of the predator effect increases with grazer richness. Data are only from ambient light treatments. Error bars represent standard error. Statistical results are reported in Table 1.

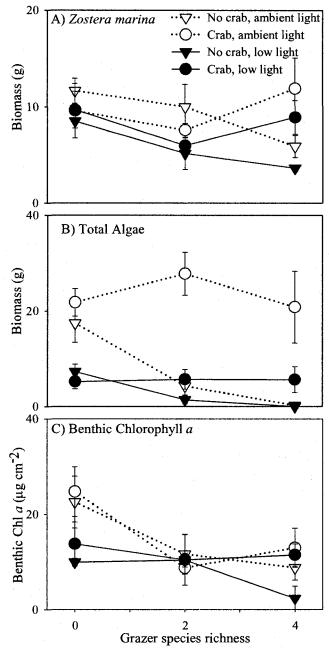
Fig. 3. Effects of light, grazers, and predators on sediment carbon and nitrogen. (A) Light increased sediment total nitrogen (%TN) and (B) total organic carbon content (%TOC). Neither grazer richness nor food chain length affected %TN or %TOC. Error bars represent standard error. Statistical results are reported in Table 1.

Fig. 4. (A) Abundance of total fatty acids (Total FA) and (B) phospholipid linked fatty acids (PLFA) normalized to total sediment organic carbon content ($\mu g m g_{TOC}^{-1}$). Light decreased total FA ($\mu g m g_{TOC}^{-1}$ (A)) but had no effect on PLFA ($\mu g m g_{TOC}^{-1}$ (B)). Error bars represent standard error. Statistical results are reported in Table 1.

Fig. 5. (A-J) Effects of light, grazers, and predators on total fatty acids (Total FA) and phospholipid linked fatty acids (PLFA) sub-classes. Light, predators, and grazers had strong singular and interactive effects on total fatty acids and phospholipid linked fatty acids. The polyunsaturated fatty acid (%PUFA) sub-class, representing fresh algal material, is comprised of: $C_{18:4}$, $C_{20:4}$, $C_{20:5}$, $C_{22:5}$, $C_{22:6}$. The branched fatty acid (%BrFA) sub-class, representing heterotrophic bacteria, includes iso- and anteiso $C_{13:0}$, $C_{15:0}$, $C_{17:0}$, $C_{19:0}$. Error bars represent standard error. See text for biomarker sources and Table 1 for statistical results.

Fig. 6. Score plots from principal component analysis for total fatty acids (Total FA) and phospholipid linked fatty acids (PLFA) in ambient light and shaded treatments. Error bars represent standard error. G denotes grazers and C refers to crab predators.





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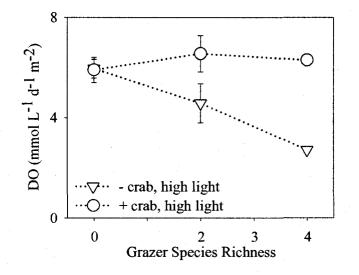
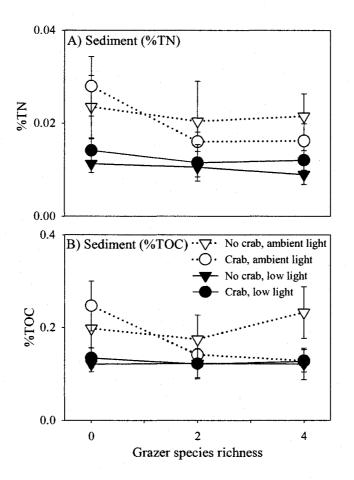
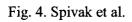


Fig. 3. Spivak et al.





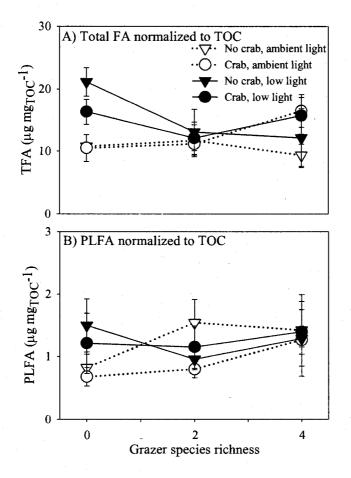
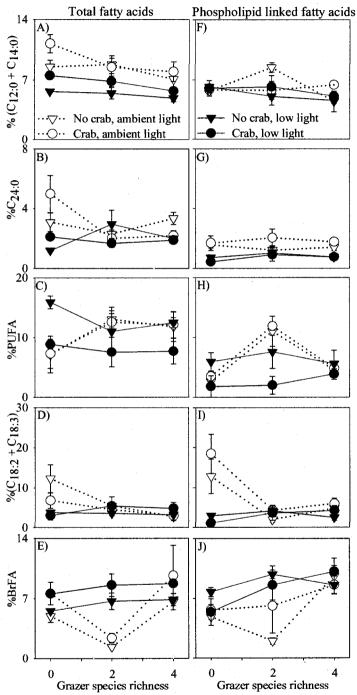
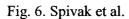


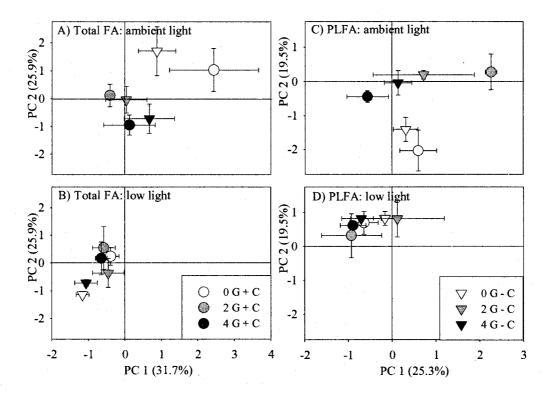
Fig. 5. Spivak et al.



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Chapter 3:

Community composition and nutrient availability alter sediment organic matter composition in a seagrass bed: a field experiment.

Amanda C. Spivak, Elizabeth A. Canuel, J. Emmett Duffy, James G. Douglass, and J. Paul Richardson.

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ABSTRACT

Eutrophication and fishing are common perturbations in aquatic ecosystems with pervasive impacts on community structure, including species diversity and abundance, that may cascade to sediment biogeochemistry. While changes in sediment processes in response to these stressors are likely important to ecosystem functioning, they are poorly understood. To address this issue, we experimentally manipulated water column nutrient levels and food web composition (i.e. predator and grazer presence and absence) in a factorial design using field enclosures situated in a Zostera marina bed. After 28 days, we quantified sediment organic matter (SOM) accumulation and composition using measures of total organic carbon and nitrogen as well as fatty acid (FA) biomarkers. Nutrient enrichment led to a rapid increase of epiphytes and a decline in Z. marina biomass. Responding to the available algae, grazers reduced epiphytes and FAs derived from microalgae. Predators reduced Z. marina abundance and possibly its ability to trap particulate OM, leading to lower sediment organic carbon content and total FA abundance. There was evidence of a trophic cascade as FA contributions from epiphytes and diatoms were higher in treatments with both grazers and predators than in treatments with grazers only. Predators increased labile diatom-derived OM, which likely resulted in the higher proportions of bacterial FA measured in predator treatments. Interactions between nutrient availability and food web composition indicated that SOM responses were complex and not predictable from single variables. Changes in SOM accumulation and composition, combined with a rapid heterotrophic bacterial response, suggest that resource availability and community structure are important to sediment biogeochemistry.

INTRODUCTION

Bottom-up (i.e. resource availability) and top-down (i.e. food chain length) controls act in concert across multi-level food webs (Carpenter et al. 1985, Hunter and Price 1992, Power 1992, Borer et al. 2006) in freshwater (Elser & Goldman 1991, Brett & Goldman 1997, Forrester et al. 1999, Chase 2003) and marine systems (Micheli 1999, Hughes et al. 2004, Burkepile & Hay 2006) to affect patterns of biomass distribution and biogeochemical cycles. Elevated resource availability and changes in top predator abundance may increase plant biomass and the delivery of plant-derived organic matter (OM) to the sediments in tri-trophic seagrass systems (Canuel et al. 2007, Spivak et al. 2007). The quality and rate of OM deposition can have large effects on bacterial decomposition and carbon burial in sediments (Hansen & Blackburn 1992, Cebrian & Duarte 2001). Consequently, resource availability and community composition may synergistically alter sediment biogeochemistry and ecosystem functioning. Here, we experimentally tested how food web structure and nutrient enrichment alter sediment organic matter (SOM) quality and content in a natural seagrass (*Zostera marina*) ecosystem.

In vegetated coastal habitats, photosynthetic carbon is channeled through grazers, exported to neighboring ecosystems, or buried in the sediments (Pergent et al. 1994, Duarte & Cebrian 1996, Cebrian & Duarte 2001, Duarte et al. 2005). Small, invertebrate grazers mainly consume nutrient-rich algae and epiphytes, leaving senesced seagrass blades as the main source of buried OM (Pergent et al. 1994, Duarte & Cebrian 1996, Cebrian 1999, Cebrian & Duarte 2001). Eutrophication may alter the proportion of algal and epiphytic carbon that is exported or buried by stimulating higher rates of production

and changing the composition of primary producer assemblages (Cloern 2001, Duarte 2002). Deposition of higher quality OM derived from labile algae can stimulate bacterial decomposition (Hansen & Blackburn 1992, Boschker and Cappenberg 1998) and, hence, the depletion of oxygen in the sediments. As anaerobic conditions develop, sulfate reduction may become a dominant pathway for OM decomposition. Thus, eutrophication may dually impact seagrass by increasing algal-mediated shading (Cloern 2001, Duarte 2002, Orth et al. 2006) and sediment dissolved sulfide concentrations (Hemminga 1998, Calleja et al. 2007, Pérez et al. 2007).

The symptoms of eutrophication may be diminished or exacerbated by food web composition and structure (Carpenter et al. 1985, Pace et al.1999). In a two level trophic system, strong grazing controls reduced the negative effects of nutrient loading by transforming algae into animal biomass (Williams & Ruckelshaus 1993, Hughes et al. 2004, Burkepile & Hay 2006, Heck & Valentine 2007). Further, grazer species identity and feeding preferences may influence the composition of the primary producer community (Duffy & Hay 2000, Duffy 2002). In a three-level trophic system, predators may exaggerate the effects of nutrient enrichment by inhibiting grazers and releasing algae and epiphytes from grazing pressures via a trophic cascade (Oksanen et al. 1981, Carpenter et al. 1985, Forrester et al. 1999, Pace et al. 1999). Therefore, the effects of nutrient enrichment in seagrass beds may, in part, be determined by trophic structure and community composition.

Despite potentially strong bottom-up and top-down effects on OM deposition and the importance of SOM quality to sediment biogeochemistry (Duffy et al. 2003, Canuel et al. 2007, Spivak et al. 2007), the synergistic effects of nutrient enrichment and

community composition on SOM are poorly understood. This is likely due to the difficulty in identifying and manipulating links between above-ground ecology and sediment processes under realistic conditions. Lipid biomarkers are a functional proxy for linking OM to its potential sources (Canuel et al. 1995, Canuel & Martens 1996), since these compounds are reliably produced by specific groups of organisms (Killops & Killops 1993). Diagnostic biomarkers often have site-specific methyl groups, double bonds, or cyclic side chains useful for tracing sources of OM (Killops & Killops 1993). Bacteria, for example, synthesize iso- and anteiso- branched fatty acids while microalgae contain highly unsaturated long chain fatty acids (Volkman et al. 1998). In addition, lipid biomarkers are sufficiently resistant to degradation to be preserved in sediments, allowing for the identification of OM that has been deposited on ecological and historical timescales (Meyers 1997, Zimmerman & Canuel 2002). Here, we used fatty acids, a class of lipid biomarkers with high source fidelity and a range of chemical reactivity (Canuel et al. 1995, Canuel & Martens 1996), to experimentally quantify links between the above-ground community and SOM content and composition.

To assess the effects of changing resource availability and food web structure on carbon fate and storage in a natural seagrass bed, we conducted an experimental manipulation of bottom-up forcing (water column nutrient availability) and community composition (grazer and predator presence) and measured their interacting effects on SOM quantity and quality. Specifically, we built on previous mesocosm studies examining the effects of community diversity (Canuel et al. 2007) and light availability (Spivak et al. 2007) on SOM composition to test several hypotheses in a field experiment. First, we predicted that nutrient enrichment will increase algal biomass and the deposition

of algal-derived OM to the sediments. The increased lability of SOM will, in turn, stimulate sediment heterotrophic bacterial activity and the deposition of bacterial FA. Second, algae will indirectly decrease *Zostera marina* abundance by increasing competition for light and nutrients. The presence of a grazer community will reduce algae and the abundance of their characteristic FA in the sediment but will increase *Z. marina*. Finally, the presence of predators will result in a trophic cascade in which grazer abundance is reduced and algal biomass and OM contributions to the sediments are increased.

METHODS

Experimental design

We conducted a field experiment to examine the main and interactive effects of food web structure (i.e. grazer and predator presence) and water column nutrient availability on SOM content and composition. Grazer treatments had two levels, either zero grazers or an assemblage of three species. Predator presence was manipulated by exposing parallel sets of these two grazer treatments to a generalist predator, the blue crab, *Callinectes sapidus*. Nutrient availability was controlled through OsmocoteTM fertilizer additions to half of the cages. In total, there were eight treatments, each replicated five times for a total of forty experimental field cages. To control for caging effects, we established no-cage control plots which only received nutrient treatments, since it was impractical to maintain grazer and predator treatments without cages. There were two no-cage treatments (with nutrients versus without nutrients), each replicated five times for a total of ten no-cage control plots.

Treatments were applied to caged enclosures (51 cm² x 81 cm) and no-cage control plots (51 cm²) situated in a *Zostera marina* bed adjacent to Goodwin Islands, an archipelago in the York River estuary, VA. The cages were covered with 250 μ m Nitex mesh which permitted water circulation and passage of propagules but prevented predator and grazer immigration and emigration. Before experimental treatments were applied, caged enclosures and no-cage control plots were defaunated with a liquid insecticide, SevinTM. Douglass et al. (2007) described cage design and the defaunation process in greater detail. The experiment ran for 28 days during Summer 2005. This time period was chosen to minimize the risk of invasion by non-target grazer species and to permit development of the animal and plant community and of surface sediment characteristics. During this time temperature and salinity ranged from 23.76 °C – 27.00 °C and 15.67-19.51 psu, respectively (K.A. Moore *unpubl.*).

Four days after defaunation, grazer, predator, and nutrient treatments were applied to the caged enclosures. Grazer treatments consisted of an assemblage of three species, including an amphipod crustacean (*Gammarus mucronatus*, 40 individuals) and two isopods (*Idotea balthica*, 40 individuals, and *Erichsonella attenuata*, 20 individuals). Predator treatments were stocked with two blue crabs (*Callinectes sapidus*), with carapace widths of 20 - 40 mm. Grazers and blue crabs were collected from the surrounding *Zostera marina* bed immediately before addition to the cages and were stocked in proportions and abundances that reflected those in the field at the time of the experiment. Nutrient treatments were applied by suspending two perforated PVC tubes containing OsmocoteTM slow release fertilizer (N:P = 3:1) above the sediments. We added 200 g of OsmocoteTM during the first week and 400 g thereafter to achieve the

desired and sustained level of enrichment. Weekly, and immediately before the fertilizer was refreshed, 25 mL of water from three replicates of each treatment were filtered through a pre-combusted (450° C) glass fiber filter. Water samples were initially chilled and later frozen (-20 °C) until analysis for NH_4^+ , $NO_2^- + NO_3^-$, and PO_4^{-3} concentrations by standard methods with a Lachat auto-analyzer (Smith & Bogren 2001, Knepel & Bogren 2002, Liao 2002).

Bulk sediment organic matter (SOM)

At the end of the experiment, three sediment cores each of 2.6 cm diameter and 2.1 cm diameter were collected from every caged enclosure and no-cage control plot. Larger cores were analyzed for sediment total organic carbon (TOC), total nitrogen (TN), and fatty acid content (FA) while smaller cores were used to determine benthic chlorophyll *a* concentration (Chl *a*; a measure of microalgal biomass). The upper 1 cm from each core was removed; sub-samples from each core were combined into a composite sample in a pre-combusted (450 °C) jar (bulk SOM and FAs) or scintillation vial (benthic Chl *a*). Samples were stored at -80 °C (bulk SOM and FAs) or at -20 °C (benthic Chl *a*) until analysis. Samples of benthic Chl *a* were analyzed within six weeks of collection according to Neubauer et al. (2000). TOC and TN were analyzed by standard methods using a Fisons Flash EA (Model 1112) after removing inorganic carbon (Hedges & Stern 1984); acetanilide was used as the standard.

Fatty acid analyses

Fatty acids (FA) were analyzed using a Bligh & Dyer (1959) method revised according to Macnaughton et al. (1997). Briefly, sediment samples were extracted with methanol : chloroform : K₂HPO₄ 50 mM buffer (2:1:0.8, v:v:v) using an accelerated solvent extraction system (Dionex ASE 200). Following extraction, the samples were partitioned and the organic phase removed. Anhydrous Na₂SO₄ was added to the sample to remove water overnight. The samples were concentrated to 1 mL (Zymark Turbo Vap 500) and then saponified using procedures described in Arzayus & Canuel (2004). Following saponification, the residue was extracted under basic (saponified-neutral) and acidic pH (saponified-acid). The saponified acid fraction was methylated using BF₃-CH₃OH and purified using silica gel chromatography. Before analysis by gas chromatography (GC), samples were evaporated to dryness under N_2 and a small volume of hexane was added. The FAs, as methyl esters, were analyzed by gas chromatography following previously-published methods (Canuel & Martens 1993, Zimmerman & Canuel 2001). Peaks were quantified relative to an internal standard, methyl heneicosanoate, added just prior to GC analysis. Peak identities were verified using reference standards and by combined gas chromatography-mass spectrometry using a Hewlett-Packard 6890 GC interfaced with a mass selective detector operated in electron impact mode. FAs are designated as A:B ω C, where A is the total number of carbon atoms, B is the number of the double bonds, and C is the position of the first double bond from the aliphatic " ω " end of the molecule. The prefixes "i" and "a" refer to iso and anteiso methyl branched FAs (see Canuel et al. 1995 and references therein).

Statistical analyses

The experiment was analyzed as a fully factorial three-way analysis of variance (ANOVA), with grazer treatment (df = 1), predator treatment (df = 1), and nutrient availability (df = 1) as fixed variables using SAS version 9.1 for Windows. Analyses of FA were conducted on percent of total FA abundance. Data were transformed by log or arcsine square root functions as necessary to maintain homogeneity of variance as determined by the Cochran's C test. From the ANOVAs we calculated the magnitude of main and interactive effects (ω^2 , percentage of variance explained). Due to failure of caged enclosures (e.g., tears or holes in Nitex mesh) seven replicates were removed from the final statistical analyses. No-cage control plots were also excluded from the final ANOVA since their inclusion would have resulted in an unbalanced statistical design. However, contrasts were performed to determine the effect of cage presence on primary producer biomass and sediment organic matter (SOM) content and composition. Thus, 33 replicates were used in statistical analyses; caged control treatments had four replicates in each nutrient condition, grazer treatments had four replicates with nutrients and five without, crab treatments had three replicates with nutrients and four without, combined grazer and predator treatments had five replicates with nutrients and four without. Results presented use the type III sum of squares (SS) from the ANOVA models.

To interpret the bulk SOM and fatty acid data, we performed multiple regression and principal components analyses (PCA; Minitab 14). Multiple regression tests modeled %TOC, %TN, and the FA groups as functions of *Zostera marina* biomass, epiphytic Chl a, and benthic Chl a. The partial r^2 was calculated by dividing the type III SS for each response variable by the total SS. In the PCA, we included *Z. marina* biomass, epiphytic Chl a, benthic Chl a, %TOC, %TN, and FA groups. PCA yielded loadings and scores,

which described correlations between dominant principal components and response variables (loadings) and observations (scores). PCA loadings were regressed against Z. *marina* biomass, epiphytic Chl a, and benthic Chl a to help interpret the non-dimensional results.

RESULTS

Cage effects

Field cages reduced photosynthetically active radiation by 66% relative to ambient, to an average of 262 μ E s⁻¹ m⁻², which is within the range of saturating irradiance for *Zostera marina* (see Douglass et al. 2007). Contrast analyses showed that field cages reduced *Z. marina* biomass (p < 0.001), epiphytic Chl *a* (p = 0.006), benthic Chl *a* (p = 0.013), total FA abundance (p = 0.002), and OM contributions from diatoms (C_{20:503} : C_{22:603}, p = 0.001) (Figs. 1-3) but increased abundances of %(C_{22:5} + C_{22:6}) (p = 0.022), %BrFA (p = 0.015), and %10Me17 (p = 0.001) (Figs. 3, 4). Overall, caged enclosures reduced primary producer biomass and OM contributions to the sediment but increased FA from sediment heterotrophic bacteria.

Nutrient concentrations

During the first week of the experiment, nutrient treatments received 200 g of OsmocoteTM which increased the concentration of $(NO_2^- + NO_3^-)$ (p < 0.001) but not of NH_4^+ or of PO₄⁻³. For the remainder of the experiment, OsmocoteTM additions were increased to 400 g, thereby raising the concentrations of $(NO_2^- + NO_3^-)$, NH_4^+ , and PO₄ (all p < 0.001; Table 1).

Primary producers

Nutrients, predators, and grazers altered final above-ground primary producer abundances (Fig. 1, Table 2). Nutrients and predators each decreased *Zostera marina* biomass while grazers decreased epiphytes. In contrast, benthic Chl *a* was insensitive to all three treatments.

Bulk sediment organic matter (SOM)

Measurable levels of TOC and TN accumulated in the surface sediments during the experiment (Fig. 2A, B, Table 2). Predators decreased %TOC while grazers increased %TN. Neither %TOC nor %TN was influenced by nutrients nor was either variable correlated to the final biomass of any primary producer group (Table 3).

Total fatty acids (total FA)

Within caged enclosures, predators decreased total FA abundance ($\mu g g^{-1}$ sediment; Fig. 2C, Table 2), which was positively correlated to *Zostera marina* biomass (Table 3). Although predators had the only significant effect on total FA concentration, all three treatment variables influenced FA composition. To analyze composition, total FA was divided into sub-classes based on chain length, degree of saturation, and carbon branching patterns as these groups represent different OM sources.

The proportion of short chain saturated FA (SCFA; $\%(C_{12:0} + C_{14:0})$), representing algal and microbial sources, in the sediment was decreased by nutrients (Fig. 3A, Table 2). Grazers increased $\%(C_{12:0} + C_{14:0})$ in the absence of predators, resulting in a

significant interaction between grazer and predator effects (Table 2). Overall, bottom-up and top-down controls were both important determinants of algal and microbial contributions to the sediment.

The proportion of long chain saturated FA (LCFA; %($C_{24:0} + C_{26:0} + C_{28:0}$)), comprising 3-7% of total FA, was consistently increased by grazers (Fig. 3B, Table 2). Nutrients increased %LCFA in the presence of predators but tended to decrease %LCFA in the absence of predators, creating a nutrient by predator interaction effect. %LCFA correlated positively with benthic Chl *a* and negatively with epiphytic Chl *a* (Table 3), suggesting that benthic microalgae became a proportionately greater source of LCFA as grazers consumed epiphytes. %LCFA was positively correlated with abundances of two grazer species, *Gammarus mucronatus*, an amphipod, and *Erichsonella attenuata*, an isopod (p = 0.004, $r^2 = 0.21$ and p = 0.031, $r^2 = 0.11$, respectively; data not shown). Thus, food web composition and nutrient availability interactively altered LCFA contributions from epiphytic and benthic algae.

Polyunsaturated FA (PUFA; %($C_{20:4}+C_{20:5}$) and %($C_{22:5}+C_{22:6}$)), indicative of labile algal OM, were affected by nutrient and food web manipulations (Fig. 3C, D, Table 2). Grazers decreased %($C_{20:4}+C_{20:5}$) but the grazing effect was eliminated in the presence of predators, resulting in a grazer by predator interaction. Predators increased %($C_{20:4}+C_{20:5}$) in non-nutrient treatments only, creating a predator by nutrient interaction. %($C_{20:4}+C_{20:5}$) was correlated negatively with benthic Chl *a* and positively to epiphytic Chl *a* (Table 3). Biomasses of the grazers *Gammarus mucronatus* and *Erichsonella attenuata* were negatively correlated with %($C_{20:4}+C_{20:5}$) (p = 0.008, r² = 0.18 and p = 0.012, r² = 0.16, respectively; data not shown). Predators decreased

 $(C_{22:5}+C_{22:6})$ in the absence of grazers, resulting in a grazer by predator interaction. Overall, the main and interactive effects of community composition and resource availability were important determinants of labile algal OM deposition and accumulation.

We used two ratios ($C_{16:1\omega7}$: $C_{16:0}$ and $C_{20:5\omega3}$: $C_{22:6\omega3}$) to determine the relative contributions of diatom-derived OM to the sediments (Budge & Parrish 1998, Shin et al. 2000). Grazers decreased both ratios and hence the abundance of diatom-derived FA relative to contributions from other microalgae (Fig. 3E, F, Table 2). Predators increased diatom:dinoflagellate FA ($C_{20:5\omega3}$: $C_{22:6\omega3}$), but the magnitude was weaker in the presence of grazers and resulted in a grazer by predator interaction. Epiphytic Chl *a* was positively correlated to both ratios while benthic Chl *a* was negatively correlated to $C_{20:5\omega3}$: $C_{22:6\omega3}$ (Table 3). Biomass of the grazing isopod *Idotea balthica* was positively related to $C_{20:5\omega3}$: $C_{22:6\omega3}$ (p = 0.019, $r^2 = 0.12$; data not shown). Combined, these data suggest that epiphytes were a major source of diatom OM in the sediments and that above-ground animal activities altered SOM supply and composition.

FAs representative of sediment microbial and bacterial OM (10Me17:0, and isoand anteiso- C $_{13:0}$, C $_{15:0}$, C $_{17:0}$, C $_{19:0}$) comprised 10% - 14% of total FA (Fig. 4). Branched odd-numbered FAs (%BrFA; iso- and anteiso- C $_{13:0}$, C $_{15:0}$, C $_{17:0}$, C $_{19:0}$), representative of sediment heterotrophic bacteria (Volkman & Johns 1977, Perry et al. 1979), were increased by predators (Fig. 4A, Table 2) and negatively correlated to *Zostera marina* biomass and to epiphytic Chl *a* (Table 3). 10Me17:0, indicative of sulfate reducing bacteria, comprised 1% - 2% of total FA. Nutrients and predators increased %10Me17:0 (Fig. 4B, Table 2), which was correlated negatively to *Z. marina* and positively to benthic Chl *a* (Table 3). These data suggest that food web structure, particularly predator presence, and resource availability influenced the sediment heterotrophic bacterial and microbial community.

Using PCA, we evaluated the effects of nutrients, grazers, and predators on primary producer abundance, bulk SOM, and FA groups. Principal components 1 (PC1) and 2 (PC2) explained 26.0% and 21.8%, respectively, of the variance in the data. PC1 tended to separate treatments according to grazer effect; variables increased by grazers $(%TN, %(C_{12:0} + C_{14:0}), %(C_{24:0} - C_{28:0})$, and $%C_{16:0}$ had negative loadings while those decreased by grazers (epiphytic Chl a, $%(C_{20:4}+C_{20:5})$, and $%C_{16:107}$) had positive loadings (Fig. 5A). PC1 was correlated positively to epiphytic Chl a and negatively to Zostera marina (Table 4). PC2 tended to separate variables according to predator effect; Z. marina biomass, total FA, %TOC, and %($C_{22:5} + C_{22:6}$) were decreased by predators and had positive PC2 loadings while %BrFA and %10me17:0br were increased by predators and had negative PC2 loadings (Fig. 5A). PC2 was positively correlated to Z. marina biomass and epiphytic Chl a (Table 4). Similar to PC loading results, PC scores separated treatments according to grazer and predator presence (Fig. 5B). Treatments with only grazers were generally negative on PC1 while those with only predators had more positive scores. Along PC2, caged control treatments had positive scores while grazer and predator treatments were more negative. The combined grazer and predator treatment was near zero on PC1 and PC2 in the absence of nutrients and negative on PC2 in the presence of nutrients. Since the scores of the grazer and predator treatment and the predator-only treatment were similar in the presence of nutrients it is likely that under eutrophic conditions predators were stronger determinants of SOM composition than grazers. Combined, our PCA results suggest that food web composition strongly

influences FA contributions from primary producers and that nutrient additions tended to shift the composition of the primary producer community towards a dominance of epiphytes and a loss of *Z. marina*.

DISCUSSION

Patterns of biomass distribution and accumulation in marine systems are well known to be influenced by both top-down and bottom-up forcing (Paine 1980, Menge 2000 and references therein, Borer et al. 2006). Since carbon storage, export, and deposition are related to biomass production (Duarte & Cebrian 1996, Cebrian 1999, Cebrian & Duarte 2001), top-down and bottom-up controls may extensively influence ecosystem properties and biogeochemical cycling. For example, increased deposition of plant-derived OM can stimulate sediment bacterial decomposition and, in turn, can affect dissolved inorganic nutrient pools and fluxes (Hansen & Blackburn 1992). The importance of understanding such feedbacks is necessary for effective conservation and management of sensitive coastal habitats (Cloern 2001, Duarte 2002). This experiment is one of the first to identify and quantify the effects of epibenthic community structure and nutrient availability on SOM composition in a natural seagrass bed.

Nutrient enrichment and SOM composition

Eutrophication is a central cause of many coastal ills including algal blooms and seagrass decline (Cloern 2001, Duarte 2002, Orth et al. 2006). Nutrient enrichment stimulates rapid growth of algae which may, in turn, increase light attenuation and shade seagrass (Short et al. 1995, Hughes et al. 2004 and references therein). Increased algal biomass has the potential to translate into higher rates of labile OM deposition to the sediments, if grazer controls are not sufficiently strong. Under low nutrient conditions most algal and epiphytic carbon is consumed or exported, leaving vascular plant material as a main constituent of SOM (Duarte & Cebrian 1996, Cebrian 1999). Since the availability of labile OM is an important determinant of decomposition rates, shifts in the proportion of algal versus vascular plant OM in the sediments may affect bacterial activity and remineralization processes (Hansen & Blackburn 1992, Boschker & Cappenberg 1998, Holmer et al. 2004). A goal of this experiment was to determine whether water column nutrient enrichment could precipitate changes in SOM composition and if these shifts were related to primary producer abundance and species composition.

In our experiment, nutrient enrichment stimulated an early increase in epiphytes $(p < 0.05, \omega^2 = 0.41, Douglass et al. 2007)$ which likely reduced light availability to *Zostera marina*, leading to a decline in its abundance (Fig. 1A, Table 2). By the end of the experiment, there was no evidence of a nutrient effect on epiphytes suggesting that grazer population growth and consumption effectively controlled the initial pulse (Douglass et al. 2007; Fig. 1B, Table 2). Strong grazing pressure on epiphytes may have resulted in a compensatory increase in *Z. marina* biomass had the experiment lasted more than four weeks. An alternative hypothesis, that nutrient enrichment increased the palatability of seagrass and, consequently, its susceptibility to grazing (McGlathery 1995), seems unlikely since we did not detect a statistical interaction between nutrients and grazers.

In the sediment, nutrient enrichment singularly and interactively affected OM contributions from benthic algae, epiphytes, and heterotrophic bacteria. Surprisingly, nutrients decreased SCFA (%($C_{12:0} + C_{14:0}$)), proxies for algal and microbial biomass (Fig. 3A, Table 2). OM contributions from benthic algae and epiphytes were influenced by interactions between nutrients and predators. Nutrient enrichment increased the abundance of LCFA (%($C_{24:0} - C_{28:0}$)), which correlated positively with benthic Chl *a* (Table 3), when predators were present (Fig. 3B, Table 2). In contrast, when predators were absent, nutrients increased %($C_{20:4} + C_{20:5}$) (Fig. 3C; Table 2), which was positively correlated with epiphytic Chl *a* (Table 3). Thus, strong nutrient and nutrient by predator interactions influenced the relative dominance of primary producer groups and, hence, their FA contributions to SOM.

