Trophic Ecology of Gelatinous Zooplankton in a Pelagic Upwelling System: Fatty Acid, Gut Content, and Methodological Insights

by

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A dissertation accepted and approved in partial fulfillment of the requirements for the degree of Doctor of Philosophy in Biology

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DISSERTATION ABSTRACT

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Doctor of Philosophy in Biology

Title: Trophic Ecology of Gelatinous Zooplankton in a Pelagic Upwelling System: Fatty Acid, Gut Content, and Methodological Insights

Gelatinous zooplankton are often treated as a homogenous, nutritionally poor group with minimal trophic importance in marine food webs. This dissertation challenges that paradigm by integrating fatty acid (FA) analysis with species-specific and comparative approaches to illuminate the trophic roles of gelatinous zooplankton in the Northern California Current (NCC), a productive eastern boundary upwelling system.

In Chapter II, I examined the trophic ecology of the ctenophore *Pleurobrachia bachei* through paired gut content and FA analyses. I found that *P. bachei* acts as both an influential predator and prey in this system, through its consumption of copepods and eggs and through its high concentration of essential fatty acids (EFA). Seasonal and latitudinal patterns further revealed how the trophic role of *P. bachei* shifts with oceanographic conditions.

In Chapter III I expanded my scope to include a diverse suite of co-occurring gelatinous taxa. FA profiles revealed that gelatinous zooplankton generally have higher proportions of EFA and poly-unsaturated fatty acids (PUFA) compared to non-gelatinous zooplankton, but that they are also a highly heterogenous group. Inter-taxonomic variation in FA profiles was far larger than intra-taxonomic variation and functional groupings based on diet also explained FA variability. I found that gelatinous predators of soft-bodied prey were particularly proportionally rich in PUFA, EFA and ARA, indicating those taxa may be especially important in pelagic food webs as quickly digestible rich prey sources. These findings underscore the functional diversity

of gelatinous zooplankton and the importance of resolving the often-overlooked “jelly web.”

In Chapter IV, I assessed how storage conditions affect FA degradation in organismal tissues. Using a fully-crossed experimental design, I demonstrated that FA degradation is highly taxon- and compound-specific, and driven more by storage duration than temperature. Despite intra-taxon variability, inter-taxonomic differences remained detectable across treatments, supporting the ecological validity of FA comparisons even under suboptimal storage conditions.

Together, these studies highlight the complex and dynamic trophic roles of gelatinous zooplankton and validate FA biomarkers as powerful tools for resolving their ecological function in changing oceans.

This dissertation includes previously published co-authored material.

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I conducted my PhD research on the land and water that are the traditional homelands of the original peoples of the Pacific Northwest since time immemorial. I taught classes, organized outreach events, and performed the majority of my laboratory work at the Oregon Institute of Marine Biology (OIMB), which is located on the lands and waters of the Confederated Tribes of the Coos, Lower Umpqua, and Siuslaw (CTCLUSI) peoples. I lived, worked, and taught in Eugene at the University of Oregon, which is located on Kalapuya Ilihi, the traditional indigenous homeland of the Kalapuya people; descendents of the Kalapuya are now citizens of the Confederated Tribes of Grand Ronde Community of Oregon and the Confederated Tribes of Siletz Indians of Oregon. I collected my zooplankton samples for chapters II and III from the waters traditionally fished by the Yaqo'n (Yaquina), Yurok, Wiyot, and Chilula peoples. I collected samples for chapter IV from the tidepools of the CTCLUSI peoples. The lands of all these communities were stolen from them, and the people were forcefully removed through violence that broke the ancient link between the people and the lands and waters here. Having lived, worked, and studied these beautiful areas, I recognize what a tremendous loss this was and recognize that my work was only possible because of this very dark history. I will continue to strive to live and work in ways that honor the land, the water, and all the living creatures here. To quote Robin Wall Kimmerer, “For what good is knowing, unless it is coupled with caring? Science can give us knowing, but caring comes from someplace else.” (Braiding Sweetgrass: Indigenous Wisdom, Scientific Knowledge, and the Teachings of Plants).

There is a saying among academics that in doing each of our relatively small contributions to science, we are all “standing on the shoulders of giants.” This was undoubtedly true for me, and I’ll go further to add that I was standing on the shoulders of giants, and leaning

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DEDICATION

For my mom Sandy Masterman: “I am always doing that which I cannot do in order that I may learn how to do it.”

TABLE OF CONTENTS

LIST OF FIGURES

Figure Page

LIST OF TABLES

CHAPTER I

INTRODUCTION

Marine food webs are shaped by the flow of energy through interwoven and complex predator-prey interactions. Identifying and describing these trophic relationships remains a central challenge in marine ecology. These dynamics are particularly difficult to characterize for gelatinous zooplankton, a diverse group of soft-bodied planktonic animals, defined by their high water content (>95%) and fragile nature (Luskow *et al.*, 2021). Truly ubiquitous, gelatinous zooplankton are found in all parts of the world's oceans, occupying an enormous range of habitats and environmental conditions (Lucas *et al.*, 2014). Gelatinous zooplankton can reproduce rapidly and form dense "blooms," which have been linked to ecological and socio-economic consequences such as reduced fish stocks through both direct predation and competition (reviewed in Purcell *et al.*, 2007).

Yet despite their ubiquity and significant trophic impacts, gelatinous zooplankton have historically been excluded from most food web models (Dadou *et al.*, 1996; Fenchel, 1988; Hopkins *et al.*, 1989) or included as trophic dead-ends (Sommer *et al.*, 2002; Verity and Smetacek, 1996). The assumption that gelatinous zooplankton are rarely consumed and trophically unimportant stems in part from their low caloric and carbon content (Doyle *et al.*, 2007), as well as the difficulty of detecting them in gut content analyses due to their lack of hard structures. This paradigm has begun to slowly shift. New technologies are revealing the widespread regular consumption of gelatinous zooplankton by a variety of animals (Thiebot and McInnes, 2019), leading to calls to consider the dietary value of these organisms beyond their caloric content (Hays *et al.*, 2018).

Fatty acids (FA) present a powerful tool to explore the trophic role of gelatinous zooplankton in pelagic food webs. FA occur universally across all living organisms as structural components of cellular membranes, as storage compounds for energy, and as biochemical precursors to eicosanoid hormones (Dalsgaard *et al.*, 2003). Structurally, FA consist of a carboxylic acid head attached to a long aliphatic chain which varies in length and in the presence/absence of double-bonds between carbons. As FA are highly diverse in both their chemical structures and in their biological functions, they may be grouped in a variety of ways, one of which is according to levels of saturation: saturated (SAFA), monounsaturated (MUFA), or polyunsaturated (PUFA) (Budge *et al.*, 2006).

FA may be used as biomarkers to identify and characterize trophic links. This makes FA a tool well suited to studying gelatinous zooplankton, whose lack of hard parts excludes them from accurate measurements via more traditional gut content studies (Pitt *et al.*, 2009). Ecologists are able to use FA as biomarkers in that many primary producers exhibit characteristic FA signatures which are then transferred with minimal or predictable modification up through higher trophic levels (Budge *et al.*, 2006; Galloway *et al.,* 2012; Galloway and Winder, 2015; Kelly and Scheibling, 2012). In addition, certain FA are synthesized in notably high concentrations by a restricted set of taxa, rendering them taxon-specific tracers (Arts *et al.*, 2009). For example, calanoid copepods synthesize *de novo* 20:1ω9/11 and 22:1ω9/11, while the PUFAs eicosapentaenoic acid (EPA, 20:5ω3) and docosahexaenoic acid (DHA, 22:6ω3) are used as markers for relative abundances of diatoms and dinoflagellates, respectively (Taipale *et al.,* 2013; Taipale *et al.,* 2016).

FA analyses can also lend insight into the nutritional quality of an organism as a prey source. This may be done through measuring the essential fatty acid (EFA) content, where EFA

are those nutritionally critical FA that limit the growth and reproduction of a consumer (Dalsgaard *et al.*, 2003). Three EFA that have been identified as being most commonly limiting in diverse aquatic organisms are EPA, DHA, and arachidonic acid (ARA, 20:4ω6) (Arts *et al.*, 2001). Diets that are rich in EFA have been shown to result in higher fecundity and faster growth rates in zooplankton and fish (Brett *et al.*, 2009; Tocher, 2003). Through these effects, changes in the EFA availability in a marine ecosystem may constrain species' abundances and even cause entire regime shifts within an aquatic community (Litzow *et al.*, 2006).

In this dissertation, I used FA analysis to investigate the trophic ecology of gelatinous zooplankton in the Northern California Current (NCC). This highly productive upwelling system supports many large fisheries (Checkley and Barth, 2009) and exhibits strong seasonal variability in primary production, making it a highly dynamic environment in which to study trophic interactions. Gelatinous zooplankton are both abundant and diverse in this system (Pearcy, 1972), yet their functional roles here remain poorly resolved. By combining dietary analysis techniques with targeted methodological evaluation, this dissertation seeks to clarify the trophic role of gelatinous zooplankton in pelagic food webs.

In Chapter II, I focused my study on the trophic role of the ctenophore *Pleurobrachia bachei*, through paired gut content and FA analyses. The trophic role of *Pleurobrachia bachei* in the NCC is poorly understood, despite its high local abundance and its recognized trophic importance in other upwelling systems (Pavez *et al.,* 2006). Through these complementary trophic analysis methods, I studied the role of *P. bachei* in the NCC as both predator and prey, and describe the seasonal and latitudinal variability in both of these roles. Chapter II was published on September 21, 2025 by the *Journal of Plankton Research* with co-authors Dr. Kelly R. Sutherland and Dr. Aaron W. E. Galloway. Dr. Sutherland contributed to hypothesis

development, assisted in sample collection, and secured the funding for sample collection and materials used in gut dissections. Dr. Galloway secured funding for and provided the resources for FA extractions and GC-MS analyses. I performed all laboratory and data analyses. All authors contributed to writing and editing the manuscript.

While gelatinous zooplankton are now more frequently included in food web models, they are often treated as a taxonomically and functionally uniform group labeled simply as "jellyfish" (reviewed in Pauly *et al.*, 2009). This representation is misguided as gelatinous zooplankton are highly diverse, spanning a wide range of phyla and feeding strategies, from the small filter feeding appendicularians to the large predatory scyphomedusae. To explore this diversity, in Chapter III, I expanded the scope of analysis to characterize the trophic ecology of a broad assemblage of co-occurring gelatinous zooplankton in the NCC. Using FA profiles from 16 gelatinous taxa spanning 6 phyla, I described the similarities and differences among taxa, both taxonomically and functionally. I further underscored the value of using FA to evaluate trophic diversity and importance of these gelatinous taxa. Dr. Kelly R. Sutherland contributed to hypothesis development and also secured the funding for and assisted in the collection of all zooplankton samples. Dr. Aaron W. E. Galloway secured funding for materials used in FA extractions and GC-MS analyses. I performed the laboratory and data analyses. Dr. Galloway and I both contributed to writing and editing the manuscript.

In conducting the research for Chapters II and III, the first step was to collect zooplankton specimens at sea. In FA studies, once a sample of biomass is collected, the best practice is to either extract the FA immediately or to store the sample at ultra-low temperatures with antioxidants added, then followed by prompt extraction (Couturier *et al.*, 2020). This recommendation derives from the observation that lipids in a sample will continue to change

post-mortem through various enzymatic and chemical reactions (Christie, 1984; Petillo *et al.*, 1998). Unfortunately, these ideal conditions are rarely met, due to infrastructural, monetary, and time constraints, and indeed were not met for my samples collected in Chapters II and III, which were stored at T-80°C for periods ranging from 1–3.5 years prior to extraction. Despite widespread reliance on stored samples, the effects of storage temperature and duration on FA composition remain poorly understood, particularly across different taxa and tissue types. In Chapter IV, I directly addressed this gap through a systematic evaluation of FA degradation in tissue samples of widely varying lipid content and FA profiles. Taxa sampled spanned four phyla: Ochrophyta, Mollusca, Echinodermata, and Chordata. I conducted a fully-crossed experiment whereby samples from consistent source tissue of each representative organism were stored at temperatures T-20°C and T-80°C and extracted at five time points after collection: 0 days, 3 months, 1 year, 2 years, and 3 years. I tested whether temperature and storage duration affected FA profiles in measure of FA concentrations or FA proportions for each species. This chapter provides practical recommendations for sample storage and contributes to a growing body of work aimed at improving the reliability of FA-based approaches. Dr. Aaron Galloway and Michael D. Thomas are co-authors on this work, assisting with writing and editing the manuscript. Dr. Galloway conceived of the initial experimental design and provided funding/materials used in fatty acid extractions and GC-MS analyses. I performed the sample collection and preparation as well as all laboratory and data analyses.

Together, these studies shed light on the complex and often underappreciated trophic roles of gelatinous zooplankton in pelagic ecosystems. This work highlights the powerful potential of FA analysis as a tool for unraveling the trophic ecology of these delicate organisms and informs best practices for applying FA biomarkers in marine food web studies.

CHAPTER II

GUT CONTENT AND FATTY ACID ANALYSES REVEAL TROPHIC ROLE OF THE CTENOPHORE *PLEUROBRACHIA BACHEI* IN THE NORTHERN CALIFORNIA CURRENT

From Masterman, J. A., Sutherland, K. R. and Galloway, A. W. E. (2025) Gut content and fatty acid analyses reveal trophic role of the ctenophore *Pleurobrachia bachei* in the Northern California Current. *J. Plankton Res.*, **47**, fbaf052. doi:10.1093/plankt/fbaf052. Minor editorial changes have been made for dissertation consistency.

1. INTRODUCTION

Gelatinous zooplankton are integral components of pelagic food webs, and though there is increasing recognition of their trophic ecology (Chi *et al.,* 2021), their feeding impact remains understudied (Hays *et al.,* 2018). With high fecundity and the ability to consume large amounts of biomass, gelatinous zooplankton can form massive blooms that have the potential to alter both the surrounding ecosystem and human populations that depend upon those systems (Purcell, 2012). Among the gelatinous zooplankton, members of the phylum Ctenophora can be impactful predators (e.g., Greve and Reiners, 1980; Auth and Brodeur, 2006) and prey to many organisms, including commercially important fishes (Brodeur *et al.,* 2021). *Pleurobrachia bachei* is a cydippid ctenophore with a wide distribution, in temperate regions of the Pacific and Atlantic oceans (WoRMS: *Pleurobrachia bachei* A. Agassiz, in L. Agassiz, 1860).

Tentaculate ctenophores like *P. bachei* are classified as ambush entangling predators, using their retractile tentacles to ensnare hard-bodied motile prey (Greene, 1985). *Pleurobrachia*

bachei sets its trap by orienting its oral pole upward and extending the two main retractile tentacles with numerous lateral tentacles in a "sit and wait" mode. When a tentacle successfully entangles a prey item, *P. bachei* contracts the tentacles and draws them across the mouth to transfer the prey into the oral opening (Greene *et al.,* 1986). While the mechanism of prey capture by *P. bachei* is relatively well understood, the prey taxa of *P. bachei* remains to be fully resolved. Diet studies indicate that *P. bachei* feed primarily on crustacean prey, although gut contents vary considerably with geographic location (Hirota, 1974; Larson, 1987; Purcell, 1990; Purcell and Sturdevant, 2001).

The Northern California Current (NCC) is an eastern boundary upwelling system with high productivity which supports important fisheries in the Northeast Pacific (Checkley and Barth, 2009). The NCC provides a dynamic background to study food web patterns along gradients of upwelling strength across season and latitude. More southern sections of the NCC experience consistent and strong upwelling throughout the year, while the more northern sections of the NCC (e.g., north of Cape Mendocino) typically experience downwelling in the winter and upwelling in the summer (Bograd *et al.,* 2009). This variability in upwelling strength and duration has pronounced effects on the zooplankton community composition (Hooff and Peterson, 2006). Efforts to quantify gelatinous zooplankton abundance in the NCC are rare due to the fragile nature of these organisms but suggest that gelatinous zooplankton are abundant. Francis *et al.* (2012) found that gelatinous zooplankton comprise an average density of at least 200 ind m^{-3} in this region, while Swieca *et al.* (2020) found ctenophores in particular at an average density of 2.01±0.04 ind m^{-3}.

Though the trophic role of *P. bachei* has not been investigated in the NCC, previous studies in the eastern Pacific Ocean point to *P. bachei* as consumers of a diverse suite of

primarily motile crustacean prey (Hirota, 1974; Larson, 1987; Purcell, 1990; Purcell and Sturdevant, 2001). *Pleurobrachia bachei* have the potential to act as a significant competitor to other predators who rely on these resources, including many larval fishes (e.g., Purcell and Sturdevant, 2001). Furthermore, *P. bachei* may serve as an important link within the food web, providing nutritional value to higher trophic levels.

The methodologies used to determine predation patterns by marine invertebrate predators can include direct observations of prey selection, gut contents, trophic "biomarkers" (including stable isotopes, fatty acids, gut content DNA), and inferences in the lab made from feeding rates and modeling. However, gelatinous zooplankton feeding measurements in the lab are heavily influenced by experimental conditions such as container size or presence of alternative prey (Purcell and Arai, 2001). In the current study, we integrated gut content and fatty acid biomarker approaches in order to get a holistic view of the trophic ecology of *P. bachei*. Gut content analyses are limited in that they provide only a short-term snapshot view of predation. Typically, only the most recently ingested prey will be present and identifiable in the guts, while earlier consumed prey will have been either fully digested and expelled or may be too heavily digested to identify (Båmstedt and Martinussen, 2000). A second drawback to gut content analyses is that soft-bodied prey become quickly unidentifiable during digestion (Sutela and Huusko, 2000). Despite these caveats, gut content analyses have been successfully utilized to describe predation patterns in ctenophores (e.g., Purcell and Sturdevant, 2001).

Fatty acid analyses integrate predation over time to complement the shorter-term view obtained through gut content analyses. Fatty acids are a diverse set of biomolecules that occur in all living organisms as integral components of various lipid classes with important roles in the function of cellular membranes, as energy reserves, and as precursors to hormones known as

eicosanoids (Dalsgaard *et al.,* 2003). The use of fatty acids as biomarkers is based on the observation that the different primary producer phylogenetic groups (e.g., phytoplankton, macroalgae, and seagrasses) exhibit a characteristic fatty acid composition (Galloway *et al.,* 2012; Galloway and Winder, 2015). Once consumed, these characteristic fatty acid profiles may then be traced up through increasing trophic levels (Dalsgaard *et al.,* 2003; Budge *et al.,* 2006). When primary production at the base of a food web is dominated by either diatoms or dinoflagellates, this may be reflected in the fatty acid profiles of consumers as higher amounts of either eicosapentaenoic acid (EPA) or docosahexaenoic acid (DHA), respectively. Elevated ingestion of bacteria by primary consumers is reflected in higher trophic levels as greater concentrations of branched and odd-chain fatty acids. Predation on calanoid copepods is marked in consumers by the presence of 20:1ω9, 20:1ω11, 22:1ω9, and 22:1ω11, which are biosynthesized de novo in large amounts by this prey type. This method of trophic analysis using fatty acids along with gut content or other biomarkers has been used to infer trophic relationships in several groups of gelatinous zooplankton (e.g., Pitt *et al.,* 2009; Milisenda *et al.,* 2018; Schram *et al.,* 2020), including ctenophores (Falk-Peterson *et al.,* 2002; Graeve *et al.,* 2008).

In addition to their use identifying trophic links, fatty acids can also describe the nutritional quality of a prey item and the relative health of a predator. In examining the trophic role of *P. bachei*, the nutritional quality, rather than energy or carbon content, may lend insight into their trophic importance (Hays *et al.,* 2018). One such measure of nutritional quality is essential fatty acid (EFA) content which exerts strong control over the growth and reproduction of a consumer (Dalsgaard *et al.,* 2003). EFA include EPA, DHA, and arachidonic acid (ARA). Through promoting higher fecundity and more rapid growth in zooplankton and fish, diets rich in EFA underpin key demographic processes (Tocher, 2003; Brett *et al.,* 2009; Winder *et al.,* 2017).

Alterations in EFA availability in a food web may thus generate far-reaching effects, even triggering abrupt regime shifts within aquatic communities (Litzow *et al.,* 2006).

Through the complementary use of gut content and fatty acid analyses, we sought to answer two questions: (1) what is the trophic role of the potentially highly influential gelatinous predator *P. bachei* in the NCC pelagic food web? and (2) how does this role change spatially and temporally? Samples of *P. bachei* were collected from the NCC via net sampling during four cruises in the winter and summer seasons of 2018 and 2019. We sampled transects that extended across-shelf from two locations within the NCC to allow for determination of spatial patterns in the results. Our results indicate that within the NCC pelagic food web, *P. bachei* functions both as a major predator – competing with many larval fishes – and as a valuable prey item, providing a consistent source of essential nutrients to its predators.

2. MATERIALS AND METHODS

2.1. Sample collection

Two transect lines were sampled within the NCC. The northern Newport Hydrographic (NH) transect ran 65 km, beginning 18 km off the coast of Newport, Oregon (44.65˚ N). The southern Trinidad (TR) transect line ran 40 km and began 10 km off the coast of Trinidad, California (41.05˚ N). Five stations were sampled per cross-shelf transect in each of four cruises in the summers and winters of 2018-2019 (coordinates listed in Table S2.1; see map in Fig. 1 of Corrales-Ugalde *et al.*, 2021). Sampling dates were as follows: Winter 2018 (02/17/18 – 02/23/18), Summer 2018 (07/05/18 – 07/11/18), Winter 2019 (03/04/19 – 03/12/19), and Summer 2019 (07/17/19 – 07/24/19).

Pleurobrachia bachei were sampled from the NH and TR transect lines using a coupled Multiple Opening and Closing Net and Environmental Sensing System (MOCNESS) (Guigand *et al.,* 2005). Each of the 10 stations was sampled twice during each of the four cruises with the exception of 15 missed sampling events due to weather or equipment constraints, resulting in a total of 65 deployments. Samples in this study were limited to those collected from the last net fired before retrieval to limit potential net-feeding of *P. bachei*; this net had mouth size of 1 m^2, a mesh size of 333 μm, and a sampling depth of 0-25 m. The upper 25 m at each station was sampled twice, with station-replicates collected separately in time by at least 24 hours. Upon net retrieval, the contents of the net were immediately poured into chilled picking trays, where individuals of *P. bachei* were removed within 30 minutes of net retrieval and either preserved in 5% buffered formalin for gut content analyses or pooled (approx. 10-50 ind.) and frozen at -80 ˚C for fatty acid analyses.

An additional ship-board experiment was performed to determine if the presence of prey inside the guts of *P. bachei* alters the fatty acid results – i.e., due to the intermixing of fatty acids present in the prey with those of the predator *P. bachei* itself. At two different stations during the summer 2018 cruise, upon collection of *P. bachei* individuals from the nets, approximately half of the individuals were pooled and immediately frozen at -80 ˚C. The remaining half of *P. bachei* were divided into jars of filtered seawater with three individuals per jar and placed into a 5 ˚C incubator undisturbed for 24 hours to complete gut evacuation (reviewed in Purcell, 2018). After twenty-four hours, all gut-evacuated *P. bachei* individuals were pooled and frozen at -80 ˚C.

2.2. Gut content analysis

Guts of *P. bachei* preserved in 5% buffered formalin were dissected under a stereo microscope and prey items were identified to the lowest taxonomic level possible. For each prey taxon, counts of abundance and proportional abundance were noted. For each *P. bachei* individual, relative proportional abundance values were calculated for each prey item category by dividing the count of items in each prey category by the total count of prey items in the gut. Values of proportional prey contribution to *P. bachei* gut contents were transformed from counts per prey to carbon content per prey using the carbon conversion values listed in Table S4.

Prey items were split into 15 categories: appendicularians, barnacle larvae, chaetognaths, cladocerans, adult copepods, copepod nauplii, crab zoea, doliolids, large (>100 μm) eggs, small (<100 μm) eggs, euphausiids, planula larvae, gastropods, unknown crustaceans, and unknown gelatinous. Barnacle larvae included both nauplius and cyprid stages. Cladocerans included both Evadne and Podon varieties. Copepods were primarily calanoid within the genera *Centropages* and *Acartia*, and cyclopoid copepods were rare. Eggs were split into two size categories (diameter <100 μm and >100 μm) based on a natural separation seen in the spread of egg sizes. "Small" eggs ranged in size from 50 – 100 μm, while "large" eggs ranged from 125 – 400 μm averaging at 320±120 μm. The small (<100 μm) eggs were determined to be most likely copepod eggs, based on size, appearance, and after seeing similar eggs in casings still attached to copepods. The large (>100 μm) eggs were classified as invertebrate eggs based on size and appearance. Crustacean and gelatinous prey too heavily digested to be identified were counted as "unknown crustacean" and "unknown gelatinous," respectively. A prey item was counted if at least 50% of the organism remained undigested to avoid double-counting.

2.3. Fatty acid analysis

Each sample of *P. bachei* was weighed frozen, freeze-dried, weighed dry, and homogenized using a stainless-steel mortar and pestle. Samples were then analyzed for 54 unique fatty acids using the extraction method described by Schram *et al.* (2018) and gas chromatography mass spectrometry (GC-MS) method described by Taipale *et al.* (2013). The GC-MS used was Shimadzu Model QP2020 equipped with a DB-23 column (30 X 0.25 mm X 0.15 µm, Agilent). Quantification of fatty acids was based on calibration curves created using serial dilutions of GLC standard mixture 566C (Nu-Chek Prep), under a strict quality control of Pearson correlation coefficients ≥ 0.99 for all standard curves. An internal standard (nonadecanoic acid) was used to ensure extraction efficacy remained consistent between samples. Fatty acid values are expressed as a percentage of each fatty acid to the total concentration of fatty acids per sample.

2.4. Statistical analysis

Differences in gut contents and fatty acids in *P. bachei* samples across season (summer vs. winter) and transect (NH vs. TR) were investigated using a one-way Permutational Analysis of Variance (PERMANOVA) and Permutest (R, vegan package v. 2.5-7). Gut contents and fatty acid contents of *P. bachei* samples were investigated for drivers of dissimilarity between seasons and between transects using SIMPER (R, vegan package v. 2.5-7). Mann Whitney U Tests (R, stats package v. 4.3.2) were used to explore seasonal and spatial differences in *P. bachei* gut fullness and FA summation content. Fatty acid results were quantitatively compared between *P. bachei* samples that had been allowed to evacuate their guts and those concurrently collected samples which were preserved with guts still filled.