Changes in OM delivery and composition stimulated responses by two functionally distinct groups of heterotrophic bacteria. Nutrient enrichment increased %10Me17:0, a FA in sulfate reducing bacteria (Dowling et al. 1986), but had no effect on %BrFA, biomarkers for heterotrophic bacteria (Fig. 4, Table 2). It is curious that nutrients did not elicit similar responses in both bacterial FA groups, however, BrFA and 10Me17:0 may reflect different communities of organisms. For instance, %BrFA was negatively related to epiphytic Chl *a* while %10Me17:0 correlated positively with benthic Chl *a* (Table 3). This suggests that bacteria represented by BrFA responded to early epiphytic OM deposition, which gradually decreased as grazer populations grew. As benthic Chl *a* became a proportionately greater source of labile SOM, sulfate reducing bacterial metabolism and production of 10Me17:0 likely increased. Higher rates of heterotrophic bacterial activity may have reduced sediment oxygen availability and

increased sulfide production, creating conditions which can be toxic to seagrass (Hemminga 1998, Calleja et al. 2007, Pérez et al. 2007). This is supported by the negative correlations between *Zostera marina* and both bacterial FA groups (Table 3). Consequently, nutrient availability may have indirectly affected seagrass survival by altering SOM composition, heterotrophic bacterial activity, and thus sediment oxidizing conditions.

In summary, our data suggest that increased nutrient availability altered the composition of above-ground primary producer communities, SOM composition, and sediment microbial communities (Canuel et al. 2007, Spivak et al. 2007). The rapid sediment heterotrophic community response to OM inputs may have implications for nutrient recycling and seagrass survivability.

Above-ground community structure and SOM composition

The ongoing depletion of commercially valuable predators from coastal habitats has broad implications for ecosystem functioning and nutrient cycling (Jackson et al. 2001, Scheffer et al. 2005, Halpern et al. 2006). Predator loss can lead to increased grazer biomass as well as more intense intraspecific competition which could affect grazer community composition (Shurin & Allen 2001, Duffy 2006). Subsequent shifts in grazer species richness and, hence, grazer food preferences may then cascade to alter plant species abundance and identity (Lubchenco 1978, Schmitz 2004). The deposition of plant and algal biomass to the sediments may alter SOM lability, which is a determinant of bacterial activity and an important food source for benthic communities (Boschker & Cappenberg 1998, Hansen & Blackburn 1992, Danovaro et al. 1999). A goal of this

experiment was to determine whether changes in food web structure indirectly affect SOM composition by altering primary producer biomass and its deposition to the sediments.

By the end of the experiment, predators decreased Zostera marina biomass, sediment TOC, and total FA abundance (Figs. 1, 2, Table 2). Unnatural confinement of predators may have contributed to Z. marina decline through crab destruction of the grass blades (Douglass et al. 2007). Loss of Z. marina corresponded with lower %TOC and total FA abundance, possibly due to lower effectiveness of the grass in trapping fine sediment and particulate OM (Fig. 2, Table 2). This is consistent with the positive correlation between Z. marina and total FA abundances (Table 3). In addition to decreasing Z. marina biomass and bulk SOM content, predators influenced SOM composition by decreasing labile OM from algal and microbial sources ($(C_{12:0} + C_{14:0})$ and $%(C_{22:5} + C_{22:6})$ and $%(C_{24:0} - C_{28:0})$ (non-nutrient treatments only; Fig. 3, Table 2). This was opposite to previous findings demonstrating the role of blue crabs in reducing grazers and increasing algal biomass in similar experiments (Duffy et al. 2005, Canuel et al. 2007, Spivak et al. 2007). Benthic microalgae were the likely source of LCFA (C24:0 - $C_{28:0}$), as suggested by positive correlations with benthic Chl *a*; LCFA were negatively correlated with epiphytic Chl a (Table 3). LCFA are the dominant FA in vascular plants but may also occur in microalgae at trace levels and have been identified in benthic diatoms (Volkman et al. 1980, Viso & Marty 1993), cyanobacterial mats (Edmunds & Eglinton 1984), and microalgae (Volkman et al. 1998 and references therein). Although predators decreased FAs representing algae and microbes in general, they increased FA specifically deriving from diatoms (e.g., higher ratio of $C_{20:5\omega3}$: $C_{22:6\omega3}$; Fig. 3, Table 2)

and, perhaps as a result, sediment heterotrophic bacterial FAs (%BrFA and %10Me17:0; Fig. 4, Table 2). The positive predator effect on %BrFA is consistent with previous seagrass mesocosm experiments (Canuel et al. 2007, Spivak et al. 2007) and suggests that the above-ground community's effects on primary producers can penetrate to influence sediment bacteria. Thus, food chain length could have important indirect effects on sediment bacterial processes such as OM decomposition and remineralization.

The grazer community influenced primary producer abundance and SOM content and composition. Grazers consumed epiphytes, reducing epiphytic Chl a and the abundance of FAs positively correlated to epiphytic Chl a (%($C_{20:4} + C_{20:5}$), $C_{16:1\omega7}$: $C_{16:0}$, and $C_{20:5\omega3}$: $C_{22:6\omega3}$) (Fig. 1, 3, Tables 2, 3). "Fresh" algae are generally the source of $(C_{20:4} + C_{20:5})$ (Canuel & Martens 1993) while diatom prevalence, relative to the microalgal community, is expressed by ratios of $C_{16:107}$: $C_{16:0}$ and $C_{20:503}$: $C_{22:603}$ (Budge & Parrish 1998, Shin et al. 2000). Although algal and microbial OM, sources of $(C_{12:0} + C_{12:0})$ $C_{14:0}$), and benthic algae, a source of $(C_{24:0} - C_{28:0})$ (Table 3), were potential food sources, abundances of these FA groups increased in grazer-only treatments. This suggests that grazers selectively consumed other food sources, likely epiphytes, allowing OM sources of $%(C_{12:0} + C_{14:0})$ and $%(C_{24:0} - C_{28:0})$ to accumulate. Thus, grazers likely reduced the relative contributions of epiphytic FAs to the sediments but increased the relative OM contributions from the microphytobenthos. The importance of grazers in mediating seagrass ecosystem properties is well recognized (reviewed by Valentine & Duffy 2006). Our field results confirm previous findings from mesocosm experiments (Canuel et al. 2007, Spivak et al. 2007) that grazers influence SOM quality and lability and that these impacts indirectly influence bacterial community composition and activity.

The importance of the above-ground animal community in determining primary producer biomass and SOM content and composition is summarized by the PCA results (Fig. 5). In the absence of nutrients, PC1 separated treatments according to predator or grazer presence, as treatments with crabs only had positive scores while those with grazers only had negative scores (Fig. 5B). Thus, response variables that grazers increased (%TN, %($C_{12:0} + C_{14:0}$), and %($C_{24:0} - C_{28:0}$)) and predators decreased (*Z. marina* biomass, total FA, %TOC, %($C_{22:5} + C_{22:6}$)) had negative PC1 loadings (Fig. 5A). The addition of nutrients shifted grazer, predator, and control treatment scores to more positive values for PC1, which appeared to be related to increased abundance of epiphytes as epiphytic Chl *a* and PC1 were positively correlated (Table 4).

PC2 separated the scores of caged control treatments from those of grazers and/or predators. Consequently variables that were higher in the absence of grazers and predators (epiphytic Chl *a*, total FA, $%(C_{22:5} + C_{22:6})$, and $%(C_{20:4} + C_{20:5})$) had positive PC2 loadings. PC1 and PC2 regressed positively with epiphytic Chl *a* (Table 4), indicating that epiphytes were most abundant in the absence of animals or when predators controlled grazing effects. This is supported by the positive loadings of epiphytic Chl *a* and $%(C_{20:4} + C_{20:5})$ on PC1 and PC2 (Fig. 5). *Z. marina* regressed negatively with PC1 and positively with PC2, likely because of the strong negative effects of predators on plant biomass (Table 4). These results confirm the patterns shown by the individual FA classes that the presence and composition of above-ground communities were strong determinants of SOM content.

Interactive effects of nutrients and trophic structure on SOM composition

Coastal habitats are often impacted by multiple stressors, including commercial fishing and nutrient pollution, that alter seagrass food web structure and nutrient cycling (Cloern 2001, Duarte 2002, Orth et al. 2006). Previous studies have addressed top-down and bottom-up controls on biomass accumulation and seagrass productivity (Hughes et al. 2004, reviewed by Valentine and Duffy 2006). Our study is novel in addressing the potential impacts of these interactions on sediment biogeochemistry, as detected in SOM accumulation and composition.

Interactions between grazers and predators altered abundances of FAs derived from epiphytic and benthic microalgae. In the absence of predators, grazers consumed epiphytes and reduced accumulation of FA from epiphytic diatoms (%($C_{20:4} + C_{20:5}$) and $C_{20:563}$: $C_{22:663}$; Fig. 3, Table 3), while increasing the abundance of %SCFA (%($C_{12:0} + C_{14:0}$); Fig. 3). Accumulation of FA from epiphytic diatoms in predator treatments is consistent with crabs suppressing or inhibiting grazers, creating a trophic cascade (Douglass et al. 2007). In contrast, predators reduced %($C_{22:5} + C_{22:6}$); these FA are dominant in dinoflagellates and microalgae other than diatoms (Budge & Parrish 1998 and references therein). Interactions between nutrients and predators also affected OM contributions from epiphytes and benthic microalgae. Nutrient enrichment increased FAs associated with epiphytes (%($C_{20:4} + C_{20:5}$)) in the absence of predators and increased FAs from benthic microalgae (%($C_{24:0} - C_{28:0}$)) in the presence of predators (Fig. 3, Table 3). Combined, these data suggest that interactions between grazers, predators, and basal resources influenced algae differentially with subsequent effects on SOM composition.

Largely, our results support the premise that grazer communities benefit seagrass by reducing algal biomass and that epiphytes and *Zostera marina* are equally important in

a tri-trophic system. Nutrient enrichment shifted the PC1 scores indicating that nutrients increase epiphytes and decrease *Z. marina* biomass despite the presence of a grazer assemblage (Fig. 5, Table 4). Since the PC scores of the predator only and the combined grazer and predator treatments were similar, predators may more strongly influence SOM composition than grazers under elevated nutrient conditions and the short timescale of our experiments. Overall, our data demonstrate that interactions between grazers, predators, and nutrients strongly influence the primary producer community, its contributions to the sediments and the sediment microbial responses.

Inter-experimental comparisons

Previous experiments in this system have varied food web composition and light levels using mesocosms (Canuel et al. 2007, Spivak et al. 2007). The value of results from these experiments depends in part on how accurately the system mimics the natural environment. Here, we briefly compare the results from this field experiment with the mesocosms. In both the present field experiment and a previous mesocosm experiment (Canuel et al. 2007), grazer presence and richness, respectively, increased algal and microbial contributions to SOM. Predators decreased "fresh" OM, represented by polyunsaturated FA (e.g., %(C_{18:4} + C_{20:4} + C_{20:5} + C_{22:5} + C_{22:6}) in Spivak et al. (2007) and by %(C_{22:5} + C_{22:6}) here). Shading (Spivak et al. 2007) and nutrients (this study) decreased *Zostera marina* biomass and SOM deriving from algae and microbes (C_{12:0} + C_{14:0}). Finally, in all three experiments, predators increased the abundance of sediment heterotrophic bacteria (%BrFA). The general similarities between this and previous experiments are encouraging and suggest that conditions in the mesocosms reflected the natural environment in important ways.

Overall, our results demonstrate that SOM composition reflected changes in the abundance and composition of the primary producer community precipitated by shifts in trophic structure and resource availability. Nutrients increased epiphytes early in the experiment leading to a decline in Zostera marina (Fig. 1). Grazer populations responded rapidly to the available algae, decreasing epiphytes (Fig. 1) and their contribution of representative FAs in the sediments ($((C_{20:4} + C_{20:5}), C_{20:5\omega3} : C_{22:6\omega3}, C_{16:1\omega7} : C_{16:0}; Fig.$ 3).Grazer control of algae did not increase Z. marina abundance, however, perhaps due to the short timeframe of the experiments. Predators reduced Z. marina and evidently its ability to trap particulate OM, leading to lower sediment organic carbon content and total FA abundance (Figs. 1, 2). There was some evidence of a trophic cascade as FA contributions from epiphytes (%($C_{20:4} + C_{20:5}$)) and diatoms ($C_{20:5\omega3} : C_{22:6\omega3}$) were higher in treatments with both grazers and predators than in treatments with grazers only (Fig. 3). In addition, predators increased diatom derived OM which may have stimulated sediment heterotrophic bacteria (%BrFA) in general and sulfate reducing bacteria (%10Me17:0) in particular (Fig. 4). The sensitivity of SOM composition to nutrient availability and food web structure suggest that sediment biogeochemistry is strongly influenced by both top-down and bottom-up controls. Further, the changes in SOM composition demonstrate that episodic shifts in community composition and resource availability can rapidly influence sediment processes and ecosystem functioning.

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Table 1. Average concentration (μ M) of water column nutrients sampled on days 14 and 23 of the experiment when OsmocoteTM additions were 400 g per treatment. Concentrations were higher in nutrient vs. non-nutrient treatments (p < 0.001).

Response	Nut	rients	No Nutrients				
	Day 14	Day 23	Day 14	Day 23			
$NO_2 + NO_3$	5.55	6.31	0.11	0.29			
NH4 ⁺	4.98	8.45	0.69	2.28			
PO ₄ ⁻³	0.27	0.57	0.01	0.09			

Table 2. Tests of significance and estimated magnitudes of effect (ω^2) for nutrient availability, predator presence, grazer presence, and their interactions on plant biomass, sediment total nitrogen, sediment organic carbon, and sediment fatty acid abundance. Except where noted, analyses were performed on un-transformed data. When an interaction between nutrients and predators or grazers was significant, the data set was divided according to the interaction (i.e., nutrients vs. no nutrients), and an analysis of variance was performed again. For interactive effects: G, grazers; P, predators; N, nutrients. MS refers to the mean squared. Significant relationships (p < 0.05) are in bold.

Response	n e name e proporte no maneror	Nutrients		P	Predators		nana mananini katarina dina dalamini in	Grazers			Interactions			Ептог	
· · ·	MS	р	ω ²	MS	р	ω ²	MS	p	ω²		MS	р	ω ²	MS	ω²
Zostera marina (AFDM)	3.76	0.001	0.21	1.79	0.017	0.09	0.68	0.128	0.02					0.27	0.65
In Epiphytic Chl a	0.10	0.468	0.00	0.48	0.119	0.02	5.93	<0.001	0.43					0.18	0.55
Benthic Chl a	0.06	0.380	0.00	0.17	0.152	0.03	0.00	0.987	0.00					0.08	1.08
%TN	0.00	0.628	0.00	0.00	0.279	0.01	0.00	0.022	0.12					0.00	0.95
%TOC	0.00	0.875	0.00	0.11	0.032	0.10	0.05	0.152	0.03					0.02	0.94
Total FA (µg g ⁻¹)	1.62	0.898	0.00	664.03	0.014	0.14	12.91	0.717	0.00					96.10	0.92
%(C _{12:0} +C _{14:0})	1.81	0.014	0.11	1.52	0.024	0.09	1.45	0.026	0.08	G*P	2.38	0.006	0.15	0.26	0.72
%C _{16:0}	0.03	0.909	0.00	0.74	0.569	0.00	20.81	0.005	0.17					2.22	0.80
%C _{18:0}	1.07	0.164	0.03	2.45	0.040	0.09	0.42	0.380	0.00					0.52	0.96
%(C _{24:0} -C _{28:0})	1.00	0.454	0.00	3.33	0.177	0.02	14.04	0.009	0.13	N*P	9.76	0.025	0.09	1.72	0.75
No Nutrients				12.78	0.014	0.20	12.32	0.015	0.19					1.58	0.56
Nutrients				0.81	0.523	0.00	3.33	0.207	0.04					1.87	1.02
%(C _{18:2} +C _{18:3})	0.01	0.901	0.00	0.04	0.738	0.00	0.49	0.267	0.01					0.68	1.04
$(C_{20:4}+C_{20:5})$	0.22	0.713	0.00	0.77	0.494	0.00	10.58	0.017	0.09	N*P	22.14	0.001	0.21	1.60	0.64
				•						G*P	11.81	0.012	0.10		
No Nutrients				16.27	0.002	0.31	4.70	0.064	0.07	G*P	8.02	0.020	0.14	1.15	0.47
Nutrients				7.03	0.092	0.09	5.89	0.120	0.07					2.10	0.80
%(C _{22:5} +C _{22:6})	0.00	0.970	0.00	2.88	0.010	0.14	0.14	0.542	0.00	G*P	1.90	0.032	0.08	0.37	0.81
%(C _{16:107})	3.92	0.608	0.00	0.51	0.852	0.00	126.60	0.007	0.18					14.50	0.91
C _{16:107} : C _{16:0}	0.02	0.526	0.00	0.01	0.756	0.00	0.65	0.002	0.23					0.05	0.85
C _{20:503} : C _{22:603}	4.41	0.291	0.00	96.83	<0.001	0.26	78.98	<0.001	0.21	G*P	43.23	0.002	0.11	3.78	0.42
arcsine (sqrt(%BrFA))*	0.00	0.323	0.01	0.01	0.043	0.09	0.00	0.343	0.00					0.00	0.97
%10me17:0	0.31	0.007	0.17	0.30	0.008	0.16	0.01	0.698	0.00		•			0.04	0.90

* %BrFA (Σ iso-, anteiso- C_{13.0}, C_{15.0}, C_{17.0}, C_{19.0})

Response	Zostera marina			I	Benthic Chl	a	E	Total		
	Coefficient Partial r ² *		р	Coeffici	ent Partial r	² * p	Coefficient Partial r ² * p			Model r ²
%TN	0.01	0.09	0.106	-0.01	0.01	0.691	0.00	0.01	0.515	0.11
%TOC	0.07	0.08	0.128	0.04	0.00	0.720	0.01	0.00	0.810	0.08
Total FA (µg g ⁻¹)	6.09	0.15	0.027	-1.02	0.00	0.886	4.34	0.06	0.145	0.21
%(C _{12:0} +C _{14:0})	0.23	0.05	0.209	0.29	0.01	0.552	-0.37	0.10	0.072	0.15
%C _{16:0}	0.40	0.02	0.376	-0.18	0.00	0.879	-0.96	0.11	0.060	0.13
%C _{18:0}	0.37	0.09	0.092	0.18	0.00	0.750	0.01	0.00	0.962	0.10
%(C _{24:0} -C _{28:0})	0.29	0.01	0.444	2.81	0.17	0.010	-1.18	0.18	0.009	0.36
%(C _{20:4} +C _{20:5})	-0.29	0.01	0.486	-2.59	0.13	0.027	1.18	0.16	0.015	0.31
%(C _{22:5} +C _{22:6})	0.26	0.06	0.173	-0.18	0.00	0.726	0.14	0.02	0.495	0.08
arcsine (sqrt(%BrFA)) [†]	-0.03	0.22	0.003	0.04	0.05	0.135	-0.04	0.25	0.002	0.52
%10me17:0br	-0.22	0.40	<0.001	0.28	0.08	0.048	-0.11	0.07	0.063	0.56
%(C _{16:1007})	-0.43	0.00	0.669	-3.32	0.04	0.225	3.38	0.24	0.005	0.28
C _{16:107} : C _{16:0}	-0.05	0.02	0.385	-0.15	0.02	0.383	0.22	0.24	0.004	0.28
$C_{20:503}: C_{22:603}$	-0.44	0.01	0.600	-5.24	0.14	0.025	2.05	0.13	0.032	0.28

Table 3. Regression analyses of *Zostera marina* (ash-free dry mass, g), benthic Chla (μ g cm⁻²), and epiphytic Chla (μ g cm⁻² blade area) against bulk SOM and the fatty acid groups (expressed as % of total FA). Signifcant relationships (p < 0.05) are in bold.

*Partial r^2 values were calculated by dividing the type III SS by the total SS.

[†] %BrFA (Σ iso-, anteiso- $C_{13:0}$, $C_{15:0}$, $C_{17:0}$, $C_{19:0}$)

Response Zostera marina				Ben	thic Chl a	!	Epi	Total		
	Coefficient	Partial r ²	* p	Coefficient Partial r ² * p			Coefficient	Model r		
PC 1	-1.30	0.17	0.004	-1.38	0.03	0.225	1.49	0.19	0.003	0.39
PC 2	1.65	0.34	<0.001	-1.67	0.05	0.086	1.77	0.32	<0.001	0.70

Table 4. Regression analyses of *Zostera marina* (ash-free dry mass, g), benthic Chl a (µg cm⁻²), and epiphytic Chl a (µg cm⁻²) blade area) against principal components 1 and 2. Significant values (p < 0.05) are in bold.

* Partial r^2 values were caculated by dividing the type III SS by the total SS.

FIGURE CAPTIONS

Figure 1. Effects of nutrients, predators, and grazers on *Zostera marina* (A), epiphytic Chl *a* (B), and benthic Chl *a* (C). The presence of cages reduced the abundances of all three primary producers. Nutrients and predators reduced *Z. marina* abundance while grazers reduced epiphytic Chl *a*. For Figures 1-4, statistical results are reported in Table 2, error bars represent standard error, and a letter in upper right hand corner designates which treatment significantly affected the response variable.

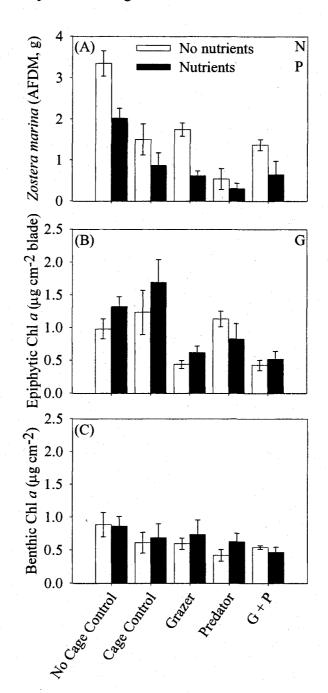
Figure 2. Effects of nutrients, predators, and grazers on sediment organic carbon (%TOC;A), sediment nitrogen (%TN; B), and sediment total fatty acid (FA) abundance (C).Predators decreased %TOC and total FA while grazers increased %TN. Nutrientenrichment did not affect %TOC, %TN, nor Total FA.

Figure 3. (A-D) Effects of nutrients, predators, and grazers on fatty acid subclasses (expressed as % of total FA) representing algal and microbial sources of organic matter (OM). Nutrients, predators, and grazers had strong singular and interactive effects on algal and microbial contributions to the sediments. (E-F) The prevalence of OM deriving from diatoms, relative to other microalgae, was influenced by grazers and predators only. See text for biomarker sources.

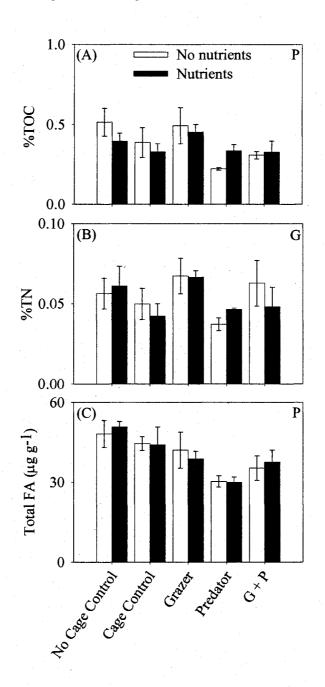
Figure 4. Effects of nutrients, predators, and grazers on the abundance of sediment heterotrophic bacterial fatty acids (expressed as % of total FA). The presence of cages increased abundances of %BrFA (A; Σ (iso-, anteiso- C_{13:0} + C_{15:0} + C_{17:0} + C_{19:0})) and

%10Me17:0 (B). Both %BrFA and %10Me17:0 were increased by predators but only %10Me17:0 was increased by nutrients.

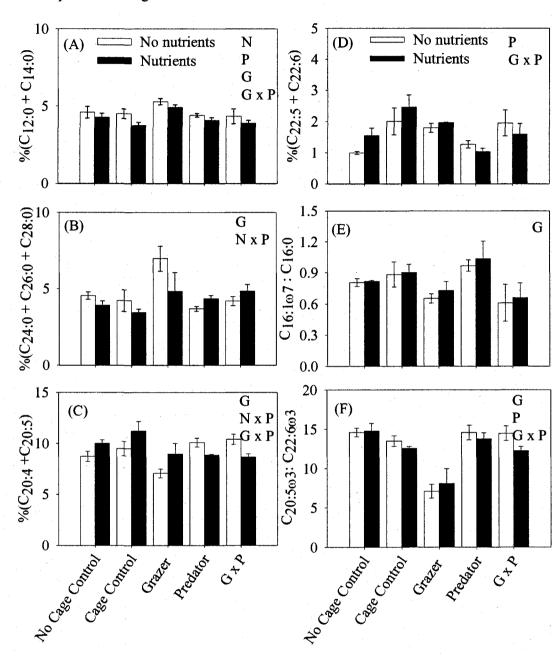
Figure. 5. Loadings (A) and score plots (B) from principal component analysis (PCA) for primary producers, sediment organic carbon, sediment nitrogen, and sediment fatty acid (FA) groups. In (A), the following abbreviations were used: TFA for total FA, E Chl a for epiphytic Chl *a*, and B Chl a for benthic Chl *a*. In (B), treatments are indicated as follows: nutrients by +N, no nutrients by –N, caged control by CC, grazers by G, predators by P, and combined grazers and predators by GP. Table 4 lists correlations between PC1, PC2, and the primary producers. Error bars represent standard error.



Spivak et al . Fig. 1

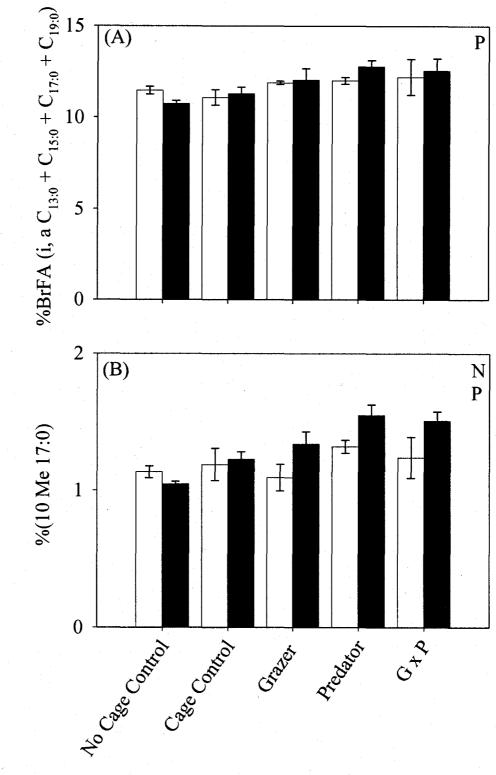


Spivak et al. Fig. 2

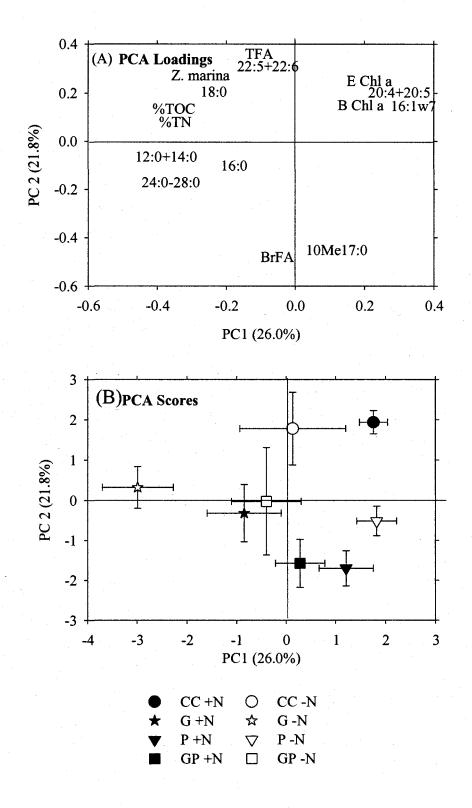


Spivak et al. Fig. 3

Spivak et al. Fig. 4



Spivak et al. Fig. 5



Chapter 4:

Nutrient enrichment and food web composition affect ecosystem metabolism in an experimental seagrass habitat.

Amanda C. Spivak, Elizabeth A. Canuel, J. Emmett Duffy, and J. Paul Richardson

Abstract.

In seagrass habitats, both bottom-up and top-down controls can influence biomass accumulation within the food web, sediment biogeochemistry, and ecosystem productivity. However it is unclear how changes in above-ground biomass and sediment organic matter quality precipitated by such shifts in bottom-up and top-down forcings also translate to changes in basic elemental cycles and fluxes. Using an experimental seagrass mesocosm system, we manipulated water column nutrient concentrations, food chain length (i.e. predator presence vs. absence), and grazer species richness (0, 1, 3, or 5)species) in a factorial design to address two main questions: (1) how do nutrient availability and food web composition affect the biomasses and stoichiometry of primary producers and grazers; (2) to what extent does ecosystem metabolism (productivity and nutrient fluxes) reflect above-ground plant and animal abundances vs. bulk sediment organic matter quality? Surprisingly, by the conclusion of the five week experiment, nutrient enrichment strongly increased secondary production but had little effect on primary production. Although the biomass of the dominant amphipod grazer, Gammarus *mucronatus*, was higher in nutrient enriched treatments it was not clear whether this effect was due to higher food availability or quality. Changes in above-ground primary producer biomass mediated by nutrient enrichment and grazer presence showed similar patterns to those of gross ecosystem production (mmol $O_2 \text{ m}^{-2} \text{ d}^{-1}$). Conversely, daily inorganic nutrient flux rates were unrelated to the biomasses of primary producers or grazers, suggesting that microbial processes in the sediments may have contributed to the observed fluxes. Combined, our data suggest that complex interactions between bottomup and top-down controls governed patterns of nutrient storage and cycling.

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Introduction.

Interactions between bottom-up influences of resource availability and top-down influences of trophic structure have important impacts on community dynamics and ecosystem functioning. For instance, nutrient enrichment of coastal waters often leads to higher abundances of algae, reduced water clarity, and, potentially, seagrass loss (McGlathery 1995; Cloern 2001; Orth et al. 2006). Conversely, top-down controls in a three-level food chain (i.e. predators – grazers – autotrophs) may moderate the effects of nutrient enrichment. For example, in seagrass systems, nutrient impacts may be exacerbated by predator inhibition of grazers or alleviated by strong grazing controls on algae (Hughes et al. 2004; Duffy et al. 2005; Heck and Valentine 2006). By extension, shifts in the relative importance of bottom-up and top-down forcings that influence the standing stocks and elemental content of primary producers and animals may also alter nutrient dynamics and, hence, energy availability to the food web (Vanni and Layne 1997; Elser and Urabe 1999). Here, we tested experimentally whether nutrient availability (i.e. bottom-up control) and food web composition (i.e. top-down control) interactively influenced plant and animal biomass and stoichiometric ratios and whether these changes were reflected by changes in ecosystem metabolism in an experimental seagrass habitat.

In seagrass beds, invertebrate grazers serve as the key intermediate trophic link between primary producers and higher levels of the food web (Klumpp et al. 1989). Consequently, the abundance and efficacy of invertebrate grazers may be affected by changes in either bottom-up or top-down controls. For instance, higher rates of primary production and, hence food availability, may lead to increased grazer biomass or grazer-

mediated nutrient recycling. In turn, grazers may fuel primary production by regenerating dissolved inorganic nutrients (Urabe 1993; Elser and Urabe 1999; Liess and Hillebrand 2006; Vanni et al. 2006). Whereas bottom-up controls tend to be strengthened by excess nutrients, trophic cascades are weakened by predator removal. For example fishing of predators may reduce predation pressure on grazers and increase grazer population growth. At high abundances or densities, grazers may be able to control algal growth stimulated by bottom-up controls (Hughes et al. 2004; Armitage et al. 2005; Heck and Valentine 2007). By reducing algal biomass, grazers can indirectly benefit seagrasses which are competitively inferior to fast-growing algae. Thus, interactions between changing bottom-up and top-down trophic controls may strongly affect community composition and ecosystem properties.

Resource availability and consumption (bottom-up and top-down controls, respectively) not only affect biomass distribution across trophic levels but also the stoichiometry of primary producers and rates of nutrient cycling. For instance, increased supply of nitrogen and phosphorous can increase the internal elemental content of primary producers, especially algae (Sterner and Elser 2002). When grazers consume the nutritionally rich algae they incorporate nutrients needed for growth and metabolism and excrete the unused elements (Elser and Urabe 1999; Sterner and Elser 2002; Anderson et al. 2005). Consuming food of higher quality may increase grazer fitness and population growth (Elser et al. 1996; Mackay and Elser 1998). By excreting the excess nutrients back into the water column, grazers can influence algal production and community composition (Sterner and Elser 2002; Vanni et al. 2002). Top-down controls, while less straightforward than bottom-up effects, can strongly alter community composition via

stoichiometric shifts (Vanni et al. 1997; Elser et al. 1998; Frost et al. 2002) as well as the more obvious effects of changing prey abundance. Thus, changing bottom-up and topdown controls can affect both plant and animal abundance and elemental cycling.