3. RESULTS

3.1. Gut contents analysis

Pleurobrachia bachei were generally abundant, collected from 68% (44/65) of the total sampling events. Out of 285 dissected *P. bachei*, 54% (n=155) individuals had one or more prey items in their guts. Of *P. bachei* with filled guts, they had an average of 9.7±14.2 prey items spanning an average of 1.9±1.0 prey categories per gut. The number of prey items and prey categories per gut ranged from 1-105 and 1-5, respectively. The oral-aboral length of formalin-preserved *P. bachei* ranged from 1 to 11 mm with an average length of 4.0±1.5 mm; this correlates to a live average length of ~8mm (Thibault-Botha and Bowen, 2004). Fifteen percent (n=42) of *P. bachei* individuals had hyperiid amphipod parasites present on the outer surface; this parasitism ranged from 0 to 11 parasites per *P. bachei*, averaging at 0.5±1.5 parasites per individual.

The three most abundant prey categories found within *P. bachei* guts were adult copepods (33.3±39.3%), copepod eggs (25.3±36.4%), and invertebrate eggs (19.9±34.3%) (Table 2.1). The other average 22% of gut contents were spread across the remaining 12 prey categories, each contributing 0.3-7.1% of gut contents across all *P. bachei*.

Table 2.1. *Pleurobrachia bachei* gut contents (15 taxonomic categories). Proportional contributions of each prey taxa to the overall gut content suite of *P. bachei* are reported as averages across individuals with standard deviations. Measurements are split up per season (Summer-Total, Winter-Total), within-season per transect (Summer-NH, Summer-TR, Winter-NH, Winter-TR), per transect (NH-Total, TR-Total), and across all *P. bachei* dissected (All-Total). (n = number of *P. bachei* with non-empty guts / number of *P. bachei* dissected).

Prey Taxa	**All**	**Summer**			**Winter**			**NH**	**TR**
	Total (n=155/285)	**NH (n=55/108)**	**TR (n=39/81)**	**Summer Total (n=94/189)**	**NH (n=55/88)**	**TR (n=6/8)**	**Winter Total (n=61/96)**	**NH Total (n=110/196)**	**TR Total (n=45/89)**
Appendicularian	1.72±12.48%	0±0%	1.71±10.68%	0.71±6.88%	3.64±18.89%	0±0%	3.28±17.96%	1.82±13.42%	1.48±9.94%
Barnacle larva	1.57±9.67%	1.55±7.57%	0±0%	0.9±5.82%	2.88±14.34%	0±0%	2.59±13.63%	2.21±11.43%	0±0%
Chaetognath	2.98±12.7%	1.97±8.63%	4.7±18.32%	3.1±13.5%	3.1±12.06%	0±0%	2.79±11.48%	2.53±10.46%	4.07±17.1%
Cladoceran	0.34±2.44%	0±0%	1.35±4.77%	0.56±3.12%	0±0%	0±0%	0±0%	0±0%	1.17±4.46%
Copepod adult	33.26±39.25%	28.04±37.66%	26.86±34.74%	27.55±36.29%	38.03±41.71%	78.9±28.61%	42.05±42.24%	33.03±39.87%	33.8±38.15%
Copepod nauplius	2.56±12.37%	4.2±15.22%	4.27±16.55%	4.23±15.7%	0±0%	0±0%	0±0%	2.1±10.92%	3.7±15.45%
Crab zoea	0.73±8.09%	0±0%	0±0%	0±0%	2.05±13.56%	0±0%	1.84±12.88%	1.02±9.6%	0±0%
Doliolid	1±6.45%	0±0%	3.97±12.52%	1.65±8.24%	0±0%	0±0%	0±0%	0±0%	3.44±11.71%
Egg - copepod	25.32±36.37%	27.83±37.58%	16.89±30.82%	23.29±35.18%	29.51±39.16%	18.59±29.03%	28.43±38.22%	28.67±38.21%	17.12±30.27%
Egg - invertebrate	19.91±34.3%	27.62±39.37%	17.51±32.2%	23.43±36.72%	16.01±30.86%	0.43±1.05%	14.48±29.65%	21.82±35.69%	15.23±30.49%
Euphausiid	1.37±8.99%	0±0%	4.78±17.38%	1.98±11.36%	0.26±1.93%	2.08±5.1%	0.44±2.41%	0.13±1.36%	4.42±16.27%
Gastropod	0.32±4.02%	0±0%	0±0%	0±0%	0.91±6.74%	0±0%	0.82±6.4%	0.45±4.77%	0±0%
Planula larva	0.65±8.03%	0±0%	0±0%	0±0%	1.82±13.48%	0±0%	1.64±12.8%	0.91±9.53%	0±0%
Unknown crustacean	7.14±24.36%	5.9±22.98%	17.48±35.16%	10.71±29.06%	1.82±13.48%	0±0%	1.64±12.8%	3.86±18.86%	15.15±33.22%
Unknown gelatinous	1.14±8.74%	2.88±14.45%	0.49±2.39%	1.89±11.18%	0±0%	0±0%	0±0%	1.44±10.28%	0.42±2.23%

Overall *P. bachei* gut contents were considerably variable. Within a single year, season, and transect, this variability was seen between stations, within a station depending on day and time of sampling, and even amongst individuals collected from a single sampling event (Fig. S2.1). Yet some patterns were observable across the large scales of season and latitude. The

proportional importance of adult copepods, copepod eggs, and invertebrate eggs varied considerably with season and latitude (Fig. 2.1). In comparisons between seasons and between transects, overall dissimilarity in *P. bachei* gut content was driven by the same four prey taxa in the same order (copepod eggs, copepod adults, invertebrate eggs, and unknown crustaceans), giving a cumulative dissimilarity of >85% between summer vs. winter and NH vs. TR (Table S2.2).

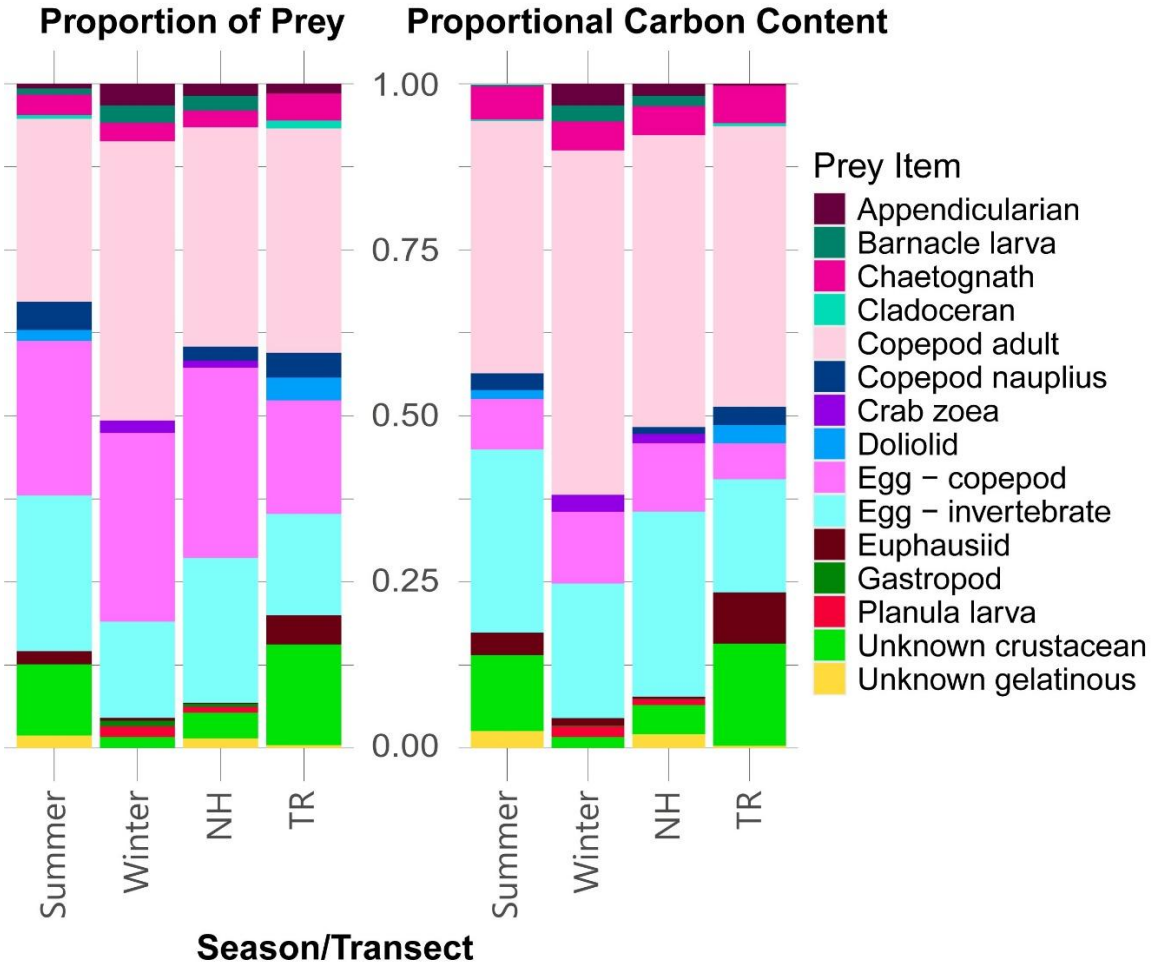

Figure 2.1. Proportional contribution of each prey taxa to *P. bachei* gut contents. Proportions are given in measure of counts of prey individuals (left) and of prey carbon content (right). Data is split to compare *P. bachei* sampled in different seasons (Summer n=94; Winter n=61) and from different transects (NH n=110; TR n=45).

Between seasons, *P. bachei* diet varied significantly on the level of whole taxonomic assemblage (Table 2.2), but not on the level of any individual prey taxa (Table S2.2).

Table 2.2. PERMANOVA and Permutests results from gut content data (in measure of prey counts) and FA data (in measure of individual FA proportions). For each dataset, results were compared for *P. bachei* collected in different seasons, transects, and season+transect combinations. Bold values indicate $p<0.05$. Footnote: * = reduced statistical testing power due to small sample size (FA samples: Winter TR n=1)

Constant	**Comparison**	**Gut content profile (counts)**			**FA profile (proportions)**		
		Permanova R^2	*Permanova p-value*	*Permutest p-value*	*Permanova R^2*	*Permanova p-value*	*Permutest p-value*
none	Seasonal (Summer vs. Winter)	0.0188	**0.009**	**0.012**	0.13648	**0.035**	0.83
none	Spatial (NH vs. TR)	0.0169	**0.02**	0.151	0.13533	**0.045**	0.596
Transect NH	Seasonal (Summer NH vs. Winter NH)	0.0181	0.065	0.131	0.21425	**0.047**	0.255
Transect TR	Seasonal (Summer TR vs. Winter TR)	0.0428	**0.047**	**0.002**	0.36983	0.144*	0.142
Season Summer	Spatial (Summer NH vs. Summer TR)	0.0161	0.136	0.226	0.14421	0.112	0.317
Season Winter	Spatial (Winter NH vs. Winter TR)	0.0375	**0.033**	0.103	0.46660	0.164*	0.128

Separating out the transects, *P. bachei* diet was statistically different between seasons within the TR transect but not within the NH transect, though this may be an artifact of low sampling size (n=8) from TR in winter. Seasonal data separated by transects can be explored further in Fig. S2.2, but was combined across transects for further interpretation here. Predation on adult copepods was higher (x1.5) in winter than in summer (Table 2.1, Fig. 2.1). Summer *P. bachei* consumed unidentifiable crustaceans at more than 6 times that of winter samples; as some of these crustaceans were likely copepods, this may narrow the consumptive difference on adult copepods between seasons. Copepod nauplii, doliolids, cladocerans, and unidentifiable

gelatinous organisms were found exclusively in summer *P. bachei*. Alternatively, crab zoea, planula larvae, and gastropods were found exclusively in winter *P. bachei*. Winter samples exhibited a shift toward higher predation on copepod eggs relative to invertebrate eggs, although the combined predation on eggs was constant between seasons (summer 47±42% and winter 43±44 %).

Between transects, *P. bachei* diet varied significantly on the level of whole taxonomic assemblage (Table 2.2) and on the level of individual taxon abundance within *P. bachei* guts for these five taxa: copepod adults, unknown crustaceans, euphausiids, doliolids, and cladocerans (Table S2.2). Separating out seasons, *P. bachei* diet was statistically different between transects in winter but not in summer. Averaged over all individuals per transect, proportional predation on adult copepods remained constant across transects at ~33% (Table 2.1, Fig. 2.1), qualified by uncertainty due to counts of unidentifiable crustaceans. Gut contents sampled from NH had more eggs than those sampled from TR. Planula larvae, barnacle larvae, crab zoea, and gastropods were only found in NH samples, while doliolids and cladocerans were only found in TR samples. Finally, euphausiids were far more common in guts of *P. bachei* from the TR transect, at about 34 times more than in *P. bachei* from the NH transect (Table 2.1).

Gut fullness as measured by either prey count or carbon content per gut varied widely among gut-filled *P. bachei* (Fig. 2.2). Prey counts ranged from 1 – 105 prey/gut and averaged at 9.7±14.2 prey/gut, while prey carbon content ranged from 0.1 – 139.1 µg C/gut and averaged at 15.3±22.1 µg C/gut. Gut fullness was seasonally consistent along the NH transect, but *P. bachei* along TR were fuller in winter as compared to summer. All differences in gut fullness between seasons, transects, or season+transect combinations were statistically non-significant (Mann Whitney U Test, α=0.05).

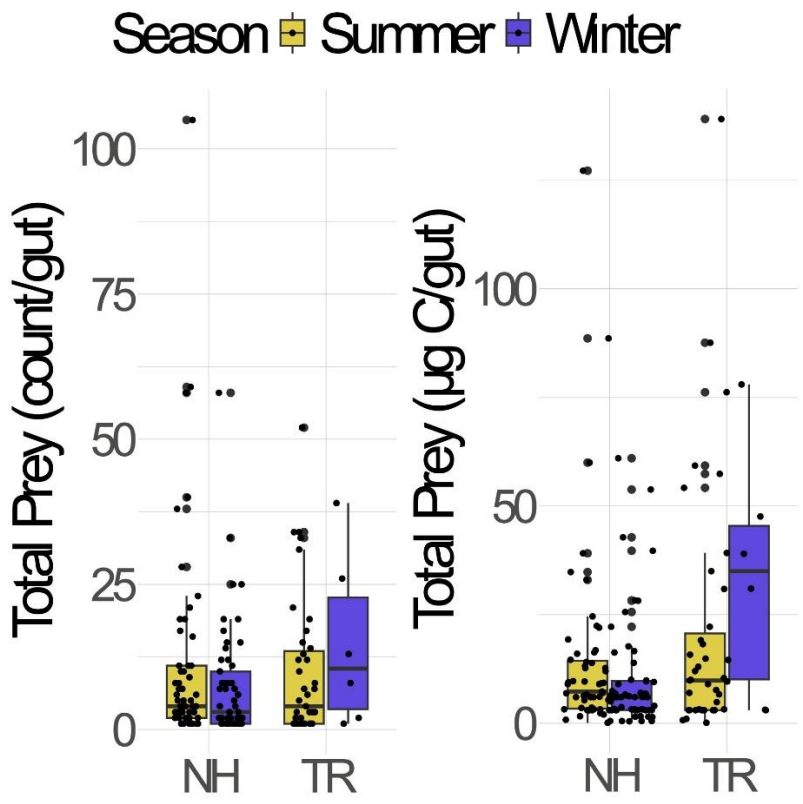

Figure 2.2. Box and whisker plots of total prey per *P. bachei* gut in non-empty *P. bachei*. Total prey is measured as either the total count of prey items (left) or total carbon content (µg C) of prey (right) per *P. bachei* gut. Data are separated per transect (NH; TR) and season (Summer, yellow; Winter, blue).

3.2. Fatty acids (FA) analysis

Pleurobrachia bachei samples were found to be consistently rich in polyunsaturated fatty acids (PUFA; 50.9±2.9%), with this FA category being the largest proportionally, followed by saturated fatty acids (SFA; 35.6±2.8%) and monounsaturated fatty acids (MUFA; 13.4±3.3%) (Table 2.3). Of the large PUFA content, nearly 90% was made up by the sum of three essential fatty acids (EFA; 44.9±3.3%), which includes EPA, DHA, and ARA. The observed patterns in these summations (SFA, MUFA, PUFA, and EFA) across all *P. bachei* samples were consistent over space and time, with no significant differences between seasons or transects.

Table 2.3. Fifty-four unique fatty acids (FA) found in *P. bachei* samples. FAs are listed in order of increasing desaturation and elongation, followed by FA summations: SFA (saturated fatty acids), MUFA (monounsaturated fatty acids), PUFA (polyunsaturated fatty acids), and SUM(EPA_DHA_ARA) (essential fatty acids). Each result is the percent contribution of that FA to the overall FA content, averaged across individuals with standard deviations. Averages are for *P. bachei* sampled from different transects (NH, TR), in different seasons (Summer, Winter), and over all *P. bachei* sampled (All). Bolded values are FAs which were found to be significantly different ($p<0.05$, SIMPER) between the two groups tested (NH vs. TR, or Summer vs. Winter).

FA	All	NH	TR	Summer	Winter
8:0	0.01±0.03	0.01±0.03	0.00±0.00	**0.00±0.00**	**0.02±0.04**
10:0	0.04±0.07	0.06±0.08	0.01±0.01	**0.01±0.01**	**0.09±0.10**
12:0	0.13±0.09	0.14±0.09	0.11±0.09	0.10±0.08	0.18±0.08
13:0	0.08±0.03	0.08±0.03	0.09±0.02	0.08±0.03	0.09±0.03
14:0	6.79±1.70	6.77±1.30	6.83±2.36	7.22±1.92	6.06±0.94
i-14:0	0.03±0.02	0.03±0.02	0.02±0.01	0.03±0.02	0.03±0.01
15:0	0.73±0.12	**0.78±0.11**	**0.66±0.10**	0.71±0.14	0.77±0.08
a-15:0	0.07±0.03	0.07±0.03	0.06±0.03	0.07±0.04	0.06±0.01
16:0	17.45±1.58	17.62±1.93	17.16±0.69	**16.69±1.04**	**18.76±1.53**
17:0	1.00±0.27	**1.13±0.20**	**0.78±0.22**	0.90±0.29	1.16±0.09
i-17:0	0.28±0.20	0.27±0.21	0.29±0.20	0.28±0.22	0.27±0.19
a-17:0	0.12±0.16	0.15±0.18	0.08±0.11	0.11±0.17	0.14±0.15
18:0	8.47±0.97	8.20±0.87	8.94±1.00	8.64±1.00	8.18±0.90
i-18:0	0.08±0.06	0.07±0.05	0.09±0.06	0.08±0.06	0.06±0.04
20:0	0.25±0.05	0.26±0.05	0.23±0.04	0.25±0.06	0.24±0.02
22:0	0.09±0.03	0.10±0.03	0.08±0.02	0.10±0.04	0.09±0.01
24:0	0.00±0.01	0.00±0.01	0.00±0.01	0.00±0.01	0.00±0.00
14:1	0.01±0.02	0.01±0.02	0.00±0.01	0.01±0.02	0.01±0.01
16:1ω5c	0.09±0.05	0.10±0.05	0.07±0.04	0.09±0.06	0.09±0.03
16:1ω7c	2.44±1.24	2.49±1.42	2.36±0.97	2.70±1.29	1.99±1.10
16:1ω7t	0.19±0.09	0.20±0.10	0.17±0.08	0.18±0.10	0.19±0.06
16:1ω9	0.08±0.15	0.09±0.16	0.06±0.15	0.06±0.15	0.09±0.16
17:1ω7c	0.03±0.06	0.04±0.06	0.02±0.06	0.03±0.05	0.04±0.06
18:1ω5c	0.05±0.02	0.05±0.02	0.04±0.02	0.04±0.02	0.06±0.01
18:1ω5t	0.13±0.07	0.14±0.08	0.11±0.05	0.13±0.07	0.13±0.08
18:1ω7c	1.31±0.54	1.19±0.52	1.51±0.55	1.32±0.41	1.28±0.74
18:1ω9c	4.49±1.34	4.39±1.26	4.65±1.55	4.26±1.33	4.87±1.36
18:1ω9t	0.11±0.04	0.11±0.04	0.10±0.05	0.11±0.06	0.11±0.01
20:1ω7	0.32±0.13	0.30±0.12	0.36±0.16	0.33±0.16	0.31±0.07
20:1ω9c	1.05±0.37	1.16±0.41	0.86±0.17	1.05±0.41	1.05±0.33
20:1ω11	0.06±0.05	0.07±0.05	0.03±0.03	0.06±0.05	0.06±0.05

Table 2.3. continued

FA	All	NH	TR	Summer	Winter
22:1ω7c	0.18±0.14	**0.14±0.11**	**0.24±0.18**	0.21±0.16	0.13±0.09
22:1ω9c	2.23±1.69	2.33±2.01	2.05±1.08	2.26±2.12	2.17±0.59
22:1ω11	0.38±0.54	0.53±0.64	0.12±0.07	0.46±0.64	0.24±0.30
24:1ω9c	0.29±0.15	0.30±0.16	0.29±0.14	**0.26±0.08**	**0.36±0.22**
24:1ω9t	0.01±0.04	0.01±0.02	0.02±0.06	**0.00±0.00**	**0.03±0.06**
16:2ω4	0.26±0.21	0.26±0.16	0.28±0.29	0.22±0.16	0.34±0.28
16:4ω1	0.12±0.30	0.09±0.18	0.17±0.46	0.05±0.15	0.23±0.46
18:2ω4	0.07±0.17	0.06±0.14	0.08±0.22	0.03±0.06	0.15±0.26
18:2ω6c	0.95±0.26	0.87±0.16	1.09±0.34	0.92±0.27	1.01±0.23
18:3ω3	0.79±0.20	0.80±0.20	0.78±0.21	0.81±0.23	0.77±0.15
18:3ω6	0.04±0.03	0.04±0.04	0.05±0.02	0.05±0.03	0.03±0.03
18:4ω3c	1.44±0.70	1.55±0.72	1.26±0.66	1.30±0.74	1.69±0.57
20:2ω6	0.31±0.09	**0.27±0.04**	**0.38±0.10**	0.33±0.10	0.28±0.02
20:3ω3	0.10±0.06	0.09±0.06	0.12±0.05	0.11±0.05	0.09±0.06
20:3ω6	0.04±0.03	0.03±0.04	0.05±0.03	0.05±0.03	0.02±0.03
20:4ω3	0.67±0.29	0.71±0.29	0.58±0.30	**0.53±0.27**	**0.90±0.12**
20:4ω6	0.68±0.34	0.68±0.41	0.68±0.16	0.78±0.37	0.51±0.18
20:5ω3	17.92±3.53	**16.28±2.89**	**20.74±2.72**	**19.47±3.19**	**15.26±2.37**
21:5ω3	0.12±0.27	0.12±0.24	0.13±0.34	0.06±0.14	0.24±0.41
22:2ω6	0.01±0.03	0.01±0.04	0.01±0.02	0.02±0.04	0.00±0.00
22:5ω3	0.80±0.20	0.74±0.22	0.90±0.12	0.81±0.20	0.77±0.22
22:5ω6	0.32±0.21	0.36±0.24	0.25±0.12	**0.28±0.16**	**0.38±0.27**
22:6ω3	26.29±3.91	27.65±3.45	23.96±3.74	**25.35±2.80**	**27.91±5.17**
SFA	35.63±2.78	35.74±3.07	35.44±2.41	35.30±2.36	36.21±3.50
MUFA	13.42±3.33	13.64±3.80	13.06±2.58	13.55±3.44	13.21±3.39
PUFA	50.94±2.93	50.62±3.26	51.5±2.36	51.15±3.30	50.58±2.35
SUM(EPA_DHA_ARA)	44.89±3.25	44.61±3.28	45.37±3.40	45.60±2.98	43.68±3.58

The essential fatty acids DHA (26.3±3.9%) and EPA (17.9±3.5%) respectively made up the first and second largest components of *P. bachei* fatty acid content. This was followed by saturated fatty acids 16:0 (17.5±1.6%), 18:0 (8.5±1.0%), and 14:0 (6.8±1.7%). Of the four calanoid copepod markers, ω9 isomers (20:1ω9 and 22:1ω9) were found in larger amounts (1.1±0.4% and 2.2±1.7%, respectively) than ω11 isomers (20:1ω11: 0.1±0.1%; 22:1ω11:

0.4±0.5%). These markers of calanoid copepod consumption remained proportionally consistent through space and time, with no significant differences found between seasons or transects.

Fatty acid profiles of *P. bachei* varied significantly between seasons (Tables 2.2 and 2.3, Fig. 2.3) overall and within the transect NH, but not within TR. Seasonal variability in FA content exceeded that observed between transects, with nine fatty acids differing significantly between summer vs. winter samples (Table 2.3). SIMPER analyses revealed that the same two essential fatty acids (EPA and DHA) that were most dissimilar between transects were also most dissimilar between seasons, with each FA contributing 17-20% to the total dissimilarity between summer vs. winter *P. bachei* samples (Table S2.3). EPA, associated with diatoms, was higher in summer (19.5±3.2%) than in winter (15.3±2.4%), while DHA, a marker of dinoflagellates, exhibited the reverse trend (summer: 25.4±2.8% vs. winter: 27.9±5.2%).

With seasons combined, FA profiles of *P. bachei* varied significantly between transects (Tables 2.2 and 2.3, Fig. 2.3) but these differences did not hold for within-season transect comparisons. While summations (SFA, MUFA, PUFA, EFA) remained consistent, five individual fatty acids varied significantly between *P. bachei* sampled from NH vs. TR transects (Table 2.3). EPA and DHA contributed the most toward the dissimilarity between FA profiles of NH vs. TR samples, with each FA contributing approximately 19% to the total dissimilarity (Table S2.3). EPA was significantly lower in *P. bachei* sampled from NH (16.3±2.9%) vs. TR (20.7±2.7%). Bacterial markers 15:0 and 17:0 were both significantly larger in NH than in TR samples.