While nutrient cycling within the water column can be affected by stoichiometric imbalances between primary producers and grazers, sediment nutrient fluxes can also be strongly influenced by the stoichiometry of deposited organic matter. For example, increased resource availability may increase the abundance and nutrient content of primary producers which may then be deposited to the sediments. Since sediment organic matter (SOM) quality and lability are partial determinants of sediment microbial activity, increased algal contributions may result in higher rates of sediment remineralization. However, not all of the remineralized nutrients will be returned to the water column as sediment bacteria may retain nutrients to maintain optimum stoichiometric balance (Elser et al. 1995). Alternatively, high rates of organic matter deposition may stimulate microbial activity leading to sediment anoxia and, consequently, nitrate influx (denitrification) and carbon burial (Hessen et al. 2004; Dahllof and Karle 2005). Further, when sediments are aerobic, phosphate is chemically bound and biologically unavailable but as anoxic conditions develop phosphate is desorbed and may by released to the overlying water column (Valiela 1995). Thus, depending on the quantity and quality of organic matter delivered to the benthos, sediments may be a source or a sink of inorganic nutrients.

Previous seagrass experiments demonstrated that resource availability and food chain length can influence above-ground biomass distribution between trophic levels (Duffy et al. 2001; Duffy et al. 2003; Douglass et al. 2007), SOM composition and

quality (Canuel et al. 2007), and gross ecosystem productivity (Spivak et al. 2007). But it remains unclear how these effects translate into changed ecosystem process rates. To assess the effects of resource availability and food web structure on seagrass ecosystem properties and fluxes, we conducted an experimental manipulation of water column nutrient enrichment and food web composition (i.e. food chain length and herbivore species richness) and measured their effects on above-ground biomass, stoichiometric ratios, and ecosystem metabolism. We predicted that nutrient enrichment would increase plant and algal biomass and this would lead to higher rates of gross ecosystem production. In turn, nutrient enrichment would increase the quality of plant and algal derived organic matter deposited to the sediments, thereby increasing sediment microbial activity, leading to higher rates of sediment dissolved inorganic nitrogen (DIN) flux. Secondly, we expected that grazers would reduce algal abundance and recycle the consumed biomass back into the water column as DIN. Finally, we predicted that predators would initiate a trophic cascade by reducing grazers and indirectly increasing primary producer abundance. The increased plant and algal biomass would, in turn, increase gross ecosystem production, sediment organic matter quality, and sediment DIN flux.

Methods

Experimental Design.

We conducted a mesocosm experiment to determine the main and interactive effects of nutrient availability, grazer species richness, and food chain length on the accumulation of primary producer and grazer biomass, flux rates of dissolved oxygen and inorganic nutrients, and the elemental ratios of seagrass, algae, and invertebrate grazers. Water column nutrient availability was manipulated by adding OsmocoteTM (N:P:K 3:1:2) fertilizer to half of the tanks. Grazer species richness varied across four levels (0, 1, 3, or 5 species); the highest richness level contained five amphipod species present in the York River, Virginia, at the time of the experiment, each replicate of the intermediate level contained random a combination of three species, and the lowest richness level only had the most abundant species, *Gammarus mucronatus*. The remaining four grazer taxa were: *Elasmopus levis*, *Melita nitida*, *Ampithoe valida*, and *Sympleustes* spp. Food chain length was manipulated by exposing parallel sets of grazer treatments to a generalist predator, the blue crab, *Callinectes sapidus*. The 16 treatments were replicated 3 times each for a total of 48 mesocosm tanks.

The outdoor mesocosm experiment was conducted over five weeks during summer 2006 in 120-liter translucent fiberglass tanks that were continuously supplied with water from the York River estuary, Virginia, USA. Water passed through a sand filter and then through 150 μ m mesh before filling 'dump buckets' which regularly spilled into the tanks, providing turbulence and aeration. The filtering process eliminated larger animals and debris and minimized invasion by non-target animals while permitting passage of invertebrate larvae and algal spores, which often colonized the tanks. The tanks were filled with a sand – mud mixture (9:2), averaging 0.80% (\pm 0.18 SE) organic matter content, to a depth of 10 cm. In contrast with previous experiments (Canuel et al. 2007; Spivak et al. 2007), we chose to use a sediment substrate with approximately 1% OM to facilitate *Zostera marina* transplant success and growth (Koch 2001). One hundred pre-weighed eelgrass (*Zostera marina*) shoots, cleaned of grazers and epiphytes

were planted in each tank. Sixteen days later, grazing invertebrates were added to each grazer mesocosm. The five-species treatment received 18 individuals of each species, the three-species treatment had 30 individuals of each species, and the one-species treatment had 90 individuals of *G. mucronatus*. Eleven days later, two juvenile blue crabs were added to each predator treatment. Each nutrient treatment received 200 g of OsmocoteTM slow release fertilizer in the first two weeks of the experiment and 100 g every week thereafter. Preliminary experiments revealed that OsmocoteTM additions resulted in a peak in dissolved inorganic nitrogen (DIN) concentrations within 24 h. After this, DIN levels declined and remained constant for the next four days before dropping again. Thus, we refreshed half the fertilizer additions twice weekly to maintain elevated and constant nutrient levels.

Nutrients were delivered through two perforated PVC tubes that were suspended from the top of the tanks. Twice a week, one nutrient PVC tube from each nutrient treatment was refreshed with new fertilizer. Water column nutrient concentrations were monitored each week by measuring NH₄⁺ concentrations from five randomly chosen tanks of each nutrient treatment using the Koroleff colorimetric method. The five week experimental incubation time was chosen to minimize the risk of invasion by non-target animals and to prevent the complete consumption of eelgrass by the grazers. This time period permitted major changes in animal (one to two grazer generations) and plant community development and in surface sediment characteristics (Duffy et al. 2003; Canuel et al. 2007; Spivak et al. 2007). Despite limitations, this experimental infrastructure simulated several aspects of the biotic and abiotic field conditions well (Duffy et al. 2001). For instance, tank water averaged 25°C while water temperatures at

Goodwin Island archipelago, the system upon which this experiment was based, averaged 23° C (Moore unpubl. data). At the end of the five week experiment we measured whole ecosystem fluxes of dissolved oxygen (DO), NH₄⁺, NO_x, and PO₄⁻³, as well as primary producer biomass and the carbon and nitrogen ratios of sediments, primary producers, and invertebrate grazers (see below). Results for the aboveground plant and animal community and for SOM accumulation and composition are reported elsewhere (Duffy et al. in prep; Spivak et al. in prep).

Primary producers.

At the end of the experiment we collected above-ground seagrass blades, macroalgae, artificial seagrass blades for epiphytic chlorophyll *a* (Chl *a*), and sediments for benthic Chl *a* to determine primary producer biomasses. Because the tanks were a flow-through system, we did not measure phytoplankton abundance. Seagrass and algae were frozen (-20 °C) until analysis when they were dried (60 °C) and then combusted (400 °C) to determine ash-free dry mass (AFDM). Epiphytic chlorophyll *a* was extracted from the artificial seagrass blades in a 90:10 (v:v) acetone : methanol solution for 24 h at -20 °C. Samples were processed according to Douglass et al. (2007). For benthic Chl *a*, three sediment cores (1.5 cm diameter) were collected from each tank and the upper 1 cm was removed. The surface sediments from the three cores were combined in a precombusted (450 °C) scintillation vial. Sediment samples were frozen (-20 °C) and analyzed within six weeks of collection according to (Neubauer et al. 2000). Since benthic microalgal distribution can be patchy, we used composite samples to increase the

likelihood that the benthic Chl *a* concentrations represented the entire surface sediments in the mesocosm tanks.

Grazers.

Invertebrate grazers were collected at the end of the experiment and stored in ethanol. Sub-samples were analyzed for grazer species identity, abundance, and size class. Grazer ash-free dry mass (AFDM) was determined using previously established calculations (Edgar 1990).

Ecosystem metabolism.

We measured fluxes of dissolved oxygen (DO), NH_4^+ , NO_x , and PO_4^{-3} to characterize whole-ecosystem metabolism. Four days before the end of the experiment, we measured DO and sampled water (25 mL) for dissolved inorganic nutrient concentrations approximately every hour over two four-hour incubation periods, one during the day (10:00 – 14:00 h) and another at night (22:00 – 02:00 h). Flux rates were estimated by regressing dissolved nutrient concentration against elapsed time (see below).

Half of the OsmocoteTM fertilizer in the nutrient treatments was refreshed three days (50 g) and half was refreshed one week (50 g) prior to measuring water column flux rates. We estimated that the NH_4^+ loading rate from the fertilizer at the time of the flux measurement incubations was 0.24 μ M h⁻¹. Immediately prior to the incubation period, the water supply was shut off and clear plastic sheeting (2 mm thickness) was placed on the water's surface to minimize oxygen exchange with the atmosphere. Before each measurement, the water was stirred to disrupt any stratification that may have formed. DO concentrations were measured using a YSI datasonde. Water samples were filtered through a pre-combusted (450 °C) glass fiber filter and frozen (-20° C) until analysis for NH_4^+ , NO_x , and PO_4^{-3} concentrations by standard methods using a Lachat auto-analyzer (Smith and Bogren 2001; Knepel and Bogren 2002; Liao 2002).

We calculated the slope of change in concentration versus the time elapsed and divided this by the area of the tank to obtain flux. Because the measured DIN and PO₄⁻³ flux rates were much higher than the dissolution rate of OsmocoteTM, we are confident that our flux rates reflect biological processes within the experimental tanks. Hourly day and night rates were scaled to the volume of the mesocosm tanks (120 l) and to 14 h of light and 10 h of darkness to estimate daily summertime gross ecosystem production (GEP) of dissolved oxygen and daily net flux rates of inorganic nitrogen and phosphorus. DIN concentrations were calculated by summing NH₄⁺ and NO_x. To calculate respiration, hourly nighttime oxygen consumption were scaled to 24 h and converted to carbon units using an assumed respiratory coefficient (RQ) of 1.0 (Hopkinson and Smith 2005; Middelburg et al. 2005). The production to respiration (P:R) was calculated by dividing estimated gross ecosystem production by respiration.

Elemental composition of primary producers, grazers, and sediments.

At the end of the experiment we collected seagrass blades, macroalgae, grazers, and sediments from each mesocosm to assess the effects of water column nutrient enrichment on their elemental composition. Twenty individuals each of the amphipods G. *mucronatus* and A. valida were collected from the treatments in which they were originally stocked. Three sediment cores (2.6 cm diameter) were collected from each tank and the top 1 cm was removed. The surface sediments from each core were combined into a composite sample. All samples were stored in separate pre-combusted (450 °C) vials and stored at -20 °C until analysis for total organic carbon (TOC) and total nitrogen (TN) content by standard methods with a Fisons Flash Elemental Analyzer (Model 1112) after removing inorganic carbon (Hedges and Stern 1984). We used acetanilide as the standard. Molar elemental ratios were calculated by first normalizing TOC and TN to the molar weight of carbon and nitrogen, respectively, and then dividing molar TOC by molar TN. We did not measure the phosphorus content of the sediments.

Statistical analyses.

The results were analyzed as a fully factorial three-way analysis of variance (ANOVA, SAS version 9.1 for Windows), with grazer treatment (df = 3), food chain length (i.e. predator presence or absence, df = 1) and nutrient availability (df = 1) as fixed factors. Data were logarithmically transformed as necessary to maintain homogeneity of variance as determined by the Cochran's C test. From the ANOVAs, we calculated the magnitude of main and interactive effects (ω^2 , estimated proportion of variance explained by the experimental variable). The analyses included three replicates of every treatment except for the no nutrient, no crab, one grazer species treatment. One replicate of this treatment was excluded because it was contaminated by more than 500 mg of ash-free dry mass of non-target grazers. One additional sample was excluded from analyses of *Z. marina* and macroalgal biomass (nutrient, no crab, five grazers) while four samples were excluded from analysis of grazer biomass (no nutrients, no crabs, five

grazers; nutrients, no crabs, five grazers; nutrients, crabs, one grazer; nutrients, crabs, three grazers) due to sample loss. Thus, we report the type III sum of squares (SS) results from the ANOVA model.

To help interpret the drivers of ecosystem flux rates, we performed multiple linear regressions of daily GEP, daily respiration, and daily fluxes of DIN and PO_4^{-3} against the abundances of the major primary producers. To detect correlations between the flux rates, we performed a multiple linear regression of daily GEP against daily DIN and PO_4^{-3} . Simple linear regressions of daily GEP, daily respiration, and daily flux rates of DIN and PO_4^{-3} . Simple linear regressions of daily GEP, daily respiration, and daily flux rates of DIN and PO_4^{-3} against sediment C:N were also performed. In addition, to understand whether respiration was related to autochthonous organic matter production or bulk sediment organic matter quality, we regressed respiration against net ecosystem production and sediment C:N.

Results

Nutrient concentrations.

During the first two weeks 200 g of OsmocoteTM fertilizer were added to each nutrient treatment, resulting in an average NH₄⁺concentration of 29.23 μ M (± 5.45 SE). OsmocoteTM additions were reduced to 100 g per nutrient treatment for the remaining three weeks and the average NH₄⁺concentration fell to 14.37 μ M (± 1.32 SE). Concentrations of NH₄⁺ were 0.95 μ M (± 0.25 SE) and 2.58 μ M (± 0.57 SE) in the nonnutrient treatments during weeks 1-2 and 3-5, respectively. Thus, the NH₄⁺ concentration of nutrient treatments was approximately 30 times ambient during the first two weeks and 5 times ambient during the remaining three weeks. The NH₄⁺ concentrations we observed in the no-nutrient treatments were typical of late spring and summer conditions in the York River estuary while the concentrations in the nutrient amended treatments were similar to or higher than late fall conditions (K. Moore *unpubl. data*).

Primary producer biomass.

Primary producer biomass was generally reduced by grazers and increased by nutrient additions. Relative to the grazer-free controls, grazers reduced epiphytic Chl *a* and nearly eliminated macroalgae (Fig. 1; Table 1). Grazers decreased *Z. marina* biomass in the three and five species treatments, but not in the one grazer species treatment which suggested that *G. mucronatus* was not responsible for eelgrass loss. Nutrient additions uniformly increased epiphytic Chl *a* but increased macroalgae only in the absence of grazers, resulting in a nutrient by grazer interaction. Overall, grazers were stronger determinants of plant and algal biomass than were predators or nutrient enrichment, as indicated by the estimated magnitudes of effect (Table 1). Benthic Chl *a* was insensitive to food chain length, grazer richness, and nutrient availability.

Grazer biomass.

In the treatments with multiple grazer species, *G. mucronatus* was the most abundant grazer and the largest contributor to total grazer biomass in both the presence (75 - 85% of total grazer biomass) and absence (66 - 68%) of predators (Fig. 2; Table 1). Because *G. mucronatus* was so abundant we divided the grazer response into two categories: *G. mucronatus* only and minor grazers (i.e. grazers other than *G. mucronatus*). Predator presence reduced minor grazer biomass but had no effect on *G*.

mucronatus, suggesting that *G. mucronatus* may was susceptible than other grazers to predation by blue crabs. Nutrient enrichment increased *G. mucronatus* biomass but had no effect on the minor grazers.

Elemental ratios.

Nutrient enrichment increased the nitrogen content of eelgrass as reflected in higher %TN and lower C:N of *Z. marina* blades (Fig. 3; Table 1). Grazers decreased *Z. marina* %TN in nutrient treatments and increased %TOC in non-nutrient treatments; resulting in grazer by nutrient interaction effects for both variables. Under ambient nutrients, predators decreased %TN which resulted in higher C:N and created predator by nutrient interaction effects. Heavy grazing prevented us from obtaining macroalgal samples for nutrient analysis from every tank. However, there was evidence of a positive nutrient effect on macroalgal quality as the C:N was 26.92 (\pm 2.02 S.E.; n = 8) in nonnutrient treatments and 14.77 (\pm 1.17 S.E.; n = 12) in nutrient treatments.

Elemental content of SOM was less sensitive than that of primary producers to changes in nutrient concentration, predator presence, and grazer richness (Fig. 4; Table 1). Predators generally increased %TOC of bulk SOM and, consequently, C:N. Grazer richness had an idiosyncratic influence on SOM %TN and %TOC, both being maximized in the three-grazer treatment under nutrient enrichment, but had no effect on the molar C:N.

At the end of the five-week experiment, there were measureable differences in the total nitrogen (%TN) and organic carbon (%TOC) content of both grazer species measured: *G. mucronatus* and *A. valida* (Fig. 5, Table 1). Elevated nutrient

concentrations increased %TN and %TOC of *G. mucronatus* but reduced the %TOC content of *A. valida*. Surprisingly, predator presence increased the %TOC content of *A. valida*. While TOC and TN content of the varied somewhat, the molar C:N ratio did not change in response to our experimental manipulations. Thus, the stoichiometric ratio of grazers was more conservative than that of their primary producer food sources.

Ecosystem fluxes.

Gross ecosystem production (GEP) and respiration were both increased by nutrient enrichment and reduced by grazers (Fig. 6; Table 1). Predators decreased GEP and respiration only at the zero and one species richness levels, resulting in a predator by grazer richness interaction. The ratio of production to respiration (P:R) was generally lower in grazer treatments compared with grazer-free controls. Predators influenced P:R in an idiosyncratic way resulting in a predator by grazer interaction effect. Daily GEP was positively correlated to the daily flux rate of DIN (p = 0.013; $r^2 = 0.13$) but was not related to PO₄⁻³ (data not shown). Net daily fluxes of DIN and PO₄⁻³ increased with nutrient enrichment but were unaffected by food web manipulations (Fig. 7; Table 1). The slope of the ratio of the fluxes of DIN:PO₄⁻³ was 15.4, which was similar to Redfield values.

Discussion.

Surprisingly, the strongest effect of nutrient enrichment in our experiment was increased accumulation of grazer, not plant, biomass. Nutrients efficiently passed through the food chain, increasing the biomass of the grazing amphipod, *Gammarus mucronatus*,

which was able to regulate primary producer abundance. Grazer consumption of plants and algae translated into lower rates of ecosystem production. While top-down (i.e. grazing) controls governed primary producer biomass and production, nutrient enrichment dominated effects on the stoichiometry of *Z. marina* and on DIN and PO_4^{-3} flux rates. Although we do not have data for carbon and nitrogen composition of macroalgae it seems likely that nutrient enrichment may have increased *G. mucronatus* biomass by increasing primary producer quality, rather than or in addition to increasing primary production per se. Our results also indicated that DIN and PO_4^{-3} were recycled at roughly Redfield proportions. Overall, grazing determined the productivity and abundance of plants and algae while nutrient enrichment influenced the storage and cycling of inorganic nitrogen and phosphorous.

Effects of nutrient enrichment and food web composition on plant and animal biomass

The nutrient enhancement of macroalgae and epiphytic algae was absent in grazer treatments, showing that grazing was a stronger determinant of algal biomass than bottom-up forcing. Grazers also decreased eelgrass biomass, but only in the three and five species treatments, which included *Ampithoe valida* a member of a family known to graze heavily on macroalgae and seagrass (Duffy and Hay 2000; Valentine and Duffy 2006). Since *Z. marina* abundance was similar in the grazer-free controls and in the monocultures, *G. mucronatus* likely had little effect on eelgrass biomass, which is consistent with previous experiments in this system (Duffy and Harvilicz 2001; Duffy et al. 2001). It is perhaps surprising that *G. mucronatus* did not indirectly increase *Z. marina* biomass by reducing competitive macroalgae and epiphytes. The minor grazers likely

reduced Z. marina biomass directly by grazing on leaves or indirectly by damaging the leaves while consuming attached algae. Overall these data corroborate previous studies showing that the individual grazer species filled different functional roles which, in turn, affected primary producer community composition.

The positive effect of nutrient enrichment on *G. mucronatus* biomass indicated that primary production stimulated by nutrient enrichment was rapidly channeled to grazing invertebrates and, by extension, higher trophic levels. Unlike *G. mucronatus*, minor grazer biomass was not elevated in nutrient enriched treatments. Minor grazers may have consumed primary producers that were unresponsive to nutrient amendments or, more likely, that they were outcompeted by *G. mucronatus*. It is also possible that the changes in grazer abundance reflected an early successional sequence; a different pattern might have emerged had the experiment run longer (Cardinale et al. 2007). However, it is likely that differences in grazer biomass were due to species-specific variations in life history and sensitivity to environmental conditions (i.e. temperature, salinity, DO, etc.) (Procaccini and Scipione 1992; Attrill et al. 1999). Since the experimental duration permitted the production of at least two amphipod generations (Duffy 2003) our results should reflect interactions between the grazer species.

Predators reduced minor grazer biomass but did not affect *G. mucronatus*, suggesting that the minor grazers, either as individuals or as a population, were more susceptible to predation by crabs. Despite the negative predator effect on minor grazer biomass, there was no evidence of a trophic cascade suggesting that the primary producer community reflected the dynamics of the most abundant grazer species. This finding is in contrast to previous experiments in which crab predators initiated a trophic cascade,

increasing biomasses of macroalgae and sediment microalgae (Duffy et al. 2005; Canuel et al. 2007; Spivak et al. 2007). It is possible that the low vulnerability of *G. mucronatus* to predation prevented a trophic cascade. The absence of predator effects underscores the importance of understanding how system productivity and community composition can affect interactions between successive trophic levels (Chase 2003; Borer et al. 2005).

Overall, both bottom-up and top-down controls regulated biomass in this system, but affected different components. Grazing tended to be a stronger determinant of primary producer abundance even under nutrient addition. This result corroborates previous studies demonstrating that grazing controls can overwhelm nutrient effects because grazer consumption of algae is immediate whereas nutrient stimulation of algal growth has a time lag (Hillebrand 2002). The relative importance of bottom-up versus top-down controls on grazers also depended on grazer identity. For instance, *G. mucronatus* was more abundant in nutrient-enriched treatments and was unaffected by predation. Whereas minor grazers did not respond to nutrient enrichment but were decreased by predators. These results confirm that grazer community composition can, in part, determine whether bottom-up controls ascend or top-down controls cascade through a food web (Chase 2003; Borer et al. 2006).

Effects of nutrient enrichment and food web composition on plant and animal stoichiometry

While grazers were the main determinant of primary producer abundance, nutrient enrichment strongly influenced the quality of producer tissues. Nutrient enrichment decreased the C:N of *Z. marina* and macroalgal tissues, thereby increasing their

nutritional value to grazing invertebrates. Conversely, there was no difference in grazer C:N in the nutrient vs. non-nutrient treatments. The less plastic stoichiometry of invertebrate grazer vs. primary producer tissues is typical (Sterner and Elser 2002).

There were two possible explanations for the lower C:N of Z. marina blades in the nutrient vs. non-nutrient treatments (Fig. 3C; Table 1). First, Z. marina was nutrient limited in the non-nutrient treatments and absorbed the nitrogen from the water column to relieve nutrient stress. Second, Z. marina might have exhibited 'luxury consumption' by absorbing more nitrogen than needed for immediate growth and metabolism (Sterner and Elser 2002). However, since C:N values of Z. marina leaves have been reported between 7.2 – 17.8 (Atkinson and Smith 1983), 'luxury consumption' seems unlikely. The lowered seagrass C:N may not have increased grazing, as observed in other systems (McGlathery 1995; Goecker et al. 2005), since Z. marina biomass was decreased in both the non-nutrient and nutrient treatments at higher levels of species richness (Fig. 1B). However, grazers reduced Z. marina %TN in nutrient-enriched treatments (Fig. 3A; Table 1). Thus, it is possible that grazers either consumed nitrogen-rich seagrass tissues or that they damaged the seagrass blades and this led to nitrogen leaching. In non-nutrient treatments, Z. marina %TOC was increased by grazers while C:N was increased by predators (Figs. 3B-C; Table 1). Mechanical damage to the plant blades caused by grazers and predators might have induced a plant physiological response, such as production of carbon-rich secondary metabolites including phenolics (Hay et al. 1994; Arnold and Targett 2002) or increased storage of carbohydrates (Alcoverro et al. 2001). Accumulation of these carbon-rich moieties, could reduce Z. marina quality as inferred by the C:N ratios. The negative effect of grazers and predators on Z. marina quality (non-

nutrient treatments) is consistent with the hypothesis that plants increase carbon-based defenses and / or store carbohydrates when resource availability is low (Bryant et al. 1983; Alcoverro et al. 2001; Massey et al. 2005). However, there is little research on seagrass physiological responses to grazing damage and more evidence is needed to support the mechanism put forth here (Heck and Valentine 2006). Nutrient effects on eelgrass and macroalgal tissues did not translate into alter SOM quality as indicated by the C:N. However, sediment C:N is a poor indicator of OM sources since SOM reflects contributions from primary producers, animals, and sediment microbes as well as the products of OM decomposition by sediment bacteria. Thus, sediment C:N likely reflected a mixture of OM sources (Elser and Foster 1998).

Due to stricter biochemical constraints, elemental ratios of animals are generally less flexible than vascular plants and algae (Elser et al. 2000; Sterner and Elser 2002; Vrede et al. 2004). As such, we expected the C:N of grazers to remain constant despite changes in plant and algal quality. Nutrient enrichment slightly but significantly increased %TN and %TOC of *G. mucronatus* but decreased %TOC of *A. valida*. Predators, however, increased the %TOC of *A. valida*. Although the nitrogen and carbon content of grazers changed in response to nutrients and food chain length, the C:N of both grazers was insensitive to our experimental manipulations. This supported our prediction that grazer stoichiometry would be less plastic than *Z. marina* and algae. Since the C:N of grazers was lower than the C:N of potential food sources (i.e. primary producers and sediments), it is likely that grazers preferentially retained nutrients to maintain an optimal stoichiometric balance. Previous studies demonstrated that C:N ratios of invertebrates (insects and crustacea) are relatively constrained, likely reflecting their body structure

and life history (Sterner and Elser 2002). Similarly, zooplankton have a narrow variation in N but are more variable in P content, which is likely due to changes in growth rate and biochemical requirements (Sterner and Elser 2002).

Ecosystem metabolism was a function of plant biomass and sediment dynamics

A final goal of this experiment was to determine whether ecosystem productivity and fluxes of inorganic nutrients reflected changes in above-ground biomass or in SOM quality. Although our measured flux rates reflected combined water column and sediment dynamics we acknowledge that sediment microbial processes are important to biogeochemical cycles and should be considered in greater detail. GEP and ecosystem respiration were increased by nutrient additions and decreased by grazers, reflecting similar changes in primary producers While GEP was correlated to above-ground primary producer biomass, ecosystem respiration appeared to be driven by benthic processes. Respiration was negatively related to surface sediment C:N but was not correlated to net ecosystem production ($r^2 = 0.03$, p = 0.195; data not shown). This suggests that sediment microbes, including benthic microalgae, rather than above-ground biomass, dominated ecosystem respiration. However, sediment C:N only explained 17% of the variation in ecosystem respiration flux. It is possible that water column processes or processes in the deeper sediments (i.e., below 0-1 cm) may explain more of the variation, but we do not have information to support or refute this hypothesis. Grazers also decreased the ratio of GEP to respiration (P:R), which is indicative of the balance between autotrophy and heterotrophy (Fig. 6C; Table 1). Combined, these data indicate

that grazers were the strongest determinant of ecosystem metabolism but that nutrient effects on SOM quality likely had indirect effects on respiration rates.

Since patterns of GEP mirrored above-ground plant and algal biomass, we expected daily flux rates of DIN to reflect uptake by plants (Hansen et al. 2000), release by grazers (Vanni 2002), and removal by sediment microbial processes (Dahllof and Karle 2005). Thus, we predicted that DIN flux rates would be low when plant biomass was high and that flux rates would be high when grazers were abundant. Instead, DIN flux rates were increased by nutrients at all levels of grazer species richness (Fig 7A; Table 1) and were not correlated to the abundances of any of the primary producers or grazers (Table 2; grazer data not shown) nor sediment C:N (Table 3). In non-nutrient treatments, DIN fluxes were negative indicating that inorganic nitrogen was being removed, likely by sediment microbial processes. However, in the presence of nutrient enrichment, DIN fluxes were consistently positive suggesting high rates of regeneration. It is possible that the short experimental duration combined with the high abundances of macroalgae and grazers prevented or reduced benthic microalgal productivity in nutrientenriched treatments. This community is particularly important to sediment redox conditions and oxygen sensitive processes that mediate in nitrogen transformations and cycling (McGlathery et al. 2007).

In this system, the most likely contributors to PO_4^{-3} flux were grazers and sediments. Grazers recycle PO_4^{-3} , from ingested plants and algae, back into the water column while PO_4^{-3} is effluxed from sediments under anaerobic conditions (Nixon et al. 1980; Valiela 1995). Consequently, we predicted that PO_4^{-3} flux rates would increase with grazer abundance and the availability of labile SOM. At the end of the five week

experiment, daily flux rates of PO_4^{-3} were increased by nutrients but were unaffected by predator presence or grazer species richness (Fig. 7B; Table 1). This indicates that grazer recycling of PO_4^{-3} was not a large contribution to the daily flux rate. PO_4^{-3} flux correlated positively to epiphytic Chl a and negatively to surface sediment C:N (Tables 2, 3). It is possible that nutrient enrichment increased epiphytic biomass, which contributed labile OM to the sediments and increased SOM quality. Sediment microbial activity likely increased in response to higher quality OM, potentially leading to lower sediment oxygen concentrations and increased efflux of PO_4^{-3} . Sediment release may be a more likely source of inorganic phosphorous than bacterial remineralization as microbes might retain some of the recycled nutrient to maintain internal stoichiometric balance (Elser et al. 1995). Since epiphytic Chl a and surface sediment C:N only cumulatively explain 20% of the variation in PO_4^{-3} other processes must also be important determinants of PO_4^{-3} flux. Another possibility is that the C:N ratio of surface sediments (0-1 cm) was not representative of the entire sediment pool (10 cm depth). If oxygen concentrations decreased with increasing depth, as is typical of coastal sediments, release of PO_4^{-3} from the deeper anoxic sediments would be likely. Combined, these data suggest SOM quality and likely, sediment reducing conditions, were likely stronger determinants of daily PO₄-³ flux than grazer richness or predator presence.

In coastal areas, relative fluxes of inorganic nitrogen and phosphorus are generally lower than the Redfield ratio of 16:1, possibly due to the removal of nitrogen by denitrifying bacteria (Nixon et al. 1980; Valiela 1995). In this experiment, daily fluxes of DIN and PO_4^{-3} were being regenerated at roughly the Redfield ratio, suggesting that algal organic matter is being recycled and that denitrification may not be an important

process in this system (McGlathery et al. 2007). Nutrient enrichment increased the relative flux of DIN to PO_4^{-3} , from 16.06 (± 3.38 S.E.) to 28.83 (± 3.29 S.E.) in non-nutrient and nutrient treatments, respectively. The higher DIN flux in nutrient enriched treatments suggest that fertilizer additions may have fueled the microbial community and increased recycling. In addition, there was no correlation between the ratio of DIN:PO₄⁻³ fluxes and grazer species richness nor predator presence (data not shown). Combined, these data suggest that both water column and sediment processes contributed to fluxes of inorganic nutrients and that DIN and PO_4^{-3} were regenerated at rates in ratios consistent with Redfield organic matter.

Our results largely supported our initial hypotheses and demonstrated that bottomup and top-down controls affected where biomass accumulates within the food web, the stoichiometric ratios of primary producers, and ecosystem metabolism. Nutrient enrichment increased_macroalgae and epiphytic Chl *a* which, in turn, increased GEP and *G. mucronatus* biomass. The grazing community effectively controlled algal and epiphytic production stimulated by nutrient enrichment, lending support to the hypothesis that invertebrate grazers can alleviate negative effects of eutrophication (Armitage et al. 2005; Burkepile and Hay 2006; Heck and Valentine 2007). Surprisingly, predators did not initiate a trophic cascade. Although there were few main predator effects, predator interactions with grazers and nutrient enrichment underscore the complexity of the system. However, the absence of strong predator effects may lend support to the notion that community composition can, in part, determine the strength of trophic cascades. Combined, our results indicate that shifts in resource availability and food web composition influence nutrient storage (as biomass) and cycling in seagrass habitats.

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Table 1. Tests of significance and estimated magnitude of effects (ω^2) of nutrient enrichment, food chain length, and grazer species richness and their interactions on biomass, elemental ratios, and daily flux rates. When an interaction was significant the dataset was divided according to the interaction (i.e. predators vs. no predators and nutrients vs. no nutrients) and single factor ANOVAs were run. For interactions, P refers to predators, G to grazers, and N to nutrients. Significant p. values are listed in bold.