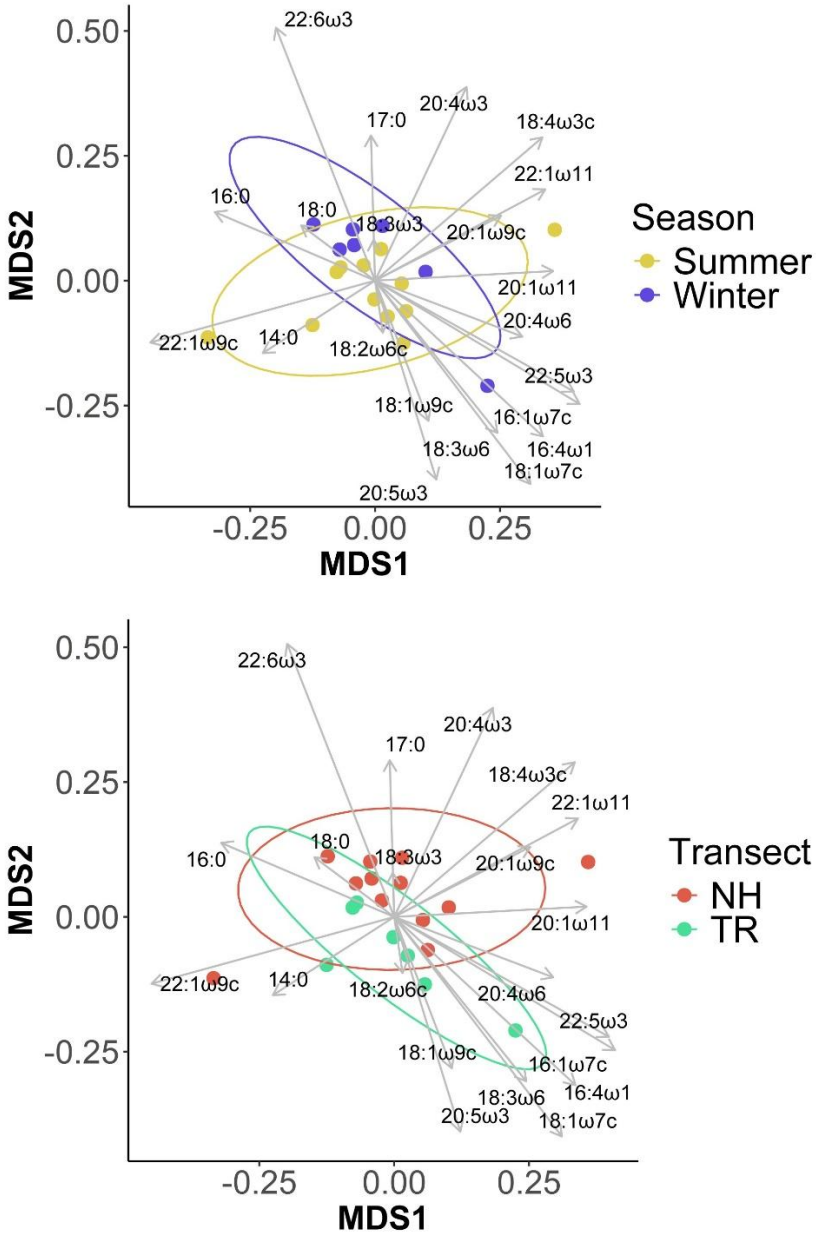

Figure 2.3. NMDS plots of *P. bachei* fatty acid profiles. Plots include all *P. bachei* fatty acid (FA) samples and display the vectors for all FAs found in proportion of at least 1% in any one sample, plus two FAs (18:3ω6 and 20:1ω11) of ecological interest. Samples are colored according to sampling season (top: Summer=yellow, n=15; Winter=Blue, n=7) or transect (bottom: NH=red, n=15; TR=green, n=7). Ellipses indicate 95% confidence intervals. NMDS stress = 0.098.

Calanoid copepod markers (20:1ω9, 22:1ω9, 20:1ω11, and 22:1ω11) were found in similar summed proportions between seasons and transects (Fig. 2.4). Two FA summations indicative of bacterial influence at the base of the food web were compared between seasons and transects: the sum of branched and odd-chain FA, and the sum of 15:0 and 17:0 isomers. Both FA summations were found to be generally higher in *P. bachei* sampled during winter as compared to summer, and those sampled from NH as compared to TR transects. Mann-Whitney U tests revealed all these seasonal and spatial differences to be non-significant except for the sum of 15:0 and 17:0 isomers between transects (W = 75, p = 0.004).

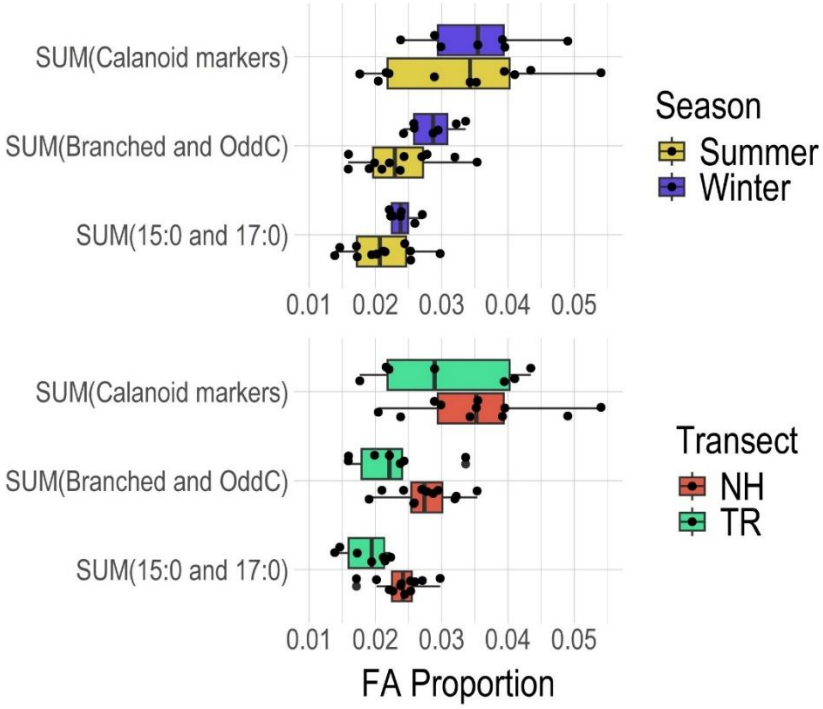

Figure 2.4. Summations of fatty acid proportions indicative of trophic relationships. Sum of calanoid markers (20:1ω9, 22:1ω9, 20:1ω11, and 22:1ω11) indicate predation on calanoid copepods. Sum of branched and odd-chain FAs as well as sum of 15:0 and 17:0 are each indicative of bacterial importance within the food web. These plots display FA summations for all *P. bachei* samples and are color coded according to sampling season (top: Summer=yellow, n=15; Winter=Blue, n=7) or transect (bottom: NH=red, n=15; TR=green, n=7). One datapoint plots beyond x-axis limits and is not displayed here: one sample of *P. bachei* collected in summer from NH transect yielded sum(calanoid markers) at 0.101 (10.1%) of total fatty acid concentration.

3.2.1. FA: Effects of gut evacuation

Little differences were found in the comparison of FA profiles of *P. bachei* samples that were allowed to evacuate their guts to those with filled guts. Averaging across paired samples, only four FAs differed more than 1% proportionally between gut-evacuated vs. gut-filled *P. bachei*. Compared to gut-filled *P. bachei*, gut-evacuated *P. bachei* saw a decrease in DHA, 14:0, and 16:0 by an average of 2.5±2.0%, 2.2±3.0%, and 1.1±0.4% respectively, but an increase in 16:1ω7c by an average of 1.2±1.5%.

4. DISCUSSION

Our analyses of *P. bachei* predation and fatty acid trophic biomarkers suggest that this ctenophore acts as both an influential predator and a rich prey source in the NCC, an eastern boundary current upwelling system. *Pleurobrachia bachei* are relatively abundant, can have high predation rates and consume prey that overlaps with many larval fishes. In providing a consistent source of quickly digestible concentrated essential fatty acids, *P. bachei* also serve as a critical source of nutrition in the NCC.

4.1. P. bachei *role as predator*

Over half of *P. bachei* sampled had prey in their guts, suggesting they feed frequently, which agrees with previous studies (Larson, 1987). Their diet was dominated by copepods (eggs and adults) and invertebrate eggs (Table 2.1), which are also critical food sources for other NCC predators, including many commercially important larval fishes (Scott, 1973; Arthur, 1976; Grover, 1991). This dietary overlap between *P. bachei* and larval fishes was similarly found in Prince William Sound (Purcell and Sturdevant, 2001). *Pleurobrachia bachei* have been found to

strongly influence pelagic food webs in other locations as well, such as through predation on small copepods off the coast of Chile (Pavez *et al.,* 2006).

Our analyses of predation patterns focused on comparisons as prey counts (i.e., taxonomic counts of prey items per gut as a percentage of total prey items per gut). Transforming the data from prey counts to prey carbon content using published conversion values (Table S2.4) did not greatly alter the overall trends seen in *P. bachei* predation patterns, with the most notable change being a greater emphasis on carbon-rich adult copepods and invertebrate eggs and less emphasis on carbon-poor copepod eggs. Thus, either measurement (prey count or carbon content) could be used to accurately characterize predation by *P. bachei* in the NCC.

Crustacean prey are generally thought to make up a major component of *P. bachei* diet. Our finding of crustaceans as about half (47±42%) of *P. bachei* prey aligns well with previous studies (32– 97%) (Hirota, 1974; Larson, 1987; Purcell, 1990; Purcell and Sturdevant, 2001). Copepods in particular made up a large (>29%) proportion of *P. bachei* diet, further supported by consistent detection of calanoid copepod FA markers. Interestingly, of the typical 20:1 and 22:1 calanoid copepod markers, ω9 isomers were found in larger amounts than ω11 isomers. This may be a reflection of the copepod taxa consumed by *P. bachei* (largely *Acartia* spp. and *Centropages* spp.). These two genera have been found to contain these ω9 but not ω11 isomers (Martynova *et al*., 2011), possibly as a result of their omnivorous feeding style or due to storing lipids as triacylglycerols rather than wax esters (Dalsgaard *et al*., 2003; Hagen and Auel, 2001).

One incongruence between our data and previous research in the temperate eastern Pacific Ocean is that three of the four previous studies (Hirota, 1974; Purcell, 1990; Purcell and Sturdevant, 2001) found cladocerans to make up a sizable (>10%) component of *P. bachei* diet, whereas our study found cladocerans in only one individual, putting its proportion at 0.3%. This

was likely due to low abundance of cladocerans at our sites and unlikely due to negative selection by *P. bachei*, as Purcell and Sturdevant (2001) found *P. bachei* exhibit strong positive selection for cladocerans. Other crustacean taxa found in *P. bachei* guts include copepod nauplii, barnacle larvae, crab zoea, and euphausiids (this study; Hirota, 1974; Larson, 1987).

Another difference between our findings and previously published work is the large (45±43%) component of copepod and invertebrate eggs in *P. bachei* guts. Hirota (1974) measured copepod eggs as the most abundant (43%) prey, while Larson (1987) also found small (>16%) and large (>19%) eggs in *P. bachei*. Yet other studies either grouped eggs into miscellany (Purcell and Sturdevant, 2001) or reported no eggs (Purcell, 1990). The invertebrate eggs that made up 20±34% of gut contents in our study were only named as a prey source in Larson (1987) and were not included in the previously referenced studies (Hirota, 1974; Purcell, 1990; Purcell and Sturdevant, 2001). Our finding of frequent predation on eggs was unexpected for *P. bachei*, whose feeding response is triggered by the movement of prey stuck to the colloblasts on its tentacles, meaning inert prey like eggs should fail to trigger feeding. We interpret this egg ingestion as incidental during the consumption of gravid adults rather than as active selection. This interpretation is supported by gut content observations in which we found copepod and invertebrate eggs in *P. bachei* guts, as well as the probable adults from which these eggs likely came detached post-consumption.

Gelatinous prey were found infrequently in our *P. bachei*, consistent with previous reports of minor (<1%) predation on appendicularians (Hirota, 1974; Larson, 1987; Purcell, 1990), chaetognaths (Hirota, 1974), and doliolids (Hirota, 1974). Gelatinous prey were unmentioned in Purcell and Sturdevant (2001). We also found that *P. bachei* consistently prey on

molluscan veligers (this study; Larson, 1987; Purcell, 1990; Purcell and Sturdevant, 2001), albeit at low (<1%) frequencies.

Fish larvae and fish eggs have been found in *P. bachei* guts from previous studies (Hirota, 1974; Purcell, 1990), yet were absent from *P. bachei* guts in this study, despite being observed as present in both our MOCNESS net collections and in concurrently collected imaging tows (Schmid *et al.,* 2023). Thus we expect that either fish larvae and eggs were not sufficiently abundant for *P. bachei* to encounter them with its ambushing tentacles or, especially in the case of fish larvae, it may be that these prey were able to successfully evade *P. bachei* capture.

Pleurobrachia bachei diet composition differed significantly between seasons. Copepod prey consistently dominated *P. bachei* diet, but predation per life stage varied seasonally. Copepod eggs and adults were more prominent in winter samples, while copepod nauplii were exclusively summer prey. As copepod abundance in the NCC typically declines in the winter (Peterson and Miller, 1977), the increased predation on copepod adults likely reflects reduced availability of alternative prey. A late-winter phytoplankton bloom induces copepod reproduction in the NCC (Peterson and Miller, 1977), which may explain the higher proportion of eggs – likely consumed via gravid females – in winter samples. The absence of copepod nauplii in winter guts may reflect sampling prior to when peak hatching occurred.

Eggs remained a consistently important prey item for *P. bachei* with a notable seasonal shift in egg source. Summer *P. bachei* fed evenly on copepod eggs and invertebrate eggs. Winter *P. bachei* consumed less invertebrate eggs, possibly due to many invertebrates being reproductively immature at this time. For comparison, *P. bachei* in nearby Saanich Inlet preyed on euphausiid eggs at rates corresponding to their seasonal abundance (Larson, 1987). An expected winter increase in appendicularian and chaetognath abundance in the NCC (Peterson

and Miller, 1977) likely explains the higher predation on appendicularians by *P. bachei* during this season, but leaves unexplained the consistent predation on chaetognaths across seasons.

Seasonal variation in *P. bachei* predation was also reflected in our FA results, where nine FAs were significantly differently concentrated in *P. bachei* between summer and winter. We interpret this as a reflection of seasonal shifts in the food web base and, reinforcing our gut content results, shifts in prey availability. Previous studies of ctenophores have similarly found FA content to track such seasonal shifts (Ju *et al.,* 2004; Graeve *et al.,* 2008).

Pleurobrachia bachei prey differed between the two latitudes sampled; although both transects were within the northern part of the California Current with a distance of only ~400km between them, predation patterns still differed significantly. This highlights the variability in both *P. bachei* predation patterns and in the Northern California Current ecosystem. One pattern that remained consistent across transects was predation on adult copepods at ~33% proportionally. More larval zooplankton and eggs were found in *P. bachei* from the NH transect, suggesting NH may host a more consistently reproducing population of zooplankton. Euphausiids were far more common in the guts of TR samples, possibly reflecting the stronger and more consistent upwelling at that latitude.

Considering that ctenophores co-occur with other carnivorous gelatinous zooplankton in the NCC, our results add to a growing literature on the trophic impact of these understudied predators. Tentaculate cnidarians including scyphomedusae (Suchman *et al.,* 2008; Zeman *et al.,* 2016) and hydromedusae (Corrales-Ugalde *et al.,* 2021) have been shown to be strong consumers of copepods and invertebrate eggs. In contrast, the drifting neustonic hydrozoan *Velella velella* (Zeman *et al.,* 2018) focuses on less motile prey such as cladocerans and anchovy eggs (*Engraulis mordax*) along with a small number of copepods.

4.2. P. bachei *role as prey*

Gelatinous zooplankton like *P. bachei* have been historically underappreciated as prey due to perceived low nutritional value, yet we found that this ctenophore is rich in essential fatty acids (EFA), with EPA and DHA together making up nearly half of its total fatty acid content. This rich source of summed EFA is consistent over space and time, making consumption of *P. bachei* a reliable way to meet these nutritional needs for *P. bachei* predators. Notably, although the summed EFA content was consistent through time, the relative concentrations of components EPA and DHA shifted seasonally. Summer *P. bachei* had higher EPA and lower DHA content, likely due to a seasonal shift in upwelling strength. Upwelling in the NCC is stronger in the summer than in the winter (Bograd *et al.,* 2009), which supports more diatoms in the NCC in spring-summer while dinoflagellates are more abundant in autumn-winter (Schmid *et al.,* 2023). These shifts at the base of the food web then become reflected in FA profiles of secondary consumers like *P. bachei*.

NH and TR transects also yielded *P. bachei* with significantly different FA profiles, with EPA and DHA driving this dissimilarity. Though diatom abundance was similar at the two transects during the study period (Schmid *et al.,* 2023), nitrate and nitrite (μM per L) levels were overall higher along the TR transect (Schmid *et al.,* 2023). This nutrient supply may have supported more sustained diatom growth at the base of the food web along TR, leading to the observed significantly higher EPA in *P. bachei* sampled from this transect.

Two FA summations indicative of bacterial activity at the food web base were higher in NH vs. TR and in winter vs. summer samples of *P. bachei*. This pattern likely reflects upwelling strength, which is weaker and more variable at NH and generally weaker during winter across the NCC (Bograd *et al.,* 2009). Weaker upwelling at the NH transect, especially during winter,

was confirmed via the Cumulative Coastal Upwelling Transport Index (CUTI) over 10 days prior to sampling (Schmid *et al.,* 2023). Weaker upwelling is expected to shift the food web toward greater microbial loop activity and reduced primary productivity, which we see reflected in the bacterial FA markers of *P. bachei*.

The consistently rich EFA found in *P. bachei* here mirrors that found in other studies of ctenophore fatty acids. Vansteenbrugge *et al.* (2016) found EFA ranged from 56.2-60.5% across three ctenophore species. Congener *Pleurobrachia pileus* has been found with similar EFA makeup in British Columbia (DHA: 33.59%, EPA: 18.58%, ARA: 0.87%; Arai *et al.,* 1989) and the southern North Sea (DHA: 34.4%, EPA: 22.5%, ARA: 3.6%; Vansteenbrugge *et al.,* 2016). To our knowledge, *P. bachei* has only been measured for FA content in one previous study along the southern California coast, where they contained much lower EFA content (PUFA: 28.20%, 22:6: 12.50%, 20:5: 12.10%, 20:4: 0.50%; Winnikoff *et al.*, 2021). It may be that the rich (44.9 ± 3.3%) EFA content of *P. bachei* in the NCC is, at least partially, owed to its frequent consumption of eggs. Compared to organisms of similar size, eggs of marine animals can have exceptionally high amounts of EFA, up to 360 times that predicted by known scaling relationships (Fuiman *et al.,* 2015).

Due to its relatively high EFA content, *P. bachei* may have an underappreciated influence in the NCC pelagic food web. EFA availability within a food web can have far-reaching consequences, causing entire regime shifts (Litzow *et al.,* 2006). EPA and DHA in particular have been identified as limiting in fish, with deficiencies linked to decreased fecundity, growth, and survival of early life stages (Tocher, 2010). As a gelatinous zooplankter, *P. bachei* is poor in total lipid content, requiring predators to consume many individuals to match the EFA mass obtained from a lipid-richer but EFA-poorer prey. However, *P. bachei* can be digested incredibly

rapidly - over 20 times faster than a shrimp (Arai *et al.*, 2003). We propose that as a quickly digestible concentrated source of EFA, *P. bachei* in the NCC serve an essential function in this food web. Schram *et al.* (2020) also found high (>25%) EFA content in another gelatinous zooplankter in the NCC, *Pyrosoma atlanticum*. Together, these findings support the call by Hays *et al.* (2018) to consider the nutritional value of gelatinous zooplankton beyond caloric content.

4.3. P. bachei *influence on NCC food web*

As part of a larger NCC research effort, planktonic community data were collected using the In Situ Ichthyoplankton Imaging System (ISIIS) alongside MOCNESS samples. Abundance and distribution of plankton from ISIIS imagery, including *P. bachei* and potential prey items, were previously published (Schmid *et al.,* 2023) and can be used to estimate trophic impact. The mean *P. bachei* abundance in the sampling region across transects, seasons, and years was 0.27±0.18 ind m^{-3}. Along the TR transect, winter abundance (0.12±0.18 ind m^{-3}) was significantly lower than in summer (0.34±0.15 ind m^{-3}) (Asymptotic Wilcoxon-Mann-Whitney Test; $Z = 2.12$, $p = 0.03$). Our abundances are comparable to those found by Pavez *et al.* (2010) off the Chilean coast, where high *P. bachei* densities (0.10±0.13 ind m^{-3} neritic; 0.33±0.52 ind m^{-3} oceanic) contribute to notable trophic impact (Pavez *et al*., 2006). Nine of the fifteen prey taxa identified from *P. bachei* guts were also quantified from ISIIS imagery. The abundance of these potential prey (Fig. S2.3, plotted from data in Schmid *et al.,* 2023) varied substantially between seasons, with total abundance in summer approximately twice that of winter (504±65 vs. 249±149 ind m^{-3}, respectively). The total prey abundance did not vary with transect (NH: 400±149 ind m^{-3}; TR: 404±184 ind m^{-3}).

By combining prey counts from *P. bachei* guts (this study) with data on abundances of *P. bachei* and background prey (Schmid *et al.,* 2023), the prey consumption (μg C m^{-3}) can be estimated (Table 2.4).

Table 2.4. *Pleurobrachia bachei* ecosystem level prey consumption in the NCC. Consumption rates per *P. bachei* individual (in measures of count and carbon content) from this study were scaled up using estimates of *P. bachei* abundance from Schmid *et al.* (2023).

Subset	***P. bachei* Abundance (ind/m^3)**	**Prey Consumption (count)**		**Prey Consumption (carbon)**	
		count/ind	*count/m^3*	μg *C/ind*	μg *C/m^3*
All	0.27±0.18	5.28±11.50	1.44±3.87	8.31±18.00	2.27±6.06
Summer	0.31±0.16	5.33±12.46	1.63±4.40	8.52±19.59	2.60±6.92
Winter	0.23±0.20	5.20±9.39	1.17±2.98	7.89±14.45	1.77±4.58
NH	0.29±0.16	5.28±12.03	1.55±4.12	6.89±14.74	2.02±5.07
TR	0.25±0.20	5.30±10.31	1.34±3.46	11.43±23.46	2.90±7.84

Seasonally, summer *P. bachei* were more abundant and consumed more zooplankton, both in prey count and carbon content. Prey field abundance was also higher in summer, making it unclear whether competition with other NCC predators is more intense in summer or winter. Consumptive impact also varied by latitude. *Pleurobrachia bachei* from the NH transect consumed a higher number of prey, while those from the TR transect ingested more carbon. Whether this reflects active selection for carbon-rich prey (e.g., euphausiids), avoidance of carbon-poor prey (e.g., eggs), or differences in prey availability remains unresolved. As a consistently abundant and frequently feeding predator in the NCC, *P. bachei* have a substantial consumptive impact in this ecosystem, feeding on an average of 1.44±3.87 prey m^{-3}, or 2.27±6.06 μg C m^{-3} (Table 2.4). This is comparable to the 2.09±3.49 μg C m^{-3} day^{-1} *P. bachei* consumes in small copepods along coastal Chile, an amount which is estimated to modulate the

copepod community size structure there (Pavez *et al*., 2006). As such, *P. bachei* in the NCC pose a considerable source of competition for the zooplankton that sustain commercial fisheries.

4.4. Conclusions

This study provides a detailed characterization of the trophic role of the tentaculate ctenophore *Pleurobrachia bachei* in the Northern California Current (NCC), a highly productive eastern boundary current. As prey, *P. bachei* serves as a reliable and quickly digestible source of essential fatty acids to its predators. As a predator, *P. bachei* acts as a major competitor through its consumption of copepods, copepod eggs, and invertebrate eggs. Patterns in *P. bachei* predation and nutritional quality both tracked seasonal and latitudinal differences in this dynamic upwelling system, with seasonal changes the more pronounced of the two. As abundant, frequently feeding, and nutritionally rich, we estimate that *P. bachei* is far more impactful to the NCC pelagic food web than previously understood. This highlights the need to consider the trophic importance of oft-underappreciated gelatinous zooplankton beyond their carbon content and more readily include them in models of pelagic food webs.

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BRIDGE

In Chapter II, I investigated the trophic role of the ctenophore *Pleurobrachia bachei* in the Northern California Current and described the influence this abundant zooplankter has here as both predator and prey. This study was limited to a single species, but there are many other gelatinous zooplankton that inhabit this upwelling system and the trophic ecology of most of these species is poorly understood. In Chapter III, I broadened my focus to characterize the trophic roles of a wide variety of co-occurring gelatinous zooplankton in the Northern California Current through the use of multivariate fatty acid analyses.

CHAPTER III

TROPHIC ECOLOGY OF CO-OCCURRING GELATINOUS ZOOPLANKTON IN A PELAGIC UPWELLING SYSTEM

This work will include coauthors Dr. Aaron Galloway and Dr. Kelly Sutherland as contributors to the final manuscript preparation. Dr. Sutherland designed sampling hypotheses and secured funding for sample collection. Sample collection using the MOCNESS sampling system was performed by members of the lab of project co-PIs Dr. Su Sponaugle and Dr. Robert Cowen. Microbial sampling was conducted by members of the lab of Dr. Anne Thompson; those results are addressed in other studies but not in the present study. Dr. Sutherland, myself, and many members of the labs of Dr. Sutherland, Dr. Anne Thompon, Dr. Su Sponaugle, and Dr. Robert Cowen participated in sample retrieval and preservation. Dr. Galloway provided all necessary materials and instrumentation for fatty acid extractions and analyses. I performed all fatty acid extractions and data analyses.

1. INTRODUCTION

Plankton encompass a functionally and taxonomically diverse assemblage, linked by the shared feature of a limited capacity to swim against currents. In categorizing this diversity, a frequently used class is “gelatinous zooplankton.” This plankton category is defined by their high (>95%) water content and fragile nature (Luskow *et al.*, 2021), which makes them very difficult to sample as traditional methods like nets destroy these delicate organisms (Purcell, 2018). Gelatinous zooplankton also have very low energy content relative to other pelagic groups, with up to 60x fewer calories per wet weight than fishes (Doyle *et al.*, 2007). For these reasons,

gelatinous zooplankton historically have been excluded from many pelagic food web models (Dadou *et al.*, 1996; Fenchel, 1988; Hopkins *et al.*, 1989), despite estimates that this globally ubiquitous group represents a demand of up to 12% of the mean annual global primary production (Lucas *et al.*, 2014).