Response	Nutrient enrichment			Food	chain length		Grazer community			Interactions	Model error	
	р	MS	ω²	р	MS	ω²	p	MS	ຄີ	-	MS	ω²
ant biomass											••	
Zostera marina (AFDM, g)	0.086	29.62	0.01	0.086	29.71	0.02	<0.001	184.00	0.38	PxG 0.023 (34.51)	9,39	0.54
Predators	0.260	16.11	0.01				0.012	59.31	0.29		11.82	0.64
No predators	0,173	16.65	0.02				<0.001	149.59	0.70		6.61	0.2
Macroalgae (AFDM, g)	0.018	116.88	0.02	0.472	9.95	0.00	<0.001	846.81	0.53	NxG <0.001 (194.85) NxPxG 0.041 (58.15)	18.71	0.32
Nutrients				0.286	26.79	0.00	<0.001	918.32	0.81		21.87	0.11
No nutrients				0.859	0.51	0.00	0.002	125.56	0.42		15.55	0.54
Epiphytic Chl a (µg cm ⁻²)	0.003	54.88	0.09	0.279	6.50	0.00	0.006	27.21	0.12		5.36	0.8
log Benthic Chl $a (\mu g \text{ cm}^{-2})$	0.297	0.20	0.00	0.121	0.45	0.02	0.912	0.03	0.00		0.18	1.12
razer Biomass												
log Gammarus mucronatus	0.034	2.16	0.05	0.419	0.28	0.00	0.219	0.68	0.02		0.41	0.9
log Minor Grazers	0.799	0.01	0.00	<0.001	3.10	0.20	0.205	0.28	0.03		0.16	0.83
oichiometry												
Z. marina %TN	<0.001	12.37	0.53	0,154	0.21	0.01	0.019	0.37	0.04	NxP 0.024 (0.55) NxG 0.007 (0.47) PxG 0.038 (0.31)	0.10	0.3
Nutrients				0.574	0.04	0.00	0.008	0.71	0.31	1 x0 0.0.0 (0.51)	0.13	0.6
No nutrients				0.006	0.69		0.147	0.14	0.07		0.07	
Predators	<0.001	9 14	0.83	01000			0.950	0.01	0.00		0.11	
No predators	<0.001	3.75	0.52				0.002	0.65	0.16	NxG 0.005 (0.51)	0.08	
Z. marina %TOC	0.471	5.08	0.00	0.777	0.78	0.00	0.012	41.02	0.10	NxP 0.036 (45.95) NxG 0.013 (39.93)	9.53	
Nutrients				0.203	17.92	0.03	0.053	32.26	0.19		10.15	0.7
No nutrients				0.093	28.50	0.08	0.009	49.10	0.33		8.87	0.6
Predators	0.095	42.06	0.10				0.212	22.34	0.06		13.33	0.8
No predators	0.198	9.94	0.02				0.022	23.77	0.19	NxG 0.006 (34,14)	5.48	0.5
Z. marina C:N (molar)	<0.001	1374.60	0.57	0.058	46.13	0.01	0.315	14.64	0.00	NxP 0.042 (53.29)	11.88	0.4
Nutrients				0.847	0.13	0.00	0.045	11.71	0.20	· · · · ·	3.47	0.70
No nutrients				0.048	96.37	0.18	0.813	6.17	0.00		20.81	0.8
Predators	<0.001	1015.37	0.83				0.903	2.69	0.00		14.34	0.2
No predators	<0.001	430.26	0.67				0.059	28.50	0.06		9.24	0.2
SOM %TN	0.834	0.00	0.00	0.148	0.00	0.01	0.040	0.00	0.07		0.00	0.9
SOM %TOC	0.925	0.00	0.00	0.035	0.15	0.05	0.045	0.09	0.07		0.03	0.93

	SOM C:N (molar)	0.051	4.92	0.03	<0.001	18.86	0.15	0.404	1.20	0.00		1.19	0.83	
	G. mucronatus %TN	0.043	12.50	0.04	0.676	0.49	0.00	0,274	3.74	0.01		2.73	0.99	
	G. mucronatus %TOC	0.028	189.32	0.05	0.818	1.86	0.00	0.153	69.66	0.04		34.20	0.96	
	G. mucronatus C:N (molar)	0.151	2.25	0.02	0.834	0.05	0.00	0.102	2,58	0.06		1.02	0.98	
	A. valida %TN	0.421	3.93	0.00	0.766	0.53	0.00	0.958	0.02	0.00	NxPxG 0.045 (27.15)	5.76	0.97	
	log Ampithoe valida %TOC	0.027	0.01	0.05	0.002	0.02	0.12	0.092	0.00	0.06		0.00	0.71	
	A. valida C:N (molar)	0.299	0.06	0.00	0.905	0.00	0.00	0.477	0.03	0.00		0.05	1.03	
Daily F	ux rates													
	GEP (mmol $O_2 m^{-2} d^{-1}$)	<0.001	9.70E+04	0.09	0.084	1.83E+04	0.01	<0.001	1.58E+05	0.44	PxG 0.0318 (1.91E+04)	5727.31	0.44	
	Predators	0.002	6.40E+04	0.21				<0.001	7.56E+04	0.47		4480.88	0.28	
	No predators	0.040	3.55E+04	0.09				<0.001	1.03E+05	0.57		7056.85	0.38	
	Respiration (mmol C m ² d ⁻¹)	<0.001	6.48E+04	0.28	0.024	8.70E+03	0.03	0.001	1.01E+04	0.11	PxG 0.017 (6069.89)	1534.90	0.54	
	Predators	<0.001	3.95E+04	0.51				0.784	843.09	0.00		2352.66	0.58	
	No predators	<0.001	2.61E+04	0.38				<0.001	1.54E+04	0.44		662.61	0.18	
	Production : Respiration (P:R)	0.098	0.26	0.02	0.408	0.06	0.00	<0.001	1.01	0.27	PxG 0.044 (0.266)	0.09	0.69	
	Predators	0.182	0.18	0.02				<0.001	1.04	0.52		0.09	0.45	
	No predators	0.326	0.09	0.00				0.064	0.25	0.19		0.08	0.87	
	DIN (mmol $m^2 d^{-1}$)	<0.001	5.26E+04	0.48	0.352	538.21	0.00	0.145	116.26	0.02		602.95	0.45	
	PO_4^{-3} (mmol m ⁻² d ⁻¹)	<0.001	109.82	0.38	0.517	0.91	0.00	0.060	5.83	0.04		2.13	0.61	
	DIN : PO4 3	0.002	4171.45	0.12	0.400	275.86	0.00	0.537	279.04	0.00		377.93	0.94	

Table 2. Regression of daily ecosystem flux rates against biomass of the major primary producer groups. The coefficient indicates the directionality of the relationship while the partial r^2 indicates the goodness of fit. Significant p values are in **bold**.

Ecosystem function		Zostera marina				Epiph	iytic Chl a		Mac	roalgae		Benthic Chl a			Total Model	
GEP (mmol O ₂ m ⁻² d ⁻¹) Respiration (mmol C m ⁻²		Coefficient P	artial r ² *	р	Co	efficient P	artial r ² *	p	Coefficient Pa	artial r ² *	p	Coefficient Pa	artial r ² *	р	r²	
	GEP (mmol O ₂ m ⁻² d ⁻¹)	9.17	0.09	<0.001		5.15	0.01	0.310	9.35	0,26	<0.001	32.36	0.01	0.327	0.36	
	Respiration (mmol C m ⁻² d ⁻¹)	3.34	0.06	0.054		6.32	0.05	0.064	1.75	0.05	0.086	0.96	0.00	0.965	0.16	
	DIN (mmol $m^2 d^{-1}$)	-2.21	0.06	0.083		3.00	0.03	0.229	0.23	0.00	0.754	7.35	0.00	0.649	0.10	
	$PO_4^{-3} \pmod{m^2 d^1}$	-0.11	0.06	0.090		0.30	0.10	0.025	-0.05	0.03	0.191	-0.37	0.00	0.662	0.20	

* partial r² was calculated by dividing the type III SS by the corrected total SS.

sediment organic matter quality (C:N). The coefficient indicates the directionality of the relationship while r^2 indicates the goodness of fit. Significant <i>p</i> values are in bold.										
Ecosystem function	C:N (mol:									
(Coefficient	r ²	р							
$GEP (mmol O_2 m^{-2} d^{-1})$	-34.06	0.10	0.029							
Respiration (mmol C $m^{-2} d^{-1}$)	-21.82	0.21	0.001							

-6.62

-0.53

0.04

0.10

0.153

0.026

DIN (mmol $m^{-2} d^{-1}$) PO₄⁻³ (mmol $m^{-2} d^{-1}$)

Table 3. Regressions of daily ecosytem flux rates against

Table 4. Ecosystem respiration as a function of sediment organic matter quality and gross ecosystem production (i.e. autochthonous organic matter). The coefficient indicates the directionality of the relationship while the partial r^2 indicates the goodness of fit. Significant p values are in bold.

Flux	Sediment	t C:N (mol	lar)	GEP (mn	Total Model			
	Coefficient Pa	rtial r ² *	p	Coefficient Pa	artial r ² *	p	r ²	
Respiration (mmol C m ⁻² d ⁻¹)	-20.09	0.17	0.003	34.64	0.03	0.195	0.20	

* partial r^2 was calculated by dividing the type III SS by the corrected total SS.

Figure Captions.

Figure 1. The effects of nutrients (N), predators (P), and grazer richness (G) on primary producer biomass. Nutrient enrichment increased macroalgae (A) and epiphytic Chl *a* (C). Grazers reduced abundances of macroalgae (A), *Z. marina* (B), and epiphytic Chl *a* (C). Benthic Chl *a* (D) was unaffected by the experimental manipulations. For this and the following figures, all error bars are standard error and the statistical results are reported in Table 2.

Figure 2. The effects of nutrients (N) and predators (P) on grazer biomass. Nutrients increased the biomass of *G. mucronatus* (B) while predators reduced the abundance of minor grazers (C).

Figure 3. The effects of nutrients (N), predators (P), and grazer richness (G) on *Z. marina* elemental content. (A) %TN was increased by nutrients and decreased by grazers. (B) %TOC was increased by grazers but only in non-nutrient treatments, resulting in a grazer by nutrient interaction. (C) Nutrients decreased C:N (mol:mol) and, hence, increased the nutritional quality of *Z. marina*.

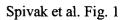
Figure 4. The effects of nutrients (N), predators (P), and grazer richness (G) on sediment organic matter (SOM) elemental content. (A) %TN was influenced by grazer richness but was unaffected by nutrients and predators. (B) %TOC was increased by predators and influenced by grazers but unaffected by nutrients. (C) C:N was increased by predators.

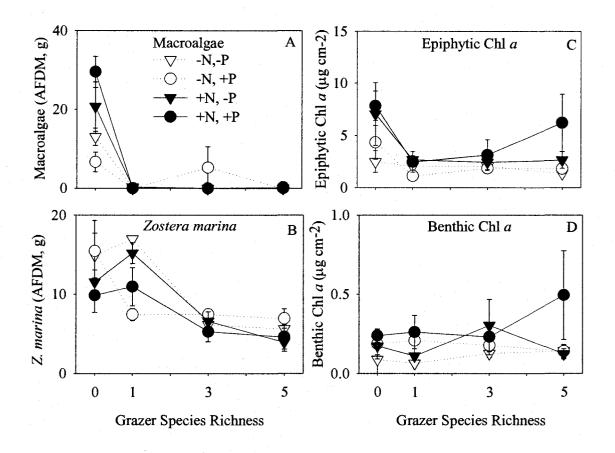
As SOM had a lower C:N than Z. marina or macroalgae, it is likely that SOM derived from multiple sources of varying quality.

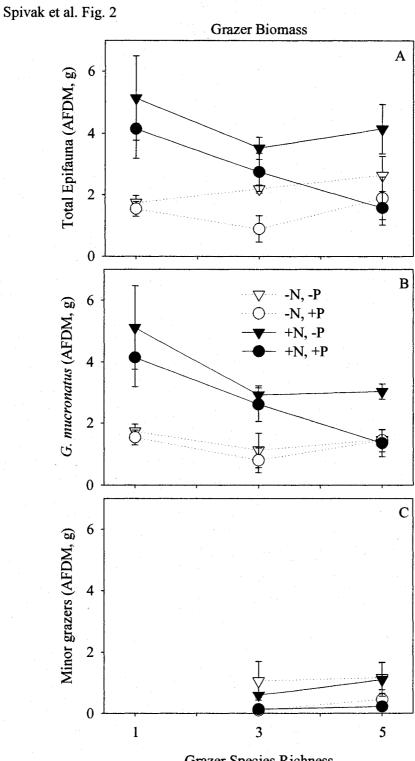
Figure 5. (A-C) Nutrients (N) increased *G. mucronatus* %TN and %TOC, but did not affect C:N. (D-F) Nutrients decreased and predators (P) increased the %TOC of *A. valida* (E). However, both %TN and C:N were insensitive to nutrient and food web manipulations. These data indicate that grazer stoichiometric ratios were less flexible than primary producers.

Figure 6. (A) Nutrients (N) increased and grazers (G) decreased gross ecosystem production. (B) Ecosystem respiration was increased by nutrients but decreased by grazers and predators (P). (C) The ratio of production to respiration was decreased by grazers. Values below or above one (marked by the horizontal line) are indicative of net heterotrophy or autotrophy, respectively.

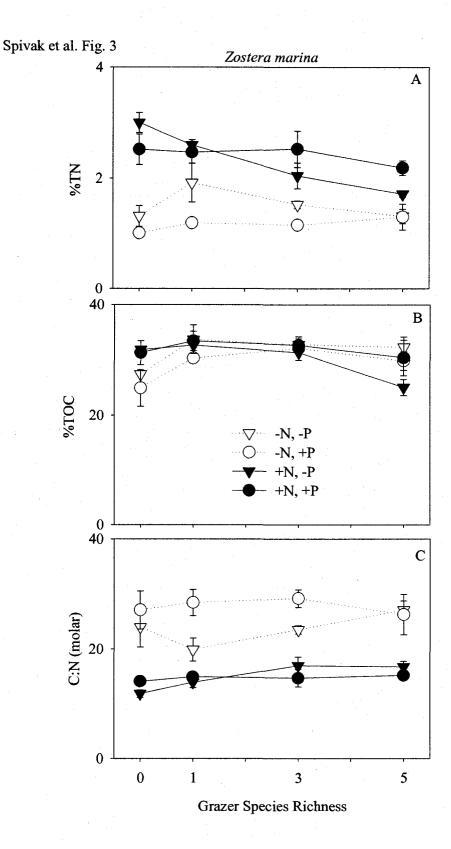
Figure 7. Nutrients increased the daily flux rates of DIN (A) and PO_4^{-3} (B). DIN and PO_4^{-3} ³ (C) were positively correlated ($r^2 = 0.64$; p < 0.001). The equation of the line was : y = 15.40x + 12.16, with a slope similar to Redfield organic matter (N:P = 16).

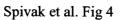


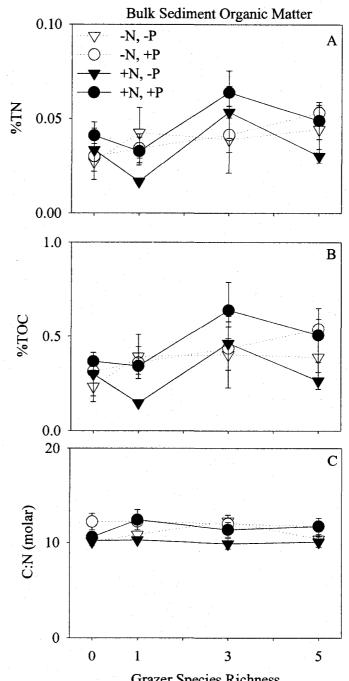




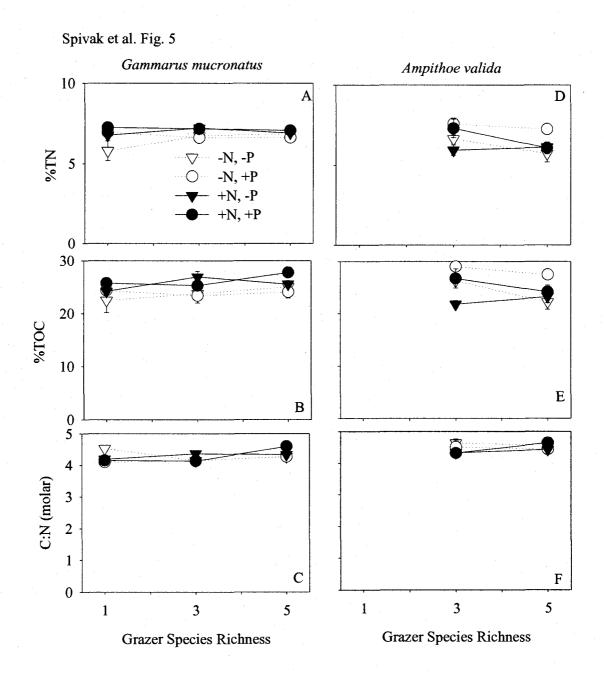
Grazer Species Richness



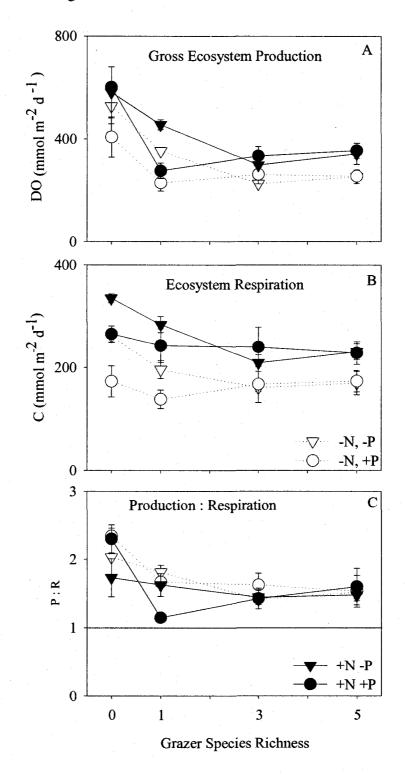


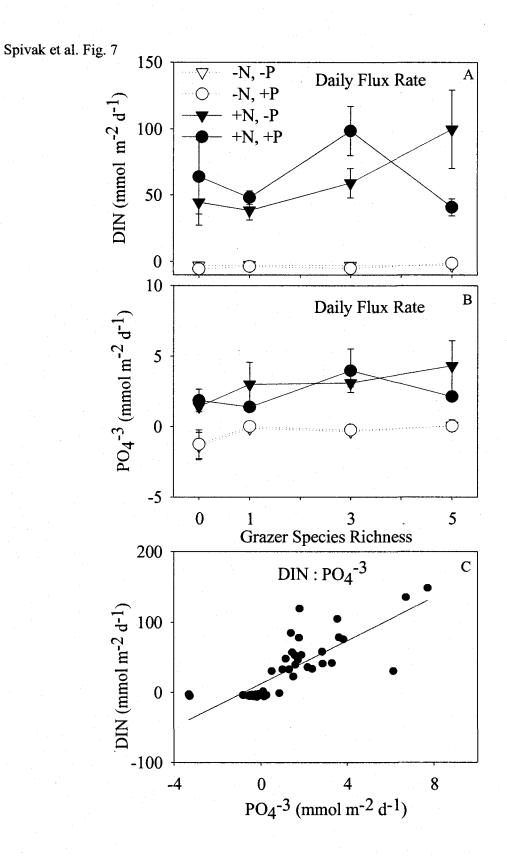


Grazer Species Richness



Spivak et al. Fig. 6





Chapter 5:

Community composition and nutrient enrichment influence sediment organic matter composition in an experimental seagrass ecosystem.

Amanda C. Spivak, Elizabeth A. Canuel, J. Emmett Duffy, J. Paul Richardson

Abstract.

Above-ground animal and plant communities may influence sediment microbial processes through the production of detrital organic matter (OM). Consequently, changes in OM sources and quality, as precipitated by above-ground communities, may have implications for sediment biogeochemistry. Here, we experimentally tested how sediment organic matter (SOM) composition changes in response to shifts in grazer species richness, trophic structure, and resource availability in a seagrass habitat. We manipulated community composition and nutrient levels since fishing and coastal nutrient enrichment, respectively, are two common perturbations to seagrass ecosystems. Our mesocosm experiment utilized a factorial design manipulating water column nutrient levels, food chain length (i.e. predator presence vs. absence), and grazer species richness (0, 1, 3, or 5 species). At the end of the five-week experiment, we analyzed the sources and quality of surface SOM using fatty acid (FA) biomarkers. We found that nutrient enrichment increased macroalgal and epiphytic biomass but resulted in lower abundances of algal and microbial FA in the sediments. Predator effects varied with grazer identity and did not cascade to primary producer abundance. In the sediments, predator presence increased the abundance of FA deriving from heterotrophic bacteria. In general, grazer effects on primary producer abundance and SOM composition were stronger than nutrient enrichment and food chain length.

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Introduction.

Declining biodiversity coupled with increasing anthropogenic stresses have prompted questions about how these disturbances affect ecosystem functioning (Hooper et al. 2005; Balvanera et al. 2006; Cardinale et al. 2006). This has generated studies exploring the effects of above-ground trophic structure (Shurin et al. 2002; Petchey et al. 2004; Byrnes et al. 2006), diversity within and between trophic levels (Tilman et al. 1997; Naeem and Li 1998; Duffy 2003), resource availability (Ware and Thomson 2005; Hulot and Loreau 2006; Cloern 2007), and their interactions (Menge 2000; Chase 2003; Borer et al. 2006) on a variety of ecosystem functions across habitats. These changes in above-ground communities and resource availability may also extend to microbial communities in terrestrial soils (Mikola and Setala 1998; Wardle et al. 2004) and marine sediments (Canuel et al. 2007; Spivak et al. 2007). The link between animals and plants above-ground and microbes in soils and sediments is often detritus. As soil and sediment bacteria govern rates of decomposition and nutrient regeneration (Boschker and Cappenberg 1998; Holmer et al. 2004; Dahllof and Karle 2005), it is important to understand how these communities are affected by changes in the quality and composition of detrital organic matter (OM) as precipitated by above-ground communities. To this end, we conducted a mesocosm experiment testing the singular and interactive effects of trophic structure, herbivore species richness, and nutrientconcentrations on sediment organic matter (SOM) composition in a seagrass habitat.

We used a coastal seagrass (*Zostera marina*) ecosystem as a model habitat for several reasons. First, animal and primary producer species within seagrass habitats are well studied (Duffy 2006; Heck and Valentine 2006). Resident invertebrate grazers

consume a variety of primary producers, including macroalgae, epiphytes, and occasionally seagrass blades (Duffy and Harvilicz 2001; Heck and Valentine 2006). Through their feeding habits and preferences, grazers can influence the delivery and composition of sediment organic matter (SOM) (Duffy 2003; Canuel et al. 2007). As SOM quality is an important determinant of sediment bacterial activity grazer mediated shifts in SOM composition may influence remineralization rates and carbon storage (Hansen and Blackburn 1992;(Cebrian and Duarte 2001).

Second, seagrass communities are affected by fishing efforts that reduce foodchain length (Duffy et al. 2005) and by coastal eutrophication that increases water column nutrient concentrations and reduce light availability (Cloern 2001; Orth et al. 2006). The loss of commercially important predators (e.g., fish and blue crabs) that live in seagrass systems may influence grazer community composition and strengthen grazer controls on primary producers (Heck and Valentine 2007). Coastal eutrophication is cited as a leading cause of two factors that contribute to seagrass loss, algal overgrowth and low water quality (Cloern 2001; Orth et al. 2006). Elevated water column nutrient concentrations may strengthen bottom-up controls since resource availability is a predictor of primary producer biomass and the abundances of organisms at higher trophic levels (Duarte et al. 2000; Ritchie 2000; Ware and Thomson 2005). However, in seagrass beds top-down controls by grazing invertebrates generally negate the stimulatory effects of nutrient resources on algae (Hughes et al. 2004; Armitage et al. 2005).

Finally, seagrass and benthic microalgae are sensitive to bacterial transformations of nitrogen, sulfur, and other nutrients in the sediments (Holmer et al. 2005; McGlathery et al. 2007; Perez et al. 2007). Bacterial decomposition of SOM regenerates inorganic

nitrogen that may rapidly be taken up by benthic microalgae in the surface sediments (Hansen et al. 2000; Eyre and Ferguson 2002; McGlathery et al. 2007). Deeper in the sediments, or if oxygen availability is depleted, sulfate reduction may become an important pathway for OM decomposition. However, an accumulation of sulfides may negatively affect seagrass health (Calleja et al. 2007; Perez et al. 2007). Thus, changes in SOM that affect the sediment bacterial community may, in turn, influence the primary producer community.

We assessed SOM composition and quality by analyzing fatty acid biomarkers. These compounds serve as functional proxies linking OM to potential sources since they are reliably produced by specific groups of organisms (Canuel and Martens 1996; Napolitano 1998; Dalsgaard et al. 2003). Diagnostic biomarkers often have site-specific methyl groups, double bonds, or branching patterns that are useful for tracing sources of OM (Napolitano 1998; Dalsgaard et al. 2003). For example, bacteria synthesize iso-, anteiso-, and methyl-branched fatty acids while microalgae produce highly unsaturated long chain fatty acids (Volkman et al. 1998). Here, we analyzed total fatty acids (TFA) and a sub-class of the TFAs, phospholipid-linked fatty acids (PLFA), to compare OM contributions from detrital and viable or recently viable sources, respectively.

Previously, we conducted mesocosm experiments to asses the influence of community composition (Duffy et al. 2003; Canuel et al. 2007) and light availability (Spivak et al. 2007) on SOM composition. These experiments revealed that both topdown and bottom-up controls affected the relative abundance of SOM deriving from primary producers and bacteria. One of the motivations of this experiment was to determine whether the type of bottom-up control (i.e. light vs. nutrients) is important to

SOM composition. To this end, we manipulated water column nutrient levels, food chain length (predator presence vs. absence), and grazer species richness (0, 1, 3, or 5 species)and measured their effects on primary producer abundance and sediment fatty acid (FA) biomarker composition. In addition, we examined whether primary producer abundance and sediment FA responses were more or less variable at the low (0-species) or high (5species) levels of grazer richness. Specifically, we tested three main hypotheses. First, nutrient enrichment would increase algal biomass and algal contributions to SOM. This would, in turn, increase SOM lability and sediment bacterial activity. Second, the presence of a grazer community would control algal production stimulated by nutrient enrichment. Thus, grazer feeding preferences would indirectly increase seagrass abundance, by reducing algae and increasing light, thereby influencing SOM composition. Third, the presence of predators would reduce grazer biomass and activity, thereby increasing the accumulation of algae, SOM quality, and sediment heterotrophic activity. Consequently, predators may exacerbate the effects of nutrient enrichment by negatively affecting the grazer community. Finally we compared the primary producer and SOM composition results from this mesocosm experiment to those from a previous field experiment with a similar design (Chapter 3).

Methods

Experimental Design.

We conducted a mesocosm experiment to test the main and interactive effects of nutrient availability, grazer species richness, and food chain length on sediment fatty acid biomarker composition. Results for primary producer and grazer biomass, ecosystem metabolism, and bulk SOM content are reported in Chapter 4. Water column nutrient concentrations were manipulated by adding OsmocoteTM slow release fertilizer (N:P:K = 3:1:2) to half of the tanks. Grazer species richness was varied across four levels (0, 1, 3, or 5 species). The highest richness level contained five amphipod species present in the York River estuary, VA, at the time of the experiment, the intermediate level contained random combinations of three species, and the lowest richness level only had the most abundant and annually persistent species, the amphipod *Gammarus mucronatus*. The remaining four grazer species were also amphipods: *Elasmopus levis*, *Melita nitida*, *Ampithoe valida*, and *Sympleustes* spp. Food chain length was manipulated by exposing parallel sets of grazer treatments to a generalist predator, the blue crab, *Callinectes sapidus*. The 16 treatments were each replicated 3 times for a total of 48 mesocosm tanks.

The outdoor mesocosm experiment was conducted over five weeks during summer 2006 in 120 liter translucent fiberglass tanks that were continuously supplied with water from the York River estuary, VA. Water passed through a sand filter and then through 150 μ m mesh before filling 'dump buckets' which regularly spilled into the tanks, providing turbulence and aeration. The filtering process eliminated larger, nontarget animals while permitting passage of invertebrate larvae and algal spores, which often colonized the tanks. The tanks were filled with a mixture of sand : mud (9:2 w:w), averaging 0.80% (\pm 0.18 S.E.) organic matter (OM) content, to a depth of 10 cm. In contrast with previous experiments (Canuel et al. 2007; Spivak et al. 2007), we used a sediment substrate with approximately 1% OM to facilitate *Zostera marina* transplant success and growth (Koch 2001). One hundred pre-weighed eelgrass (*Z. marina*) shoots, cleaned of grazers and epiphytes, were planted in each tank. Sixteen days later, grazing

invertebrates were added to each grazer mesocosm. The five-species treatment received 18 individuals of each species, the three-species treatment had 30 individuals of each species, and the one-species treatment had 90 G. *mucronatus* individuals. Eleven days later, two juvenile blue crabs were added to each predator treatment. Each nutrient treatment received 200 g of Osmocote[™] slow release fertilizer in the first two weeks of the experiment and 100 g every week thereafter. We reduced the fertilizer dosage since the target concentration was five times ambient and 200 g resulted in higher than target concentrations. The 200 g and 100 g additions of Osmocote[™] increased NH₄⁺ concentration to 30.6 (29.23 μ M) and 5.6 (14.37 μ M) times ambient, respectively (Spivak et al. in prep). Nutrients were delivered through two perforated PVC tubes that were suspended from the top of the tanks. Twice a week, one nutrient PVC tube from each nutrient treatment was refreshed with new fertilizer. Water column nutrient concentrations were monitored each week by measuring NH₄⁺ concentrations from five randomly chosen tanks of each nutrient treatment using the Koroleff colorimetric method. The five-week experimental incubation time was chosen to minimize the risk of invasion by non-target animals. This time period permits major changes in animal (one to two grazer generations) and plant community development and in surface sediment characteristics (Duffy et al. 2003; Canuel et al. 2007; Spivak et al. 2007). Despite limitations, this experimental infrastructure simulates several aspects of the biotic and abiotic field conditions well (Duffy et al. 2001). Results for the aboveground plant and animal community and for ecosystem metabolism and stoichiometric ratios are reported elsewhere (Duffy et al. in prep; Chapter 4).

Sediment fatty acid analyses.

At the end of the five week experiment, sediments were collected and analyzed for fatty acid biomarker composition. Three sediment cores (2.6 cm diameter) were collected from every mesocosm tank; the upper 1 cm from each was removed and combined to form a composite surface sediment sample which was stored in a precombusted (450 °C) jar. Samples were immediately put on ice following collection and were later frozen at -80 °C until analysis.

Fatty acids (FA) were analyzed using a revised Bligh & Dyer (1959) method (Macnaughton et al. 1997). Briefly, sediment samples were extracted with methanol:chloroform :K₂HPO₄ 50 mM buffer (2:1:0.8, v:v:v) using an accelerated solvent extraction system (Dionex ASE 200). Following extraction, the samples were partitioned and the organic phase removed and allowed to sit over anhydrous Na₂SO₄ overnight to remove traces of water. The samples were concentrated to 1 mL (Zymark Turbo Vap 500). The total lipid extracts were separated into non-polar (F1/2) and polar (F3) fractions using silica gel columns; each fraction was then eluted with solvents of increasing polarity (Guckert et al. 1985). F1/2 (neutral and glyco-lipids) and F3 (phospholipids) were each saponified, using procedures described in Canuel et al. (2007). Following saponification, the residue was extracted under basic (saponified-neutral) and acidic pH (saponified-acid). The saponified acid fraction was methylated using BF₃-CH₃OH and purified using silica gel chromatography. Before analysis by gas chromatography (GC), samples were evaporated to dryness under N_2 , and a small volume of hexane (100 μ L for the polar fraction and 400 μ L for the non-polar) was added. The FAs, as methyl esters, were analyzed by gas chromatography following previously-

published methods (Canuel and Martens 1993; Zimmerman and Canuel 2001). Peaks were quantified relative to an internal standard, methyl heneicosanoate, added just prior to GC analysis. Peak identities were verified using reference standards and by combined gas chromatography-mass spectrometry using a Hewlett-Packard 6890 GC interfaced with a mass selective detector operated in electron impact mode. FAs are designated as A:B ω C, where A is the total number of carbon atoms, B is the number of the double bonds, and C is the position of the first double bond from the aliphatic " ω " end of the molecule. The prefixes "i" and "a" refer to *iso* and *anteiso* methyl branched FAs (see Canuel et al. 1995 and references therein). Results for two classes of fatty acids are presented: phospholipid-linked fatty acids (PLFA) which represent viable or recently viable biomass and total fatty acids (TFA) which represent neutral, glyco-, and phospholipids and include the sum of the viable and detrital contributions.

Statistical analyses.