This paradigm has begun to slowly shift and gelatinous zooplankton are increasingly being included in pelagic food web models (reviewed in Hays *et al.*, 2018; Clerc *et al.*, 2023; Luo *et al.*, 2020; Wright *et al.*, 2021). However, when gelatinous zooplankton are included, they are often grouped together as a single entity (Pauly *et al.*, 2009; Fuiman *et al.*, 2015; Lamb *et al.*, 2019) or considered to be trophic "dead ends" (Sommer *et al.*, 2002; Verity and Smetacek, 1996) in that they act as predators but are not considered specifically as prey. Both of these aspects of the inclusion of gelatinous zooplankton within pelagic food web models are understandable given the dearth of information on these organisms, but they are still misguided. First, gelatinous zooplankton encompass a wide variety of feeding strategies. Some are powerful predators; for example, the ctenophore *Beroe* sp. employs a raptorial feeding mode, and consumes prey by either engulfing it completely or biting off pieces using tooth-like macrocilia that line *Beroe*'s wide mouth (Haddock, 2007). Other gelatinous zooplankton are grazers; for example, the appendicularian *Oikopleura* sp. uses internal and external mucous mesh filters to collect tiny (pico- to micro-) plankton, including phytoplankton, microzooplankton, bacteria and viruses (Conley *et al.*, 2018). Hence, lumping all gelatinous zooplankton taxa together as one entity can turn into a problematic oversimplification. Second, modeling gelatinous zooplankton as trophic dead ends in pelagic food webs discounts the large number of species known to prey on gelatinous zooplankton, including many birds, mammals, reptiles, crustaceans, other gelatinous zooplankton, and fishes (Hays *et al.*, 2018; Thiebot and McInnes, 2020). With their rapid

digestibility and lack of hard parts to leave a trace, traditional gut content analyses are generally insufficient to determine predation on gelatinous zooplankton. Trophic "biomarkers" or "biochemical tracers" based on analysis of molecules, isotopes, or trace elements (e.g., reviewed in Pethybridge *et al.*, 2018) can be especially valuable for filling in this knowledge gap.

Fatty acids (FA) are molecules that are found in all living organisms and serve a wide variety of important biological functions, including acting as precursors to eicosanoid hormones, structuring cellular membranes, and storing biochemical energy (Dalsgaard *et al.*, 2003). Each FA is composed of a carboxylic acid head attached to a long aliphatic chain which varies widely both in its length and level of saturation, leading to groupings based on both these features: saturated (SAFA), monounsaturated (MUFA), polyunsaturated (PUFA), long chain polyunsaturated (LC-PUFA), etc. (Budge *et al.*, 2006). The basis of using FA as biomarkers stems from the observation that many primary producers synthesize a unique combination of FA, yielding a characteristic FA profile for that taxon (Galloway and Winder, 2015). Upon consumption, these FA are then transferred up to higher trophic levels with relatively little modification, allowing researchers to use FA profiles to trace trophic pathways (Budge *et al.*, 2006). There are certain FA that are generally useful as biomarkers for particular primary producer groups (Kelly and Scheibling, 2012). For example, when primary production is dominated by diatoms, consumers exhibit higher amounts of eicosapentaenoic acid (EPA, 20:5ω3) and 16:1ω7 in their tissues (Budge and Parrish, 1998). When dinoflagellates dominate primary producer communities, consumers exhibit higher amounts of docosahexaenoic acid (DHA, 22:6ω3) (Budge and Parrish, 1998). Consumers of bacteria exhibit markedly higher concentrations of branched and odd-chain fatty acids while consumers of calanoid copepods exhibit calanoid markers (20:1ω9, 20:1ω11, 22:1ω9, and 22:1ω11) (Budge and Parrish, 1998).

Across PUFAs, it has been observed that as trophic level increases, organisms tend to have larger proportions of longer-chain, more highly-modified PUFAs (e.g., EPA and DHA) while lower trophic levels tend to have proportionally more shorter-chain, less modified PUFAs such as linoleic acid (LA, 18:2ω6) and alpha-linolenic acid (ALA, 18:3ω3) (Galloway and Budge, 2020).

The FA content in a consumer's tissues is generally determined by 1) unmodified dietary FA, 2) dietary FA that is modified in predictable ways, and 3) endogenously derived FA from *de novo* synthesis by the consumer (Budge *et al.*, 2006). The combination of these determinants results in most taxa have a somewhat unique multivariate FA profile, a "signature" that typically varies more inter-taxonomically than intra-taxonomically. Note that intra-taxonomic variation in FA proportions does still occur, typically stemming from variability in extrinsic factors such as prey availability or shifts in primary production (Budge *et al.,* 2002, Hiltunen *et al.,* 2022). In addition to using FA to identify trophic relationships, we can also use FA profiles to infer the nutritional quality of an organism as a prey item. An organism can be considered nutritionally rich prey through having high concentrations of PUFA, especially of the essential fatty acids (EFA) which are those nutritionally critical FA that limit the growth and reproduction of a consumer (Dalsgaard *et al.*, 2003). Three EFA that have been identified as being most commonly limiting in diverse aquatic organisms are EPA, DHA, and arachidonic acid (ARA, 20:4ω6) (Arts *et al.*, 2001). When pelagic consumers such as zooplankton and fish have access to large amounts of EFA in their diet, they experience accelerated growth rates and increased fecundity (Brett *et al.*, 2009; Tocher, 2003). As a result, shifts of EFA supply within marine ecosystems can have cascading effects (Litzow *et al.*, 2006). A variety of gelatinous zooplankton have been found to be proportionally rich in PUFA (Joseph, 1979) and EFA (Schram *et al.*, 2020),

suggesting that fatty acids may be an insightful measure of the trophic importance of this group in pelagic food webs (Hays *et al.*, 2018).

One pelagic ecosystem boasting large populations of gelatinous zooplankton is the Northern California Current (NCC), an eastern boundary upwelling system that runs along the west coast of North America, extending from Cape Mendocino, California, to Vancouver Island, British Columbia. The high productivity of this system sustains many large fisheries (Checkley and Barth, 2009), necessitating a thorough understanding of the pelagic food web in this region. Gelatinous zooplankton in the NCC are both abundant and diverse. In comparisons of biomass (measured as dry weight biomass per volume of water) in the NCC among various groups, Pearcy (1972) found that of medusae to be higher than that of euphausiids and nearly equivalent to that of copepods. Pearcy (1972) also noted the wide variety of gelatinous zooplankton in the NCC, cataloguing 33 Hydrozoa, 5 Scyphozoa, 2 Ctenophora, 1 Appendicularia, and 8 Thaliacea. More recent work (Francis *et al.*, 2012) has estimated that gelatinous zooplankton have an average abundance of >200 ind m^{-3} in this region.

To better understand the trophic role of gelatinous zooplankton in marine food webs, we sampled from the NCC a variety of gelatinous zooplankton, along with some crustaceans and larval fishes to allow for comparisons to these non-gelatinous groups. We then compared the FA composition of these organisms using several categorical frameworks that enabled us to both compare gelatinous taxa with one another and contrast them with non-gelatinous taxa. Categorization schemes were chosen to address both the intrinsic and extrinsic factors that determine a consumer's FA composition. Phylogenetic groupings derived from the expectation that samples would exhibit taxonomic FA "signatures" (Budge *et al.*, 2006). Trait-based groupings are another way to categorize zooplankton (Kiørboe, 2011; Martini *et al.,* 2021) and

have been effectively used to compare FA profiles among a variety of zooplankton (Gonçalves *et al*., 2012; Hiltunen *et al.*, 2022; Stevens *et al*., 2022). We grouped samples according to "plankton categories" (gelatinous, crustacean, fish) based on the observation that this is a separation frequently used in the literature (e.g., Bode *et al*., 2013; Opdal *et al*., 2019; Wright *et al.*, 2021). We next grouped samples based on the broad feeding styles of "grazer" or "predator" where grazers feed via a mucous mesh or web as opposed to predators which feed by direct consumption. Lastly, we used known prey preferences to split predators according to more detailed "feeding guilds": "hard-body consumer (HB consumer)," "soft-body consumer (SB consumer)," "mixed-body consumer (MB consumer)," or "grazer.". This categorization approach derives from the observation that gelatinous predators generally fall into either of the two main groups, as consumers of primarily either hard- or soft-bodied prey, as noted by Robison (2004) and as used in other inter-taxonomic comparisons of gelatinous zooplankton (Costello and Colin, 2002). Altogether, this strategy yielded the following five categorization approaches through which we compared FA profiles among our samples: plankton categories, taxon, phylum, feeding styles, and feeding guilds.

2. MATERIALS AND METHODS

2.1. Sample collection

Samples of zooplankton were collected from two cross-shelf latitudinally parallel transect lines within the Northern California Current (Masterman *et al.*, 2025; Schmid *et al.*, 2023). The Newport Hydrographic Line at 44.65˚ N ran from 18-83 km off the coast while the Trinidad transect line at 41.05˚ N ran from 10-50 km off the coast. Transects were sampled during four cruises in the summers and winters of 2018-2019 over the following dates: Winter 2018

(02/17/18 – 02/23/18), Summer 2018 (07/05/18 – 07/11/18), Winter 2019 (03/04/19 – 03/12/19), and Summer 2019 (07/17/19 – 07/24/19).

Zooplankton were sampled from the Northern California Current using a coupled Multiple Opening and Closing Net and Environmental Sensing System (MOCNESS) (Guigand *et al.*, 2005). Samples in this study were restricted to those collected from the last net fired before retrieval to limit potential net-feeding that may confound trophic interpretations. This net had mouth size of 1 m^2, mesh size of 333 μm, and sampling depth of 0-25 m. Immediately after net retrieval, cod-end contents were poured into chilled picking trays. Within 30 minutes, individual zooplankton were hand-picked from the trays, pooled by taxon to ensure adequate biomass for FA extraction, and frozen at –80°C.

2.2. Fatty acid analysis

Each sample of zooplankton was weighed frozen, freeze-dried, weighed dry, and homogenized using a stainless-steel mortar and pestle. Samples were then analyzed for fatty acid content using the extraction method described by Schram *et al.* (2018) and gas chromatography mass spectrometry (GC-MS) method described by Taipale *et al.* (2013). The GC-MS used was Shimadzu Model QP2020 equipped with a DB-23 column (30 X 0.25 mm X 0.15 μm, Agilent). Quantification of fatty acids was based on calibration curves created using serial dilutions of GLC standard mixture 566C (Nu-Chek Prep), under a strict quality control of Pearson correlation coefficients ≥ 0.99 for all standard curves. An internal standard (nonadecanoic acid) was used to ensure extraction efficacy remained consistent between samples.

2.3. Dietary categorizations

As diet is a primary determinant of FA content in a consumer's tissues, we sought to investigate trophic drivers of inter-taxonomic variability in gelatinous FA profiles. We

accomplished this through categorizing each taxon first into a broad "feeding style," as either a "predator" (primarily feeding on other zooplankton) or "grazer" (primarily feeding on primary producers or heterotrophic microbes) (Table 3.1). We then followed this with a more detailed characterization of predation based on whether a taxon ate primarily hard-bodied prey, primarily soft-bodied prey, or a roughly equal mix of the two (Table 3.1). Based on known prey preferences, each taxon was thus put into one of four feeding guilds: "hard-body consumer (HB consumer)," "soft-body consumer (SB consumer)," "mixed-body consumer (MB consumer)," or "grazer" (Table 3.1). "Hard-body consumer" includes all taxa whose known diet is composed of primarily (>75%) hard-bodied prey including crustaceans and fish larvae. "Soft-body consumer" includes all taxa whose known diet is composed of primarily (>75%) soft-bodied prey including other gelatinous zooplankton and eggs. "Mixed-body consumer" includes all taxa whose known diet is composed of approximately equal (35-65%) amounts of hard- and soft-bodied prey. Lastly, "grazer" includes all taxa who feed via a mucous mesh or web to graze on tiny (pico- to micro-) plankton, including viruses, bacteria, cyanobacteria, phytoplankton and microzooplankton.

Table 3.1. Trophic information for gelatinous taxa. For each gelatinous taxon sampled, feeding style and common prey items were determined from the literature. From this, taxa were placed into feeding styles of "predator" or "grazer." Taxa were placed into feeding guilds of "hard-body consumer (HB consumer; H_BC)," "soft-body consumer (SB consumer; S_BC)," "mixed-body consumer (MB consumer; M_BC)," or "grazer" depending on whether known prey are primarily (>75%) soft-bodied (gelatinous zooplankton and eggs), hard-bodied (crustaceans and fish larvae), a mix of both, or feeding is done by grazing through mucous mesh or webs.

Taxon	**Sample Size (n)**	**Feeding Style**	**Feeding Guild**	**Known Prey**	**Sources**
Tomopteris sp.	5	predator	S_BC	chaetognaths, tunicates, fish larvae (minor)	Rakusa-Suszczewski, 1968
Chaetognatha	36	predator	H_BC	copepods, small crustaceans, fish larvae	Terazaki, 2000
Appendicularia	6	grazer	grazer	diatoms, dinoflagellates, bacterioplankton	Troedsson *et al.*, 2005
Doliolida	9	grazer	grazer	diatoms, dinoflagellates, coccolithophores	Hiebert *et al.*, 2025
Pyrosoma atlanticum	3	grazer	grazer	diatoms, dinoflagellates, coccolithophores	Hiebert *et al.*, 2025
Salpidae	8	grazer	grazer	diatoms, dinoflagellates, coccolithophores, small crustaceans (minor)	Hiebert *et al.*, 2025
Aequorea sp.	4	predator	S_BC	appendicularia, eggs, small medusae, copepods (minor)	Costello and Colin, 2002
Clytia sp.	9	predator	S_BC	appendicularia, eggs (copepod or invertebrate), chaetognatha, copepods (minor)	Corrales-Ugalde *et al.*, 2021
Eutonina sp.	2	predator	S_BC	appendicularia, eggs (copepod or invertebrate), chaetognatha, copepods (minor)	Corrales-Ugalde *et al.*, 2021
Mitrocoma sp.	4	predator	S_BC	appendicularia, eggs, copepod nauplii, crustaceans (minor)	Corrales-Ugalde *et al.*, 2021 (supp.); Costello and Colin, 2002
Siphonophorae Calycophorae	11	predator	M_BC	copepods, appendicularia, salps	Hetherington *et al.*, 2022; Damien-Serrano *et al.*, 2022
Siphonophorae Physonectae	3	predator	H_BC	euphausiids, small crustaceans, large crustaceans, maybe fishes	Choy *et al.*, 2017; Damien Serrano *et al.*, 2021
Beroe sp.	7	predator	S_BC	exclusively ctenophores	Haddock, 2007
Pleurobrachia bachei	19	predator	M_BC	copepods, eggs (copepod or invertebrate), chaetognatha	Masterman *et al.,* 2025 (see Chapter II)
Pteropod Gymnosomata	2	predator	S_BC	exclusively *Limacina* sp.	Conover and Lalli, 1972
Pteropod Thecosomata	7	grazer	grazer	diatoms, protists, small copepods, juvenile *Limacina* sp.	Gilmer and Harbison, 1991; Hiebert *et al.*, 2025

2.4. Data analysis and statistics

Several categorization approaches were used to group zooplankton: 1) plankton categories (gelatinous, crustacean, and fish), 2) taxon (i.e. lowest level of taxonomic resolution), 3) phylum, 4) feeding style (predator vs grazer), and 5) feeding guild (HB consumer, MB consumer, SB consumer, or grazer). Qualitative seasonal comparisons were made for all taxa sampled in both winter and summer, while statistical seasonal comparisons were limited to Chaetognatha samples. FA profiles were compared between groups using permutational multivariate analysis of variance (PERMANOVA; Anderson *et al*., 2001) and using Bray-Curtis dissimilarity in order to test for significant differences in FA proportions between groups. Permutests were used to test for significant differences in multivariate dispersion of FA proportions between groups, with the understanding that a significant result from permutest might contribute to a false positive significant result from PERMANOVA. Similarity Percentages (SIMPER) analyses were used to determine which FAs drove differences in FA profiles between the groups in each categorization approach. Non-metric multidimensional scaling (NMDS) plots were used to visualize variability in FA profiles, with ellipses for each group in the plot depicting 95% confidence intervals of the multidimensional spread. FA summations were compared between groups using barplots and tested for significant differences using Mann Whitney U tests. Boxplots were used to compare R^2 results from the aforementioned PERMANOVA tests to compare the explanatory power offered by each of the categorization approaches. All statistical tests were performed in R version 2023.12.1+402 (R Core Team, 2023) using vegan package version 2.6-4 (Oksanen *et al.*, 2022).

In performing so many PERMANOVA tests, researchers sometimes apply a correction (e.g., Bonferroni or Benjamini-Hochberg) to resulting p-values in order to control for inflated

false positives. In our PERMANOVA tests comparing FA profiles, we found most comparisons to yield significant ($p<0.05$) results without a correction, while a Bonferroni correction yielded almost no significant results. Considering both of these overall conclusions, neither seems to adequately represent the reality of our dataset. Notably, in our permutests comparing FA profiles, we found that these tests also frequently yielded significant results, indicating that in many of our PERMANOVA comparisons, it may be the significantly different dispersions that are causing the significant PERMANOVA result. Thus, we opted to leave the PERMANOVA p-values un-corrected and instead look at both PERMANOVA and permutest results to interpret patterns in our FA data. It should also be noted that sample sizes varied greatly among our comparisons, especially in intertaxonomic comparisons where samples sizes ranged from n=2 to n=36. This great variability in sample sizes also likely affected some of our statistical comparisons.

3. RESULTS

3.1. Zooplankton sampled

Through this focused sampling effort, we collected a total of 16 gelatinous taxa, that we identified to the lowest taxonomic level possible (Table 3.1). For some taxa, we were able to identify down to species (e.g., *Pyrosoma atlanticum*) while others were limited to order (e.g., Doliolida). Gelatinous taxa spanned six phyla with most phyla encompassing more than one taxon. Also included in this study are three crustaceans and two fishes to allow for comparisons of gelatinous zooplankton to these non-gelatinous plankton categories.

Table 3.2. List of zooplankton collected with phylogenetic classifications. A total of 16 gelatinous zooplankton (top section) taxa were sampled for this study as well as 3 crustacean (middle section) taxa and 2 species of fish larvae (bottom section). All taxa were identified to the lowest taxonomic level possible (taxon), as well as noted for what was the lowest level of identification achieved: ID = class (C), order (O), sub-order (O), family (F), genus (G), or species (S). Sample sizes are given by n.

Phylum	Class	Order	Family	Genus & species	ID	Taxon	n
Annelida	Polychaeta	Phyllodocida	Tomopteridae	*Tomopteris*	G	*Tomopteris* sp.	5
Chaetognatha	Sagittoidea	-	-	-	C	Chaetognatha	36
Chordata	Appendicularia	Copelata	-	-	O	Appendicularia	6
Chordata	Thaliacea	Doliolida	-	-	O	Doliolida	9
Chordata	Thaliacea	Pyrosomatida	Pyrosomatidae	*Pyrosoma atlanticum*	S	*Pyrosoma atlanticum*	3
Chordata	Thaliacea	Salpida	Salpidae	-	F	Salpidae	8
Cnidaria	Hydrozoa	Leptothecata	Aequoreidae	*Aequorea*	G	*Aequorea* sp.	4
Cnidaria	Hydrozoa	Leptothecata	Campanulariidae	*Clytia*	G	*Clytia* sp.	9
Cnidaria	Hydrozoa	Leptothecata	Eirenidae	*Eutonina*	G	*Eutonina* sp.	2
Cnidaria	Hydrozoa	Leptothecata	Mitrocomidae	*Mitrocoma*	G	*Mitrocoma* sp.	4
Cnidaria	Hydrozoa	Siphonophorae; sub-order Calycophorae	-	-	Sub-O	Siphonophorae Calycophorae	11
Cnidaria	Hydrozoa	Siphonophorae; sub-order Physonectae	-	-	Sub-O	Siphonophorae Physonectae	3
Ctenophora	Nuda	Beroida	Beroidae	*Beroe*	G	*Beroe* sp.	7
Ctenophora	Tentaculata	Cydippida	Cydippidae	*Pleurobrachia bachei*	S	*Pleurobrachia bachei*	19
Mollusca	Gastropoda	Pteropoda; sub-order Gymnosomata	-	-	Sub-O	Pteropod Gymnosomata	2
Mollusca	Gastropoda	Pteropoda; sub-order Thecosomata	-	-	Sub-O	Pteropod Thecosomata	7
Arthropoda	Malacostraca	Amphipoda; sub-order Hyperiidea	-	-	Sub-O	Amphipoda Hyperiidea	5
Arthropoda	Hexanauplia; sub-class Copepoda	Calanoida	-	-	O	Copepoda	21
Arthropoda	Malacostraca	Euphausiacea	Euphausiidae	-	F	Euphausiidae	22
Chordata	Actinopterygii	Perciformes	Scorpaenidae	*Sebastes*	G	*Sebastes* spp.	24
Chordata	Actinopterygii	Myctophiformes	Myctophidae	*Stenobrachius leucopsarus*	S	*Stenobrachius leucopsarus*	19

3.2. "Gelatinous Zooplankton" as a group: comparisons to other plankton categories

FA profiles of plankton categories exhibited a large amount of overlap in multidimensional space (Fig. 3.1).

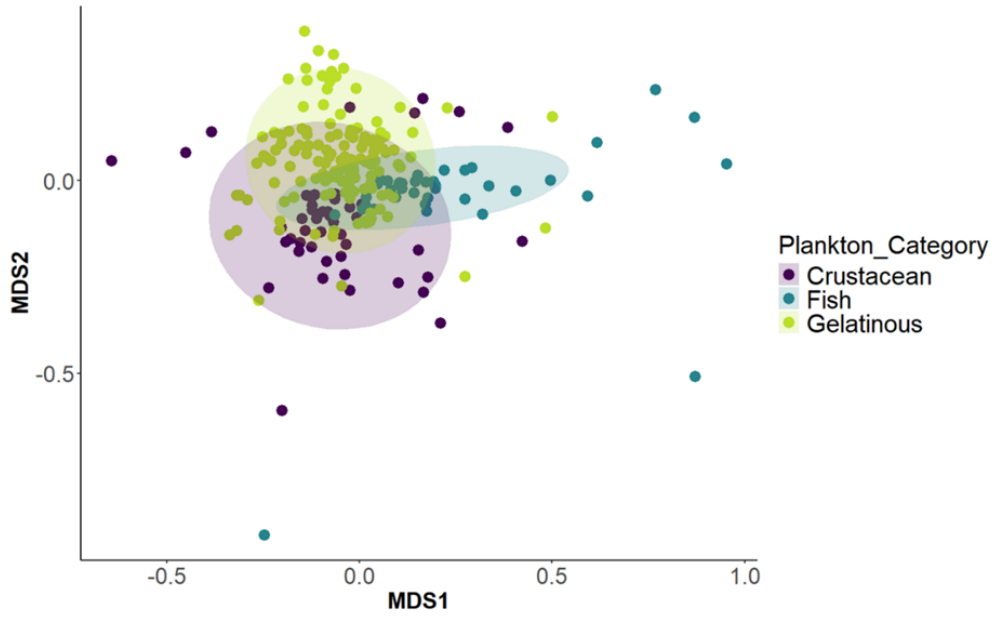


Figure 3.1. NMDS plot of FA profiles for all zooplankton samples. Includes both gelatinous (green, n=135) and non-gelatinous (fish: blue, n=43; crustacean: purple, n=48) zooplankton. All FAs are included and FAs were measured as proportions. Datapoints are colored by plankton category. Ellipses indicate 95% confidence intervals. NMDS Stress = 0.192.

Despite the visual overlap in multidimensional space, FA profiles differed significantly between each pair of plankton categories (Table 3.2). Across paired PERMANOVA comparisons, this categorization approach of "plankton category" explained 8.4-17.4% of the observed variability in FA profiles.

Table 3.3. PERMANOVA and Permutest comparisons based on plankton category. PERMANOVA and permutests were run to compare the FA profiles of all gelatinous and non-gelatinous zooplankton to each other based on "plankton category" (gelatinous, fish, or crusctacean). FA profiles were compared across samples as proportional contributions of each FA to the total FA concentration per sample. Bolded values indicate significance ($p<0.05$).

Comparison: Plankton Category		**Sample sizes (n)**		**PERMANOVA**			**Permutest of dispersion**	
Group A	**Group B**	**A**	**B**	**Pseudo-F**	**R^2**	**p**	**F**	**p**
Crustacean	Fish	48	43	18.76	0.174	**0.001**	0.46	0.473
Crustacean	Gelatinous	48	135	16.54	0.084	**0.001**	6.06	**0.011**
Fish	Gelatinous	43	135	33.92	0.162	**0.001**	0.78	0.375

Among these plankton categories, gelatinous zooplankton had significantly higher PUFA proportions (48.26±7.06%) (Table S3.1) than in fishes (Mann Whitney U: $p<0.001$) and crustaceans (Mann Whitney U: $p=0.043$). Gelatinous zooplankton also boasted significantly higher EFA proportions (39.3±6.36%) than in both other groups [Mann Whitney U: $p<0.001$ (fishes), $p=0.027$ (crustaceans)]. Proportional MUFA was significantly lower in gelatinous zooplankton (18.42±6.70%), than in crustaceans (Mann Whitney U: $p<0.001$) but not significantly lower than in fishes (Mann Whitney U: $p=0.151$). FAs driving dissimilarity (Table S3.2) between gelatinous zooplankton and each of the other two categories were primarily DHA, EPA, 18:1ω9, and various SAFA. Among all three, gelatinous zooplankton had the highest proportion of DHA and the lowest proportion of 18:1ω9. Proportional EPA content in crustacean zooplankton was higher than in gelatinous zooplankton. Average proportions of each FA per taxon sampled are given in supplemental Tables S3.3 (gelatinous zooplankton), S3.4 (crustaceans), and S3.5 (fishes).

3.3. Gelatinous zooplankton: high inter-taxonomic variability in FA profiles

FA profiles of co-occurring gelatinous zooplankton varied greatly inter-taxonomically (Fig. 3.2, Table S3.3).

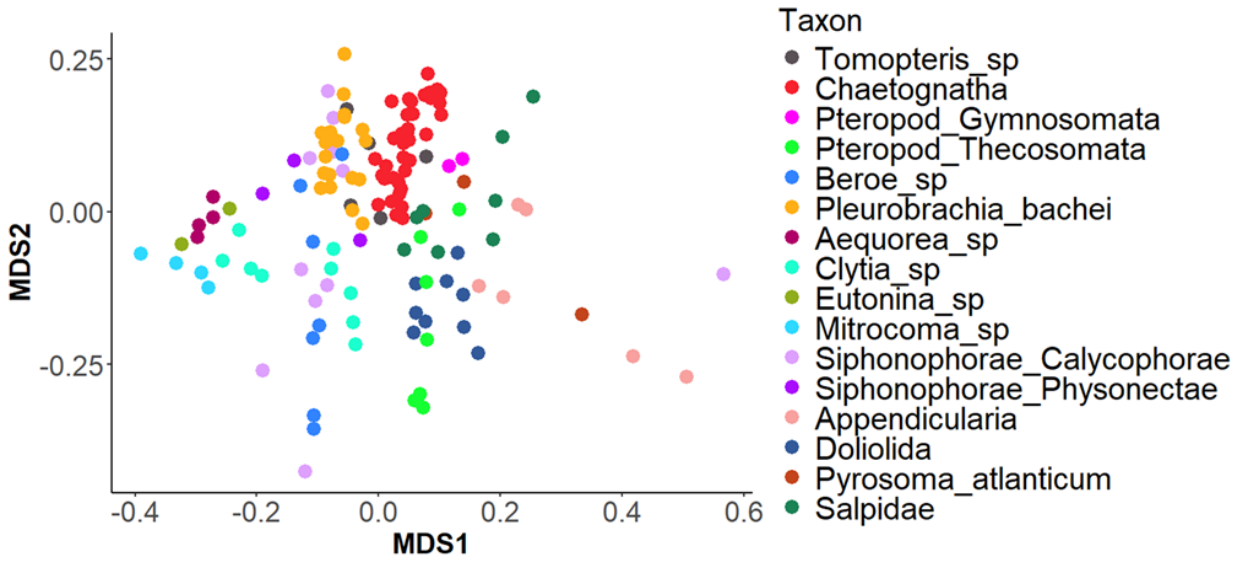


Figure 3.2. NMDS plot of FA profiles for gelatinous zooplankton, by taxon. All FAs are included and measured in proportions. Datapoints are colored by taxon. Stress = 0.229.

Of the 120 inter-taxonomic comparisons of FA profiles, PERMANOVA results showed a significant difference in nearly every (105/120) case (Table S3.6). In these comparisons of FA profiles across all gelatinous samples, taxon identification explained on average nearly half (45.9±16.7%) of the variability seen in FA profiles, in some cases explaining nearly all (94.2%) of the variability. Yet dispersions in FA profiles within taxa also varied greatly, leading to the Permutest detection of significant differences in dispersion in about half (64/120) of inter-taxonomic comparisons. Inter-taxonomic comparisons involving gymnosome pteropods were all non-significant, likely due to the low sample size (n=2). Comparisons among taxa within the order Leptothecata were also frequently non-significant, suggesting some strong within-order similarity among leptothecates.

In addition to varying among taxa, FA profiles also varied intra-taxonomically. Of the sixteen gelatinous taxa, ten were sampled in both summer and winter seasons: Appendicularia, Chaetognatha, *Clytia* sp., *Pleurobrachia bachei*, Pteropod Thecosomata, *Pyrosoma atlanticum*, Salpidae, Siphonophore Calycophorae, Siphonophore Physonect, and *Tomopteris* sp.. Across these taxa, winter samples were generally enriched in DHA and depleted in both EPA and 16:1ω7. Replication per season was only high enough to allow for further investigation for *Pleurobrachia bachei* (see Chapter II) and Chaetognatha. Chaetognatha exhibited a clear seasonal shift in FA proportions in multidimensional space (Fig. S3.1). Compared to summer (n=15), winter (n=21) samples were significantly (SIMPER $p<0.05$) richer in DHA and significantly depleted in EPA. MUFA 18:1ω9 was significantly higher in winter samples. Together these three FA (DHA, EPA, and 18:1ω9) drove about a third (34.4%) of the dissimilarity between seasons in Chaetognatha. MUFAs 16:1ω7, 22:1ω9, and 24:1ω9 also drove dissimilarity with the first being higher in summer and remaining two being higher in winter samples.

3.4. Drivers of inter-taxonomic variability: Phylum

With the high degree of inter-taxonomic variability in FA profiles among gelatinous zooplankton, we sought to identify drivers of this variability. Separating gelatinous zooplankton based on phylum yielded some notable separation in multidimensional space (Fig. 3.3). Some phyla (Cnidaria, Chordata) showed a wide distribution in FA space, likely owing to the grouping of numerous taxa within each of these phyla (Cnidaria taxa n=6; Chordata taxa n=4). In contrast, Chaetognatha (taxa n=1) grouped very tightly in multivariate space. Those phyla containing two taxa (Mollusca and Ctenophora) both exhibited a wide spread along just one axis, likely due to

encompassing the two centroids of each taxon split in space. Annelida (taxa n=1) exhibited a relatively wide spread, possibly due to low replication of its only taxon (*Tomopteris* sp. n=5).

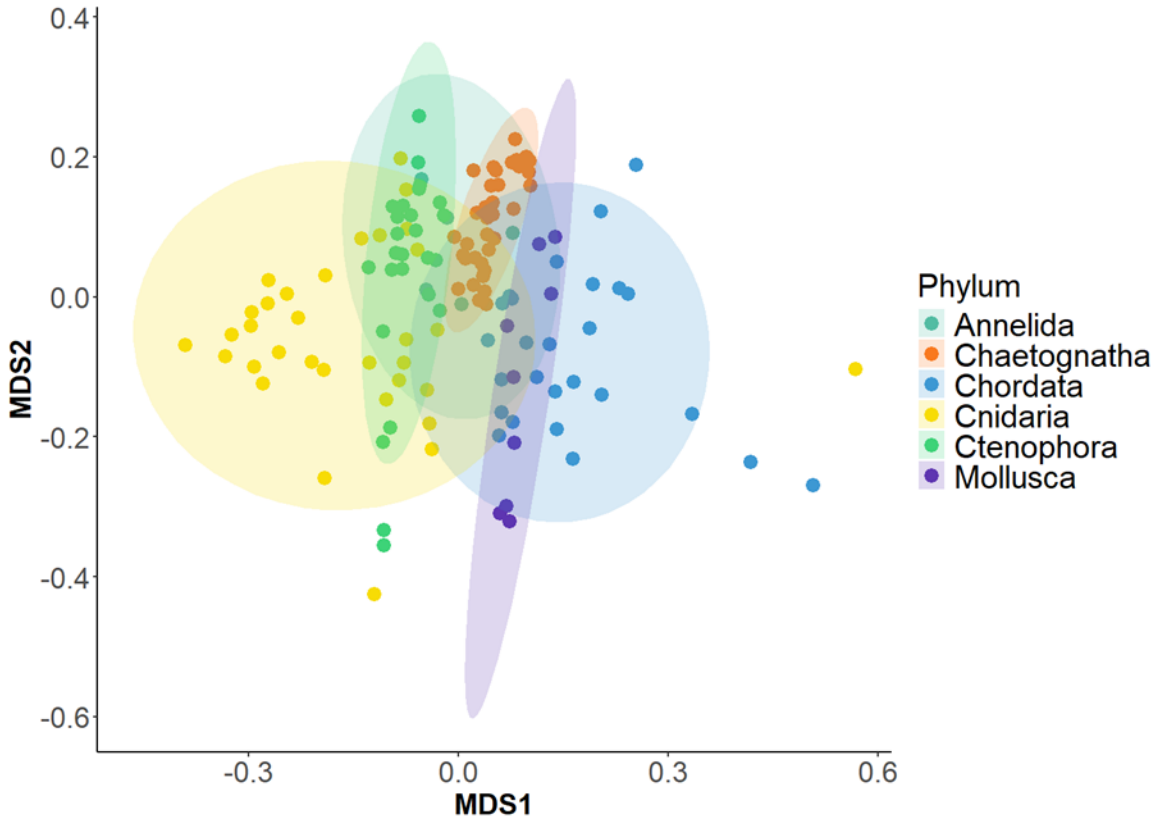


Figure 3.3. NMDS plot of FA profiles for gelatinous zooplankton, categorized by phylum. All FAs are included and measured in proportions. Datapoints are colored by phylum. Ellipses indicate 95% confidence intervals. Stress = 0.229.

PERMANOVAs showed significant ($p<0.05$) differences in every inter-phyla comparison, but note that dispersions were also significantly different between most phyla (Table 3.3). The explanatory power of this categorization approach was much higher (13.1-42.8%) than that of "plankton categories" (8.4-17.4%) in describing the observed variation in FA proportions.

Table 3.4. PERMANOVA and Permutest comparisons based on phylum. PERMANOVA and permutests were run to compare the FA profiles of all gelatinous zooplankton to each other based on phylum. FA profiles were compared across samples as proportional contributions of each FA to the total FA concentration per sample. Bolded values indicate significance ($p<0.05$).

Comparison: Phylum		**Sample sizes (n)**		**PERMANOVA**			**Permutest of dispersion**	
Group A	**Group B**	**A**	**B**	**Pseudo -F**	**R^2**	**p**	**F**	**p**
Annelida	Chaetognatha	5	36	9.66	0.199	**0.001**	1.11	0.302
Annelida	Cnidaria	5	33	5.42	0.131	**0.001**	10.35	**0.01**
Chaetognatha	Chordata	36	26	28.82	0.324	**0.001**	30.5	**0.001**
Chaetognatha	Cnidaria	36	33	32.91	0.329	**0.001**	45.65	**0.001**
Chaetognatha	Ctenophora	36	26	23.87	0.285	**0.001**	8.63	**0.004**
Chaetognatha	Mollusca	36	9	32.17	0.428	**0.001**	5	**0.03**
Chordata	Cnidaria	33	26	19.04	0.25	**0.001**	0.35	0.561
Chordata	Ctenophora	26	26	19.68	0.282	**0.001**	3.8	0.065
Chordata	Mollusca	9	26	7.88	0.193	**0.001**	3.16	0.086
Cnidaria	Ctenophora	26	33	12.18	0.176	**0.001**	7.47	**0.004**
Cnidaria	Mollusca	9	33	12.35	0.236	**0.001**	5.48	**0.029**
Ctenophora	Mollusca	9	26	11.59	0.26	**0.001**	0.13	0.711
Annelida	Chordata	5	26	6.15	0.175	**0.002**	7.33	**0.02**
Annelida	Mollusca	5	9	8.53	0.416	**0.003**	3.95	0.07
Annelida	Ctenophora	5	26	4.93	0.145	**0.014**	2.95	0.086

Differences in FA profiles between phyla were primarily driven by EFA (EPA, DHA, and ARA) (Table S3.7). In any inter-phyla comparison, a commonly observed pattern was to find EPA higher in one phylum and DHA higher in the other phylum; yet altogether the summed EFA was relatively consistent across phyla, ranging from an average of 34.81±7.82% in Chordata to 44.2±4.44% in Ctenophora (Table S3.8). MUFA 18:1ω9 was also a frequent driver of dissimilarity, ranging from an average of 1.47±0.41% in Mollusca to 7.09±2.63% in Chaetognatha.

3.5. Drivers of inter-taxonomic variability: Diet - Feeding Style

FA profiles of gelatinous zooplankton categorized by feeding style differed significantly (PERMANOVA: Pseudo-F=21.04, R^2=0.137, p=0.001) from one another with no significant

difference in dispersion (Permutest: F=0.076, p=0.795). Samples split clearly in multidimensional space based on feeding style (Fig. 3.4).

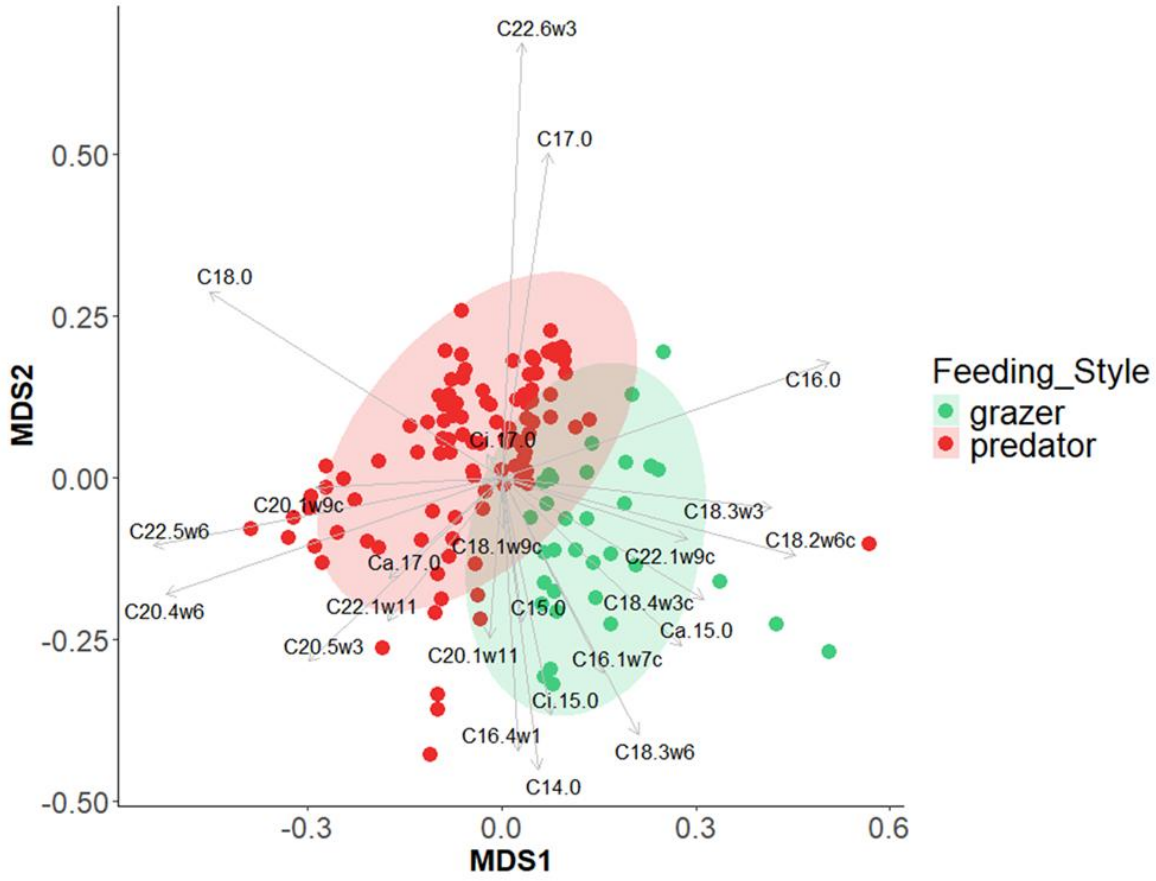


Figure 3.4. NMDS plot of FA profiles of gelatinous zooplankton comparing feeding style: predator (red) vs. grazer (green). Datapoints are colored according to feeding style and ellipses indicate 95% confidence intervals. FA vectors displayed are a subset of FA that were found to frequently drive dissimilarity across comparisons throughout this study, as well as FA that are of ecological importance. Stress = 0.229.

Between gelatinous predators (n=102) and gelatinous grazers (n=33), PUFAs DHA and EPA were the first and third drivers of dissimilarity, respectively, with each being higher in predators than in grazers (DHA: 21.6% vs 19.0%; EPA: 16.3% vs 15.42%) (Table S3.9). The PUFA ARA was also higher in predators. MUFA drivers of dissimilarity included 18:1ω9 which was higher in predators, and MUFAs 22:1ω9 and 16:1ω7 which were both higher in grazers. In

general, grazers were higher in most saturated and branched odd-chain FAs (14:0, 15:0, i-15:0, a-15:0, i-17:0, and a-17:0) as well as shorter-chain PUFAs [18:2ω6 (LA), 18:3ω3 (ALA), 18:3ω6 (GLA), and 18:4ω3] (Fig. 3.4, Table S3.10). In contrast, predators were higher in many MUFAs (18:1ω9, 20:1ω9, 20:1ω11, and 22:1ω11, but notably not 22:1ω9) and longer-chain PUFAs (ARA, EPA, DHA, and 22:5ω6).

FA summations indicative of trophic relationships differed between the two feeding styles (Fig. 3.5). Bacterial indicators (sum of branched and odd-chain FA) and ecologically important short-chain PUFAs (ALA+LA) were both significantly (MWU: $p<0.05$) higher in grazers than in predators. In contrast, the summation of long-chain EFA PUFAs (EPA+DHA+ARA) was significantly higher (MWU: $p<0.05$) in predators than in grazers. A summation indicative of calanoid copepod consumption (sum of Calanoid markers) was nearly identical in both groups, with averages differing by just 0.1%, yet this summation was still found to be significantly (MWU: $p<0.05$) higher in grazers than in predators.

With the categorization approach of "feeding style" able to explain just 13.7% of the variability in FA profiles of our gelatinous zooplankton, we further explored the driving effects of diet on this variability using the more detailed trophic categorizations of "feeding guilds."

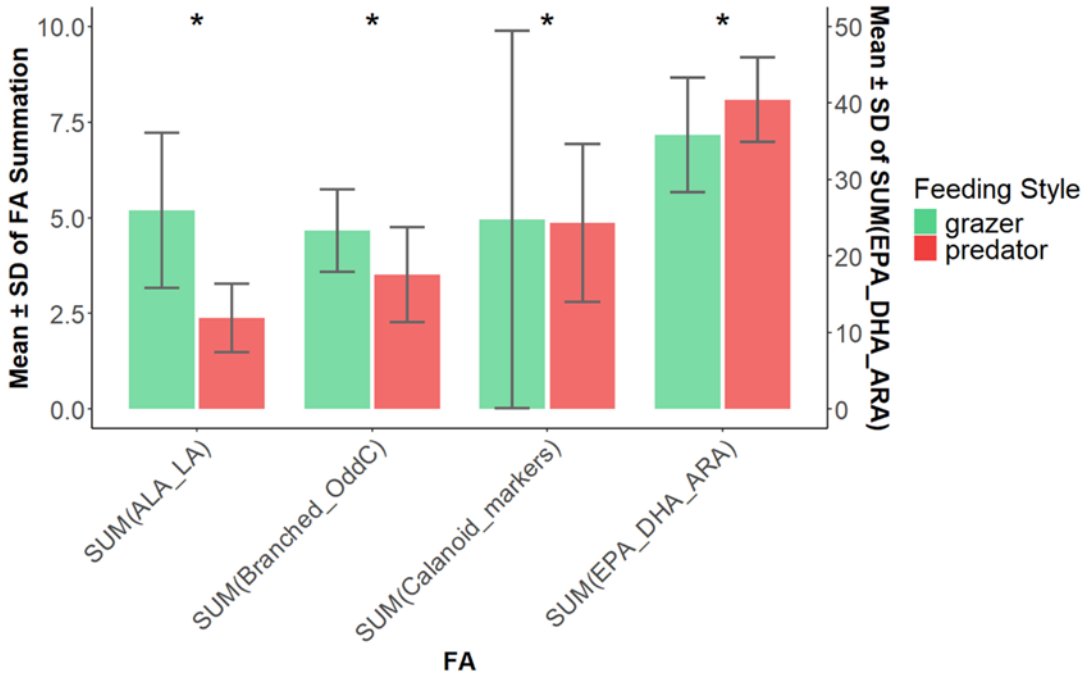


Figure 3.5. Bar plot of FA summations comparing feeding styles predator (red) vs. grazer (green). Bar heights indicate the average sum of FAs indicated per group, with FAs measured as percent of total FA concentration per sample. Error bars indicate standard deviations. The y-axis on the right side of the plot gives the values for SUM(EPA_DHA_ARA); the y-axis on the left side of the plot gives values for all other summations. Asterisks above an FA summation denote significant differences (Mann Whitney U test $p<0.05$) found between groups for that summation.

3.6. Drivers of inter-taxonomic variability: Diet - Feeding Guilds

In multidimensional space, feeding guilds exhibited considerable overlap with SB consumers and grazers each showing a wide spread in multivariate FA signatures (Fig. 3.6). Despite this observation, PERMANOVAs detected significant differences in FA profiles between each pair of feeding guilds (Table 3.5). As with previous categorization approaches, dispersion was also significantly different in most inter-guild comparisons.

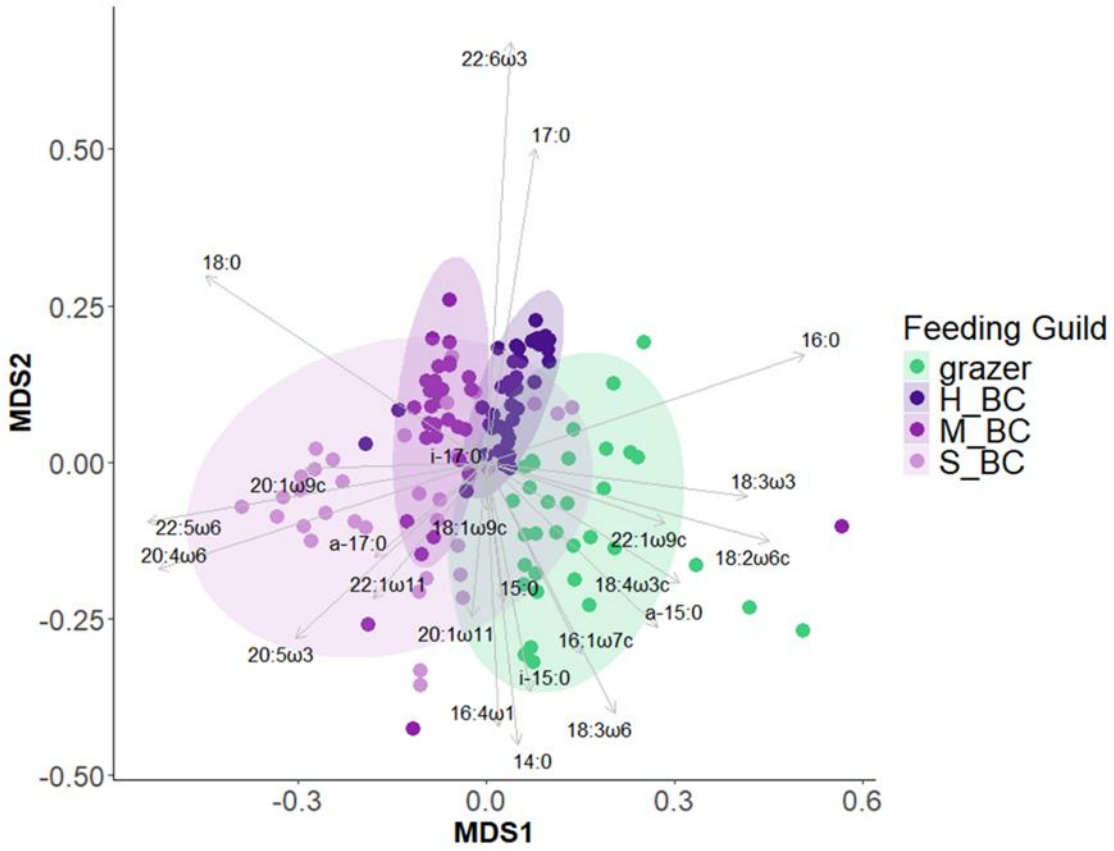


Figure 3.6. NMDS plot of FA profiles of all gelatinous zooplankton comparing feeding guilds. Feeding guild categories are: "grazer" (green), "hard-body consumer" (HB consumer; H_BC, dark purple), "mixed-body consumer" (MB consumer; M_BC, medium purple), and "soft-body consumer" (SB consumer; S_BC, light purple). Datapoints are colored according to feeding guild and ellipses indicate 95% confidence intervals. FA vectors displayed are a subset of FA that were found to frequently drive dissimilarity across comparisons throughout this study, as well as FA that are of ecological importance.

Table 3.5. PERMANOVA and Permutest comparisons based on feeding guild. PERMANOVA and permutests were run to compare the FA profiles of all gelatinous zooplankton samples to each other based on feeding guild: "hard-body consumer" (HB consumer; H_BC), "mixed-body consumer" (MB consumer; M_BC), "soft-body consumer" (SB consumer; S_BC), or "grazer." FA profiles were compared across samples as proportional contributions of each FA to the total FA concentration per sample. Bolded values indicate significance ($p<0.05$).

Comparison: Feeding Guild		**Sample sizes (n)**		**PERMANOVA**			**Permutest of dispersion**	
Group A	**Group B**	**A**	**B**	**Pseudo-F**	**R^2**	**p**	**F**	**p**
S_BC	H_BC	33	39	26.22	0.272	**0.001**	48.49	**0.001**
S_BC	M_BC	33	30	10.25	0.144	**0.001**	4.1	**0.048**
S_BC	grazer	33	33	17.2	0.212	**0.001**	0.09	0.755
H_BC	M_BC	39	30	14.83	0.181	**0.001**	7.76	**0.008**
H_BC	grazer	39	33	27.62	0.283	**0.001**	29.72	**0.001**
M_BC	grazer	30	33	17.79	0.226	**0.001**	2.48	0.119

In all inter-guild comparisons, DHA was the leading FA driving dissimilarity (Table S3.11) DHA was high (~23%) in both HB consumers and MB consumers and was noticeably lower (17-19%) in SB consumers and grazers (Table S3.12). EPA also drove dissimilarity, steadily decreasing in average proportion from SB consumers to MB consumers to HB consumers. ARA was a major driver of dissimilarity only in inter-guild comparisons involving SB consumers. This was likely due to the high concentration of ARA in SB consumers at an average of 5.87±4.8%, roughly 4x higher than in any other feeding guild. MUFA 18:1ω9 was a frequent driver of dissimilarity in all comparisons, averaging at its lowest in grazers (3.53±1.62%) and highest in MB consumers (7.63±5.98%). MUFA 22:1ω9 also contributed heavily to dissimilarity and was the highest in grazers (3.89±4.77%). As the proportional predation on soft-bodied prey increased (i.e. from HB consumer to MB consumer to SB consumer), so too did the average proportion of PUFA. In contrast, as the proportional predation on soft-bodied prey increased, the average proportion of MUFA showed a clear decrease. Grazer PUFA and MUFA proportions fell in the middle range amongst the other feeding guilds.

FA summations indicative of trophic relationships varied with feeding guild (Fig. 3.7).