Results of the experiment were analyzed in a fully factorial three-way analysis of variance (ANOVA, SAS version 9.1 for Windows), with grazer treatment (df = 3), food chain length (i.e. predator presence or absence, df = 1) and nutrient availability (df = 1) as fixed factors. Data were logarithmically transformed as necessary to maintain homogeneity of variance as determined by the Cochran's C test. From the ANOVAs, we calculated the magnitude of main and interactive effects (ω^2 , percent of variance explained). To determine whether abundance of sediment fatty acid groups varied among replicates, we conducted the Levene's test of homogeneity of variance (Schultz 1985). The three species treatment was excluded from the Levene's analysis as it contained

random combinations of grazer species (whereas the one and five species treatments had constant composition among replicates) and, consequently, was expected to be the most variable treatment. All analyses included all three replicates of every treatment except for two: (1) one replicate of the no-nutrient, no-crab, one-grazer species treatment was excluded due to contamination by more than 500 mg of grazer ash-free dry matter; and (2) a replicate of the no-nutrient, crab, five-grazer species treatment was excluded from the total fatty acid analyses because of low internal standard recovery. Thus, we reported the type III sum of squares (SS) results from the ANOVA model. Analyses were performed on fatty acid biomarker concentrations (ng g⁻¹sediment). Results for primary producer and grazer abundances were reported in Chapter 4.

To aid data interpretation, we performed multiple regression and principal components analyses (PCA). We examined relationships between the fatty acid groups and the major primary producers (*Z. marina*, macroalgae, and epiphytic Chl *a*) and invertebrate grazers using multiple linear regressions. Since *G. mucronatus* was the most abundant grazer at all levels of richness, we divided the grazer response into two categories, *G. mucronatus* only and "minor" grazers (i.e., total epifauna less *G. mucronatus*; see Chapter 4). The partial r^2 was calculated by dividing the type III SS for each response variable by the total SS. We conducted principal components analysis (PCA; using Minitab 15) to better elucidate relationships between manipulated and response variables. We only performed PCA on SOM variables, as these responded to primary producer abundance determined by food web composition and nutrient concentrations. PCA loadings describe the relationships between the response variables and the dominant principal components. PCA loadings were also regressed against the

major primary producer groups (Z. marina, macroalgal biomass, and epiphytic Chl a) to help interpret the results.

Results

Above-ground biomass.

Results for above-ground biomass of primary producers were reported in Chapter 4. Here, we present the results for grazer community composition and relative abundance in the one and five species treatments (Fig. 1). We compared the one and five grazer treatments since the one species treatment only contained *G. mucronatus* and the five species treatment included the full complement of grazers. Since *G. mucronatus* is the most perennially abundant grazer, a comparison between the monoculture and the five species treatment reflects a realistic hypothesis of grazer community composition after and before, respectively, a grazer extinction event. The three species treatment was excluded because it consisted of random grazer combinations, some of which did not include *G. mucronatus*.

Nutrients increased grazer biomass in the one and five species treatments (Fig. 1; Table 1). This effect was stronger for *G. mucronatus* in the one species treatment ($\omega^2 = 0.19$) than for total epifaunal biomass in the five grazer treatment ($\omega^2 = 0.12$). Predators reduced total epifaunal biomass but had no effect on *G. mucronatus* biomass in the one species treatment. There was no difference in total grazer biomass in the one versus five grazer species treatments, however, *G. mucronatus* achieved higher biomass in the monoculture than in the polyculture .It is possible that the changes we observed in grazer biomass reflect early successional dynamics in grazer community development and that, had the experiment run longer, different patterns might have emerged (Cardinale et al. 2007). However, the experimental duration did permit the production of several grazer generations (Duffy et al. 2003) and likely allowed for competitive interactions between grazer species.

Total fatty acids.

At the end of the experiment the abundance of total fatty acids (TFA) was lowest in the one grazer species treatment but was unaffected by nutrient enrichment or predator presence (Fig. 2A; Table 2). Variation in TFA abundance (among replicates) in the one and five species treatments was similar (Table 3). TFA abundance correlated negatively to biomasses *Z. marina* and *G. mucronatus* and positively to minor grazers (Tables 4, 5). Patterns in TFA and phosopholipid-linked FA (PLFA) were qualitatively very similar, however, PLFA abundance was not significantly affected by any of the manipulated variables (Fig. 2B; Table 2). Since TFA and PLFA derive from detrital and recently viable OM sources, respectively, we normalized the abundance of PLFA to TFA to determine the relative contributions from each OM pool (Fig. 2C). Nutrients increased PLFA:TFA which is consistent with higher abundances of any of the primary producers but was negatively correlated to minor grazer abundance (Tables 4, 5). Since the PLFA contributions to the TFA pool were small and the trends in PLFA and TFA sub-classes were similar, we only present results for the TFA hereafter.

We partitioned the TFA into five sub-classes based on FA chain length and saturation and branching patterns (Table 6). Saturated, short-chain FAs $(C_{12:0} + C_{14:0})$,

which constituted 3-6% of the TFAs, are indicative of algal and microbial sources of OM. Abundance of this group was lower in treatments with nutrients but was unaffected by predators and grazers (Fig. 3; Table 2). $C_{12:0} + C_{14:0}$ was negatively correlated to *G*. *mucronatus* biomass (Table 5). Abundances of saturated long chain FA ($\Sigma(C_{24:0} - C_{30:0})$; 5-11% of TFA), $C_{16:0}$ (20-30% of TFA), and $C_{18:0}$ (3-9% of TFA) were insensitive to all of the experimental manipulations (data not shown).

Polyunsaturated FAs (PUFA), which are indicative of labile, algal-derived OM accounted for approximately 15% of TFA. We analyzed two PUFA groups, $C_{20:4} + C_{20:5}$ (i.e. C_{20} PUFA) and $C_{22:5} + C_{22:6}$ (i.e. C_{22} PUFA) which represent OM contributions from diatoms and dinoflagellates, respectively (Fig. 3; Table 2). Grazers were the strongest determinant of PUFA abundance as C_{20} PUFA was lowest and C_{22} PUFA was highest in the *G. mucronatus* monocultures. Minor grazer biomass correlated positively with C_{20} PUFA and negatively with C_{22} PUFA (Table 5), suggesting that grazer diet preferences influenced the composition of sedimentary PUFA... Grazers also affected the variance of the PUFA groups (Table 3). C_{20} PUFA was more variable in the five- than in the one-species grazer treatments whereas C_{22} PUFA was more variable in the one- than in the five-species treatments. In summary, the results for saturated FAs and PUFA indicate that grazer community composition can influence the importance of different primary producer taxas to SOM through their feeding preferences.

Branched fatty acids (iso- and anteiso $C_{13:0} + C_{15:0} + C_{17:0} + C_{19:0}$; BrFA) representative of sediment heterotrophic bacteria, accounted for 5-11% of TFA (Fig. 3; Table 2). Grazer richness and predator presence increased the abundance of BrFA but there was no effect of nutrients. Abundance of this TFA sub-class correlated negatively to biomasses of *G. mucronatus* and *Z. marina* (Tables 4, 5). The data indicate that food web structure and composition, and their effect on the primary producer community, influenced the sediment heterotrophic community.

We also analyzed the ratio $C_{20:5\omega3}$: $C_{22:6\omega3}$ to estimate diatom-derived OM contributions to the sediments (Budge and Parrish 1998; Shin et al. 2000). The ratio was lower in the *G. mucronatus* (1 species treatments) suggesting that this grazer reduced FA contributions from diatoms relative to dinoflagellates (Fig. 3; Table 2). In addition, there was less variability of the ratio (across replicates) in the one versus five species treatments, suggesting that *G. mucronatus* was a more effective consumer of diatoms in the monoculture than in the polyculture (Table 3). This hypothesis is further supported by positive correlations between the ratio $C_{20:5\omega3}$: $C_{22:6\omega3}$ and minor grazer biomass (Table 5). Predators decreased the ratio $C_{20:5\omega3}$: $C_{22:6\omega3}$, but only in the three and five grazer species treatments which created a predator by grazer interaction effect. $C_{20:5\omega3}$: $C_{22:6\omega3}$ was negatively correlated to *Z. marina* biomass but not the biomass of any of the algal groups (Table 4). Thus, grazing by *G. mucronatus* and, to a lesser extent, the presence of crab predators tended to shift the composition of SOM from diatom to dinoflagellate contributions.

PCA provided a summary of TFA composition in response to grazer richness, predator presence, and nutrient availability (Fig. 4). PC1 and PC 2 described 42.6% and 17.5% of the variance, respectively and were both negatively correlated to *Z. marina* biomass (Table 7). The negative correlation between PC1 and *Z. marina* was supported by the loadings of TFA, short chain FA, C₂₀ PUFA, BrFA, and C_{20:503} : C_{22:603} (all negatively related to *Z. marina*; Table 8). PC1 tended to separate SOM variables

according to grazer effects especially in nutrient enriched treatments. For instance, TFA, C_{20} PUFA, and $C_{20:5\omega3}$: $C_{22:6\omega3}$ had positive PC1 scores and were lowest in the one grazer treatments while C_{22} PUFA and PLFA:TFA had negative PC1 scores and were highest in the one grazer treatments. PC2 separated the one grazer treatment (positive scores) from all other grazer treatments (negative scores). PC2 also provided some information about predator effects as SOM C:N, C_{22} PUFA, and BrFA, had positive scores and were increased by predators.

We analyzed PC scores in the presence and absence of nutrients to determine whether enrichment affected relationships between grazer and predator treatments (Fig. 4). One grazer species treatments were distinct from the rest of the grazer treatments despite nutrient concentrations. In the absence of nutrients, the zero, three, and five grazer species treatments tended to cluster together. In the presence of nutrients, however, there were three distinct groupings according to species richness: (1) the one species treatment, (2) the zero species treatment, and (3) the multi-species treatments. The clustering of the three and five grazer treatments suggests that the species rich communities were more similar to each other than they were to the zero or one species treatments. In addition, predator effects tended to be stronger under nutrient enrichment as treatments with predators tended to have more positive PC2 scores than those with grazers only. In summary, the PCA results indicate that grazer identity (i.e. G. *mucronatus*) was a strong determinant of SOM composition. Secondarily, nutrient enrichment increased the importance of predator presence and grazer richness to sediment geochemistry. Finally, despite differences in the composition of three- and fivespecies treatments, they consistently grouped together.

In summary, nutrient enrichment increased the abundance of macroalgae and epiphytes (Chapter 4) and this translated into higher *G. murcronatus* biomass (Fig. 1) and a greater proportion of PLFA relative to TFA (Fig. 2). The grazer community reduced above-ground primary producer biomass (Chapter 4) but SOM composition was most influenced by grazer identity. This is suggested by low abundances of TFA, $C_{20:4} + C_{20:5}$, and $C_{20:5\omega3}$: $C_{22:6\omega3}$ in the *G. mucronatus* monocultures (i.e. one-species treatments; Figs. 2, 3). Predators reduced minor grazer biomass (Chapter 4) but did not initiate a trophic cascade, as evidenced by an absence of predator effects on primary producer biomass and representative FAs in the sediments. Surprisingly predator presence and grazer richness both increased BrFAs, suggesting that the above-ground trophic structure is important to the sediment heterotrophic community (Fig. 3).

Discussion.

Grazer community composition and richness had much stronger effects, on average, than nutrient enrichment or predators, on SOM composition (Table 2). Specifically, the amphipod, *G. mucronatus*, sharply reduced the abundance of SOM deriving from diatoms in the one-species treatment (Fig. 3). However, similar SOM composition in the three and five grazer species treatments suggested that the strong effects of *G. mucronatus* were dampened in more diverse communities. It was somewhat surprising that grazer effects on sediment FA groups were stronger than nutrient enrichment since light availability, another bottom-up force, was a main determinant of SOM composition in a previous experiment (Spivak et al. 2007). It is probable that nutrient enrichment in this experiment did not lead to reduced light availability because

grazers were able to control primary producer abundance (Chapter 4). Thus, grazing invertebrates appear to lessen the effects of nutrient enrichment in this seagrass habitat as shown in others (Hughes et al. 2004; Armitage et al. 2005; Heck and Valentine 2007).

Grazer species identity and richness affected SOM composition.

In this experiment, one of the clearest trends was that SOM composition differed in the one versus the three and five grazer species treatments. This strongly suggested that G. mucronatus exerted a much greater influence over SOM composition in the absence of competition with other grazer species. These differences may have been due to G. mucronatus accruing more biomass in monoculture than in a multi-species community (Fig. 1; Table 1). However, the strong effect of nutrient enrichment on G. *mucronatus* biomass and the general lack of nutrient by grazer interaction effects on SOM composition suggest that the influence of this grazer was not proportional to its abundance. Thus, despite relatively high G. mucronatus biomass in the five species treatments, direct or indirect interactions between grazer species attenuated the influence of G. mucronatus on SOM composition. This suggests that grazer diversity may weaken trophic effects that extend to SOM composition (Finke and Denno 2002; 2004). Alternatively, minor grazers may have had a disproportionate influence on SOM composition despite their low abundance. This hypothesis is in accord with other experiments suggesting that grazer identity rather than biomass is important to ecosystem properties (Duffy et al. 2001; Canuel et al. 2007; Jaschinski and Sommer 2008). However, from this dataset we can not discern which hypothesis provides the most likely

explanation for differences in SOM composition between the grazer monocultures and polycultures.

Differences in SOM composition in the one- versus three- and five-species treatments hint that grazer community makeup and interactions can impact sediment biogeochemistry (Duffy and Harvilicz 2001; Canuel et al. 2007; Spivak et al. 2007). For instance, diatom-derived OM (i.e. C_{20:4}+C_{20:5}, C_{20:503}:C_{22:603}; Fig. 3) was less abundant in the grazer monocultures compared to the polycultures. This is consistent with a previous study where G. mucronatus decreased the accumulation of benthic microalgae (chlorophyll *a*) and the relative abundance of polyunsaturated FAs (Canuel et al. 2007). Since algal OM is particularly labile, SOM quality might have been lower in the monoculture than in the more species rich treatments (Canuel and Martens 1996). The higher abundances of diatom-derived FAs ($C_{20:4} + C_{20:5}$ and $C_{20:5\omega3}$: $C_{22:5\omega3}$) in the threeand five-species treatments might have been the indirect result of minor grazers reducing Z. marina, thereby increasing light availability and, hence, sediment microalgal production (Chapter 4). This hypothesis is supported by negative correlations of Z. marina with TFA and FAs indicative of diatom OM ($C_{20:4} + C_{20:5}$, and $C_{20:5\omega3}$: $C_{22:6\omega3}$; Table 4). Increased abundance of labile, algal-derived SOM may also stimulate sediment microbial activity as BrFA (sediment heterotrophic bacteria) abundance was higher in the mixed grazer species treatments than in monoculture (Fig. 3; Table 2). Supporting this hypothesis was the negative correlation between Z. marina biomass and abundance of iso- and anteiso-BrFA, which are abundant in gram positive bacteria (Kaneda 1991) (Table 4). Thus, an indirect effect of reduced Z. marina biomass might have been a heightened sediment bacterial response, suggesting that shifts in SOM composition

precipitated by grazer effects on primary producers influenced the sediment bacterial community. Cascading effects of above-ground animals on organic matter composition and the bacterial community have been observed in soil systems as well (Lavelle et al. 1997; Bardgett et al. 1998; Wardle et al. 2004). This suggests that above-ground community composition and structure may affect biogeochemical cycles in a variety of ecosystems.

We tested whether our data supported the portfolio hypothesis, which predicts that variability will decrease as species richness increases (Tilman 1999; Lhomme and Winkel 2002), by comparing the variance of SOM properties among replicate mesocosms at low (1) and high (5) grazer species richness. There was little evidence that the fivegrazer species community conferred stability since the variance of many fatty acid groups was similar in monocultures and mixed species treatments (Table 3). However, when variance in FA abundance differed between the one- and five-species treatments, the pattern was opposite of the prediction. For example, there was less variance in the abundance of diatom-derived FAs ($C_{20:4} + C_{20:5}$, $C_{20:5\omega3} : C_{22:6\omega3}$) in the one- versus fivespecies treatments (Fig. 3; Table 3). This was likely the result of G. mucronatus efficiently consuming diatoms in the one species treatment. In contrast, grazer interactions in the multi-species community, may have reduced G. mucronatus' ability to consume diatoms and, consequently, resulted in higher and more variable concentrations of representative FAs (i.e. $C_{20:4} + C_{20:5}$, $C_{20:5\omega3} : C_{22:6\omega3}$). While diatom FAs were less variable in the one-species treatment, dinoflagellate FAs $(C_{22:5} + C_{22:6})$ were variable in the five-species community ((Budge and Parrish 1998)Table 2). It is possible that algal sources of C₂₂ PUFA were more efficiently grazed in the mixed species community than

in the monoculture. Overall, these data suggested that grazer species richness did not consistently influence the variance in algal contributions to SOM.

Combined, our results indicated that grazer community composition (identity and richness) were important determinants of SOM composition. Despite the high biomass of *G. mucronatus*, relative to the minor grazers in the five species treatment, SOM patterns were not controlled solely by this species. Instead, minor grazers moderated the effects of the more abundant *G. mucronatus* and may have disproportionately affected SOM composition. Consequently, it is important to consider the entire grazer community rather than focus on the most abundant species (Jernakoff and Nielsen 1997; Matthiessen et al. 2007; Jaschinski and Sommer 2008).

Bottom-up and top-down controls on SOM composition.

Effects of nutrients and predators on primary producers and grazers in this experiment (Chapter 4) also affected SOM composition. For instance, nutrients increased the relative abundance of labile FAs (PLFA:TFA) in the sediment (Fig. 2; Table 2). Thus, algal growth, stimulated by nutrient enrichment, increased the lability and quality of SOM. Curiously, abundance of sediment microbial and algal FAs ($C_{12:0} + C_{14:0}$) was lower in nutrient enriched treatments (Fig. 3; Table 2). Predators increased sediment bacterial FA abundance (BrFA; Fig. 3; Table 2), possibly by increasing SOM lability, physically altering sediment conditions, or both. Previous studies demonstrated that grazers can stimulate sediment microbes by fragmenting POM and increasing surface area, by changing the chemical composition of OM, by irrigation and sediment resuspension which reduce build-up of metabolites, etc. (see papers by Aller; Lee 1991;

(Zimmer et al. 2002; Mermillod-Blondin et al. 2003; Zimmer et al. 2004) While we are unable to resolve the mechanism, the positive effect of predators on bacterial FAs is consistent with previous experiments (Canuel et al. 2007; Spivak et al. 2007) and suggests that food chain length was an important determinant of the sediment heterotrophic bacterial community and microbial processes. Shifts in sediment bacterial activity may have important implications for *Z. marina* and algal productivity. For instance, an increase in sediment bacteria that leads to anoxic conditions and a build up of sulfides may negatively affect seagrass health (Holmer et al. 2006; Calleja et al. 2007; Perez et al. 2007). Alternatively, an increase in sediment bacteria and bacterial activity in aerated surface sediments may lead to higher rates of mineralization and nitrogen availability to benthic microalgae (Eyre and Ferguson 2002; McGlathery et al. 2007).

Although there were few main predator effects on SOM variables, it is possible that the influence of predators was moderated by nutrient enrichment. Evidence for this comes from PCA (Fig. 4). There was little distinction between treatments according predator presence in the absence of nutrients, whereas treatments separated along PC2 according to crab presence in nutrient enriched treatments (Fig. 4). In addition, SOM variables increased by predators (BrFA, SOM C:N) had positive PC 2 loadings (Table 8). This suggests that interactions between bottom-up and top-down controls may produce different SOM patterns than either variable singularly.

Although primary producer abundance and SOM composition were sensitive to bottom-up (i.e. nutrient enrichment) and top-down (i.e. food web composition) controls, grazer effects were generally stronger and more pervasive (see ω^2 values in Table 2). The importance of grazer effects was also supported by the PCA as the one-species treatment was consistently separated from the other treatments despite nutrient enrichment or predator presence. Thus, the grazing community was likely a stronger determinant of ecosystem properties than resource availability and trophic structure. The importance of grazing, relative to nutrient enrichment and predation, is consistent with previous studies and suggests that grazers may play a pivotal ecological role in seagrass habitats (Heck et al. 2000; Hughes et al. 2004; Armitage et al. 2005) and in other systems (Hillebrand et al. 2000; 2002; Borer et al. 2006; Burkepile and Hay 2006).

Experimental comparisons.

Although mesocosm experiments allow for controlled manipulations, their value partly depends on how accurately the system mimics the natural environment. To this end, we tested the interactive effects of nutrient enrichment and seagrass community composition on ecosystem functioning in a mesocosm (Chapter 4; this study) and a field experiment (Douglass et al. 2007; Chapter 3).

In both the mesocosm and field experiments, nutrients increased above-ground algae and reduced *Z. marina* biomass (Douglass et al. 2007; Chapters 3, 4) as often found in other experiments (McGlathery 1995; Hauxwell et al. 2003; Hughes et al. 2004). In addition, changes in the primary producer community were reflected in SOM composition. For instance, nutrients decreased the abundance of FAs deriving from algae and microbes (short-chain FA) in both this mesocosm study and in the field experiment (Chapter 3). The declines in *Z. marina* abundance and benthic algal and microbial

production were likely the indirect results of nutrients reducing light availability by stimulating above-ground epiphytic algal growth (Havens et al. 2001; Bintz et al. 2003; Hauxwell et al. 2006).

In both the mesocosm and field experiments, the above-ground animal community strongly influenced primary producers and SOM composition. For instance, grazers decreased epiphytic Chl *a* but had no effect on benthic microalgae. The latter result may seem surprising since grazers reduced benthic Chl *a* in two previous mesocosm experiments (Canuel et al. 2007; Spivak et al. 2007). Instead grazer effects on above-ground algae translated into changes in SOM composition and quality. For example, diatom-derived contributions to SOM, as indicated by $C_{16:107}$: $C_{16:0}$, and $C_{20:503}$: $C_{22:603}$, were reduced in the mixed grazer community of the field experiment (Chapter 3) and in the one species treatment of this study. It was curious that the mixed grazer community did not decrease diatom-derived OM in both the mesocosm and field experiments. However, the mixed grazer treatments in each experiment contained different grazer species. The field experiment included one amphipod (*G. mucronatus*) and two isopods (*Erichsonella attenuata*, *Idotea balthica*) while this study contained five different amphipod species.

These differences in the deposition of plant derived OM may be a function of grazer feeding preferences and interactions. The importance of grazer identity on SOM composition was demonstrated in a previous mesocosm experiment. Duffy and Harvilicz (2001) showed that grazer feeding preferences significantly influenced the accumulation of different types of macroalgae. For example, red algae, such as *Polysiphonia*, increased significantly in treatments with the amphipod *G. mucronatus*. Canuel et al. (2007) found

that long chain fatty acids, indicative of vascular plant OM, were more abundant in *G. mucronatus* monocultures while short chain fatty acids, deriving from algae and microbes, were more abundant in monocultures of the isopod *Erichsonella attenuata*. In monoculture, *G. mucronatus* and *E. attenuata* had strong effects on FA sub-groups. SOM composition in grazer species polycultures, however, largely reflected the entire community rather than a single species (Canuel et al. 2007). The averaging effect of a mixed grazer species on SOM composition was largely consistent with the results of this experiment. For example, the abundance of C₂₀ PUFA and the ratio C_{20.503} : C_{22.603} were lowest in the one grazer species treatment but were more abundant in the mixed species treatments. Thus, despite the high *G. mucronatus* biomass, minor grazers strongly influenced SOM composition. Consequently, it may be important to consider the effects of the entire grazer community rather than the influence of the most abundant species.

SOM composition was also influenced by food chain length in both the field and mesocosm experiments. Abundances of BrFA and MeBrFA (sulfate reducing bacteria) were increased by predators in both experiments. Since this result was congruous with previous mesocosm experiments (Canuel et al. 2007; Spivak et al. 2007), it is likely that predators enhance sediment heterotrophic activity by increasing SOM quality or by physically altering the sediment environment (Mermillod-Blondin et al. 2003; Wardle et al. 2004; Zimmer et al. 2004). For example, crab burrowing may increase oxygen penetration into the sediments, creating more favorable conditions for microbial decomposition (Morrisey et al. 1999; Fanjul et al. 2007). Crabs may also fragment plant detritus increasing the surface area available for grazing. Thus, heavy harvesting of this

invertebrate may have implications for rates of OM decomposition and carbon storage in the sediments.

Overall, SOM patterns in the field experiment (Chapter 3) and in this study were largely consistent. While field experiments would be preferable to mesocosm experiments, the mesocosm setup allowed us to control grazer community composition and measure ecosystem metabolism (Chapter 4) which would have been unfeasible in the field. Risk of contamination by non-target grazers species in the field experiment prevented us from manipulating grazer species more precisely than the presence or absence of a mixed species community. Thus the use of complementary mesocosm and field experiments yielded information about grazer species and community effects on SOM composition and demonstrated that nutrient enrichment and trophic structure can rapidly influence SOM quality, despite the presence of previously deposited OM and variance in environmental conditions typical of field situations. Literature Cited.

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Table 1. Tests of significance and estimated magnitude of effect (w2) of nutrient enrichment, food chain length, and species richness on grazer community composition. We only analyzed differences in grazer abundance in the one versus the five-species treatments. Data were log transformed to obtain homogeneity of variance. Significant p (<0.05) values are in bold.

Response	Nutrie	ent enrichm	ent	Foo	d chain lengt	h	Grazer	Richness (1	vs. 5)	Interactions	Model e	TOF
	р	MS	ω²	р	MS	ω²	p	MS	ω²		MS	ω²
log G. mucronatus biomass +1	0.004	0.39	0.19	0.097	0.10	0.04	0.021	0.21	0.10	,	0.03	0.63
log total epifauna biomass + 1	0.017	0.29	0.12	0.046	0.19	0.07	0.345	0.04	0.00		0.04	0.73

Table 2. Tests of significance and estimated magnitude of effects (p²) of nutrient enrichment, food chain length, and grazer community on SOM composition. In order to determine whether grazer-free controls and grazer richness levels differed in their effects on the response variable we conducted Student-Newman-Keuls (SNK) analyses; different means are designated by letters. When an interaction was significant, the dataset was divided according to the interaction (i.e. with vs. without nutrients) or with vs. without predators) and the ANOVA was run again. Significant interactions are followed by the *p* value for significance and the mean squared in parentheses. N refers to nutrient enrichment; G to grazer community; P to predators. Fatty acid analyses were conducted on abundance normalized to sediment (ing g⁺). See text for description of fatty acid organic matter sources.

Response		Nutri	ent enrichment		Foo	d chain length		Gra	zer community		Interactions	Model erro	r	SNK
		р	MS	0) ²	p	MS	w ²	р	MS	ω²		MS	ω²	
Total FA		0.242	2.80E+08	0.01	0,251	2.70E+08	0.00	0.002	1.19E+09	0.17	-	1.97E+08	0.88	0*1*3*5*
LFA		0.838	208244.11	0.00	0.317	5053530.36	0.00	0.109	10709661.01	0.04		4883030.50	0.97	0 ^{ab} 1 ^b 3 ^{ab} 5
LFA : TFA		0.022	0.00	0.05	0.967	0.00	0.00	0,002	0.01	0.15		0.00	0.76	0°1°3°5°
C12:0 + C14:0		0.033	3.38E+06	0.05	0.531	2.74E+05	0.00	0.095	1.58E+06	0.05		6.80E+05	0.96	0"1"3"5"
C(C _{24:0} - C _{30:0})		0.829	7.69E+04	0.00	0.161	2.03E+06	0.01	0.768	3.75E+05	0.00		9.86E+05	1.03	0° 1° 3° 5°
20:5 + C20:4		0.992	7.83E+01	0.00	0.979	5.31E+02	0.00	<0.001	2.82E+07	0.58		7.79E+05	0.44	0°1°3°54
22.6 + C22.5		0.187	7.74E+04	0.00	0.410	2.96E+04	0.00	<0.001	1.90E+06	0.63		4.25E+04	0.38	0° 1° 3° 5°
лFA		0.095	8.16E+06	0.02	0,066	1.00E+07	0.03	0.010	1.24E+07	0.12		2.75E+06	0.90	0°1°3°55
dd BrFA*		0.142	2.90E+06	0.01	0.031	6.75E+06	0.05	0.006	6.56E+06	0.13		1.31E+06	0.87	0°1°3°55
og even BrFA [†]		801.0	1.20E+00	0.02	0.095	1.31E+00	0.02	0.052	1.27E+00	0.07		4.40E-01	0.96	0°1°3°5°
te BrFA [§]		0.115	3.51E+04	0.02	0.038	6.29E+()4	0.05	0.145	2.58E+04	0.03		1.33E+04	0.98	0°1°3°5°
16: Jui 7 : C16:0		0.004	0.71	0.05	0.550	0.03	0.00	<0.001	1.72	0.42	NxG 0.023 (0.27)	0.07	0.49	0"1"3"5"
	nutrients				0.637	0.02	0.00	0.002	0.78	0.48		0.09	0.59	0°1°3°5°
	no nutrients				0.182	0.13	0.03	<0.001	1.18	0.72		0.05	0.27	0*1*3*5*
20:3w3 : C _{22:6w3}		0,250	12.42	0.00	0.318	9.33	0.00	<0.001	835.14	0.72	NxG 0.013 (38.15)	. 9.04	0.21	0°1°3°5°
	nutrients				0.091	22.02	0.01	<0,001	466,30	0.86		6.81	0.12	0°1°3°5°
	no nutrients				0.948	0.05	0.00	<0.001	420.49	0.73	PxG 0.012 (61.34)	11.58	0.19	0°1°3°5°
	crabs				0.972	0.01	0.00	<0.001	349.88	0.82		7.68	0.19	0"1"3"5°
	no crabs				0.151	23.85	0.01	<0.001	562.90	0.79	NxG 0.021 (45.35)	10.40	0.15	0*1*3*5*

• iso-, anteiso- $\Sigma(C_{13:0} + C_{15:0} + C_{17:0} + C_{19:0})$

[†] iso- ($C_{M;0} + C_{16;0}$)

§ 10Me17:0 + 10Me19:0

Table 3. Results from Levene's test of homogeneity of variance for fatty acid biomarker composition. Grazer richness treatments (i.e. 1 or 5 species) are listed in the Variance column according to whether the treatments were more or less variable relative to each other. The mean and standard deviation (SD) are listed for each treatment as well as the p for the Levene's test. See text for description of fatty acid organic matter sources. Fatty acid analyses were conducted on abundance normalized to dry sediment (ng g⁻¹).

Response		Variance		1 grazer	5 gra	zers	Levene's HOV	
	Less	More	I	mean S.D.	mean	S.D.	p	
Total FA		· _	2405	57.71 11214.17	49379.96	16191.87	0.467	
PLFA : TFA		=		0.17 0.03	0.13	0.02	0.565	
PLFA		=		14.31 1807.35	6546.20	2372.89	0.128	
$C_{12:0} + C_{14:0}$		=	143	86.41 812.43	2300.15	964.05	0.745	
$\Sigma(C_{24:0} - C_{30:0})$		=	244	7.22 1088.83	2830.69	.996.86	0.242	
$C_{20:5} + C_{20:4}$	1	< 5	.35	50.81 199.13	4231.04	1125.35	0.006	
$C_{22:6} + C_{22:5}$	5	< 1	105	58.60 344.06	272.17	106.98	0.001	
BrFA		=	309	06.35 1513.49	5150.83	2102.11	0.392	
odd BrFA*		=	230	7.47 1141.82	3654.77	1347.07	0.610	
log even BrFA [†]		=		6.17 0.59	6.91	0.62	0.754	
Me BrFA [§]		=	23	35.69 110.58	297.43	126.90	0.903	
$C_{16:1\omega7}: C_{16:0}$. 1	< 5		0.00 0.00	0.88	0.08	0.001	
$C_{20:5\omega3}: C_{22:6\omega3}$	1	< 5		0.00 0.00	20.81	4.17	<0.001	

* iso-, anteiso- $\Sigma(C_{13:0} + C_{15:0} + C_{17:0} + C_{19:0})$

[†] iso- $(C_{14:0} + C_{16:0})$

[§] 10Me17:0 + 10Me19:0

Table 4. Results of regression analyses of fatty acid biomarker groups against the biomass of the major primary producers. The coefficient indicates the	
directionality of the relationship. Partial r ² calculated by dividing the type III SS by the corrected total SS of the model. See text for description of fatty	
acid organic matter sources. Analyses were conducted on fatty acid abundance normalized to dry sediment (ng g ⁻¹).	

Response	Zostera n	narina (AF	DM, g)	Macroa	lgae (AFDN	1, g)	Epiphyti	Epiphytic Chl $a (\mu g \text{ cm}^{-2})$		
	Coefficient	Partial r ²	р	Coefficient	Partial r ²	p	Coefficient	Partial r ²	p	r ²
Total FA	-1514.08	0.19	0.002	-178.73	0.01	0.515	1052.53	0.03	0.237	0.23
PLFA	-146.65	0.08	0.047	-35.84	0.01	0.400	206.90	0.05	0.136	0.14
PLFA : TFA	0.00	0.07	0.088	0.00	0.01	0.485	0.00	0.01	0.488	0.09
$C_{12:0} + C_{14:0}$	-53.56	0.08	0.054	-18.09	0.03	0.262	37.40	0.01	0.470	0.12
$\Sigma(C_{24;0} - C_{30;0})$	-46.47	0.05	0.139	-9.28	0.01	0.612	97.13	0.06	0.104	0.11
$C_{20:5} + C_{20:4}$	-186.71	0.29	<0.001	-3.84	0.00	0.884	23.71	0.00	0.780	0.29
$C_{22:6} + C_{22:5}$	28.51	0.10	0.035	-11.74	0.05	0.137	16.89	0.01	0.501	0.16
Branched FA	-111.96	0.16	0.004	-39.30	0.06	0.008	80.54	0.02	0.259	0.24
odd BrFA*	-111.96	0.16	0.004	-39.30	0.06	0.079	80.54	0.02	0.259	0.24
log even BrFA [†]	-0.06	0.16	0.003	-0.02	0.06	0.071	0.09	0.09	0.022	0.31
Me BrFA [§]	-5.23	0.04	0.171	-2.47	0.03	0.272	1.00	0.00	0.889	0.07
C _{16:107} : C _{16:0}	-0.02	0.02	0.319	0.00	0.01	0.624	-0.03	0.02	0.315	0.05
$C_{20:503}: C_{22:603}$	-1.02	0.30	<0.001	0.05	0.00	0.700	-0.04	0.00	0.932	0.31

[†] iso- $(C_{14:0} + C_{16:0})$ § 10Me17:0 + 10Me19:0

Table 5. Results of regression analyses of fatty acid biomarker groups against the biomasses of G. mucronatus and minor grazers. The coefficient indicates the directionality of the relationship. Partial r^2 calculated by dividing the type III SS by the corrected total SS of the model. See text for description of fatty acid organic matter sources. Analyses were conducted on fatty acid abundance normalized to dry sediment (ng g^{-1}).

Response	G. muc	ronatus (1	ng)	log Mine	or grazers	(mg)	Total Mode
	Coefficier I	Partial r ²	р	Coefficient I	Partial r ²	р	r ²
Total FA	-3.96	0.13	0.036	7288.24	0.14	0.026	0.27
PLFA	-0.28	0.03	0.350	653.14	0.06	0.192	0.09
PLFA : TFA	0.00	0.13	0.020	-0.02	0.23	0.003	0.36
$C_{12:0} + C_{14:0}$	-0.20	0.13	0.042	253.16	0.07	0.136	0.20
$\Sigma(C_{24:0} - C_{30:0})$	-0.14	0.05	0.270	63.59	0.00	0.772	0.05
$C_{20:5} + C_{20:4}$	-0.32	0.08	0.055	1153.65	0.34	<0.001	0.42
$C_{22:6} + C_{22:5}$	0.05	0.04	0.159	-289.80	0.42	<0.001	0.46
Branched FA	-0.48	0.13	0.045	434.97	0.04	0.277	0.17
odd BrFA*	-0.35	0.14	0.038	290.50	0.03	0.299	0.18
log even BrFA [†]	0.00	0.16	0.029	0.14	0.04	0.254	0.20
Me BrFA [§]	-0.02	0.09	0.123	-3.00	0.00	0.910	0.09
$C_{16:1w7}: C_{16:0}$	0.00	0.16	0.005	0.27	0.31	<0.001	0.47
$C_{20:5w3}: C_{22:6w3}$	0.00	0.06	0.018	7.95	0.61	<0.001	0.66

[†] iso- $(C_{14:0} + C_{16:0})$ [§] 10Me17:0 + 10Me19:0

Table 6. Names and sources of fatty acid (FA) groups analyzed in this experiment.

Fatty Acid (FA) Group		Likely source	Reference
Short chain FA	$C_{12:0} + C_{14:0}$	Algae and microbes	Viso and Marty 1993
C ₂₀ Polyunsaturated FA	$C_{20:4} + C_{20:5}$	Diatoms	Viso and Marty 1993; Budge and Parrish 1998
C ₂₂ Polyunsaturated FA	$C_{22:5} + C_{22:6}$	Dinoflagellates	Viso and Marty 1993; Budge and Parrish 1998
Branched FA	iso, anteiso odd $\Sigma(C_{13:0} - C_{19:0})$	Heterotrophic bacteria	Volkman et al. 1980

Table 7. Results from regression analyses of principle components (PC) against the major primary producer groups. The coefficient indicates the directionality of the relationship. Partial r^2 was calculated by dividing the type III SS by the corrected SS of the model.

PC	Zostera m				gae (AFD		Epiphytic			Total Mod
	Coefficient	t Partial r	2 p	Coefficien	t Partial r	² p	Coefficient	Partial r	² p	r ²
PC1	-0.30	0.27	<0.001	-0.05	0.02	0.260	0.15	0.02	0.254	0.31
PC2	-0.12	0.11	0.029	0.05	0.05	0.136	-0.07	0.01	0.504	0.16

Variable	PC1	PC2
· · · · · · · · · · · · · · · · · · ·		
SOM C:N (mol:mol)	0.02	0.11
TFA	0.39	0.11
PLFA : TFA	-0.17	0.25
Monounsaturated FA	0.37	-0.15
$C_{12:0} + C_{14:0}$	0.35	0.22
Σ(C _{24:0} - C _{30:0})	0.25	0.37
$C_{20:5} + C_{20:4}$	0.34	-0.19
$C_{22:6} + C_{22:5}$	-0.11	0.49
odd BrFA*	0.35	0.23
log even BrFA [†]	0.33	0.18
Me BrFA [§]	0.21	0.19
$C_{16:1007}: C_{16:0}$	0.20	-0.40
$C_{20:5\omega 3}: C_{22:6\omega 3}$	0.23	-0.39
* iso-, anteiso- $\Sigma(C_{13:0} + C_{15:0} + C_{15:0})$	$+C_{17:0}+C_{19}$	(0:

[†] iso- $(C_{14:0} + C_{16:0})$ § 10Me17:0 + 10Me19:0

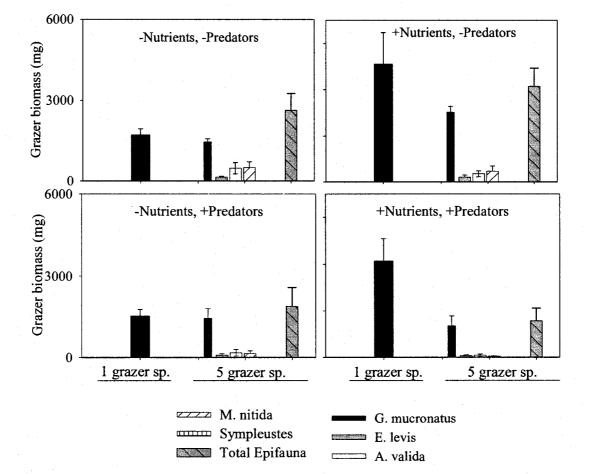
Figure Captions.

Figure 1. Biomass distribution of individual grazer species. Results are only presented for the one and five species treatments since those contained grazer communities of constant composition while the three grazer treatment contained random combinations of species.

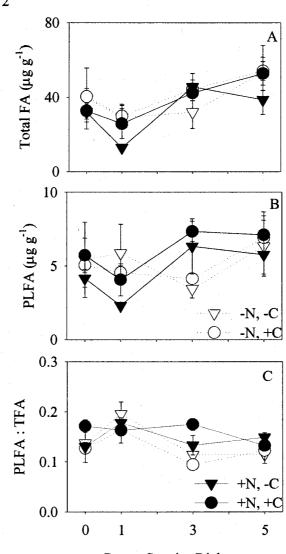
Figure 2. Effects of nutrient enrichment, food chain length, and the grazer community on the abundances of total fatty acids (TFA) and phospholipid linked fatty acids (PLFA) as well as the ratio PLFA:TFA. Results are presented for fatty acid abundance normalized to dry sediment (ng g^{-1}). See text for organic matter source assignment of each fatty acid biomarker subgroup.

Figure 3. Effects of nutrient enrichment, food chain length, and the grazer community TFA sub-classes. (A) Short-chain FA ($C_{12:0} + C_{14:0}$) abundance was reduced by nutrients and grazers. (B) C_{20} PUFA ($C_{20:4}+C_{20:5}$), representative of diatom OM, was least abundant in the one species treatment. (C) C_{22} PUFA ($C_{22:5}+C_{22:6}$), common in dinoflagellates, was more abundant in the grazer monoculture than the polycultures. (D) Branched FA (i, a $\Sigma(C_{13:0} - C_{19:0})$), from heterotrophic bacteria, were increased by predators and grazers. (E). $C_{20:5\omega3} : C_{22:6\omega3}$, indicative of diatom OM, was least abundant in the one-species treatments. Results are presented for fatty acid abundance normalized to dry sediment (ng g⁻¹).

Figure 4. Principal component scores for total fatty acid groups in treatments with and without nutrients. PC2 separated the grazer monoculture treatments from the grazer-free controls and three and five species treatments. PC1 tended to separate the treatments with three or five grazer species from the monocultures and controls; this effect was strongest in nutrient treatments.

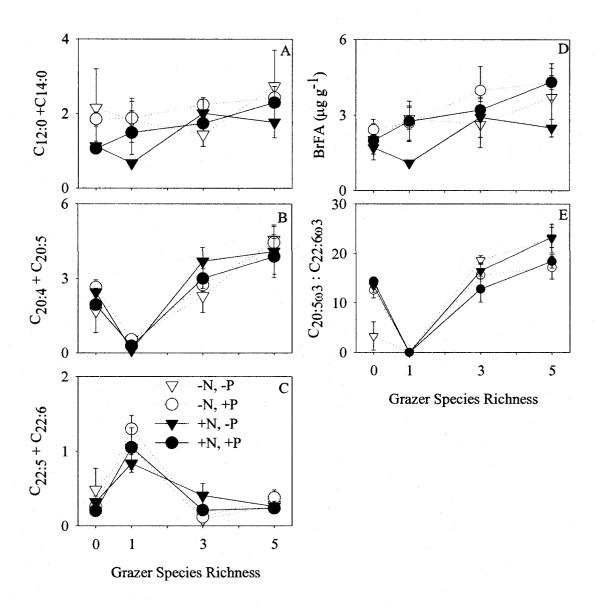


Spivak et al. Fig. 1

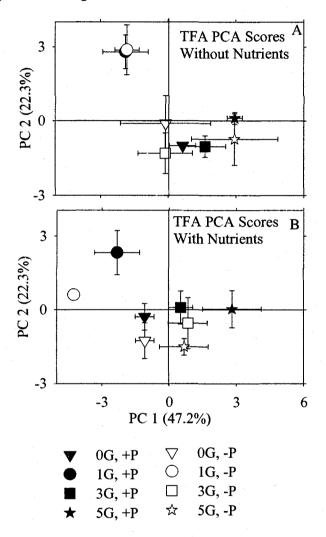


Grazer Species Richness

Spivak et al. Fig. 2



Spivak et al. Fig. 3



Spivak et al. Fig. 4

Chapter Six: A Summary

Amanda C. Spivak

Introduction.

The rapid loss of global biodiversity combined with changing environmental conditions has spurred research investigating interactions between biodiversity (Chapin et al. 1998; Balvanera et al. 2006; Bunker and Naeem 2006), community structure (Chase 2003; Burkepile and Hay 2006; Byrnes et al. 2006), and ecosystem functioning (Tilman et al. 2001; Downing 2005; Hooper et al. 2005). Changes in above-ground plant and animal communities that influence ecosystem functioning may also affect processes in soils and sediments (Wolters 2000; Liiri et al. 2002; Heemsbergen et al. 2004; Wardle et al. 2004). Detrital organic matter (OM) produced by above-ground communities often serves as substrate to below-ground organisms and, therefore, functionally links the two communities. The quality of sediment organic matter (SOM) is a partial determinant of sediment bacterial activity (Boschker and Cappenberg 1998; Holmer et al. 2004; Bouillon and Boschker 2006). Thus, changes in SOM quality that influence the sediment microbial community may have implications for nutrient cycling and regeneration. Thus, a goal of my dissertation was to address the role of SOM as a link between above- and belowground communities. I tested the interactive effects of above-ground community composition and resource availability on (1) SOM quality; and (2) ecosystem metabolism and nutrient dynamics in a seagrass habitat. I used a seagrass (Zostera marina) ecosystem as a model system because (1) the animal and plant communities are well studied (Valentine and Heck 1999; Duffy 2006; Heck and Valentine 2006); and (2) seagrass habitats are commonly influenced by perturbations that affect resource availability (i.e. eutrophication) and trophic structure (i.e. fishing) (Cloern 2001; Orth et al. 2006). The results from my dissertation will increase our understanding of seagrass ecosystem

functioning and will better elucidate the role of SOM as a link between above- and below-ground communities.

Experimental Design.

I examined the effects of resource availability and food web composition on seagrass ecosystem functioning in two mesocosm experiments and one field experiment. The first mesocosm experiment varied light levels, food chain length (i.e. predator presence), and grazer species richness (0, 2, or 4 species) in a factorial design (Chapter 2). This experiment ran for six weeks during Summer 2003. At the conclusion of this experiment I analyzed changes in gross ecosystem production (GEP), primary producer biomass, and bulk SOM content and composition. The second mesocosm experiment manipulated nutrient levels, food chain length, and grazer species richness (0, 1, 3, or 5)species) in a factorial design (Chapters 4-5). This experiment lasted 5 weeks in Summer 2006. I measured flux rates of dissolved oxygen (DO), dissolved inorganic nitrogen (DIN), and phosphate as well as changes in primary producer and grazer biomass and SOM composition. The field experiment had a similar design to the second mesocosm experiment; except that the presence (not richness) of the grazer community was varied (Chapter 3). The design of the field experiment was less complex that those of the mesocosm experiments due to the difficulty in maintaining grazer treatments and preventing contamination by non-target grazers. Field cages were situated in an eelgrass (Zostera marina) bed at Goodwin Islands in the York River, VA. This experiment ran for 4 weeks during Summer 2005. At the end of the field experiment I analyzed primary producer abundance and SOM composition. In all three experiments, SOM composition

was evaluated using fatty acid (FA) biomarkers. Please see the previous chapters for a more detailed explanation of FA biomarkers and their use. The remainder of this chapter is devoted to describing similarities and differences in the results of the three experiments and to describing the conclusions from this dissertation.

Discussion.

In general, grazer identity and community composition were stronger the determinants of FA composition than resource levels and predator presence. Predator effects on SOM composition were generally weak, suggesting that above-ground trophic cascades may not consistently affect plant contributions to SOM. Finally, resource identity was important; light availability was a stronger determinant of SOM composition than nutrient levels. The presence of interactive effects between food web composition and resource levels indicates that these factors should not be considered in isolation.

Grazers.

Grazers reduced algal biomass in all three experiments but only reduced Z. marina biomass in mesocosm experiment 2 (Tables 1, 2; Chapters 2-4). Grazer effects on the primary producer community often translated into changes in SOM composition. In mesocosm experiment 1, grazers reduced macroalgae and benthic Chl a as well as the relative abundance of algal and microbial FA ($C_{12:0} + C_{14:0}$; Table 1; Fig. 1). In mesocosm experiment 2, grazers reduced epiphytes and the relative abundance of FAs deriving from diatoms ($C_{20:4} + C_{20:5}$; Table 2). Although grazers strongly influenced both primary producer abundance and SOM composition, patterns of FA abundance were not consistent in grazer treatments across experiments (Tables 1, 2). For instance, the relative abundance of long chain FA (vascular plant OM) was decreased by grazers in ambient light treatments of mesocosm 1 ($C_{24:0}$; Chp. 2), was increased by grazers in the field experiment (C_{24:0}-C_{28:0}; Chp.3), and was unaffected by grazers in mesocosm 2 (C_{24:0}- $C_{28:0}$; Chp. 5). The relative abundance of short chain FAs (algal and microbial OM) was decreased by grazers in mesocosm experiment 1 ($C_{12:0}+C_{14:0}$; Chp. 2) but was increased by grazers in the field experiment ($C_{12:0}+C_{14:0}$; Chp. 3; Tables 1, 2; Fig. 1). While this is curious, differences in SOM composition between experiments may be the result of grazer community composition rather than grazer species richness. For example, mesocosm experiment 1 included two amphipod species (Ampithoe longimana, G. *mucronatus*) and two isopods (*Idotea baltica* and *Erichsonella attenuata*). The grazer community in the field experiment consisted of G. mucronatus, I. baltica, and E. attenuate. Finally, in mesocosm experiment 2, I used five amphipod species: G. mucronatus, Elasmopus levis, Melita nitida, Ampithoe valida, and Sympleustes spp. While there was some overlap in species composition between experiments (mainly G. mucronatus), none of the experiments used the same grazer community. Thus, differences in SOM patterns between experiments may be due to grazer community composition and the diet preferences of particular grazer species.

Previous studies demonstrated that grazer identity is important to multiple ecosystem properties (Duffy et al. 2001; Matthiessen et al. 2007; Jaschinski and Sommer 2008), including SOM composition (Duffy et al. 2003; Canuel et al. 2007). Canuel et al. (2007) found that the relative abundance of long chain FA (vascular plant OM) and short chain FA (algal and microbial OM) was higher in *G. mucronatus* and *E. attenuate*

monocultures, respectively. While these two grazer species had strong effects on FA subgroups in monoculture, SOM composition largely reflected the entire community, rather than a single species, in grazer polycultures (Canuel et al. 2007). This suggests that grazer diversity may weaken trophic effects that extend to SOM composition (Finke and Denno 2002; 2004). The averaging effect of a mixed grazer species on SOM composition was largely consistent with the results of mesocosm experiment 2 (Chp. 5). For example, C_{20} PUFA abundance and the ratio $C_{20:5\omega3}$: $C_{22:6\omega3}$ were lowest in the one grazer species treatment but were more abundant in the mixed species treatments. Consequently, it is important to consider the effects of the entire grazer community rather than the influence of the most abundant species.

Another trend was that multi-species grazer communities tended to have more similar SOM composition than treatments without grazers or with only one species. For instance, in mesocosm experiment 2, principal component (PC) scores of treatments with two- or four-grazer species were more similar to each other than either was to the grazer free controls in ambient light treatments (Chapter 2; Fig. 2). In mesocosm experiment 2, PC scores of treatments with three and five grazer species were consistently different from the scores of one grazer treatments (Chapter 5; Fig. 2). This trend was more evident with nutrient enrichment. However, it is important to note that *G. mucronatus* was the only grazer in the monoculture treatments and it was the most abundant grazer in the five species community did not resemble SOM patterns in the monocultures. This suggested that grazer identity rather than biomass is important to ecosystem properties (Duffy et al. 2001; Canuel et al. 2007; Jaschinski and Sommer 2008).

Predators.

In all three experiments, I initially predicted that the presence of crab predators would initiate a trophic cascade, whereby grazer biomass would be reduced and primary producer abundance increased. However, crab predators only had a positive effect on macroalgal biomass in mesocosm experiment 1 (Table 1; Chapter 2). This was somewhat surprising and suggested that the effect of predators may depend on the species composition of the grazer community. For instance, crabs sharply reduced total epifaunal biomass in mesocosm experiment 1 but not in mesocosm experiment 2 (Fig. 3). Thus differences in grazer community composition and grazer species susceptibility to predation by crabs likely affected the propagation of predator affects to lower trophic levels.

Positive predator effects on plants and algae may translate into increased labile algal contributions to SOM which could, in turn, stimulate sediment bacterial activity. For instance, Canuel et al. (2007) found higher abundances of polyunsaturated FA (PUFA), indicative of labile algal OM, and branched FA, deriving from heterotrophic bacteria, in treatments with predators. This suggested that predators indirectly influenced sediment biogeochemistry. However, there was no evidence of a positive predator effect on PUFA in any of the experiments described in this dissertation. Instead, predators decreased the relative abundance of PUFA in low light treatments of mesocosm 1 (Chp. 2) and in the field experiment ($C_{22:5} + C_{22:6}$; Chapter 3).. However, in both mesocosm experiments and in the field experiment, predators increased the relative abundance of branched FA (Fig. 4). Instead of increasing labile algal contributions to SOM, predators

may have influenced sediment bacteria through other processes such as fragmenting POM and increasing surface area, changing the chemical composition of OM, irrigation and sediment resuspension which reduce build-up of metabolites, etc. (Zimmer et al. 2002; Mermillod-Blondin et al. 2003; Zimmer et al. 2004). Shifts in sediment bacterial activity may have important implications for *Z. marina* and algal productivity. For instance, an increase in sediment bacteria that leads to anoxic conditions and a build up of sulfides may negatively affect seagrass health (Holmer et al. 2006; Calleja et al. 2007; Perez et al. 2007). Alternatively, an increase in sediment bacteria and bacterial activity in aerated surface sediments may lead to higher rates of mineralization and nitrogen availability to benthic microalgae (Eyre and Ferguson 2002; McGlathery et al. 2007). Consequently the positive effect of predators on the bacterial community may have implications for sediment biogeochemistry and the primary producer community.

Resources.

High resource levels increased above-ground macroalgal and epiphytic abundance in all three experiments while only light increased sediment microalgal abundance in mesocosm experiment 1 (Chps. 2-4; Tables 1, 2; (Douglass et al. 2007)). *Z. marina* biomass was increased by high light levels (mesocosm expt. 1; Chapter 2) but was decreased by high nutrient levels (field experiment; Chapter 3; Tables 1, 2). High nutrient levels increased epiphytes early in the field experiment (Douglass et al. 2007) and likely reduced *Z. marina* biomass by reducing light availability.

Changes in the primary producer community were reflected in SOM composition. For instance, algal and microbial fatty acids (FA) ($C_{12:0}+C_{14:0}$) were increased by high light availability (mesocosm expt. 1) but were decreased by nutrient enrichment (mesocosm expt. 2 and field expt.; Tables 1, 2; Fig. 1; Chps. 2-3, 5). High nutrient levels may have indirectly reduced algal and microbial FAs in the sediments by increasing shading by above-ground macroalgae. In general, however, the effects of light availability on SOM content and composition were stronger than nutrient enrichment. For example, a greater number of FA sub-groups (i.e. short and long chain FA, branched FA, polyunsaturated FA) were affected by light availability than by nutrient levels (short chain FA and branched FA in the field experiment). In addition, light availability strongly influenced where sediment FA sub-classes clustered in principal components analysis (PCA) while nutrient levels had little influence on FA groupings (Fig. 2; Chapters 2, 5). In ambient light, grazer-free treatments were clearly distinct from communities with twoor four-grazer species (Chp. 2). In low light, though, treatments were not separated by grazer richness but by predator presence or absence (Chp. 2). Combined, these results suggested that, in ambient light, treatments with grazers had more similar SOM compositions than grazer-free controls while, in low light, treatments with predators were more similar to one another than treatments without predators. Nutrient enrichment, however, had little effect on the PCA scores (Chp. 5). The results of these analyses suggested that light availability was a more important determinant of SOM composition than nutrient concentrations.

Although light was a stronger determinant of SOM composition, nutrient enrichment influenced both primary and secondary production as well as plant elemental content and dissolved nutrient fluxes (Chp 4). For instance, while light and nutrients both increased total algae in the mesocosm experiments, only nutrient enrichment extended up

a trophic level to increase biomass of the grazer *G. mucronatus* (Fig. 3). The positive effect of nutrients on *G. mucronatus* biomass might have been the result of higher abundance or higher quality of primary producers (i.e., lower C:N; Chp. 4). Consequently, both light and nutrients may be equally important determinants of ecosystem functioning but they may affect different ecosystem properties and processes.

Conclusions.

Overall, food web composition and resource availability were important determinants of seagrass ecosystem metabolism and SOM composition (Fig. 5). Importantly, resource identity had a strong influence on ecosystem nutrient fluxes, animal and plant biomass, and SOM composition. In general, light was a more important determinant of SOM composition than nutrient concentrations. However, nutrient enrichment strongly influenced nutrient storage in biomass and ecosystem metabolism (Chp. 4). Predator effects on SOM composition were generally weak and tended to vary with grazer community composition, suggesting that grazers differed in their susceptibility to predation by blue crabs. Finally, my results indicated that grazer species identity and community composition strongly influenced SOM composition. While individual grazer species may differ in their effects on FA sub-classes, multi-grazer species communities tended to have similar patterns of SOM composition, as indicated by PCA (Fig. 2). In addition to the main effects of resources and food web composition, there were a variety of interactions indicating that seagrass ecosystem functioning is influenced by multiple factors that should not be considered in isolation.

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Table 1. Comparison of results between mesocosm experiments 1 and 2. Resources were light and nutrients in experiments 1 and 2, respectively. Arrows indicate whether resource, grazers, or crabs increased or decreased the response variables. Fatty acid (FA) data are presented as percent of total FA abundance.

abundance.	Resource	Grazers	Crabs
Macroalgae	<u>ि 1</u>		
Z. marina			
Benthic Chl a		\square	
GEP	NA 1		Î
TFA : TOC			
%Short chain FA		Ţ	
%Long chain FA			
%Branched FA	IJ	1	
	esocosm Expt. 1	Mesoco	osm Expt. 2

Table 2. Comparison of results between the field experiment and mesocosm experiment 2. Arrows indicate whether nutrients, grazers, crabs increased or decreased plant biomass or fatty acid (FA) response variables. FA data are reported as percent of total FA abundance.

•	Nutrients	Grazers	Crabs
Epiphytes	1		
Z. marina		J	
%Short chain FA		1	
%Long chain FA			
%Branched FA	1	1	
%C ₂₀ PUFA			
%C ₂₂ PUFA		1	
Diatom : Dino.			
· · · ·	Field Expt.	Mesoco	sm Expt. 2

Figure Captions.

Figure 1. Comparison of short chain fatty acids (FA; $C_{12:0} + C_{14:0}$) abundance across experiments. Both nutrients and light reduced short chain FA, which are indicative of algal and microbial sources of OM. Significant (p < 0.05) effects of resources, crab predators, and grazers are indicated in the upper corner of each graph by R, C, or G, respectively. Treatments with predators are circles, without predators are triangles, with resources are closed, without resources are open.

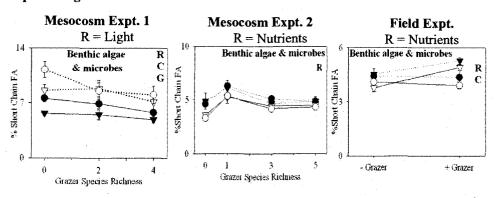
Figure 2. Comparison of PCA scores from two mesocosm experiments, one varying light availability and the other varying nutrient enrichment. In mesocosm experiment 1, circles represent treatments with crab predators and triangles represent treatments without crab predators. Open symbols represent treatments with zero grazers, shaded symbols are 2 grazers, and closed symbols are 4 grazers. In mesocosm experiment 2, triangles are zero grazers, circles one grazer, squares three grazers, and stars five grazers. Open symbols are treatments without crab predators while closed symbols denote treatments with predators.

Figure 3. Comparison of grazer biomass in two mesocosm experiments. Nutrient enrichment increased *G. mucronatus* biomass, suggesting that bottom-up forces may ascend the food web. Light availability, however, did not affect grazer biomass. Significant (p < 0.05) effects of resources, crab predators, and grazers are indicated in the upper corner of each graph by R, C, or G, respectively.

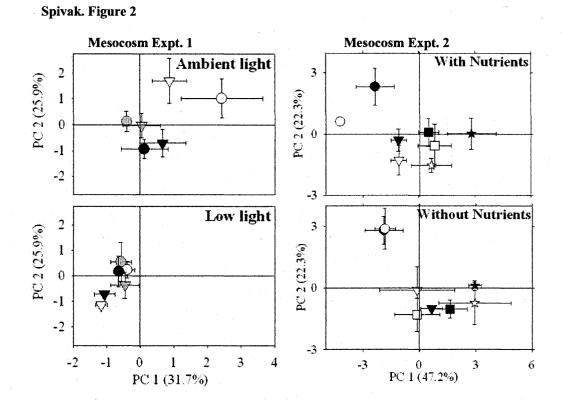
Figure 4. Comparison of branched FA abundance across experiments. Predators had a positive effect on branched fatty acids in all three experiments. Significant (p < 0.05) effects of resources, crab predators, and grazers are indicated in the upper corner of each graph by R, C, or G, respectively. Treatments with predators are circles, without predators are triangles, with resources are closed, without resources are open.

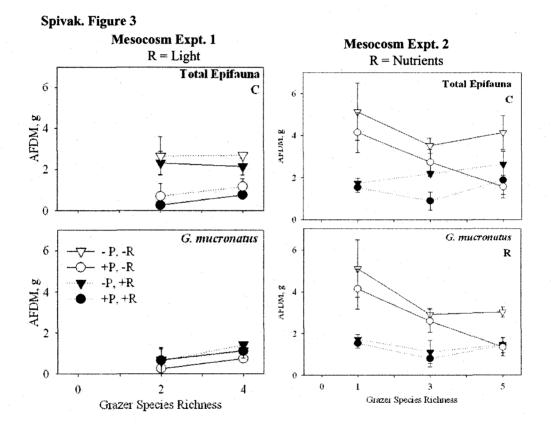
Figure 5. Comparison of the effects of resource levels, grazer richness, and predator presence on gross ecosystem production and sediment organic matter (SOM) content and composition in mesocosm experiments 1 and 2. Solid lines represent direct effects while broken lines are indirect effects. Dark lines represent main effects while light lines are interactive effects. Short chain fatty acids (FA), representing algal and microbial OM, are $C_{12:0} + C_{14:0}$. Bacterial FAs are iso, anteiso $\Sigma(C_{13:0} + C_{15:0} + C_{17:0} + C_{19:0})$. Polyunsaturated FAs, representing labile algal OM, are $\Sigma(C_{18:4} + C_{20:4} + C_{20:5} + C_{22:5} + C_{22:5})$

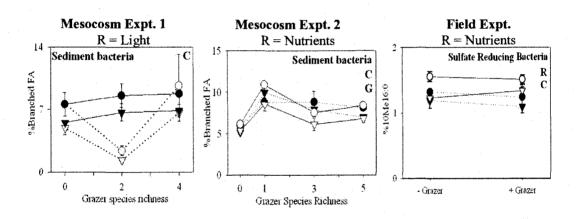
 $C_{22:6}$) except in mesocosm experiment 2 which does not include $C_{18:4}$.



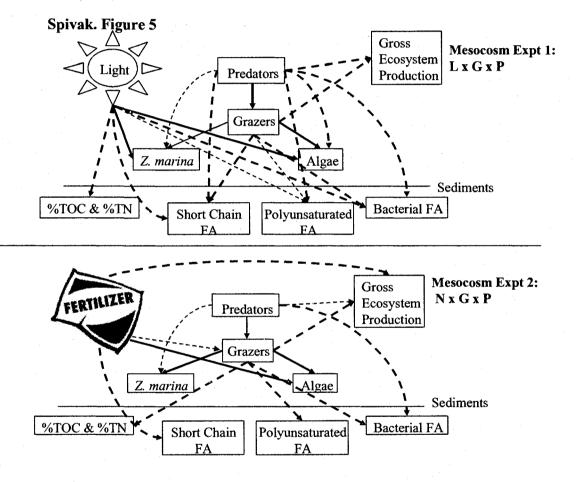
Spivak. Figure 1







Spivak. Figure 4



Appendix 1. Raw DO data from Chapter 2.