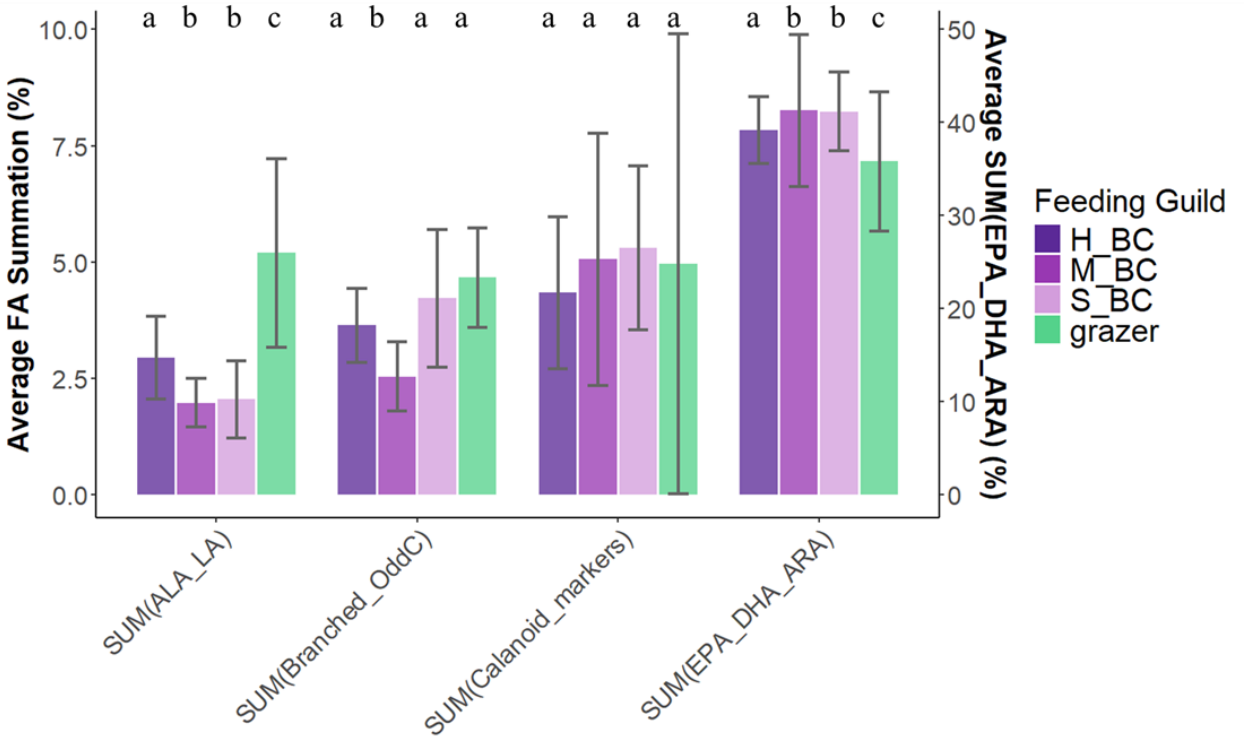


Figure 3.7. Bar plot comparing average FA summations of ecological importance, per feeding guild. Error bars indicate standard deviations. Includes all gelatinous zooplankton categorized as one of four feeding guilds: HB consumer (H_BC), MB conumser (M_BC), SB consumer (S_BC), or grazer. FA summations include short-chain PUFA [SUM(ALA_LA)], bacterial markers [SUM(Branched_OddC)], calanoid copepod markers [SUM(Calanoid_markers)], and long-chain PUFA EFA [SUM(EPA_DHA_ARA)]. The y-axis on the right side of the plot gives the values for SUM(EPA_DHA_ARA); the y-axis on the left side of the plot gives values for all other summations. Letters above bars denote feeding guild comparisons for which no significant difference (Mann Whitney U test $p<0.05$) was found for that FA summation.

Following the same trend as PUFA proportions, the sum of longer-chain PUFA EFA (sum of EPA, DHA, and ARA) increased with increasing predation on soft-bodied prey, being significantly (Mann Whitney U test $p<0.05$) higher in SB consumers than in HB consumers. Proportional EFA content in grazers was significantly lower than in all other feeding guilds. The summation of shorter-chain PUFA (sum of ALA and LA) showed the reverse trend: this summation was significantly lower with increasing predation on soft-bodied prey (SB consumer

< HB consumer), and was significantly highest in grazers. Bacterial markers (sum of branched and odd-chain FA) were highest in grazers, varied in HB consumers and SB consumers, and were significantly lowest in MB consumers relative to all other feeding guilds. The sum of calanoid FA markers varied widely per feeding guild, but especially in grazers. This summation did not significantly differ between any of the guilds.

3.7. Drivers of inter-taxonomic variability: Comparing Categorization Approaches

Categorization approaches were compared for their effectiveness in explaining the wide degree of variability observed in gelatinous FA profiles. Variability in FA profiles was best explained by "taxon," i.e. the lowest level of taxonomic identification achieved in sampling (Fig. 3.8). In inter-taxonomic comparisons via PERMANOVA, taxon identification explained an average of nearly half (45.9±16.8%) the variability in FA profiles, but ranged from explaining little (12.9%) to almost all (94.2%) variability. The next best categorization approach was by phylum, which explained an average of 25.5±9.1% of the variability in FA profiles. Categorizing by feeding guilds was about equally as effective as by phylum, with this approach explaining on average 22.0±5.3% of FA variability among samples. Finally, categorizing samples by the broader trophic grouping of "feeding style" (predator vs grazer) failed to explain much FA variation (13.7%). Finally, our broadest approach of categorizing the larger group of all zooplankton (gelatinous and non-gelatinous) into plankton categories (gelatinous, crustacean, and fish) also explained little (14.0±4.9%) of FA variability among all zooplankton.

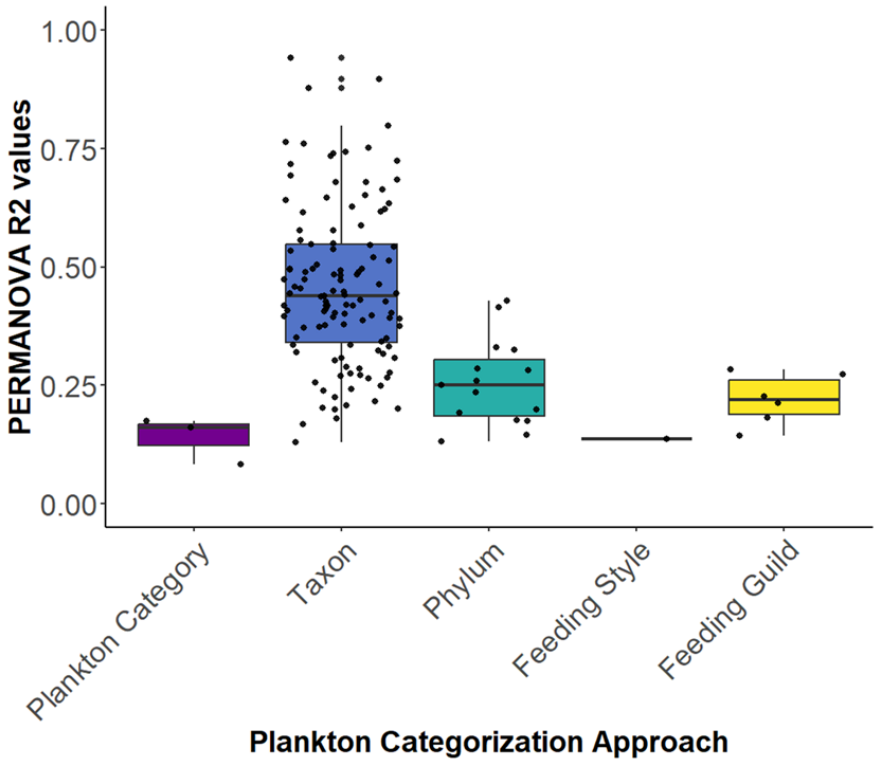


Figure 3.8. Boxplot comparing PERMANOVA R^2 values from categorization approaches. Compares the R^2 values resulting from PERMANOVAs run to compare the FA profiles of zooplankton via various categorization approaches. Zooplankton (gelatinous and non-gelatinous) were categorized by "plankton category": gelatinous, crustacean, or fish. Gelatinous zooplankton were categorized by "taxon" (lowest level of identification), phylum, "feeding style" (predator or grazer), and "feeding guild" (HB consumer, MB consumer, SB consumer, or grazer).

4. DISCUSSION

While gelatinous zooplankton exhibited higher proportions of PUFA and EFA relative to crustaceans and fishes, this grouping of taxa as "gelatinous" overall obscured substantial heterogeneity in FA profiles, phylogeny, and feeding behavior, limiting its utility for interpreting multivariate FA patterns. The best explanatory power emerged at the finest taxonomic resolution, consistent with the expectation of unique FA "signatures" for each taxon, while categorizing by phylum was less effective. Categorizing taxa by feeding style and feeding guild also revealed interesting patterns in FA profiles, especially the notably high proportions of PUFA, EFA, and

ARA in gelatinous consumers of soft-bodied prey, highlighting their potential importance as high-quality prey in pelagic food webs.

4.1. "Gelatinous zooplankton" as a category features little cohesion in FA signatures

4.1.1. Comparisons to non-gelatinous zooplankton

Separating zooplankton according to "plankton categories" (gelatinous, crustacean, or fish) was mostly ineffective in describing FA proportions. However, one notable result was the finding that gelatinous zooplankton had the highest proportions of PUFA and EFA of the three groups. This aligns with previous work that has identified gelatinous zooplankton as possessing large concentrations of PUFA (Jospeh, 1979). Within EFA, DHA was particularly high (21.2±5.6%) in gelatinous zooplankton, at levels similarly seen in other studies of gelatinous zooplankton FA. Von Harbou *et al.* (2011) found DHA ranging from 21.0-30.9% in salps. Nelson *et al.* (2000) found DHA as high as 24.8% in *Beroe cucumis*, though other gelatinous taxa in their study had DHA as low as 3.9±0.6%. In a study of the gelatinous pteropod predator-prey pair *Clione limacina* and *Limacina helicina*, Falk-Peterson *et al.* (2000) measured DHA at nearly equivalent amounts in each species at ~28%, highlighting the conservation of this FA through dietary intake.

Beyond the observation of particularly high proportions of PUFA and EFA in gelatinous zooplankton, this categorization approach of "plankton categories" was generally ineffective in explaining variability in FA profiles. This was unsurprising as FA content of a consumer is primarily driven by diet and there are many trophic links between these three groups. Crustaceans sampled in this study included hyperiid amphipods, euphausiids, and copepods. Hyperiid amphipods have long been known to frequently parasitize a variety of gelatinous zooplankton (Harbison *et al.*, 1977) and to possess a lipid profile that reflects that of their hosts

(Phleger *et al.*, 2000). Euphausiids in our sampling region are typically considered omnivores, consuming phytoplankton, protists, and copepod nauplii (Zhou *et al.*, 2021), thus showing dietary overlap with gelatinous grazers. Copepods sampled in this study were mostly not classified beyond Copepoda, although some (n=3) were identified as *Candacia* sp., likely *C. bipinnata* based on its relative abundance in this region (Batten and Walne, 2011). *Candacia bipinnata* has been identified as a consumer of exclusively appendicularians (Ohtsuka and Onbe, 1989). Fish larvae sampled in this study (*Sebastes* spp. and *Stenobrachius leucopsarus*) regularly consume copepods, copepod nauplii, and protists (Swieca *et al.*, 2023; Sumida and Moser, 1984; Walsh *et al.*, 2024) and are themselves consumed by gelatinous predators of fish larvae (see Table 3.4). Besides these numerous trophic links, there is also phylogenetic overlap between these plankton categories, with some gelatinous zooplankton and fishes being in the same phylum Chordata. Overall, these many trophic links and phylogenetic overlap together contributed to the ineffectiveness of grouping zooplankton by "plankton categories" (gelatinous, crustacean, fish) in explaining FA variability.

4.1.2. Comparisons among gelatinous zooplankton

The gelatinous zooplankton sampled in this study are diverse, spanning a wide range of phylogenetic and trophic differences. In PERMANOVA testing of inter-taxonomic differences between FA profiles, nearly every comparison yielded a significant difference. The finding that each taxon has a somewhat unique FA "signature" aligns with expectations, where inter-taxonomic variation in FA profiles is larger than intra-taxonomic variation (Iverson 1993; Hiltunen *et al.*, 2022), allowing researchers to use these signatures to distinguish and characterize species in an ecosystem (Budge *et al.*, 2002).

Even intra-taxonomic variation in FA was measurable in taxa with sufficient cross-seasonal sampling. As variability in FA content in a consumer is primarily driven by diet and many gelatinous zooplankton are known to vary diet with season (Corrales-Ugalde *et al.*, 2021; Fleming *et al.*, 2015; Masterman *et al.*, 2025; Milisenda *et al.*, 2018), we expect FA profiles of our gelatinous taxa to reflect these seasonal changes. Chaetognatha, which grouped very tightly in inter-taxonomic multivariate visualizations of FA profiles, showed a clear seasonal shift in FA profiles. Chaetognatha had significantly higher DHA (a dinoflagellate marker) in winter and significantly higher EPA (a diatom marker) in summer. Paralleling our findings for *Pleurobrachia bachei* (see chapter II), this likely reflects a seasonal shift at the base of the food web in the Northern California Current, in which stronger summer upwelling supports more diatom growth, while weaker winter upwelling leads to dinoflagellate dominance (Bograd *et al.*, 2009; Schmid *et al.*, 2023). Seasonal variability in FA content of gelatinous zooplankton has been similarly observed in previous studies (Ju *et al.,* 2004; Graeve *et al.,* 2008; Stenvers *et al.*, 2020).

4.2. Drivers of inter-taxonomic variability: Phylum

While the lowest level of taxonomic resolution best explained variability in FA profiles among gelatinous zooplankton samples, categorization by phylum also explained a notable amount of variation in FA proportions, on average ~25%. This finding is caveated by two points: 1) some phyla (Chaetognatha and Annelida) in our study contained just one taxon, and 2) phylum designation cannot be fully separated from diet, as the two are at some point inextricably linked. For example, the cnidarians in this study all possess cnidocytes distributed on tentacles; this morphological similarity can be expected to lead to similar feeding habits, relative to a zooplankter with wildly different morphology (e.g., an annelid). Yet some of the phlya here

contain taxa with very disparate predation habits. Ctenophora in our study included *Pleurobrachia bachei*, which primarily feeds on copepods and eggs via trailing tentacles (see Table 3.4) and *Beroe* sp. which feeds exclusively on ctenophores via direct consumption. Additionally, Mollusca sampled in this study contained both thecosome pteropods (grazers that feed on diatoms, protists, and other microplankton via mucous mesh) and gymnosome pteropods which feed exclusively on thecosome pteropods via ambush predation. Thus both Ctenophora and Mollusca are examples of phyla which encompassed taxa with disparate feeding behavior and prey types, but were still able to be significantly differentiated from other phyla in our study. This suggests there may indeed be a measurable effect of phylum designation on FA profiles of gelatinous zooplankton.

4.3. Drivers of inter-taxonomic variability: Diet – Feeding Style

Approaching categorization of gelatinous zooplankton at the broad dietary level of "feeding style" (predator vs. grazer) explained little (13.7%) of the variability in gelatinous FA profiles. Generally, gelatinous predators contained larger proportions of longer-chain, more highly-modified PUFAs (EPA, DHA, ARA) while grazers contained more shorter-chain, less modified PUFAs (LA, ALA, GLA). This followed expectations in which longer-chain highly modified PUFAs are known to accumulate with increasing trophic levels, while shorter-chain synthesized PUFA are more abundant at lower trophic levels (Galloway and Budge, 2020). Predators also contained higher 18:1ω9, which tracks with the use of this FA as an indicator of carnivory (Falk-Peterson *et al.*, 1990; Dalsgaard *et al.*, 2003). The FA summation indicative of bacterial influence to diet was higher in grazers; this aligns with our expectations, as their method of feeding via a mucous mesh net is expected to accumulate large amounts of bacteria (Sutherland and Thompson, 2022). Of the four typical markers for calanoid copepods (20:1ω9,

20:1ω11, 22:1ω9, and 22:1ω11; source: Dalsgaard *et al.*, 2003), all but 22:1ω9 were higher in predators, which follows expected consumption of calanoid copepods. In contrast, the remaining calanoid copepod marker (22:1ω9) was higher in grazers, suggesting that one or more of the taxa in this category may also regularly consume calanoid copepods.

4.4. Drivers of inter-taxonomic variability: Diet – Feeding Guild

Based on the observation that gelatinous predators generally fall into one of two groups, those that eat either primarily hard-bodied or primarily soft-bodied prey (Robison, 2004; Costell and Colin, 2002), we used known predation patterns to split our gelatinous zooplankton into four "feeding guilds": "hard-body consumer (HB consumer)," "soft-body consumer (SB consumer)," "mixed-body consumer (MB consumer)," or "grazer." Note that no feeding guild was monophyletic, ensuring that we did not conflate phylogenetic differences with feeding guild differences. This approach of using functional rather than phylogenetic groups to explore FA across zooplankton has been effectively used in previous studies (Stevens *et al*., 2022).

This categorization approach was about equally as effective as grouping by phylum in explaining variability in FA profiles. Some observed trends were as expected from results of feeding style comparisons, such as higher amounts of bacterial markers and shorter-chain PUFAs in grazers. One of the most compelling discoveries here was the trend of increasing proportions of PUFA and EFA with increasing proportional predation on soft-bodied prey (defined here as gelatinous zooplankton and eggs). It has long been noted (Joseph, 1979) that gelatinous zooplankton as a group are typically proportionally high in PUFA relative to other plankton categories – a trend observed again in this study. Furthermore, eggs are an incredibly rich source of EFA, typically containing one to two orders of magnitude more EFA than would be predicted given their size (Fuiman *et al.*, 2015). Eggs have been identified as an underrecognized source of

EFA in pelagic food webs (Fuiman *et al.*, 2015) and have been noted as important prey to a variety of gelatinous zooplankton (Masterman *et al.*, 2025; Purcell *et al.*, 1994; Purcell, 1989; Purcell, 1985). This suggests that through consuming PUFA- and EFA-rich prey, these gelatinous soft-body consumers themselves become especially proportionally rich in PUFA and EFA, relative to their gelatinous hard-body consumer counterparts.

Of the EFA, ARA was substantially higher (5.87±4.8%) in SB consumers than in all other feeding guilds, and was a major driver of dissimilarity between SB consumer and all other guilds. ARA has been previously found in unusually high amounts (2.2±1.7 μg ARA mg DW^{-1}) in the gelativorous hyperiid amphipods of Puget Sound, WA (Hiltunen *et al.*, 2022); notably ARA was not elevated in hyperiid amphipods sampled in our study (ARA: 1.32±0.44%). Still this trend of higher in ARA in gelatinous consumers may point to another over-looked aspect of the importance of gelatinous zooplankton in pelagic food webs, as ARA is known to be a vital eicosanoid precursor in fish tissues (Bell and Sargent, 2003).

The FA summation of calanoid copepod markers exhibited an unexpected pattern. The summation of calanoid copepod markers might be expected to follow a trend of decreasing with increasing predation on soft-bodied prey (and thus decreasing predation on hard-bodied prey such as calanoid copepods). However, this was not the case, as this FA summation did not significantly differ in any inter-guild comparison and was in fact on average larger in grazers than in HB consumers. We interpret this finding as indicating that grazers may be consuming much larger numbers of small copepods, copepod nauplii, and copepod eggs than might be assumed given their feeding style. Digested remains of calanoid copepods have been identified in the stomachs of some salps (e.g., *Thetys vagina*, Hiebert *et al.*, 2025) and all four calanoid copepod markers have been found in small amounts across a variety of salp species (von Harbou

et al., 2011). Furthermore, a recent comparative study found that salps practice substantial omnivory/carnivory through consumption of copepods and ostracods, giving salps a trophic position only just below that of Chaetognatha (Decima *et al.*, 2019). Finally, the calanoid copepod marker 20:1ω9 specifically has been found in many gelatinous grazers, including Doliolids (Pond and Sargent, 1998), *Limacina helicina* (Falk-Peterson *et al.*, 2001), appendicularians (Troedsson *et al.*, 2005), and pyrosomes (Schram *et al.*, 2020 supplementary material).

4.5. Applications

All fatty acid measurements in this study thus far have been presented in proportional measurements (i.e., concentration of each individual FA divided by summed concentration of all FAs). As part of our methods, we extracted FA from each sample per a measured amount of dry sample mass. Using the experimental recorded measurements of dry mass per sample and using estimates of water content for each taxon from the literature (Table S3.13), we can now present our FA results in measures of concentrations, as "ng FA per mg dry weight" and "ng FA per mg wet weight." These FA measurements in concentrations are given for each taxon in tables in the appendix: gelatinous zooplankton (Tables S3.14, S3.15, S3.16, and S3.17), crustaceans (Table S3.18), and fishes (Table S3.19). We also used values from the literature (Table S3.13) to convert a subset of FAs and FA summations of ecological interest into units of "mg FA per g dry weight," "mg FA per g wet weight," and "mg FA per g carbon content." We present these values as averages per each grouping used in any of the categorization approaches applied in this study (Tables S3.20, S3.21, and S.22). Interpretations of any FA concentrations presented here are subject to the following caveat. Upon collecting zooplankton samples, we strove to limit the amount of excess seawater that was intermixed with zooplankton in sample storage bags.

However, the amount of excess seawater preserved in each sample likely varied; this should result in measures of FA concentrations having greater variability (i.e., larger standard deviations associated with averages) as well as all FA concentrations being a potential underestimation (due to excess salts arbitrarily inflating our measurements of dry sample masses).

Fatty acid data given in measurements of concentration can prove highly useful in estimating the trophic impact of a particular organism or group of organisms on global scales. For example, Budge *et al.*, (2014) used FA concentrations measured from filtered seawater samples along with chlorophyll-a data to estimate the annual supply of EPA provided by diatoms across the world's oceans. Applying a similar logic, we can combine the estimated biomass of gelatinous zooplankton in the global mixed layer of the ocean (38.3 Tg C; Lucas *et al.*, 2014) along with our own estimate of gelatinous zooplankton containing an average EFA concentration of 24.65±33.57 mg EFA per g C (Table S3.20). This yields an estimated 944±1286 Gg of EFA provided by gelatinous zooplankton in the global mixed layer of the world's oceans. Our estimates also place soft-body consuming (SB consumer) gelatinous zooplankton as having intriguingly high ARA content at 2.71±1.5 mg ARA per g C (Table S3.22), nearly four times higher than any of the other gelatinous feeding guilds (HB consumer, MB consumer, or grazer; Table S3.22) and more than three times higher than in our samples of crustaceans or fishes (Table S3.20). Although beyond the scope of this paper, it would be exciting to explore the contribution of soft-body consuming gelatinous zooplankton to the global ARA budget, especially as ARA has been noted to be highly important for fish nutrition despite being also frequently overlooked in preference to EPA and DHA in many FA studies (Bell and Sargent, 2003).

4.6. Conclusion

Beyond the observed higher proportions of PUFA and EFA in gelatinous zooplankton as compared to crustaceans or fishes, categorizing zooplankton as "gelatinous" yields a group that is highly heterogenous in FA profiles, phylogeny, and feeding behavior/patterns, making this categorization approach generally ineffective in describing variability in multivariate FA signatures. The best explanatory power for FA profiles in gelatinous taxa came from the lowest taxonomic resolution, aligning with expected results of each taxon having a unique FA "signature." FA profiles varied substantially, especially inter-taxonomically but also seasonally within taxa. Drivers of this variability appear to be both phylogenetic and diet-related, although the two measures are at some point inextricably linked. In trophic comparisons, we found that those gelatinous zooplankton that are consumers of primarily soft-bodied prey (other gelatinous zooplankton and eggs) are proportionally richer in PUFA, EFA, and ARA as compared to gelatinous consumers of primarily hard-bodied prey. Due to their fragile nature, it is difficult to either sample gelatinous zooplankton or to appreciate the frequency at which they are preyed upon as they are quickly digested and leave no hard part traces. It then follows that it must be doubly difficult to appropriately quantify the predation of gelatinous zooplankton by gelatinous zooplankton, as the "ghost of a ghost." Fatty acids are one tool that we may use in trophic analyses which is not biased against these fragile organisms and has here helped to elucidate some of the underappreciated trophic importance of gelatinous zooplankton in pelagic food webs. Our findings underscore the importance of these organisms in pelagic food webs as a quickly digestible source of high nutritional value.

BRIDGE

In Chapter III, I used multivariate fatty acid analyses to explore the trophic roles of a suite of diverse co-occurring gelatinous zooplankton in a pelagic upwelling system. The use of fatty acids here has proven to be a powerful tool in the ecological analyses of these delicate organisms. Yet the use of fatty acids in food web analyses is not without its limitations, one of them being the degradation of FA that can occur with sub-optimal or prolonged sample storage. While FA degradation is known to occur in these cases, it is yet unclear to what extent. In the next chapter, I sought to fill in this knowledge gap by performing a rigorous fully-crossed experimental design that tested the effects of both storage temperature and duration on the degradation of FA in organismal tissues.

CHAPTER IV

SAMPLE STORAGE TEMPERATURE (-20°C VS. -80°C) AND DURATION (UP TO 3 YEARS) AFFECTS FATTY ACID PROFILES IN FOUR MARINE PHYLA

This work includes coauthors Dr. Aaron Galloway and Michael D. Thomas who have contributed to the writing of the manuscript. Dr. Galloway conceived of the initial experimental design and secured funding for all materials used in fatty acid extractions and GC-MS analyses. I performed all sample collection, experimental treatments, FA extractions, and data analyses.

1. INTRODUCTION

Fatty acids (FA) are biomolecules that occur in all living organisms as integral components of various lipid classes with important roles in the function of cellular membranes, as energy reserves, and as precursors to hormones known as eicosanoids (Dalsgaard *et al.*, 2003). FA are composed of a carboxylic acid head (COOH) and a long aliphatic chain with a terminal methyl group (CH_3). Each FA can be identified uniquely through a combination of four descriptors in the form "A:Bn-C cis/trans": length of carbon chain (A), number of double bonds (B), position of double bonds counted from methyl end (C), and cis/trans isomerism. Diverse in their form and function, FA are often grouped according to the level of saturation: saturated (SAFA), monounsaturated (MUFA), and polyunsaturated (PUFA) (Budge *et al.*, 2006).

FA have long been studied in aquatic sciences (e.g., Lovern 1935, Kelly *et al.*, 1959), particularly as indicators of changes in the health of individuals, populations, or communities (Parrish *et al.* 2000, Müller-Navarra *et al.*, 2004; Tocher, 2010). Their relevance extends beyond ecology, as FA can inform assessments of nutritional value with certain FA showing clear links

to human and animal health (Arts *et al.*, 2001). Particularly important FA to heterotrophs in aquatic food webs are the essential fatty acids (EFA; reviewed in Parrish, 2009), which are nutritionally critical FA that limit the growth and reproduction of a consumer and must be obtained via diet as they cannot be made in sufficient amounts *de novo* (Dalsgaard *et al.*, 2003). Two FA that are sometimes described as the "true" EFA are the "precursor" EFA, linoleic acid (LA, 18:2ω6) and α-linolenic acid (ALA, 18:3ω3). Both of these 18-carbon FA can be considered EFA as they cannot be synthesized *de novo* in mammals (Cunnane, 2000). Three FA that are more commonly considered EFA in marine ecology are the 20- and 22-carbon PUFAs: eicosapentaenoic acid (EPA, 20:5ω3), docosahexaenoic acid (DHA, 22:6ω3), and arachidonic acid (ARA, 20:4ω6) (Cunnane, 2000). These three longer-chain EFA have been identified as being most commonly limiting in diverse aquatic organisms (Arts *et al.*, 2001). High dietary concentrations of EFA have been linked to greater fitness in consumers, such as through increased growth and reproductive success in zooplankton, fish, and other aquatic consumers (Brett *et al.*, 2009; Tocher, 2003, Winder *et al.* 2017). Through these effects, shifts in EFA availability may regulate populations sizes and, at broader scales, even restructure entire aquatic communities. (Litzow *et al.*, 2006).

Scientists also successfully employ FA as trophic markers (FATM) to identify trophic relationships between species and to quantify the flow of energy and nutrients within a food web. This FATM method of trophic analysis exploits the fact that many primary producers can be characterized by unique FA profiles (Galloway *et al.* 2012; Kelly and Scheibling, 2012; Galloway and Winder, 2015). These FA signatures are then assimilated into consumer tissues with minimal or predictable modification, allowing researchers to trace these trophic pathways. (Budge *et al.*, 2006). There are also some FA that are diagnostic for specific taxa, enabling fine-

scale dietary resolution (Arts *et al.*, 2009). For example, calanoid copepods synthesize 20:1ω9/11 and 22:1ω9/1, diatoms (Bacillariophyceae) produce large amounts of 16:1ω7 and EPA, and dinoflagellates (Dinophyceae) have high proportions of DHA (Budge and Parrish, 1998; Kelly and Scheibling, 2012; Taipale *et al.* 2013, Taipale 2016). This FATM concept has progressed to where it can now provide even quantitative information in food web modelling, such as Quantitative FA Signature Analysis (QFASA) or FA-based mixing models, whereby one can estimate prey contributions to a consumer diet (Iverson *et al.*, 2004; Galloway *et al.*, 2014; Bromaghin, 2018, Litmanen *et al.*, 2020).

As the field of FA analysis progresses, with ever-expanding applications, it becomes increasingly important that we ensure the initial methodological steps within the process are carried out as soundly as possible. One of the very first steps in any FA study is to collect and temporarily preserve the tissue samples which will later be extracted for FA analysis. Once a sample of biomass is collected, ideally it would either be extracted immediately (which is not generally possible) or it would then be immediately stored at as low a temperature as possible with antioxidants added, followed by prompt FA extraction (Couturier *et al.*, 2020). This recommendation derives from the observation that lipids in a sample will continue to change post-mortem through various enzymatic and chemical reactions (Christie, 1984; Petillo *et al.*, 1998). Unfortunately, these ideal conditions are rarely able to be met, due to infrastructural, monetary, and time constraints. For example, many sampling efforts take place in remote areas without immediate access to liquid nitrogen or ultracold freezers, and samples are often just frozen in “standard” -20°C freezers for varying lengths of time until extraction or before moving to other long-term storage in -80°C freezers. The reality of sampling for most research programs results in a wide range of sample storage conditions, ranging from putting the samples on ice

(0°C) to freezing samples in liquid nitrogen (-196°C), and from extracting samples within hours to extracting samples after years.

It is currently unclear exactly how storage temperature and duration affect FA analyses. Previous studies have shown that lipid degradation depends not only on storage temperature and duration (Ohman, 1996; Rudy *et al.*, 2016; Sasaki and Capuzzo, 1984), but also varies with species and tissue type sampled (Ingemansson *et al.*, 1995; Nazemroaya *et al.*, 2011). It is generally thought that extra prudence be applied in storing samples with high (>10% wet weight) total lipid content or high amounts of PUFA, as both of these conditions can lead to greater storage sensitivity (Couturier *et al.*, 2020; Rudy *et al.*, 2016; Sasaki and Capuzzo, 1984). However, this is not always the case; for example, in a study on fishes stored at -25°C for up to 9 months, Romotowska *et al.* (2017) found greater lipid degradation in species with higher MUFA content than those with higher PUFA and SAFA content.

Most previous studies on the effects of sample storage on lipid degradation in marine organisms focus on either a single species or several closely related species, and most frequently fishes. However, as the field of FA analysis continues to grow and expand into broader food web studies, through FATM and quantitative approaches like QFASA, there exists a need to better understand how sample storage temperature and duration affect FA analyses on a wide variety of taxa, including macroalgae, invertebrate tissues, and fish tissues of varying lipid content and FA composition. Toward this goal, we sought to compare FA degradation in four taxa, which varied widely in total lipids and in FA profiles, belonging to different phyla (Ochrophyta, Mollusca, Echinodermata, and Chordata). We performed a fully-crossed experiment whereby samples from consistent source tissue of each representative organism were stored at temperatures -20°C and -80°C and extracted at five time points after collection: 0 days, 3 months, 1 year, 2 years, and 3

years. We tested whether temperature and storage duration affected FA content (FA concentrations) and composition (FA proportions) for each species.

2. MATERIALS AND METHODS

2.1. Sample collection

Four species, each from a different phylum, were selected for this study: kelp greenling (*Hexagrammos decagrammus*, phylum Chordata), gumboot chiton (*Cryptochiton stelleri*, phylum Mollusca), purple sea urchin (*Strongylocentrotus purpuratus*, phylum Echinodermata), and bullwhip kelp (*Nereocystis luetkeana*, phylum Ochrophyta). All within-species replicates in this experiment were aliquots of homogenized tissue from one single individual organism. The purpose of this study is not to characterize the variation in FA from a sample of different individuals from each taxa; the decision to sample from one homogenized individual was therefore purposefully made so that the subsequent analyses of the variation in FA were based on the different temperature and duration treatments, and the replicates were kept in different sample vials under all treatments and are not "pseudo-replicates" under this sampling design.

All samples were collected in a single day (February 4, 2022). The kelp greenling was donated by a local public aquarium, the Charleston Marine Life Center, where it had been fed a diet of primarily herring and anchovy, and occasionally shrimp, mussel, and squid; this fish was sampled opportunistically because it had coincidentally died on the day of sampling. The remaining three taxa (gumboot chiton, purple sea urchin, and bullwhip kelp) were all collected from the tide pools of South Cove, Cape Arago State Park, OR (43.303013, -124.398601). The chiton and urchin were collected directly from their habitat while the kelp was collected as a freshly washed-up specimen from deeper waters. The invertebrates and kelp were collected

under NOAA Fisheries / Oregon Department of Fish and Wildlife permit #26448 issued to Aaron Galloway and the fish was donated as a mortality collected on the Charleston Marine Life Center's 2020 Oregon Scientific Take Permit #23670.

2.2. Sample homogenization and subsampling

Prior to and in between handling different taxa, all dissection tools were cleaned with tap water, DI water, and then 70% ethanol. Each taxon was sampled for a particular tissue type, which was then homogenized and split into 60 subsamples, weighing every fifth subsample for wet weight, before finally placing all subsamples into their respective treatment freezers.

2.2.1. Fish: kelp greenling

The frozen kelp greenling measured at 260 mm standard length and weighed 337.42 g. One fillet (wet weight 29.43g) from the fish was dissected, rinsed with tap water, rinsed with DI water, and chopped into pieces sized approximately 10 mm^3 to homogenize. Preparation of fish samples lasted for 1 hour.

2.2.2. Chiton: gumboot chiton

The frozen gumboot chiton weighed 834.58 g and measured at 195 mm standard length, although the individual was slightly curled inward so the live relaxed standard length may have been slightly longer. The chiton was collected from the tidepool rocks and immediately placed in a bucket of ice. In the lab, the chiton foot was removed, measuring 134 mm and weighing 45.3 g. The foot was rinsed with tap water, DI water, and then chopped into pieces sized approximately 50 mm^3 to homogenize. Preparation of chiton samples lasted for 2 hours.

2.2.3. Urchin: purple sea urchin

The frozen purple sea urchin had a test diameter of 52 mm and weighed 71.7 g. The urchin was collected from the tidepools and immediately placed in a bucket of ice. All gonads

were removed and any debris was rinsed off using DI water. Gonads appeared to be female. Gonads were homogenized into a slurry through mixing with a metal spatula. Preparation of urchin samples lasted for 2 hours.

2.2.4. Kelp: bullwhip kelp

The bullwhip kelp was collected from tidepools where it had been washed up. It was fresh (not deteriorated) and the holdfast was still connected to a small rock. The kelp stipe was cut free from the holdfast and placed into a bucket of ice, leaving 0.20 m of stipe with the holdfast. The weight of the kelp (excluding holdfast and 0.20 m of stipe) was 1595.39 g. The total length of the kelp from holdfast to tip of longest blade was 3.88 m with the following delineations: stipe (3.34 m), pneumatocyst (0.09 m), and longest blade (0.45 m). A section of the stipe was removed, starting just below the pneumatocyst and extending 354 mm. This sample of stipe weighed 373.92 g and had an outer diameter that ranged from 38—52 mm. This sample of stipe was rinsed with tap water, DI water, then chopped into pieces sized approximately 15 mm^3 cubic to homogenize. Preparation of kelp samples lasted for 3 hours.

2.3. Subsample preparation for FA extraction

Extractions occurred at five timepoints giving the following storage durations: initial, 3 months, 1 year, 2 years, and 3 years. At each timepoint, five subsamples per taxon per freezer treatment were removed from their freezers, weighed frozen, and then placed in a lyophilizer for a time ranging from 25–87 hours. After fully drying, subsamples were weighed dry and then each was homogenized and weighed out for FA extraction. The dry mass used for extraction depended on the taxon: fish (~20 mg), chiton (~30 mg), urchin (~10 mg), and kelp (~15 or ~55 mg) and varied based on total lipid content of each tissue so that approximately the same mass of lipid was extracted from each tissue type. Fish, urchin, and kelp subsamples were all

homogenized in the same way, using a solvent-washed and dry stainless-steel mortar and pestle to homogenize each subsample into a fine powder. Chiton subsamples were found to be too stiff to homogenize using the mortar and pestle, so instead were homogenized by chopping into even smaller pieces (~10 mm^3) using a razor blade. In between subsamples of different taxa/treatments, all FA extraction preparation tools were cleaned by rinsing with tap water, DI water, 70% ethanol, then allowed to dry in a hood. In between subsample replicates of the same taxon and treatment, FA extraction preparation tools were cleaned with 70% ethanol and allowed to dry. These are the standard procedures used in our lab for all FA extractions, regardless of sample type or duration of storage, and follow methods generally described in Schram *et al.*, (2018) and Thomas *et al.* (2020).

2.4. FA extraction and total lipid determination

All samples were extracted for total lipids (gravimetric determination) and then derivatized to fatty acid methyl esters (FAME) before being analyzed on a gas chromatograph mass spectrometer (GC-MS) for fatty acid content. Extraction methods followed a modified Folch procedure; both extraction and GC-MS methods followed those described in detail by Schram *et al.* (2018) and Taipale *et al.* (2013), respectively. The GC-MS used was Shimadzu Model QP2020 equipped with a DB-23 column (30 X 0.25 mm X 0.15 µm, Agilent). Quantification of fatty acids was based on calibration curves created using serial dilutions of GLC standard mixture 566C (Nu-Chek Prep), under a strict quality control of Pearson correlation coefficients ≥ 0.99 for all standard curves. An internal standard (nonadecanoic acid) was used to ensure extraction efficacy remained consistent between samples. Fatty acid measurements were reported as both mass fractions (mg of FA per g of dry sample) and as proportions (ng of FA per ng of total fatty acid content).

To each weighed sample, 2 mL of chloroform and 1 mL of methanol was added and then capped under nitrogen. This was vortexed for 10 s, then put into -20°C freezer overnight. The next morning (~10 h later), to each sample, 0.75 mL of 0.9% NaCl solution and 70 µL of 1 mg/mL nonadecanoic acid internal standard was added. Samples were capped under nitrogen, vortexed on ice for 10 s, sonicated on ice for 10 min, vortexed for 10 s again, then centrifuged at 3000 rpm at 4°C for 5 min. The bottom chloroform layer containing organics was removed into a separate vial which was placed under nitrogen to begin evaporation. To each original sample, chloroform was replenished by adding 2 mL, and then samples were capped under nitrogen, vortexed, sonicated, vortexed again, and centrifuged as described above. The bottom chloroform layer was again removed and added to the evaporating vial. Once each vial was fully evaporated of chloroform under nitrogen, 1.5 mL of chloroform was added, samples were vortexed for 5 s, and 1.0 mL of this total lipid solution was removed for derivatization. The remaining 0.5 mL of total lipid solution was capped under nitrogen and retained at -20°C for later gravimetry.

Continuing with derivatization, the 1.0 mL of total lipid solution in chloroform was evaporated to dryness under nitrogen. Then to each was added 1 mL of toluene and 2 mL of 1% H_2SO_4 in methanol; samples were capped under nitrogen, vortexed for 10 s, then put into a hot water bath at 90°C for 90 min to trans-esterify the FA to FAME. After cooling back to room temperature, to each vial was added 1.5 mL of 2% $KHCO_3$ and 2 mL of hexane, capped under nitrogen, vortexed 10 s, then centrifuged at 1500 rpm at 4°C for 2 min. The top layer of FAME in hexane was carefully removed and put into a new vial which was placed in a <35°C water bath under nitrogen to begin evaporation. To each original vial, 1.5 mL of hexane was added, capped under nitrogen, vortexed, and centrifuged again as described above. The top layer of FAME in hexane was again removed and added to the evaporating vials in the <35°C water bath.

Once all hexane was evaporated, 1.5 mL of hexane was added to each vial, capped under nitrogen, vortexed 2 s, and kept at -20°C until GC-MS analysis.

FAME were analyzed via GC-MS on a Shimadzu Model QP2020 equipped with a DB-23 column (30 X 0.25 mm X 0.15 µm, Agilent) using helium as a carrier gas. Samples were injected at 1 µL via split/splitless injector. Following Taipale *et al.* (2013), the following heating program was used: hold at 50°C for 1 min, ramp to 140°C at 10°C/min, ramp to 190°C at 1.40°C/min, hold at 190°C for 3 min, ramp to 220°C at 5°C/min, ramp to 240°C at 13°C/min, and hold at 240°C for 2 min. From the resulting chromatograph, FA were identified based on retention times, known associated mass ions, and comparisons to mass ion (m/z) spectra library. FA were quantified based on peak areas of major mass ions (Taipale *et al.*, 2016). Concentrations of FA were calculated based on calibration curves created using serial dilutions of GLC standard mixture 566C (Nu-Chek Prep), under a strict quality control of Pearson correlation coefficients ≥ 0.99 for all standard curves. Dividing these concentrations by the dry mass of sample originally extracted gave concentrations of FA in units of "mg of FA per g of dry weight." Dividing each FA concentration by the summed concentrations of all FA present gave proportional FA data. Measured concentrations of the internal standard nonadecanoic acid were evaluated against expected concentrations to ensure extraction efficacy remained consistent between samples.

Gravimetry was performed to measure total lipid content of each sample. From each sample of total lipids in chloroform, 80 µL was dispensed in duplicate into two pre-weighed tins. After evaporating all chloroform, tins were re-weighed to determine weight of total lipids dispensed. If the standard deviation between duplicate measurements exceeded one fourth of the average of the two, gravimetry was redone. Averaging the duplicate results yielded one value of "mg total lipids per g of dry weight" per sample.

2.5. Statistical analyses

FA profiles were compared in "amounts," where amounts were measured both as proportions (proportion of total FA content) and as concentrations (mg of FA per g of dry weight). To test the effect of storage duration, permutational multivariate analysis of variance (PERMANOVA; Anderson *et al*., 2001) tests were run on Euclidean distance matrices of multivariate FA signatures between (per taxon): 1) samples stored at T-20°C extracted at t0 vs. at each later timepoint, and 2) samples stored at T-80°C extracted at t0 vs. at each later timepoint. To test the effect of storage temperature, PERMANOVAs were run on Euclidean distance matrices of multivariate FA signatures between (per taxon) at each extraction timepoint, samples stored at T-20°C vs. those stored at T-80°C. Permutests tested for significant differences in multivariate dispersion of FA signatures for all comparisons. Non-metric multidimensional scaling (NMDS) plots were used to visualize variability in FA profiles between taxa and within each taxon for different storage conditions. Similarity Percentages (SIMPER) analyses were used to identify which FAs drive dissimilarity in FA content between storage conditions. SIMPER tests were run to compare (per taxon) storage durations and temperatures. The top 10 FAs driving dissimilarities for all of these comparisons were then pooled across all taxa to yield a suite of 25 unique FAs that were identified as being the top drivers of dissimilarity across all comparisons. Heatmaps were used to visualize changes in these 25 FAs over time; these were created by color-mapping the change in each FA amount (proportion or concentration) from extraction timepoint t0 to each other timepoint, per each taxon and per storage temperature. Total lipids were compared per taxon per storage temperature across extraction timepoints by averaging across replicates and plotting via barplots. A linear model was fit to total FA data for urchin samples to describe how total FA content varies with storage duration for this taxon. Due

to instrument repair requirements at the time of the t3year extractions, total lipid data from this timepoint could not be reliably obtained and were therefore excluded from all analyses. All statistical tests were performed in R version 2023.12.1+402 (R Core Team, 2023) using vegan package version 2.6-4 (Oksanen *et al.*, 2022).

3. RESULTS

3.1. How do taxa differ in lipid & FA content?

Total lipid (TL) content varied widely and significantly between each pair of taxa (Fig. 4.1; Mann Whitney U tests: $p<0.05$), ranging from 16.3±5.4 (mg TL / g dry wt) in kelp to 242.9±15.4 (mg TL / g dry wt) in urchin. Total lipid data showed no notable variation with storage duration or temperature.

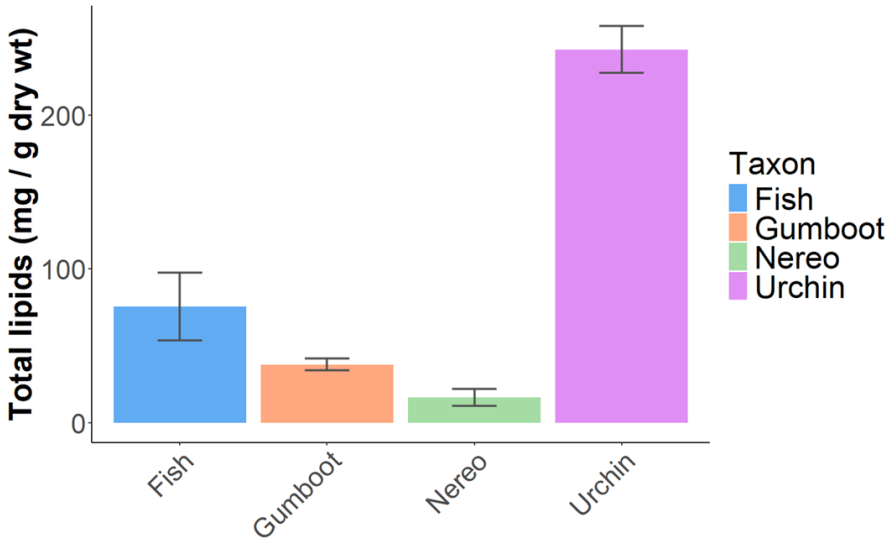


Figure 4.1. Average total lipid content per taxon. Per taxon, total lipid measurements were averaged across all storage temperatures and durations (except t3year). Error bars give standard deviations. "Nereo" is bullwhip kelp, *Nereocystis luetkeana*.

Total FA concentration also varied widely and significantly between each pair of taxa (Fig. 4.2; Mann Whitney U tests: $p<0.05$). Averaging only those samples extracted at timepoint

t0 and stored at temperature T-80°C (Table S4.1), total FA concentrations ranged from their lowest in kelp (3.12±0.05 mg total FA / g dry weight) to their highest in urchin (84.3±2.7 mg total FA / g dry weight), following a trend similar to total lipid concentrations.

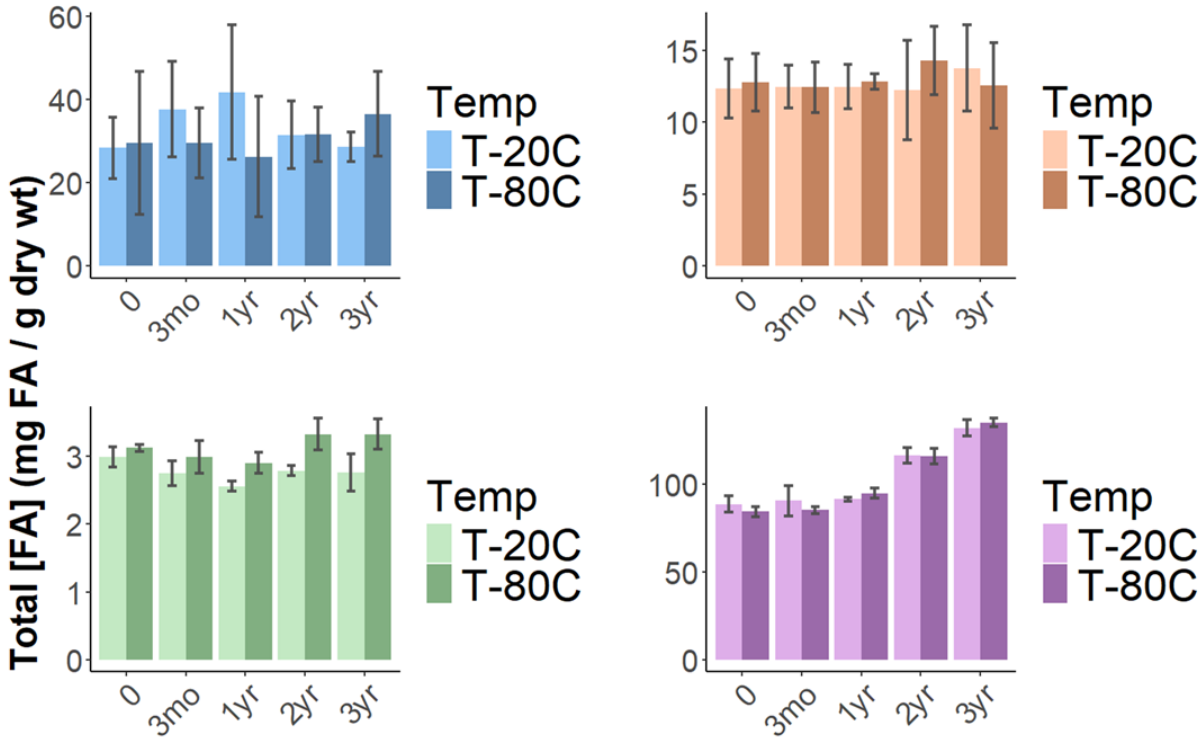


Figure 4.2. Total FA content per storage duration and temperature. Total FA content was averaged per taxon across the five replicates for each storage condition (temperature and duration). Bar heights give these averages for fish (upper left, blue), gumboot (upper right, orange), kelp (Nereo, lower left, green), and urchin (lower right, purple). "Nereo" is bullwhip kelp, *Nereocystis luetkeana*. Error bars give standard deviations.

PUFA dominated FA composition in fish (46.2±5.7%), while the remaining three taxa exhibited FA proportions roughly equally spread between SAFA, MUFA, and PUFA categories with each summation ranging from 27-37% (Table S4.1). The proportionally highest FA in fish was DHA (25.8±6.2%), which was not found in gumboot or kelp samples, but was found in urchins at small amounts (0.30±0.01%). ARA was highest in kelp (19.4±0.6%) followed by gumboot (12.7±2.0%). kelp and urchin samples boasted some of the highest proportions of 18-C PUFAs, with kelp highest in 18:2ω6 (6.2±0.3%) and urchin highest in 18:4ω3 (2.3±0.1%).

Among the MUFAs, all samples were highest in the same MUFA, 18:1ω9c, which ranged from 5.9±0.1% in urchins to 19.1±0.4% in kelp samples. Proportional SAFA content was relatively similar across taxa with each taxon being proportionally richest in 14:0, 16:0, and 18:0.

In multivariate space, taxa separated out from each other into distinct clusters with minimal overlap, indicating clear differences in FA profiles (Fig. 4.3), which was expected based on previous work with organisms in these phyla. This was true for NMDS plots of FA measured as proportions (Fig. 4.3), concentrations, or summations of proportions. Despite samples being stored across a wide range of conditions (temperature and time), the inter-taxonomic separation in FA profiles held.

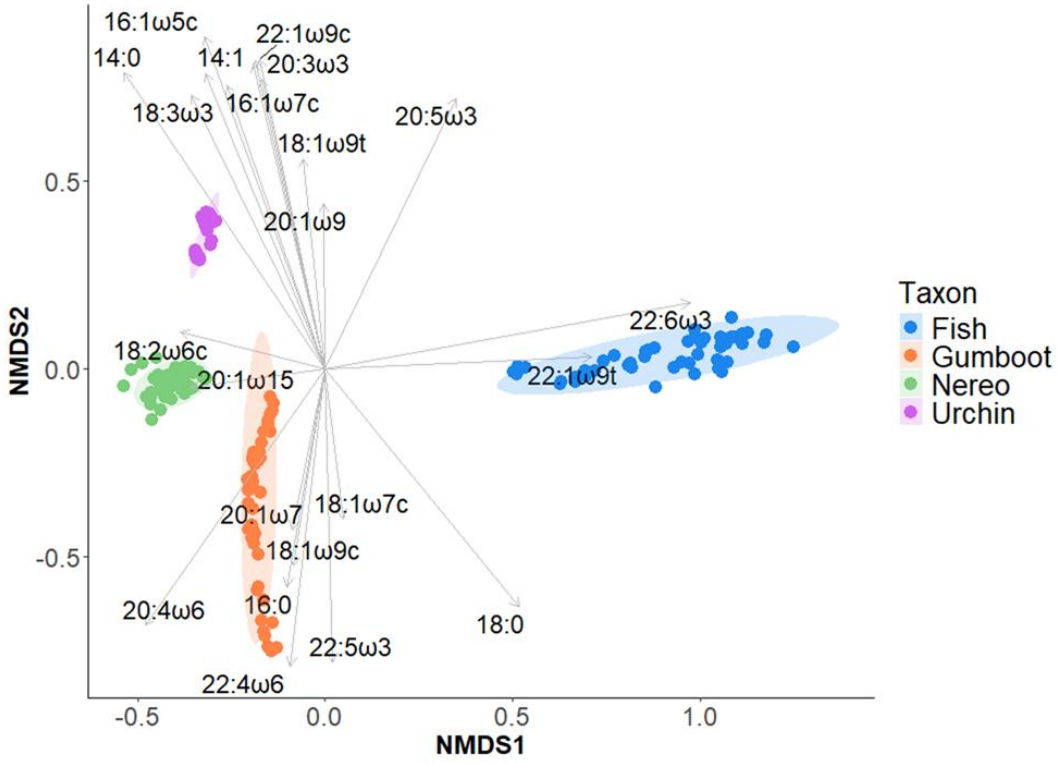


Figure 4.3. NMDS plot of FA proportion data comparing taxa. Datapoints included here are for all taxa, all extraction timepoints and all storage temperatures. All FA are included in this plot, measured as proportions, but vectors are only displayed for those 25 FA which were identified as drivers of dissimilarity across analyses. Datapoints are colored by taxon: fish (blue), gumboot (orange), kelp (Nereo, green), and urchin (purple). "Nereo" is bullwhip kelp, *Nereocystis luetkeana*. Ellipses indicate 95% confidence intervals. NMDS stress = 0.113.