L/D					L⁄D	Water Vol (cm^3)	water vol (m^3)		DO (mg/L) (T-1)	DO (mg/L) (T-2)	DO (mg/L) (T=3)	DO (mg/L) (T=4)	{DO] (mM) T=0	(DO) (mM) [T=1	DO] (mM) [1 T=2	DO] (mM) [I T=3	DO] (mM) T=4	1 me (n) 1			Elapsed Time (h) T	
		Cylinda			r craha?			DO at T=0				(1)				-		= 0	=1	T= 2	~ 3	= 4
L	2		2 0	CON		141371.67	0.14	13.53	17.61	19.37	18.90		0.44	0.57	0.62	0.61		. 0.00	0.60	1.48	2.35	
	4		30	CON		141371.67		13.46 13.99	15.41	17.90	22.10		0.43	0.50	0.58	0,71		0.00	0.60	1.62	2.36	
ĩ			3 0	CON		141371.67	0.14	10.43	15.45	20,29 15,72	21,71 18,30		0.45 0.34	0.50 0.38	0.65	0.70		0.00 0.00	0.85 0.68	1.92 1.80	2.46 2.41	
Ē.	10		4 0	CON		141371.67	0.14	12.46	15.23	17.21	18.93		0.40	0.49	0.56	0.61		0.00	0.65	1.80	2.41	
Ľ	2		4 0	CON		141371.67	0.14	11.40	12.65	13.45	18.04		0.37	0.41	0.43	0.58		0.00	0.60	1.53	2.35	
L	4		4 0	CON	Noctab L	141371 67	0.14	13 36	16.57	17.30	21.58		0.43	0.53	0.56	0.70		0.00	0.60	1.70	2.38	
L	6		20	CON		141371.67	0.14	12.91	16.30	19.30	20.77		0.42	0.53	0.62	0.67		0.00	0.80	1.90	2.45	
L	8		60	CON		141371.67	0.14	12.97	16.22	20.10	22.59		0.42	0.52	0.65	0.73		0.00	0.72	1.87	2.42	
L	10		3 0	CON		141371.67	0.14	14.29	13.74	17.75	19.71		0.46	0.44	0.57	0.64		0.00	0.62	1.75	2.38	
L	6		5 2	AE	CRAB L	141371.67	0.14	10.92	13.03	16.40	17.71		0.35	0.42	0.53	0.57		0.00	0.80	1.88	2.45	
L	10		2 2	AI	CRAB L	141371.67	0.14	14.03	16.70	18.25	21.78		0.45	0.54	0.59	0.70		0.00	0.63	1.77	2.39	
L	4		62 42	CB CE	CRAB L CRAB L	141371.67	0.14	14.78 13.03	17.69	19.10	21.92 22.60		0.48	0.57	0.62	0.71		0.00 0.00	0.60 0.72	1.72	2.38	
L	ŝ		3 2	GI	CRAB L	141371.67	0.14	9.76	16.62 13.18	20.60 16.25	22.60		0.42	0.54	0.66 0.52	0.75		0.00	0.72	1.87 1.47	2.42 2.35	
L	6		4 2	AE	Nocrab L	141371.67	0.14	11.29	13.81	15.62	17.45		0.36	0.45	0.52	0.65		0.00	0.85	1.47	2.55	
ĩ	10		6 2	AL	Nocrab L	141371.67	0.14	9.01	9.60	11.47	13.52		0.30	0.31	0.30	0.44		0.00	0.67	1.93	2.41	
ŭ	4		1 2	CB	Nocrab L	141371,67	0.14	13.40	14.13	16.50	20,11		0.43	0.46	0.53	0.65		0.00	0.57	1.57	2.30	
ĩ	8		5 2	ČE	Nograb L	141371.67	0.14	9.48	12.05	15.02	17.05		0.31	0.39	0.48	0.55		0.00	0.68	1.83	2.41	
L	2		5 2	GI	Nocrab L	141371.67	0.14	8.23	9.72	11.75	11.27		0.27	0.31	0.38	0.36		0.00	0.73	1.62	2.35	
L	2		66	ALL	CRAB L	141371.67	0.14	15.47	14.47	18.88	22.90		0.50	0.47	0.61	0.74		0.00	0.62	1.58	2.36	
L	4		2 6	ALL	CRAB L	141371.67	0.14	10.97	12.72	16.25	20.07		0.35	0.41	0.52	0.65		0.00	0.60	1.67	2.36	
L	6		36	ALL	CRAB L	141371.67	0.14	9.30	.11.69	15.15	17.40		0.30	0.38	0.49	0.56		0.00	0.75	1.87	2.43	
L	8		16	ALL		141371.67	0.14	10.26	10.38	14.24	17.12		0.33	0.33	0.46	0.55		0.00	0.68	1.80	2.41	
L	10		1 6	ALL		141371.67	0.14	10.86	11.44	14.20	18.99		0.35	0.37	0.46	0.61		0.00	0.60	1.73	2.36	
L	2		1 6	ALL		141371.67	0.14	7.50	7.94	9.10	10.27		0.24	0.26	0.29	0.33		0.00	0.63	1.50	2.35	
L	4		5 6	ALL		141371.67	0.14	7.95	8.52	9.58	11.05		0.26	0.27	0.31	0.36		0.00	0.65	1.67	2.41	
L	6		1 6	ALL		141371.67	0.14	8.08	8.70	9.98	11.38		0.26	0.28	0.32	0.37		0.00	0.75	1.85	2.43	
L	10		26	ALL ALL		141371.67 141371.67	0.14	8.10	8.73 9.19	9.96	11.05 11.77		0.26	0.28 0.30	0.32	0.36		0.00	0.70	1.85	2.41	
L.	10		56	ALL	Nocrab L	1415/1.0/	0.14	8.76	9.19	10.77	11.77		0.28	0.30	055	0.58		0.00	0.63	1.77	2.39	
Ð	2		20	CON		141371.67	0.14	7.15	6.58	5.72	5.33	4.40		0.21	0.18	0.17	0.14		0.78	1.62	2.42	3.15
D	4		3 0	CON		141371.67	0.14	7.77	7.00	6.02	5.16	4.40		0.23	0.19	0.17	0.14		0.77	1.57	2.38	2.95
D	6		6 0	CON		141371.67	0.14	12.72	11.77	9.96	9.15	8.38		0.38	0.32	0.30	0.27		0.70	1.47	2.27	2,93
D			3 0	CON		141371.67	0.14	12.45	11.13	9.46	8.49	8.69		0.36	0.31	0.27	0.28		0.78	1.60	2.40	3.07
D	10		40 40	CON CON		141371.67 141371.67	0.14	8.50 5.78	7.65 5.06	6.30 4.30	5.66 3.46	5.06		0.25	0.20 0.14	0.18 0.11	0.16		0.70 0.78	1.50 1.60	2.32 2.40	2.98 2.93
D	4		4 0	CON		141371.67	0.14	5.06	4.79	4.50	3.00	2.95		0.15	0.14	0.10	0.05		0.78	1.57	2.40	2.85
D	6		2 0	CON		141371.67	0.14	12.72	12.20	11.10	10.63	9.68		0.19	0.36	0.34	0.31		0.77	1.53	2.38	3.00
Ď	ŝ		6 0	CON		141371.67	0.14	7,12	6.05	5.22	3.89	3.41		0.20	0.17	0.13	0.11		0.80	1.62	2.42	3.08
Ď	10		3 0	CON		141371.67	0.14	10.07	8.15	7.65	6.23	4.75		0.26	0.25	0.20	0.15		0.73	1.53	2.35	3.02
Ď	6		5 2	AE	CRAB D	141371.67	0.14	6.05	6.32	5.66	4.90	4.35		0.20	0.18	0.16	0.14		0.68	1.45	2,25	2.92
D	10		2 2	Al	CRAB D	141371.67	0.14	6.29	5.49	4.54	3.64	3.20		0.18	0.15	0.12	0.10		0.77	1.57	2.38	2.88
D	4		62	CB	CRAB D	141371.67	0.14	11.54	10.77	9.71	9.20	8.71		0.35	0.31	0.30	0.28		0.72	1.52	2.33	3.00
D	8		42	CE	CRAB D	141371.67	0.14	11.68	10.62	10.22	9.14	8.55	0.38	0.34	0.33	0.29	0.28		0.78	1.60	2.40	3.07
D	2		32	Gl	CRAB D	141371.67	.0.14	8.15	7.36	6.17	4.77	3.30	0.26	0.24	0.20	0.15	0.11	0.00	0.78	1.63	2.43	3.17
D	6		42	AE.	Nocrab D	141371.67	0.14	10.60	9.60	7,88	7,19	6.49		0.31	0.25	0.23	0.21	0.00	0.70	1,47	2,27	2.93
D	10		62	AI	Nocrab D	141371.67	0.14	6.70	6.00	5.12	4,58	4.00		0.19	0.17	0.15	0,13		0.72	1.52	2.33	3:00
D	4		1 2	CB	Nocrab D	141371.67	0.14	10.46	9.32	7.79	6.94	6.98		0.30	0.25	0.22	0.23		0.78	1.60	2.40	3.07
D	8		5 2	CE	Nocrab D	141371.67	0.14	6.55	5.37	3.60	2.70	2,04		0,17	0.12	0.09	0.07		0.77	1,58	2.40	3.07
D	2		52	GI	Nocrab D	141371.67	0.14	7.21	6.91	6.37	5.89	5.41		0.22	0.21	0.19	0.17		0.78	1.63	2.43	3.15
D	2		66	ALL		141371.67	0.14	6.73	6.33	5.68	4.96	4.35		0.20	0.18	0.16	0.14		0.78	1.52	2.32	3.03
D	4		2636	ALL	CRAB D CRAB D	141371.67 141371.67	0.14	6.32 6,20	5.43 5.39	4.51 4.66	3.66 3.88	3.05 3.30		0.18 0.17	0.15	0.12	0.10		0.77	1.57	2.38 2.33	2.90 3.00
D	6		3 0	ALL	CKAD D	141571,67	0.14	6,20	5.59	4.00	3.88	5.30	0.20	0.17	0.15	0.13	0.11	0.00	0.77	1.55	4.55	5.00

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	116.87		29.65093		104.2147		0				125.466									87.04735			
		628.5864 54.09237			646.2334 3.063863						517.5844 33.06462				496,3989 36,53303					575.0873 31.5211		975.7748 54.75743	
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	43.44156	13.30586				25.7528	2.276306								221.9921				205.97	247.6698	57.98652	1144.613	
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	176.0949		182.2764			299.592														264.9557			
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		111.8382																		13,15319			
		350.667													217.2038							490.7345	
4	199.8547		44.54668		107.1832		0	2.716862	190.1093	210.3252	86.1062	82.62687	169.3928	111.3103	73.94578	55.19978	184.0851	0	149.8818	240.6431		201.6795	
	0				337.6191															569.2064			
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		289.4523 969.1965													506,9992 229,2098			1264.444		470.2611 253.8159			
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		64.41961												1.676775		3.87427		3.907096				79.54635	
	39.1012		0	0	0	0	0		40.21777			ŏ			5,28381					3,361528		0	6.873
		82.68586																		38.49195		37.58948	
		1204.492																					
		308.3948																		572.6971		391.6758	
		749.1835				383.1155 8.588884					64.71934 136.197									1748.466		2718.057	
		193.9013				324,9087														101.7898			
		341.4839																		11.19858			
		96.35635																		45.07445			
:0	1696.733	1331.906	1313.64	1256.016	1198.98	1265.618	1213.238	939.35	1719.827	1666,763	868.0251	925.8501	887.6537	669.4764	1079.482	1239.601	813.3651	883,9331	1011.179	1302,233	1410.282	1976.69	1410
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:6w6		68.72821		0		55.35907		0			27.03213				105.3704					90.95855		205.3564	
	349.9802	137.9341 0	73.0095	0	409.0171	98.32411 0	18.37949	0.	514.7531	643,4588 0	146.1245 n	113.1603	241.369	236.7937	343.521	89.42597	215.9219	280.6085	442.9067	406.9807	408.6475	705.8287	0
		75.38913.	•	0		34,14964		0										•	•	97.51967		202.7029	
		55.24187		0	0	22.60769					5.888659				00.00031	0	0	11.76055		22.51066		0	0
		22.19528		õ											7.711331					22.88494			ō
		368.9305													190.7254							767.9847	
:0		181.3865																		184.4604			
:0 :0			14.80615		35.68356		25.98063							3.687712		8.867243					28.08308		38.1
:0 :0 :1	63.76675						367.5511	216.8559		896.174 0	293.4166 0	108,7643	408.3511	248.7116	295.4129	207.38 0	202.7696 D	477.8656	344.9494 0	508.1518 0			279.1
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9-6 plfa	1-4 pHa	3-6 pila	5-1 plfa	7-2 pita	9-5 pite	1-1pila	3-5 pita	5-5 pite	7-4 pife	9-4 pilia
0	. 0	3.243991	5.756961	3.682631	. 0	. 0	2.611853	2.158451	6,137615	4.630076
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3.326671	o	3.073962	3.976431	6.292795	1.964555	3.017897	2.468095	2.068509	3.95303	
36,16847	0	32.44735	113.9928	85.47178	55.20583	7.616705	5.859143	10.12193	59.44476	32.63173
37.10303	4,958955	180.3173	226.3874	128.106	58.34124	26.43944	66.33768	49.84056	185.8751	136.5733
5.501561	10.40352	150.8304	163,7198	54.92845	10.4058	11.56106	71.7694	57.44213	188.2313	
5.556895	5.979507	92.64906	118.5863	33.31091	10.2256	7.193574	43.67189	39.56136	111.4773	
4.357881	0	5.136227	10.11062	11.29508		3.046482	5.23286	6.193687	3.238624	7.606438
6.602844	5.185986	41.00397	50.4061	21.87616	8.166045	9.204666	24.14612	24,50674	49.85944	47.67442
. 0	0	6.286585	6.507833		0		0	0	5.683767	5.107568
0	0	0	0	0				0	0	0
3.981834	0	0	0		0		6.52107	7,848187	0	0
0	4.321488	70.81995	64,66748	23.31	4.00773		26.81541	21.99459	80.00106	
11.65996	4.933357	481.7949		112.5269				102.5733	438.6491	
6.223241	0	45.91153	47.76607	12.21008	5.575593	0	13.27078	11.47849	47.84614	
142.9181	88.0444	609.024	870.8121	472.5528	196.2079			313.8631	826.1931	606.7238
0	0	16.08849	20.32636	0	Ð	0		7.447559	25.46796	21.88878
0	4.958897	27.56194	29.93567	9.797578		5.11136		10.95746	31.82131	31.40134
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	4.776226	17.87073	23.33812				7.232693	7.923429		
18.91974	5.389798	49.9586 0	39.53283		10.9475	100.8629	70.65208	82.3175 0	42.69222	37.22497
4.944835	18.67264	41.4143	29.59519		11,21953			25.24547	33,42639	
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32,51674	10.77134	68.3443	59.43124 229 3808		2.610382			21.86908	307.4382	
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126.5528	21.8166	141,3577	20.92986		158.8600		87.05168	70,83719	98.99458	
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2.087578	0	6.826723	4.236734	7.667415				0.68544	6.419417	4.966333
3.214852	6.017385	14,90035	19,79429					12,73014	11.24132	
106.7113	105.275	108.782	102.9507	222.474	105,7828	121.9923	109.6596	110.1432	107.7255	106,1525
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107.4706	0	146.8004	5.036677	209.2072			0	12.28908	3.484063	
6.064086	4.565439	14.8639	11.64681	13,76218		16,29208		15.5821	9.362015	
48.03051	57.5623	43.3655	38.36612		53.55705				40.24136	
6.12709	0	1.07379	4.190724	12 17353		15.65456		5.724679	9.495026	3.727615
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5.428098	0	7.808642			4.606135		0	0	0	0
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17.15855	0	0	10.95074	7.851335		6.817368		11.59958	8.595819	
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Component 12:0					41 TFA 217.9196	17 TFA			45 TFA				22 TFA		40 TFA			25 TFA							43 TFA
12.0					108.3891								75.06108												
a13	31.1393	28.53665	25.21564	43.85799	52.07119	32.22024	19.75595	35.09886	34,39384	34.07938	14.65692	13.26581	40.83063	35,13925	25.40659	41.4751B	23,87682	17.70921	31.73959	40.9965	97.70433	23.68441	72.92945	58.09555	41.26304
13:1					39.84132															25.02538		0	0		26.02625
13:0 *i14*					173.0622 752.1951								108.7146				112.2312 433.0114								
14:1	94.36454		58.29828		163.0555												100.3809								
14:0					2681.619																				
i15 a15			901.6061		2159.788 2889.375								1417.579 2011.393												
a15 15:1				2346.437									2011.393												
15:0			884.4854				1504.391						910.6801												
16:4	82.94488		59.12464										82.64223												81.65637
16:3 *16:2*	0 9.528323	0	0	° °	0	0	0	0	0	0	0	0	0	0	0	0	0	0	. 0	0	0	92,94264	0	0	0 209.2208
116				893.3969					15.77808		13.76701		0 717.4827				451.1538								
16:1w7				8153.528									5088.965				8800.253	4152.26	5435.677	6385.327	7148,958	2241.114	6007.89	4298.926	5342.458
16:1w9	368.5281			435.1867				43.32657					291.7047									631.9181			
16:0	8148.682		6075.889 356 8805		12296.92																				
10Ma17br i17	537.1932 429.6717		265.525		773.3399 619.3659																				
a17			1036.927		1630.964		1045.683						607.7424												
17:1					448.9841								242.3218												
17:0 *18:4*				803.0907	1118.784 254.6999			764.8262					779.4588 106.8368							980.984				860.9645	
18:4					254.5999 509.3008																				
18:2					1078.909												690,645					382.0466			
18:1w9c					3310.664																				
18:1w9					5244,287																				
18:0			1572.216		2857.291 33.09569		2084.58 80.42127		2142.793	2431.181 64.68658			1806.095 136.5904							4.833236		1082.802			
a19					96.28326																				
19:1	31.5331	52.54722	12.95016	55.67647	89.44124	79:30027	47.35815	72.28976	105.5036	54.74934	89.32461	15.59548	78.89772	15.67042	77.75304	123.2279	61.32239	33.26529	50.54768	35.01909	64.7788	21.90999	70.44917	57.43254	82.5275
19:0					6176,625																			3940.652	
20:5w6 20:4w6				56.77219	2342.701		13.45541	14.73973 1951 AP2		68.81465			60.07489 1243.255								144.4529			55.16774	
20.5w3					2656.731																				1678.238
20:3	107.1511	118,731	111.4862	124,6829	130.7764	166.5371	190.0572	157.7226	170.0897	111.9201	888.5623	159.6522	91.65349	170.6393	439.7414	189.5853	134.5413	106.5328	117.8986	131.2194	166.9803	41.9868	109.2096	64.30395	
20:2					121.4437												164,4116								
20:1w7 20:0			94.20498 2561.902				113.23 3092.266						160.3568 2975.552				3200.704							2999.323	
21:0					2958.105												1731.517								
22:6w6					82.38139					0	0	0	0		38.82711	0	0	0	0		0	0	0	0	0
22:5w3				160.1028									145.0759												
*22.5w6 22:5w3	106.1255		125,9033	165.7077		620.979 412.2101	215.9425 248.028						204.7857 210.2097												
22:300					4,808738																				
22:1w9	89.95419	61.42263	57.16041	60.48142	82.54384	68.8633	48.04765	57.62381	58.25422	69.83849	62.87602	98,56298	68.44626	86.79127	59.36058	98.95076	64.99765	41.62877	72.39514	105.2186	20.02007	15.26219	27.4085	14.44368	46.88428
22:0					1044.712																				
23:0					586.7621 42.98869															508.6635				390.1104	363.6632
24:1 24:0					42.95869																				1258.037
25:0	122.7394	138.619	74.48169	153,2996	217.8007	206.6777	106.9127	115.8573	124.3632	122.6548	88.8569	79.34661	173.1499	118.0715	106.8291	134,8313	353,8985	58.77371	79.19319	133.472	209,1208	138.7564	191.779	157.6309	161.4437
26:0	611.0721			732.5582									813.5595										1045.061	780.0331	840.5099
27:0 28:0	0	0	0	0 339.7737	0 509.7216	0 307.0783	0 253.0127	0 259.5857	0	0	0 170.4349	214.521	0 481.7821	414 382	0	0 260,7031	0 360,5041	119 6612	178 6614	270.0040	577 5006	0 440.1869	524 4600	248 6364	430 1565
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14:1			12.10634										8.310014												
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a 15	465.9839	409.533	245.9523	307.4828	357.9167	450.1059	329.1076	308.8513	289.6457	276.6753	402.8596	241.5877	383.5505	356.8222	185.0901	495.8722	365.6645	213.5077	265,8945	441.8464	511.7136	297.7874	489.0867	582.4337	716.757
16:1 15:0													12.69015												
16:4													156,1195 14.26192												
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16:1w7													678.925												
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i17	114.786	109.0311	67.43583	73.46801	101.213	129.5181	103.4336	99.09138	64.46347	70.7975	156.7556	58.97935	106.4345	137.7996	61.65973	143.6983	111.5117	97.1767	85.32691	99.1654	135.0814	71.93007	132.8066	157.4211	158.2068
e17 17:1		139.9905 52.8394	68,12973	90.0498 29.28012		160.3491							109.9076 44.12978												
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18:4		14.88541											9.248553											10.41031	
18:3 18:2	53.10402 145.7187												54.25783 138.3963												
18:1w9c	784.4086	695.6954	642.1466	578.4634	560.3354	727.7371	775.8868	510.4441	648.4569	640.3844	692.2555	302,2303	535,4667	651.9167	576.0095	592.4751	469.8146	297.7652	464.0373	510.1913	630.7752	298,511	475.8597	753.4982	843.5836
18:1w9													787.8725												
18:0 N19*			21.34465		374.1867		632.2712 31.01972			1204,347			468.4728								519.9075				
a19	30.93681	28.87655	16.84203	20.4985	22.55859	31.70947	20.84394	21.65801	30.33507	15.60361	47.47248	13.48612	30.47712	45.05609	19,17232	32.7036	21.67003	24.60227	27.62523	33.70454	36.45966	17.37708	29.06566	39.15602	41.32631
19:1 19:0													21.13506									74 00212		10.25782	
20:5w6	9.88942			23.79276				14.73973		35.81192			20,081								20.50284				0
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20:2	19.98973	30.98758	26.08592	22.34417	21.91046	52.02772	27.75898	28.09373	41.14757	32.11689	71.13593	29.03957	28.63549	58.90679	37.03682	71.5549	42.0471	29.90817	51.34666	28.09764	0	19.47032	29.35554	26.22022	20.35324
20:1w7 20:0			22.47917	23.29186	21.65886	39.20606	32.25416	32.52952	35.52085	24.55235	9.480435	28.82754	42.75148 80.19186	9,599046	26,51374	06.74355	40.41833	68.49767	5.663912	43.245	169.2903	32.39364	62.33669	84.11952	7.969951
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22:6w6				9,416606			8.328196			0	0				38.82711							0	0	0	0
22:6w3 *22:5w6													35.46773										42.46234		
22:5w3	20.61845	36.86287	28.00648	25.73789	18.21441	93.66989	38.3354	34.85607	75.22249	29.17563	225.2389	61.67548	62.90161	261.8374	89,53086	171.5178	69.12929	118.6481	147.7688	119.3959	65.1981B	47.20604	63.13498	115.6902	108,1149
22:2 22:1w9			9.253346										8.285841 15.99654								7.404915 20.02007				
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 10.5 7 394636 235.8047 266.2957 378.4974 10.99977 136.7254 13.91542 0 4.648336 126.6426 535.7645 32.845 1416.888 95.07141 256.7438 267.0654 345.8312 12.887 133.1783 24.94967 0 0 246.1269 308.2314 9.003193 122.6462 13.1226462 13.12981 0.9.905593 118.4393 597.3508 25.30986 25.30986 25.30986 25.30986 25.30986 25.30986 25.30986 25.30986 25.30986 25.30986 25.30986 25.30986 25.30986 25.30986 25.30986 1.47805 25.50986 26.50935 10.45866 0 125.8392 20.18756 26.60423 27.747 86.94594 6,054403 0,7,852297 67,37733 302,1631 105,8012 800,5815 42,80678 46,05748 46,05748 46,05748 46,05748 46,05748 46,05748 30,06712 36,41854 7,420004 43,31163 43,31163 43,31163 43,31163 43,31163 43,31163 43,31163 43,31163 43,31163 43,31163 43,31163 43,31163 44,31163 44,31163 44,31165 10,375791 14,3757 14.64804 45.59795 248.0523 0 10.74185 14.63326 10.08693 0 71.98246 10.44301 46.67401

	Appen	dix 6.	Daytime (light) DO flu	xes from Cha	pter 4.																
				•			DO (mg/L)	DO (mg/L)	DO (mg/L)	DO (mM)	DO(mM)	DO (mM))	DO (mM)									
1		cosm			richness	T1	· T2	T3	T4	T1	T2	T3	T4	TI (min)	T2 (min)		T4 (min)			T3 (†r)	T4 (hr)	
	10	5	1	. 1	0	9.31	13.56			0.29094				0	74	145	206	0.00	1.23	2.42	3.43	
	12	6		1	0	10.33	12.49	14.61	18.31	0.32281	0.39031	0.45656	0.57219	0	70	150	213	0.00	1.17	2.50	3.55	
	14	3	_ 1	1	. 0	10.8	13.34	18.5	19.3	0.3375	0.41688	0.57813	0.60313	0	72	154	207	0.00	1.20	2.57	3.45	
	10	6	1	1	. 1	9.16	10	10.96	11.93	0.28625	0.3125	0.3425	0.37281	0	74	148	205	0.00	1.23	2.47	3.42	
	11	6	1	1	1	8.61	9.29	10.74	11.43	0.26906	0.29031	0.33563	0.35719	0	68	154	219	0.00	1.13	2.57	3.65	
	12	3	1	1	1	7.27	7.99	8.6	9.33	0.22719	0.24969	0.26875	0.29156	0	73	155	211	0.00	1.22	2.58	3.52	
	8	3	1	1	3	8.71	9.69	11.05	12.65	0.27219	0.30281	0.34531	0.39531	0	71	147	204	0.00	1.18	2.45	3.40	
	10	7	1	1	3	9.46	10.61	12.51	13.41	0.29563	0.33156	0.39094	0.41906	0	74	145	206	0.00	1.23	2.42	3.43	
	11	4	1	1	3	7.82	8.74	9.74	10.79	0.24438	0.27313	0.30438	0.33719	0	67	153	218	0.00	1.12	2.55	3.63	
	9	4	1	1	5	8.8	10.53	12.93	14.07	0.275	0.32906	0.40406	0.43969	ō	74	148	205	0.00	1.23	2.47	3.42	
	11	5	1	1	5	7.68			11.12			0.31406	0.3475	. 0	71	153	215	0.00	1.18	2.55	3.58	
	14	2	1	1	5	9.51	10.55			0.29719				ō	70	151	207	0.00	1.17	2.52	3.45	
	8	4	1	0	0	12.46				0.38938				ō	71	146	204	0.00	1.18	2.43	3.40	
	12	1	· 1	ŏ	0	7.8			15.94			0.42375		ŏ	72	154	211	0.00	1.20	2.57	3.52	
	14	4	. 1	ŏ	. 0	12.8		17.08	16.22			0.53375		ŏ	71	153	210	0.00	1.18	2.55	3.50	
	9	6	2 1	Ö	1	8.53			13.41			0.39563		ŏ	72	146	204	0.00	1.20	2.43	3.40	
	9	6	-	ő					15.56			0.39303		ö	74	148	205	0.00	1.23		3.40	
	-	-		0	-	9.87	11.5	15.61												2.47		
	12	2	1	-		10.08			15.06			0.44688		0	71	154	216	0.00	1.18	2.57	3.60	
	-	2		0	. 3	8.52				0.26625			0.375	0	72	148	205	0.00	1.20	2.47	3.42	
	11	7		0	3	7.15			10.6			0.30719		0	71	153		0.00	1.18	2.55	3.60	
	12	. 5	1	0	3	9.04	10.55		12.09			0.35281		0	72	154	209	0.00	1.20	2.57	3.48	
	9	5	1	0	5	8.35		10.9	12.6			0.34063		0	74	148	205	0.00	1.23	2.47	3.42	
	10	8	1	. 0	5	9.38			14.07			0.42094		0	74	146	203	0.00	1.23	2.43	3.38	
	12	7	1	0	5	8.8			11.31			0.34625		0	69	150	205	0.00	1.15	2.50	3.42	
	8	8		1	0	12.91	17.34			0.40344				0	70	147	204	0.00	1.17	2.45	3.40	
	10	1	0	1	0	9.9			16.47			0.38156		- 0	74	146	204	0.00	1.23	2.43	3.40	
	14	8	0	1	0	9.2	9.74	11.64	12.63	0.2875	0.30438	0.36375	0.39469	0	71	152	208	0.00	1.18	2.53	3.47	
	8	5	0	1	1	7.03	7.82	8.33	9.22	0.21969	0.24438	0.26031	0.28813	. 0	71	147	204	0.00	1.18	2.45	3.40	
	9	7	0	1	1	8.07	8.64	10.2	11.51	0.25219	0.27	0.31875	0.35969	0	73	147	204	0.00	1.22	2.45	3.40	
	10	4	0	. 1	1	8.34	9.54	10.37	10.96	0.26063	0.29813	0.32406	0.3425	0	74	148	204	0.00	1.23	2.47	3.40	
	9	8	0	1	3	8.15	8.92	10.59	11.67	0.25469	0.27875	0.33094	0.36469	0	74	148	205	0.00	1.23	2.47	3.42	
	11	2	0	1	3	11.28	12.74	13.67	14.9	0.3525	0.39813	0.42719	0.46563	0	69	153	220	0.00	1.15	2.55	3.67	
	12	4	0.	1	3	8.85	9.06	9.76	11.3	0.27656	0.28313	0.305	0.35313	0	71	152	214	0.00	1.18	2.53	3.57	
	9	3	0	1	5	7.65	8.15	9.55	11.05	0.23906	0.25469	0.29844	0.34531	0	74	148	205	0.00	1.23	2.47	3.42	
	10	2	0	1	5	7.91	8.69	9.56	10.55	0.24719	0.27156	0.29875	0.32969	0	73	147	205	0.00	1.22	2.45	3.42	
	11	3	Ō	1	- 5	7.57	8.12	9.56	10.08	0.23656	0.25375	0.29875	0.315	0	71	153	217	0.00	1.18	2.55	3.62	
	8	2	Ō	0	0	15.51	17.94		24.94			0.63063		0	71	145	202		1.18	2.42	3.37	
	9	1	ō	ō	ō	9.8		13.87		0.30625			0.5275	ō	75	148	205	0.00	1.25	2.47	3.42	
	14	1	õ	Ď	ů ř	9.5		12.56	14.37		0.34281		0.44906	. Õ	72	154	207	0.00	1.20	2.57	3.45	
	8	1	ŏ	Ď	1	8.8			13.21			0.36469		0	71	138	195	0.00	1.18	2.30	3.25	
	12	8		õ	1	9.4		12.75		0.29375				ő	71	151	213	0.00	1.18	2.52	3.55	
	14	7	ŏ	0	4	9.8		12.75		0.30625				ő	72	153	205	0.00	1.20	2.55	3.42	
	14	2	0	0	3	9.6 7.5			9.99		0.30701		0.31219	. 0	71	133	203	0.00	1.18	2.55	3.42	
	11	- 1 i	0	0	3	7.23				0.23436				0	71	153	204	0.00	1.18	2.45	3.40	
	14	5	0	0	. 3									0	72	153	206		1.10	2.55	3.62	
	14	5	U	0		8.65	9.98	10.8	11.01	0.27031	0.31166	0.00120	U.30201	U	12	104	200	0.00	1.20	∡.5/	3.43	

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Арр	endix	7. N	litetime (dar	k) DO flux	es from Chap																
							DO (mg/L)			DO (mM)		DO (mM))									
	COS		nutrients	crab	richness	T1	T2	T3	DO (mg/L) 14	T1	12	T3	T4	Ti (min)	T2 (min)	T3 (min)			T2 (hr)		
1		5	+	+	0	5.2	3.89	3.47	2.67			0.10844		0	57	114	170	0.00	0.95	1.90	2.83
1.		6	+	+	0	5.14	3.8	3.08				0.09625		0	59	127	186	0.00	0.98	2.12	3.10
1		3	· +	+	0	5.08	4.31	4.26				0.13313		0	60	135	194	0.00	1.00	2.25	3.23
1		6	+	+	1	4.94	4.18	3.63				0.11344		. 0	55	114	170	0.00	0.92	1.90	2.83
1		6	+	+	1	9.39	8.07	7.1				0.22188		0	61	126	185	0.00	1.02	2.10	3.08
1:		3	+	+	1	5.75	4.99	4.27	3.69			0.13344		0	58	127	188	0.00	0.97	2.12	3.13
	8	3	+	+ '	3	7.59	6.69	5.84	4.77		0.20906		0.14906	0	57	111	169	0.00	0.95	1.85	2.82
1		7	+	+	3	5.62	4.87	4.32			0.15219		0.12094	0	57	114	170	0.00	0.95	1.90	2.83
1		4	+	+	3	6.23	5.33	4.78				0.14938		0	64	124	189	0.00	1.07	2.07	3.15
	9	4	+	. +	5	5.56	4.91	4.43			0.15344		0.12	0	58	113	170	0.00	0.97	1.88	2.83
1		5	+	+	5	5.95	5.09	4.35	3.73			0.13594		· 0	59	.126	185	0.00	0.98	2.10	3.08
1-		2	+	+	5	5.91	5.19	3.11	3.84		0.16219		0.12	0	58	127	180	0.00	0.97	2.12	3.00
	8	4	+	÷	0	8.29	7.07	6.09	5.16			0.19031		0	61	113	171	0.00	1.02	1.88	2.85
1.		1	+	-	0	5.24	4.33	3.07				0.09594		0	58	126	187	0.00	0.97	2.10	3.12
1-		4	+	-	0.	5.64	4.48	3.37	2.25	0.17625		0.10531		0	58	128	191	0.00	0.97	2.13	3.18
;	-	6	+		1	7.32	6.31	5.42	4.6	0.22875	0.19719	0.16938	0.14375	0	61	113	172	0.00	1.02	1.88	2.87
	9	6	+	÷	1	7.17	6.33	5.71	4.9	0.22406	0.19781	0.17844	0.15313	0	57	112	169	0.00	0.95	1.87	2.82
1.	2	2	+	-	1	5.07	4.1	3.07	2.42	0.15844	0.12813	0.09594	0.07563	0	57	<u> </u>	174	0.00	0.95	1.95	2.90
	9	2	+	-	3	5.31	4.67	4.2	3.65			0.13125		0	57	112	169	0.00	0.95	1.87	2.82
1		7	+	•	3	5.58	4.81	4.06	3.64			0.12688	0.11375	0	58	126	185	0.00	0.97	2.10	3.08
1.		5	+	-	3	5.04	4.18	3.53	2.88	0.1575	0.13063	0.11031	0.09	0	57	111	171	0.00	0.95	1.85	2.85
	9	5	+	-	5	5.48	4.73	4.09	3.37	0.17125	0.14781	0.12781	0.10531	0	54	112	167	0.00	0.90	1.87	2.78
1	0	8	+	-	5	4.96	4.82	3.45	2.91	0.155	0.15063	0.10781	0.09094	- 0	55	114	170	0.00	0.92	1.90	2.83
1.		7	+	-	5	5.88	5.16	4.45	3.87			0.13906		0	59	130	190	0.00	0.98	2.17	3.17
	8	8	-	+	0	6.95	6.23	5.62	4.91	0.21719	0.19469	0.17563	0.15344	0	59	112	170	0.00	0.98	1.87	2.83
1		1		+	0	5.31	4.78	4.32					0.11938	. 0	- 56	114	170	0.00	0.93	1.90	2.83
1.	4	8		+	0	7.61	7.26	6.65	6.41	0.23781	0.22688	0.20781	0.20031	0	59	128	193	0.00	0.98	2.13	3.22
	8	5		+	1	7.81	7.53	7.19	6.92			0.22469		0	58	112	169	0.00	0.97	1.87	2.82
1	9	.7	-	+	1	5.11	4.59	4.07	3.71			0.12719		0	54	113	168	0.00	0.90	1.88	2.80
1		4	•	+	1	5.22	4.79	4.28	3.89			0.13375		0	55	114	170	0.00	0.92	1.90	2.83
	9	8	-	+	3	5.98	5.46	5.07	4.66			0.15844		0	57	112	170	0.00	0.95	1.87	2.83
1		2	-	+	3	6.4	5.62	4.79	4.1	0.2	0.17563	0.14969	0.12813	0	63	123	188	0.00	1.05	2.05	3.13
1.		4	-	+	3	6.4	5.81	5.54	5.19			0.17313		0	- 58	128	186	0.00	0.97	2.13	3.10
1	9	3	-	+	5	5.56	5.17	4.78	4.41	0.17375	0.16156	0.14938	0.13781	0	55	112	167	0.00	0.92	1.87	2.78
1	0	2	-	+ -	5	4.87	4.29	3.69	3.14	0.15219	0.13406	0.11531	0.09813	0	52	111	166	0.00	0.87	1.85	2.77
1		3	•	+	5	6	5.22	4.64	4.13		0.16313		0.12906	0	59	126	185	0.00	0.98	2.10	3.08
	8	2	-	-	0	9.52	8.46	7.49	7.17			0.23406		0	61	. 112	170	0.00	1.02	1.87	2.83
1	9	1	-	-	0	5.07	4.23	3.49	2.99	0.15844	0.13219	0.10906	0.09344	0	55	112	168	0.00	0.92	1.87	2.80
1	4	1	-	-	0	5	3.94	3.05	2.19	0.15625	0.12313	0.09531	0.06844	0	60	129	194	0.00	1.00	2.15	3.23
	8	1		•	1	6.64	6.04	5.42	4.76	0.2075	0.18875	0.16938	0.14875	0	- 58	111	169	0.00	0.97	1.85	2.82
1	2	8	-	-	1	6	5.26	4.7	4.22	0.1875	0.16438	0.14688	0.13188	0	58	127	187	0.00	0.97	2.12	3.12
1	4	7	-	-	1	6.65	6.08	5.35	4.31	0.20781	0.19	0.16719	0.13469	0	59	115	181	0.00	0.98	1.92	3.02
	8	7	•	-	3	7.45	6.97	6.54	6.16	0.23281	0.21781	0.20438	0.1925	0	57	112	169	0.00	0.95	1.87	2.82
1	1	1		-	3	6.22	5.56	5.02	4.5	0.19438	0.17375	0.15688	0.14063	0	60	126	186	0.00	1.00	2.10	3.10
. 1	4	5	•	•	3	6.09	5.56	4.86	4.49	0.19031	0.17375	0.15188	0.14031	0	60	129	195	0.00	. 1.00	2.15	3.25

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Light	Tank	cosm	nutriente	crab	richnees	NH4 time 1	NU 14 77 0	NH4 Time 3	NH4 Time 4	T. (1.)	70 (1-)	T0 (h.)	T. ()
Day	8	2	0	Crab O	0	31.27	1.22	1.23	1.04	T1 (hr) 0.00	T2 (hr) 1.18	T3 (hr) 2.42	T4 (hr) 3.37
Day	9	1	0	õ	0	4.02	3.81	3.37	3.70	0.00	1.16	2.42	3.42
Day	14	1	ŏ	õ	õ	2.98	2.93	2.82	2.35	0.00	1.20	2.57	3.42
Day	8	;	õ	õ	1	3.99	3.41	2.75	2.83	0.00	1.18	2.30	3.45
Day	12	8	õ	ŏ	1	5.56	6.36	6.04	2.03 6.64	0.00	1.18	2.50	3.25
Day	14	7	õ	ŏ	1	3.94	3.35	3.06	2.34	0.00	1.20	2.52	3.55
Day	8	7	õ	0	3	5.94	6.03	5.71	2.04 5.45	0.00	1.18	2.35	3.40
Dev	11	1	õ	õ	3	8.52	8.15	8.22	5.45 8.27	0.00	1.18	2.45	3.40
Day	14	5	0	0	3	5.18	4.40	4.11	8.27 3.50	0.00	1.20	2.55	3.62
Day	10	3	õ	ŏ	5	7.72	7.68	7.92	7.50	0.00	1.22	2.43	3.40
Day	11	8	ŏ	õ	5	8.01	8.14	8.22	7.32	0.00	1.18	2.57	3.63
Day	14	6	õ	õ	5	6.35	6.38	5.80	5.22	0.00	1.18	2.55	3.47
Day	8	8	õ	1	õ .	2.98	2.20	1.56	1.48	0.00	1.17	2.45	3.47
Day	10	1	ŏ	1	õ	3.07	2.49	1.91	1.56	0.00	1.23	2.43	3.40
Day	14	8	õ	1	õ	3.15	2.40	2.10	1.40	0.00	1.18	2.53	3.40
Day	8	5	0	1	1	4.27	3.72	3.23	3.37	0.00	1.18	2.45	3.47
Day	9	7	ŏ	- i	i	7.10	6.74	6.31	6.22	0.00	1.22	2.45	3.40
Day	10	4	ō	i	1	7.31	7.27	6.83	6,40	0.00	1.23	2.47	3.40
Day	9	8	0	1	3	6.12	5,61	4.94	4.57	0.00	1.23	2.47	3.42
Day	11	2	õ	1	3	3.34	2.54	2.23	2.25	0.00	1.15	2.55	3.67
Day	12	4	õ	1	3	6.43	5.92	5.38	4.63	0.00	1.18	2.53	3.57
Day	9	3	ŏ	i	5	6.59	6.54	0.00	6.19	0.00	1.23	2.47	3.42
Day	10	2	ō	1	5	10.28	11.17	10.61	11.31	0.00	1,22	2.45	3.42
Day	11	3	0	1	5	6.83	6.56	7.08	5.68	0.00	1.18	2.55	3.62
Day	8	4	1 .	0 .	õ	10.36	10.30	10.48	32.55	0.00	1.18	2.43	3.40
Day	12	1	i	õ	õ	14.62	16.02	20.49	23.93	0.00	1.20	2.57	3.52
Day	14	4	1	ō	ō	13.47	14.81	17.01	15.66	0.00	1.18	2.55	3.50
Day	8	6	i	ō	1	32.36	31.17	33.10	30.01	0.00	1.20	2.43	3.40
Day	9	6	1	õ	1	39.03	48.57	43.14	38.78	0.00	1.23	2.47	3.42
Day	12	2	1	ō	1	11.53	19.20	22.02	24.71	0.00	1.18	2.57	3.60
Day	9	2	1	ō	3	16.77	29.18	31.48	36.23	0.00	1.20	2.47	3.42
Day	11	7	1	0	3	19.44	21.95	27.32	31.13	0.00	1.18	2.55	3.60
Day	12	5	1	ō	3	16.44	22.94	21.91	25.00	0.00	1.20	2.57	3.48
Day	9	5	1	ō	5	30.77	46.41	49.08	74.84	0.00	1.23	2.47	3.42
Day	10	8	1	õ	5	20.84	27.81	34.76	49.20	0.00	1.23	2.43	3.38
Day	12	7	1	ō	5	18.34	22.21	25.95	28.13	0.00	1.15	2.50	3.42
Day	10	5	1	1	ō	2.82	1.71	2.52	5.12	0.00	1.23	2.42	3.43
Day	12	6	1	1 .	ō	13.07	13.70	37.61	57.27	0.00	1.17	2.50	3.55
Day	14	3	1	1	0	13.35	19.74	22.45	21.26	0.00	1.20	2.57	3.45
Day	10	6	1	1	1	15.71	19.20	20.43	19.96	0.00	1.23	2.47	3.42
Day	11	6	1	1	1	25.14	28.94	30.81	35.62	0.00	1.13	2.57	3.65
Day	12	3	1	1	1	24.63	28.01	32.23	32.66	0.00	1.22	2.58	3.52
Day	8	3	1	1	3	1.51	33.32	36.96	39.52	0.00	1.18	2.45	3,40
Day	10	7	1	1	3	27.28	36.50	37.92	42.83	0.00	1.23	2.42	3.43
Day	11	4	1	1	3	22.14	53.07	43.88	55.53	0.00	1.12	2.55	3.63
Day	9	4	1	i	5	17.66	20.16	22.75	29.05	0.00	1.23	2.47	3.42
Day	11	5	1	1	5	17,94	20.87	23.17	27.09	0.00	1.18	2.55	3.58
Day	14	2	1	1	5	18.33	21.26	24.86	25.82	0.00	1,17	2.52	3.45
		-		•	-								

Appendix 8. Day and night NH₄ fluxes from Chapter 4.

Nig	2	0	0	0	1.77	0.58	0.65	0.50	0.00	1.02	1.87	2.83
Nig	1	0	0	0	3.77	3.40	2.88	2.61	0.00	0.92	1.87	2.80
Nig	1	0	0	0	2.05	1.93	1.65	1.27	0.00	1.00	2.15	3.23
Nig	1	0	. 0	1	4.22	3.84	3.34	2.96	0.00	0.97	1.85	2.82
Nig	8	0	0	1	3.06	3.17	2.73	2.74	0.00	0.97	2.12	3.12
Nig	7	. 0.	0	1	1.38	2.31	1.96	1.75	0.00	0.98	1.92	3.02
Nig	7	0	0	3	5.71	5.74	5.51	5.15	0.00	0.95	1.87	2.82
Nig	1	0	0	3	6.28	7.12	5.40	5.01	0.00	1.00	2.10	3.10
Nig	5	0	0	3	2.00	3.18	2.72	2.83	0.00	1.00	2.15	3,25
Nig	3	0	0	5 5	8.71	8.78	9.09	8.74	0.00	0.93	1.90	2.82
Nig	8	0	0		6.15	4.97	4.84	4.51	0.00	1.00	2.08	3.07
Nig	6		0	5	4.05	3.98	3.96	3.80	0.00	0.97	2.12	3.17
Nig	8	0	1	0	30.08	1.15	0.61	0.53	0.00	0.98	1.87	2.83
Nig	1	0	1	0	3.99	3,17	2.94	2.17	0.00	0.93	1.90	2.83
Nig	8	0	1	0	1.33	0.94	0.89	0.71	0.00	0.98	2.13	3.22
Nig	5	0	1	1	2.80	2.75	2.32	2.09	0.00	0.97	1.87	2.82
Nig	7	0	1	1	7.43	7.73	7.70	6.71	0.00	0.90	1.88	2.80
Nig	4			1	8.23	7.61	7.54	7.35	0.00	0.92	1.90	2.83
Nig	8	0	1 1	3	6.01	5.92	5.73	5,11	0.00	0.95	1.87	2.83
Nig	2	0		3	3.51	2.50	1.50	1.38	0.00	1.05	2.05	3.13
Nig	4 3	0	1	3	2.87	2.80	2.49	2.52	0.00	0.97	2.13	3.10
Nig	2	0	1	5	6.32	7.04 10.37	6.49	5.70	0.00	0.92	1.87 1.85	2.78
Nig	2		1	5 5	9.80		10.54	10.39	0.00	0.87		2.77
Nig	4	0	0	0	4.82	4.90 14.52	4.76 14.68	4.62 15.20	0.00	0.98	2.10	3.08
Nig	4	1	0	0		14.52		15.20 8.84	0.00	1.02 0.97	1.88 2.10	2.85
Nig	4	1	0	0	8.49 11.96	13.11	7.82 14.94	14.62	0.00	0.97	2.10	3.12 3.18
Nig	6	1	0	1	2.09	32.07	34.88	36.19	0.00	1.02	1.88	2.87
Nig	6	1	0	1	30.88	32.38	40.71	42.24	0.00	0.95	1.87	2.87
Nig	. 2	1	0	1	11.18	12.30	15.30	42.24	0.00	0.95	1.95	2.90
Nig	2	÷	õ	3	23.08	22.73	30.22	29.31	0.00	0.95	1.87	2.80
Nig	7	1	ŏ	3	16.68	20.33	24.59	29.51	0.00	0.93	2.10	3.08
Nig	5	1	Ď	3	14.41	14.84	18.74	18.36	0.00	0.97	1.85	2.85
Nig	5	1	õ	5	29.94	34.26	39.46	42.92	0.00	0.90	1.87	2.35
Nig	8	1	ő	. 5	25.32	27.01	30.00	33.12	0.00	0.92	1.90	2.83
Nig	7	1	. 0	5	14,71	17.65	18.76	20.51	0.00	0.98	2.17	3.17
Nig	5	i	1	õ	27.33	40.52	42.87	53.23	0.00	0.95	1.90	2.83
Nig	6	i	1	ŏ	10.99	8,73	10.11	10.50	0.00	0.98	2.12	3.10
Nig	3	1		õ	10.14	8.31	11.42	9.30	0.00	1.00	2.25	3.23
Nig	6	1	1	1	21.69	27.15	32.28	33.15	0.00	0.92	1.90	2.83
Nig	6	, t	1	1	37.74	39.88	42.27	44.30	0.00	1.02	2.10	3.08
Nig	3	1	1	1	20.08	24.21	25.95	31.30	0.00	0.97	2.12	3.13
Nig	3	1	1	3	28.82	29.94	35.98	35.70	0.00	0.95	1.85	2.82
Nig	7	1	1	3	32.73	35.64	41.76	43.85	0.00	0.95	1.90	2.83
Nig	. 4	1	i	3	21.06	23.15	23.93	26.07	0.00	1.07	2.07	3.15
Nig	4	i	1	5	18.48	19.14	22.47	25.74	0.00	0.97	1.88	2.83
Nig	5	1	1	5	16.56	19.43	18.04	19.35	0.00	0.98	2.10	3.08
Nig	2	i	1	5	17.61	20.37	16.90	21.83	0.00	0.97	2.12	3.00
	 -			2				2.100	2.00			

Appendix 9. Day and night NO_x fluxes from Chapter 4.

day 8 day 9 day 14 day 8 day 12 day 12 day 12 day 12 day 12 day 12 day 14 day 10 day 14 day 10 day 14 day 14 day 14 day 10 day 10 day 8 day 9 day 10 day 9 day 12 day 9 day 11 day 8 day 11 day 8 day 11 day 8 day 12	2 1 1 8 7 7 1 5	-	-	0 0 1	18.46 0.55 0.82 0.46	0.04 0.44 0.91 0.42	0.03 0.32 0.59	0.00 0.41 0.46	0.46 0.18 0.21	0.03 0.14 0.21	0.04 0.10 0.25	0.01 0.13 0.19	18.00 0.38 0.61	0.01 0.29 0.70	-0.01 0.22 0.34
day 14 day 8 day 12 day 12 day 12 day 14 day 14 day 14 day 14 day 14 day 14 day 10 day 14 day 14 day 14 day 10 day 14 day 8 day 10 day 8 day 9 day 9 day 11 day 11 day 11 day 11	1 8 7 7 1 5	-	-	0	0.82 0.46	0.91	0.59	0.46							
day 8 day 12 day 12 day 14 day 14 day 10 day 14 day 10 day 14 day 14 day 14 day 10 dey 14 day 8 day 10 day 9 day 9 day 10 day 9 day 9 day 11 day 9 day 11 day 11 day 11 day 11 day 11 day 11	B 7 7 1 5	-	-	1	0.46				0.21	0.21	0.25	0.19	0.61	0.70	
day 12 day 14 day 11 day 14 day 10 day 14 day 14 day 14 day 14 day 14 day 10 day 14 day 8 day 10 day 9 day 9 day 9 day 9 day 11 day 11 day 11	B 7 7 1 5	-	-	•					0.00		0.45				
day 14 day 8 day 11 day 14 day 14 day 14 day 14 day 14 day 14 day 8 day 10 day 8 day 9 day 10 day 9 day 11 day 11 day 11 day 11	7 7 1 5	-	-				0.27	0.23	0.22	0.23	0.15	0.15	0.24	0.19	0.12
dey 8 day 11 day 12 day 11 day 14 day 8 day 10 day 14 day 8 day 14 day 9 day 11 day 11 day 11 day 8	7 1 5	-		•	0.87	0.88	0.65	0.56	0.43	0.44	0.30	0.33	0.44	0.44	0.35
day 11 day 14 day 10 day 11 day 14 day 10 day 14 day 14 day 14 day 14 day 14 day 10 day 14 day 8 day 10 day 9 day 11 day 111 day 11 day 8	1 5		-	1	0.95	1.42	0.65	0.45	0.33	0.30	0.36	0.24	0.62	1.12	0.29
day 14 day 10 day 11 day 14 day 8 day 10 day 8 day 8 day 9 day 10 day 9 day 9 day 11 day 9 day 9 day 9 day 11 day 11 day 11 day 8	5	-	-	3	0.47	0.46	0.45	0.40	0.24	0.24	0.24	0.21	0.23	0.23	0.21
day 10 day 11 day 14 day 8 day 10 day 14 day 8 day 9 day 11 day 11 day 11 day 8	-	-	•	3	1.48	1.45	1.10	1.04	0.61	0.56	0.52	0.47	0.87	0.88	0.59
day 11 day 14 day 10 day 10 day 14 day 14 day 10 day 14 day 14 day 14 day 14 day 10 day 9 day 11 day 11 day 11 day 11 day 8		-	-	3	1.29	1.37	0.87	0.80	0.41	0.38	0.42	0.38	0.88	0.99	0.45
day 14 day 8 day 10 day 10 day 9 day 9 day 10 day 9 day 10 day 9 day 9 day 9 day 12 day 9 day 9 day 9 day 9 day 11 day 11 day 8	3	-		5	0.86	0.62	0.58	0.52	0.32	0.26	0.26	0.22	0.55	0.36	0.32
day 8 day 10 day 14 day 8 day 9 day 10 day 9 day 10 day 9 day 10 day 9 day 12 day 9 day 12 day 9 day 11 day 11 day 11	- 8	-	-	5	1.14	1.13	0.93	0.77	0.50	0.46	0.44	0.39	0.64	0.67	0.49
dey 10 day 14 day 10 day 9 day 10 day 9 dey 11 day 9 day 12 day 9 day 10 day 11 day 11 day 8	6		-	5	1.25	1.49	0.92	0.89	0.44	0.41	0.43	0.40	0.82	1.08	0.49
day 14 day 8 day 9 day 10 day 9 day 11 day 12 day 9 day 12 day 9 day 11 day 11 day 9 day 11 day 11 day 11 day 11	8	-	+	0	0.47	0.23	0.14	0.06	0.16	0.12	0.12	0.07	0.31	0.10	0.01
day 8 day 9 day 10 day 11 day 12 day 9 day 12 day 9 day 11 day 8	1	-	+	0	0.45	0.32	0.22	0.19	0.19	0.19	0.09	0.10	0.26	0.13	0.13
day 9 day 10 day 11 day 11 day 12 day 9 day 9 day 11 day 8	8	-	+	0	0.86	1.08	0.61	0.45	0.28	0.26	0.28	0.21	0.59	0.82	0.33
day 10 day 9 dey 11 day 12 day 9 day 10 day 11 day 8	5	-	+	1	0.63	0.37	0.32	0.29	0.20	0.17	0.17	0.19	0.43	0.20	0.15
day 9 day 11 day 12 day 9 day 10 day 11 day 8	7	-	+	1	1.01	0.58	0.54	0.48	0.36	0.28	0.25	0.22	0.64	0.30	0.29
day 11 day 12 day 9 day 10 day 11 day 8	4	-	+	1	0.80	0.68	0.59	0.50	0.29	0.29	0.30	0.24	0.51	0.39	0.30
day 12 day 9 day 10 day 11 day 8	8	•	+	3	0.89	0.57	0.53	0.45	0.31	0.28	0.23	0.21	0.58	0.28	0.30
day 9 day 10 day 11 day 8	2	-	+	3	0.73	0.59	0.41	0.27	0.34	0.25	0.21	0.13	0.39	0.33	0.20
day 10 day 11 day B	4	-	+	3	1.26	1.10	0.94	0.60	0.56	0.47	0.47	0.39	0.70	0.64	0.48
day 11 day B	3	• ·	+ .	5	1.02	0.65		0.62	0.36	0.30		0.27	0.67	0.35	
day 11 day B	2	-	+	5	0.87	0.72	0.65	0.64	0.30	0.30	0.27	0.24	0.57	0.42	0.37
day B	3	-	+	5	1.42	1.31	1.07	0.92	0.58	0.52	0.52	0.44	0.84	0.79	0.55
	4	+	-	0	14.92	17.77	20.57	39.64	1.33	1.54	1.78	4.12	13.59	16.23	18.79
	1	+	-	ō	8.16	8,75	13.93	17.66	0.85	1.16	1.50	1.98	7.32	7.59	12.43
day 14	4	+		0	11.29	15.09	17.95	17.03	0.82	1.09	2.10	1.57	10.47	14.00	15.85
day 8	6	+	-	1	23.31	24.17	31.22	30.58	0.68	0.74	0.84	0.91	22.63	23.43	30.38
day 9	6	+	-	1	27.30	35.84	33.52	32.00	0.72	0.82	0.91	1.00	26.56	35.02	32.61
day 12	2	+	-	1	5.09	10.63	12.78	16.84	0.57	0.62	0.66	0.71	4.52	10.01	12.12
day 9	2	+		3	7.36	17.20	18.60	22.74	0.42	0.47	0.53	0.55	6.93	16.73	18.07
day 11	7	+	-	3	9.70	11.98	20.82	20.68	0.78	0.82	0.85	0.95	8.91	11.16	19.97
day 12	5	+	-	3	7.20	13.34	13.84	18.41	0.70	0.87	0.83	0.77	6.50	12.47	13.01
day 9	5	÷	-	5	16.98	29.63	31.87	48.35	0.58	0.77	0.96	1.18	16.40	28.86	30.91
day 10	8	+	-	5	9.21	14.66	20.45	32.01	0.66	0.75	0.89	1.14	8.54	13.91	19,56
day 12	7			5	8.41	10.75	14.65	17.27	0.77	0.90	0.98	1.04	7.63	9.85	13.67
day 12 day 10	5	+	+	õ	29.25	52.79	87.86	92.88	0.74	1.27	1.43	1.49	28.51	51.53	86.43
day 10 day 12	6	+	+	0	7.76	9.07	28.93	43.54	0.74	0.69	0.62	0.73	7.05	8.38	28.31
	3	+	+	n	7.25	13.67	16.60	15.58	0.45	0.64	0.56	0.59	6.80	13.03	16:04
,	6	+	+	1	8.96	10.50	12.69	12.66	0.43	0.45	0.45	0.44	6.42	10.05	12.24
,	6	+	+	1	18.31	22.57		27.20	0.34		0.43	0.80	17.54	21.77	22.95
	3	+	+	1	15.11	18.35	23.78	24.14	0.77	0.80		0.80		17.53	22.95
	3	-	+	3	0.39		23.07	24.14		0.82	0.81 0.52	0.59	14.34 0.37	20,37	26.59
,		+		3		20.84	27.11		0.02	0.47					
day 10			+	3	13.43	21.54	23.60	27.41	0.42	0.47	0.49	0.51	13.01	21.07	23.11 [°] 30.16
day 11	7														
day 9	7	+	+	3	13.60	40.85	30.96	41.03	0.73	0.75	0.80	0.79	12.87	40.10	
day 11	7 4 4	+ +	+	5	8.73	10.50	13.20	18.64	0.36	0.41	0.41	0.46	8.36	10.09	12.79
day 14	7	+ +													

0.07 0.15 0.22 0.38 0.40 0.22 0.30 0.41 0.29 0.29 0.29 0.29 0.29 0.29 0.29 0.29 0.29 0.29 0.29 0.29 0.29 0.29 0.29 0.29 0.29 0.29 0.23 0.44 0.22 0.37 0.41 0.22 0.33 0.44 0.22 0.33 0.44 0.22 0.33 0.44 0.22 0.33 0.44 0.22 0.33 0.44 0.22 0.33 0.44 0.22 0.34 0.50 0.64 0.75 0.64 0.79 0.64 0.79 0.64 0.79 0.40 0.79 0.40 0.79 0.40 0.79 0.40 0.79 0.40 0.79 0.40 0.79 0.40 0.79 0.40 0.79 0.40 0.79 0.55 0.55night night 8 9 14 8 12 14 8 11 10 11 14 8 01 8 9 10 9 11 29 10 11 8 12 14 8 9 12 9 11 29 10 12 10 12 14 10 11 12 8 10 11 9 11 14 2111877153868185748243234146622275587563663374452 0 0 1 1 0.16 0.19 0.27 0.26 0.37 0.26 0.36 0.36 0.45 0.46 0.48 0.48 0.48 0.48 0.37 0.20 0.36 0.47 0.30 0.37 0.20 0.43 0.20 0.45 0.40 0.20 0.43 0.20 0.45 0.40 0.20 0.45 0.40 0.20 0.45 0.40 0.20 0.45 0.40 0.20 0.45 0.40 0.20 0.68 0.57 0.79 0.83 0.56 0.661 0.57 0.56 0.661 0.57 0.57 0.56 0.57 0.0.00 0.10 0.15 0.07 0.21 0.10 0.14 0.19 0.21 0.24 0.19 0.24 0.19 0.24 0.10 0.24 0.10 0.24 0.10 0.24 0.36 0.05 0.07 0.07 0.07 0.07 0.07 0.07 0.07 0.07 0.07 0.33 0.28 0.00 0.36 0.36 0.36 0.36 0.36 0.36 0.36 0.36 0.34 10.54 11.54 11.93 25.27 18.73 5.97 18.73 21.23 19.24 11.54 13.49 13.20 11.54 13.20 13. 0.09 0.10 0.22 0.29 0.32 0.32 0.32 0.32 0.32 0.32 0.32 0.32 0.32 0.32 0.32 0.33 0.47 0.33 0.04 0.33 0.09 0.32 0.39 0.32 0.39 0.32 0.39 0.32 0.39 0.32 0.39 0.32 0.39 0.32 0.39 0.32 0.39 0.32 0.39 0.32 0.39 0.32 0.37 0.33 0.39 0.32 0.37 0.33 0.39 0.32 0.37 0.33 0.39 0.32 0.37 0.33 0.39 0.32 0.37 0.33 0.90 0.27 0.33 0.90 0.27 0.37 0.92 0.93 0.92 0.55 0.58 0.583 3 3 5 5 5 0 0 0 1 1 1 3 3 3 5 5 5 0 0 0 1 1 1 3 3 3 5 5 5 0 0 0 1 1 1 3 3 3 5 5 5 5 0 0 0 1 1 1 3 3 3 5 5 5 5 + + + + + + +

NO3 time 4	T1 (hr)	T2 (hr)	T3 (hr)	T4 (hr)
-0.01	0.00	1.18	2.42	3.37
0.28	0.00	1.25	2.47	3.42
0.27	0.00	1.20	2.57	3.45
0.08	0.00	1.18	2.30	3.25
0.23	0.00	1.18	2.52	3.55
0.20	0.00	1.20	2.55	3.42
0.19	0.00	1.18	2.45	3.40
0.57	0.00	1.18	2.55	3.62
0.41	0.00	1.20	2.57	3,43
0.29	0.00	1.22	2.43	3.40
0.37	0.00	1.18	2.57	3.63
0.49	0.00	1.18	2.55	3.47
0.00	0.00	1.17	2.45	3.40
0.09	0.00	1.23	2.43	3.40
0.24	0.00	1.18	2.53	3.47
0.10	0.00	1.18	2.45	3.40
0.26	0.00	1.22	2.45	3.40
0.26	0.00	1.23	2.47	3.40
0.24	0.00	1.23	2.47	3.42
0.15	0.00	1.15	2.55	3.67
0.41	0.00	1.18	2.53	3.57
0.35	0.00	1.23	2.47	3.42
0.40	0.00	1.22	2.45	3.42
0.48	0.00	1.18	2.55	3.62
35.52	0.00	1.18	2.43	3,40
15.68	0.00	1.20	2.57	3.52
15.46	0.00	1.18	2.55	3.50
29.67	0.00	1.20	2.43	3,40
31.00	0.00	1.23	2.47	3.42
16.13	0.00	1.18	2.57	3.60
22.19	0.00	1.20	2.47	3.42
19.73	0.00	1.18	2.55	3.60
17.64	0.00	1.20	2.57	3,48
47.17	0.00	1.23	2.47	3.42
30.87	0.00	1.23	2.43	3.38
16.23	0.00	1.15	2.50	3.42
91.40	0.00	1.23	2.42	3.43
42.81	0.00	1.17	2.50	3.55
14.99	0.00	1.20	2.57	3.45
12.22	0.00	1.23	2.47	3.42
26.40	0.00	1.13	2.57	3.65
23:32	0.00	1.22	2.58	3.52
30.56	0.00	1.18	2.45	3,40
26.90	0.00	1.23	2.42	3,43
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0.07	0.00	0.97	2.12	3.12
0.08	0.00	0.98	1.92	3.02
0.20	0.00	0.95	1.87	2.82
0.20	0.00	1.00	2.10	3.10
0.14	0.00	1.00	2.15	3.25
0.28	0.00	0.93	1.90	2.82
0.08	0.00	1.00	2.08	3.07
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0.09	0.00	0.93	1.90	2.83
0.04	0.00	0.98	2.13	3.22
0.11	0.00	0.97	1.87	2.82
0.33	0.00	0.90	1.88	2.80
0.33	0.00	0.92	1.90	2.83
0.32	0.00	0.95	1.87	2.83
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0.36	0.00	0.92	1.87	2.78
0.41	0.00	0.87	1.85	2.77
0.15	0.00	0.98	2.10	3.08
29.20	0.00	1.02	1.88	2.85
7.63	0.00	0.97	2.10	3.12
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35.73	0.00	1.02	1.88	2.87
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14.59	0.00	0.95	1.87	2.82
12.90	0.00	0.97	2.10	3,08
11.83	0.00	0.95	1.85	2,85
25.30	0.00	0.90	1.87	2.78
16.18	0.00	0.92	1.90	2.83
13.72	0.00	0.98	2.17	3.17
31.13	0.00	0.95	1.90	2.83
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25.37	0.00	0.97	2.12	3.13
31.84	0.00	0.95	1.85	2.82
24.53	0.00	0.95	1.90	2.83
15.12	0.00	1.07	2.07	3.15
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Appendix 10. Day and night PO4-3 fluxes from Chapter 4.

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VITA

Amanda Cecelia Spivak

Born November 1979 in New Jersey. Attended Pitman High School and graduated in 1997. Graduated *magna cum laude* from Bryn Mawr College in 2001, earning an A.B. in Biology (with honors) with a concentration in Environmental Science and a minor in English. Entered the School of Marine Science graduate program at the College of William and Mary in 2002.