3.2. Time: How did FA change with storage duration?

3.2.1. Across all taxa

Generally, longer storage durations resulted in more significant differences in FA profiles (Table 4.1). FA profiles changed significantly over time for several taxa, especially after 2 and 3 years of storage. These patterns of significance were largely similar whether measuring FA as proportions or concentrations, although the t0 vs. t1yr comparison at T-80°C was significant for kelp and urchin when using concentration data, but was non-significant when using proportional data.

Per taxon, the top 10 FAs driving dissimilarity in comparisons between storage duration and temperatures were averaged for their contribution to overall dissimilarity across these comparisons. These averages are given for both proportional and concentration data per taxon (Table 4.2).

Table 4.1. Results of PERMANOVA tests, separated for proportional and concentration data. The top set results are for PERMANOVA comparisons run on proportional FA data and the bottom set are for PERMANOVA comparisons run on FA concentration data. In each set of results, taxa are listed per row: fish (blue), gumboot (orange), kelp (Nereo, green), and urchin (purple). "Nereo" is bullwhip kelp, *Nereocystis luetkeana*. The left five comparisons are comparing temperatures (T-20°C vs T-80°C) at each extraction timepoint. The right eight comparisons are comparing storage duration (t0 vs tX) at either temperature (T-20°C vs T-80°C). Listed in each comparison is the PERMANOVA R^2 value and p -value. Significant results ($p<0.05$) are shaded in gray.

PERMANOVAs on FA Proportional data														
Datapoints included:	*t0*	*t90*	*t1yr*	*t2yr*	*t3yr*	*T-20C*	*T-80C*	*T-20C*	*T-80C*	*T-20C*	*T-80C*	*T-20C*	*T-80C*
PERMANOVA comparison:	**T-80C vs T-20C**	**T-80C vs T-20C**	**T-80C vs T-20C**	**T-80C vs T-20C**	**T-80C vs T-20C**	**t0 vs. t90**	**t0 vs. t90**	**t0 vs. t1yr**	**t0 vs. t1yr**	**t0 vs. t2yr**	**t0 vs. t2yr**	**t0 vs. t3yr**	**t0 vs. t3yr**
Fish	R2=0.005215959, p=0.951	R2=0.1916222, p=0.21	R2=0.2557158, p=0.1	R2=0.1337234, p=0.307	R2=0.04741236, p=0.614	R2=0.1079217, p=0.346	R2=0.06896053, p=0.481	R2=0.1840383, p=0.184	R2=0.04579841, p=0.486	R2=0.04357172, p=0.579	R2=0.1166493, p=0.334	R2=0.2302558, p=0.159	R2=0.1756003, p=0.219
Gumboot	R2=0.00346726, p=0.935	R2=0.1611616, p=0.225	R2=0.02326214, p=0.835	R2=0.05710589, p=0.519	R2=0.2132171, p=0.166	R2=0.03805243, p=0.641	R2=0.09728442, p=0.358	R2=0.1448907, p=0.321	R2=0.1216036, p=0.386	R2=0.08523154, p=0.416	R2=0.1553305, p=0.266	R2=0.1612258, p=0.255	R2=0.1046725, p=0.339
Nereo	R2=0.1490124, p=0.229	R2=0.3430872, p=0.032	R2=0.6790342, p=0.007	R2=0.8971293, p=0.007	R2=0.92935786, p=0.007	R2=0.3810205, p=0.007	R2=0.1562627, p=0.227	R2=0.7980607, p=0.007	R2=0.2257824, p=0.119	R2=0.8887232, p=0.007	R2=0.576632, p=0.007	R2=0.8804325, p=0.007	R2=0.6483846, p=0.007
Urchin	R2=0.1392029, p=0.293	R2=0.197788, p=0.134	R2=0.08973813, p=0.493	R2=0.1924202, p=0.159	R2=0.0564143, p=0.728	R2=0.04656845, p=0.715	R2=0.1586618, p=0.248	R2=0.06310258, p=0.676	R2=0.1137647, p=0.415	R2=0.91113111, p=0.007	R2=0.92241175, p=0.007	R2=0.92430073, p=0.007	R2=0.93691433, p=0.007

PERMANOVAs on FA Concentration data													
Datapoints included:	*t0*	*t90*	*t1yr*	*t2yr*	*t3yr*	*T-20C*	*T-80C*	*T-20C*	*T-80C*	*T-20C*	*T-80C*	*T-20C*	*T-80C*
PERMANOVA comparison:	**T-80C vs T-20C**	**T-80C vs T-20C**	**T-80C vs T-20C**	**T-80C vs T-20C**	**T-80C vs T-20C**	**t0 vs. t90**	**t0 vs. t90**	**t0 vs. t1yr**	**t0 vs. t1yr**	**t0 vs. t2yr**	**t0 vs. t2yr**	**t0 vs. t3yr**	**t0 vs. t3yr**
Fish	R2=0.009725009, p=0.895	R2=0.1645245, p=0.242	R2=0.2448648, p=0.093	R2=0.06806556, p=0.479	R2=0.2994779, p=0.111	R2=0.2359723, p=0.165	R2=0.03854625, p=0.61	R2=0.2703491, p=0.131	R2=0.0136495, p=0.578	R2=0.09592839, p=0.406	R2=0.102662, p=0.412	R2=0.184327, p=0.17	R2=0.250991, p=0.108
Gumboot	R2=0.01025062, p=0.851	R2=0.06383759, p=0.47	R2=0.02899861, p=0.737	R2=0.1053684, p=0.411	R2=0.1193772, p=0.275	R2=0.01284591, p=0.846	R2=0.05313521, p=0.524	R2=0.06220206, p=0.514	R2=0.05267673, p=0.595	R2=0.03270818, p=0.669	R2=0.1691207, p=0.214	R2=0.150289, p=0.237	R2=0.03317652, p=0.624
Nereo	R2=0.2725261, p=0.032	R2=0.336954, p=0.06	R2=0.6848069, p=0.007	R2=0.8627846, p=0.007	R2=0.7150737, p=0.007	R2=0.4392283, p=0.031	R2=0.2527026, p=0.104	R2=0.8047849, p=0.007	R2=0.5153021, p=0.007	R2=0.7904623, p=0.007	R2=0.5868115, p=0.007	R2=0.5585703, p=0.007	R2=0.5024403, p=0.007
Urchin	R2=0.2502488, p=0.114	R2=0.1835724, p=0.197	R2=0.3057831, p=0.083	R2=0.04467877, p=0.56	R2=0.1496443, p=0.275	R2=0.01102415, p=0.836	R2=0.0741809, p=0.595	R2=0.07689392, p=0.463	R2=0.7219326, p=0.007	R2=0.93763641, p=0.007	R2=0.9657616, p=0.007	R2=0.96688286, p=0.007	R2=0.990787205, p=0.007

Table 4.2. Average contribution to dissimilarity per FA per taxon across comparisons. Per taxon, the top 10 FAs driving dissimilarity in comparisons between storage duration and temperatures were identified via SIMPER and then averaged for their contribution to overall dissimilarity across these comparisons. These averages are given for both proportional (Prop.) and concentration (Conc.) data per taxon: fish (blue), gumboot (orange), kelp (Nereo, green), and urchin (purple). "Nereo" is bullwhip kelp, *Nereocystis luetkeana*. Each result is the average (± standard deviation) percent contribution to dissimilarity across comparisons given by that FA for that taxon. FA are listed in order of decreasing saturation and increasing carbon chain length.

	Fish		Gumboot		Nereo		Urchin	
FA	Prop.	Conc.	Prop.	Conc.	Prop.	Conc.	Prop.	Conc.
C14:0	3.29 ±0.33	3.39 ±0.57	5.43 ±0.81	6.48 ±0.62	8.58 ±2.44	6.42 ±2.57	11.73 ±5.11	14.58 ±3.65
C15:0				2.66 ±0.37				
C16:0	11.75 ±1.7	12.11 ±1.36	7.82 ±3.65	17.18 ±1.57	16.2 ±4.61	11.71 ±4.16	10.18 ±4.56	17.68 ±3.87
C18:0	3.22 ±0.39	3.4 ±0.58	5.62 ±1.51	4.2 ±1.2	4.67 ±2.26	3.26 ±1.51	5.44 ±1.84	5.01 ±1.55
C14:1							3.41 ±0.43	2.58 ±0.38
C16:1ω5c					3.33 ±1.39	3.15 ±0.92	3.12 ±0.44	5.08 ±0.81
C16:1ω7c	5.46 ±0.37	6.26 ±0.53	4.13 ±0.34	4.86 ±0.24	4.11 ±1.15	3.23 ±1.39	5.45 ±na	4.56 ±0.5
C18:1ω7c	2.48 ±0.26	5.06 ±0.35	4.32 ±0.87	5.74 ±0.97				4.28 ±0.3
C18:1ω9c	16.32 ±1.52	20.36 ±1.65	23.26 ±2.08	26.64 ±1.49	10.85 ±3.26	11.21 ±5.47	3.8 ±0.66	4.89 ±0.77
C18:1ω9t	2.78 ±0.57		6.88 ±0.9	4.31 ±1.37			5.58 ±2.22	4.32 ±1.09
C18:2ω6c					4.51 ±0.65	6.07 ±1.33	2.54 ±0.07	
C18:2ω6t							2.56 ±0.03	
C18:3ω3					4.28 ±1.83	4.44 ±1.43		
C18:4ω3c					6.93 ±1.86	6.49 ±1.69	3.46 ±0.67	
C20:1ω7			5.95 ±0.42	3.94 ±0.25				
C20:1ω9	3.25 ±0.26	3.46 ±0.4					8.89 ±3.68	6.03 ±1.92
C20:1ω15	1.98 ±na		4.11 ±0.42	5.46 ±0.28			7.65 ±4.66	5.31 ±2.67
C20:3ω3							2.47 ±0.31	
C20:4ω6	1.96 ±na		14.25 ±2.03	5.85 ±1.43	18.88 ±5.82	26.92 ±8.35	3.29 ±0.65	4.81 ±0.53
C20:5ω3	6.44 ±1.04	8.32 ±1.04	4.88 ±1.17	4.31 ±0.82	11.29 ±1.96	12.53 ±3.41	9.22 ±3.5	11.76 ±2.83
C22:1ω9c							3.42 ±0.62	
C22:1ω9t	3.63 ±0.38	3.27 ±0.52						
C22:4ω6			6.12 ±0.65	2.86 ±0.25				
C22:5ω3			7.86 ±0.84	3.02 ±0.25				
C22:6ω3	27.43 ±2.56	15.64 ±5.99						

Whether FAs were measured as proportions or concentrations, these top 10 FAs were largely (19/25) the same with a few exceptions: different from when FA were measured as concentrations, the top 10 FA list for FA as proportions included 18:2ω6t, 20:3ω3, 22:1ω9c, and 22:4ω6 but excluded 14:1 and 15:0. The top 3 FA in any comparison often included a SAFA, MUFA, and PUFA. Across taxa, the #1 FA in any comparison was not reliably of any particular

saturation level. Differences in the top 10 FA list between FAs measured as proportions vs. those measured as concentrations were minimal. The same FAs generally appeared in both lists at around the same position number; for example, 18:1ω9c appeared in 31/32 comparisons at average position 3.1±2.7 and 28/32 comparisons at average position 2.6±1.9 in lists of concentrations and proportions, respectively. Some FAs (14:1 and 15:0) appeared in lists of concentrations but not in proportions and the opposite was also true (18:2ω6t, 20:3ω3, 22:1ω9c, and 22:4ω6), but these were typically at high positions (>9) and were rare in occurrence (<5/32). Some notable exceptions were 18:1ω7c, which featured much more prominently in lists of concentrations at 23/32 occurrences and average position 6.3±1.7, as compared to the 12/32 occurrences at average position of 9.3±0.9 in proportions. Two FAs, 20:1ω7 and 22:1ω9t, each had equal occurrences in both lists, but appeared at roughly double the position in lists of concentrations as compared to proportions (20:1ω7: 9±0.7 vs. 5.5±0.5; 22:1ω9t: 9±1 vs. 6.3±0.4). FAs 22:1ω9c and 22:4ω6, both absent from concentrations list, occurred in 7/32 and 8/32 comparisons in proportions at average positions 6.7±1.3 and 6.3±1.0, respectively. Finally, 22:5ω3 featured much more prominently in proportions lists, appearing in 8/32 comparisons at position 3.6±0.7, as compared to only 3/32 comparisons only in position 10 in lists of concentrations.

The PUFA EPA showed up within the top 10 FA for every taxon for every timepoint comparison, (except for Gumboot t0 vs. t3yr at T-80°C for which EPA was #11). The second highest occurring PUFA in dissimilarity measurements was ARA, occurring in about 2/3 of comparisons, but especially in SIMPER comparisons of gumboot and kelp data.

From SIMPER analyses, generally across taxa it was true that longer storage duration resulted in a higher number of FAs being significantly dissimilar between that timepoint and t0;

this was true for FA measured in concentrations and in proportions. This was also generally true at both storage temperatures, although the effect was greater for samples stored at T-20°C than at T-80°C.

Analyzing differences in FA through heatmaps revealed that with increased storage duration, changes in FA proportions were often bidirectional (some increasing with time, some decreasing) (Fig. 4.4), while changes in concentrations were mostly unidirectional increases over time (Fig. 4.5).

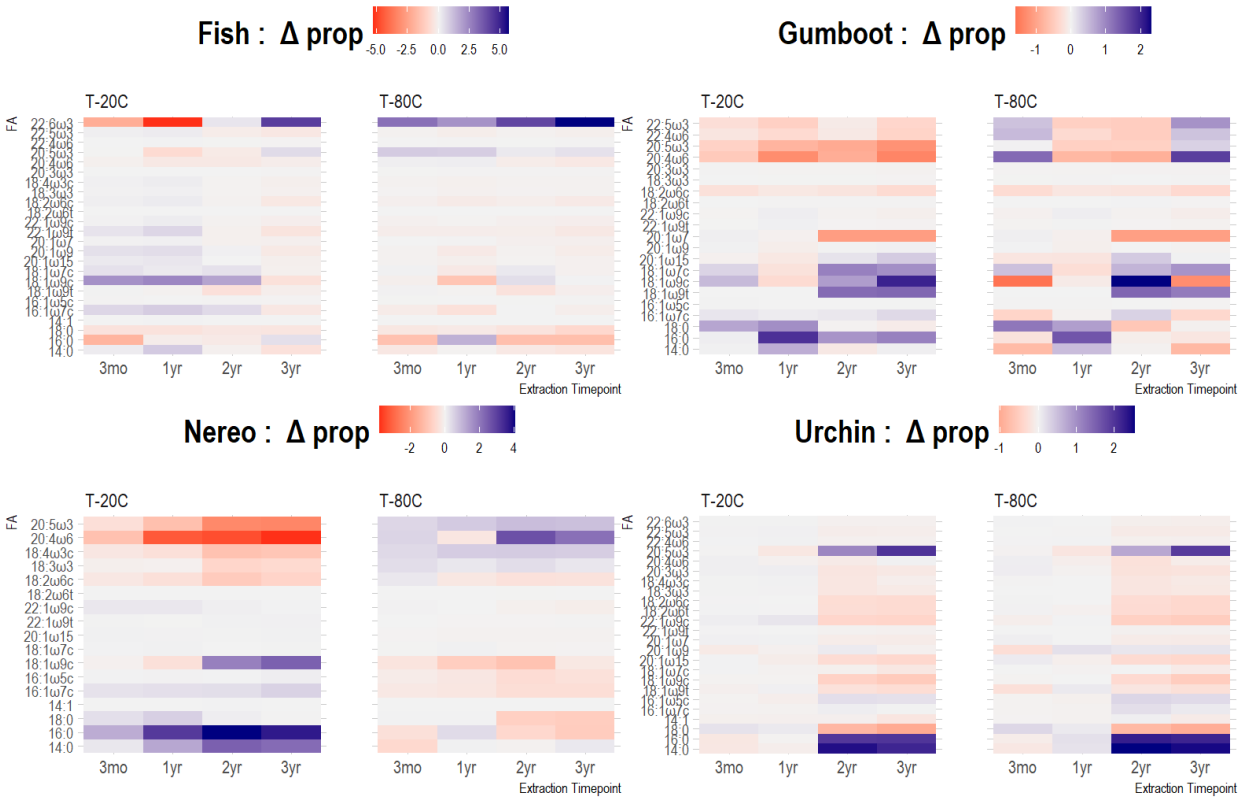


Figure 4.4. Heatmap of changes in FA proportions. For each taxon stored at each temperature, the change in proportions for each of the FA identified as drivers of dissimilarity (suite of 25) was calculated as (proportion of FA at timepoint tX – proportion of FA at timepoint t0). The resulting values are displayed in this heatmap; the color gradient (specific to each taxon) shows how certain FA are relatively enriched (blue) or depleted (red) between the initial extraction and the extraction timepoint depicted. "Nereo" is bullwhip kelp, *Nereocystis luetkeana*.

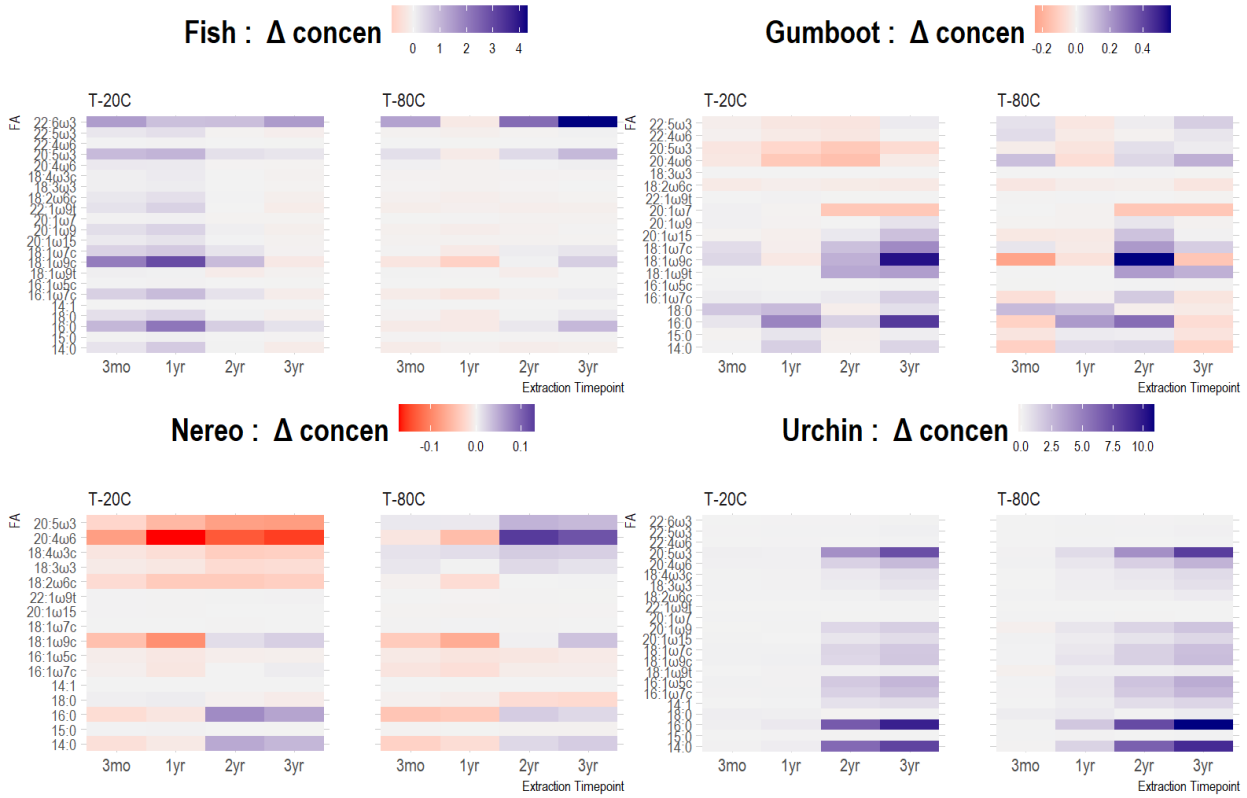


Figure 4.5. Heatmap of changes in FA concentrations. For each taxon stored at each temperature, the change in concentrations for each of the FA identified as drivers of dissimilarity (suite of 25) was calculated as (concentration of FA at timepoint tX – concentration of FA at timepoint t0). The resulting values are displayed in this heatmap; the color gradient (specific to each taxon) shows how certain FA are relatively enriched (blue) or depleted (red) between the initial extraction and the extraction timepoint depicted. "Nereo" is bullwhip kelp, *Nereocystis luetkeana*.

In either concentrations or proportions, increases in PUFA with time were generally limited to samples stored at T-20°C, while increases in MUFA or SAFA with time occurred at both storage temperatures. One PUFA in particular (18:2ω6c) instead of following the trend of other PUFAs as dictated by taxon-specific trends, followed its own trend of decreasing in proportion with time, at either temperature for all taxa (Fig. 4.4, 4.5). Trends in concentration of this FA were more variable with taxon, temperature, and timepoint.

3.2.2. Taxon-Specific: Fish

FA profiles were not significantly different between fish samples that were immediately extracted compared to those that were stored for up to 3 years at either T-20°C or T-80°C, as measured by proportions or concentrations (Table 4.1; Fig. 4.6).

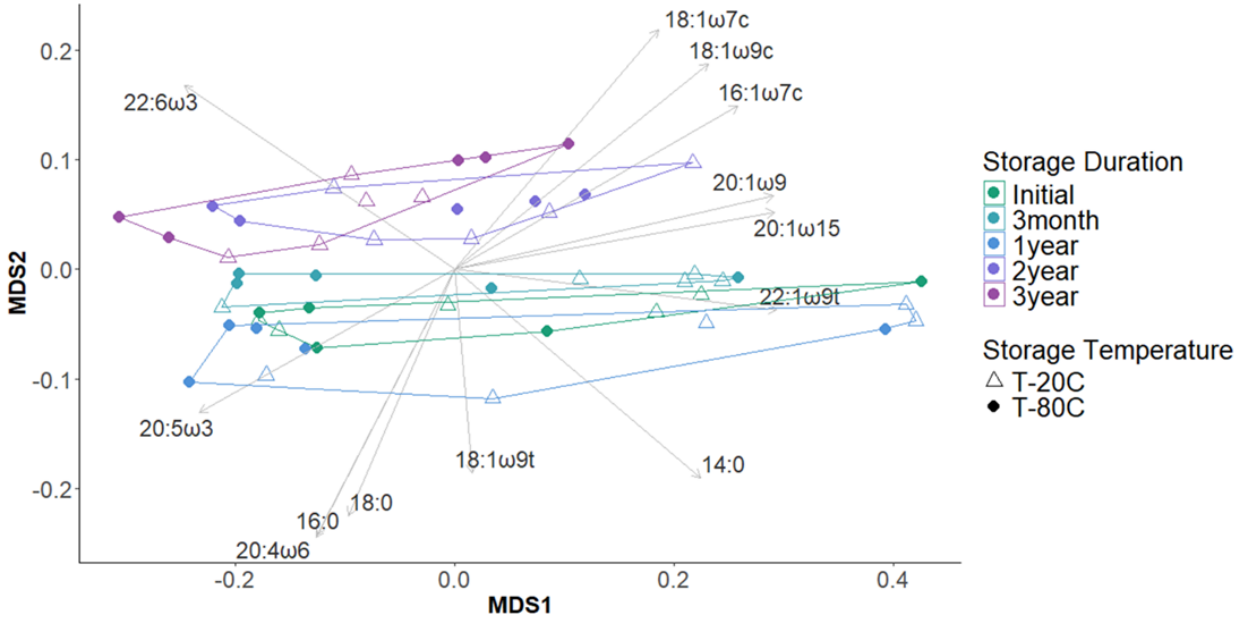


Figure 4.6. NMDS of fish FA proportions. Datapoints include all FAs measured in proportions, colored by storage duration and shaped by storage temperature. Vectors are drawn only for those FA that were identified by SIMPER analyses as the top 10 FA driving dissimilarity between any timepoint or temperature comparison for this taxon. Points are hulled per storage duration. NMDS stress = 0.044.

There were some significant differences for individual FA found via SIMPER analyses. In proportion data at either temperature, the only PUFAs that were significantly dissimilar between t0 vs. any other extraction timepoint were all ω-6 PUFAs (20:2ω6, 20:3ω6, 22:3ω6, and 22:5ω6) and did not include any ω-3 PUFAs although ω-3 PUFAs were present in about equal numbers and were proportionally higher than ω-6 PUFAs. This finding was only observed in fish and no other taxon. This finding also did not hold for concentration data, where both ω-3 and ω-

6 PUFAs were significantly dissimilar from t0 at various timepoints, at both temperatures - notably EPA and DHA for samples stored at T-80°C for 2 years and 3 years, and nearly half of FAs (27/55) stored at T-20°C for 1 year. This was different from proportion data, where the same temperature and timepoint yielded only six significantly dissimilar FAs. Several FAs, including DHA and EPA, generally increased in concentration over time, particularly for samples stored at T-80°C (Fig. 4.5). Proportionally, these two FAs were more abundant at all timepoints compared to t0 when stored at T-80°C, but showed initial decrease and then later increase when stored at T-20°C (Fig. 4.4). For all FAs, this trend was generally true at either temperature: proportional data showed increases or decreases in any FA depending on timepoint, while concentration data suggested mostly net gains with time. Heatmaps (Fig. 4.4, 4.5) indicated DHA in fish showed the widest spread in proportional change of any FA across all taxa, changing substantially, from -5.29% at T-20°C at timepoint 1 year to +5.68% at T-80°C and timepoint 3 years – giving a total spread of 10.97%. Furthermore, DHA was an extremely important driver of dissimilarity in simper analyses of fish data, being the number one driver of dissimilarity for all timepoint comparisons at both temperatures when FA was measured as proportions. Measured as concentrations, DHA still featured high in the list for fish, appearing in every timepoint comparison at both temperatures with an average position of 2±0.9. This FA did not appear in the top 10 FA list for any other taxon.

3.2.3. Taxon-Specific: Gumboot

FA profiles were not significantly different between gumboot samples that were immediately extracted compared to those that were stored for up to 3 years at either T-20°C or T-80°C, as measured by proportions or concentrations (Table 4.1, Fig. 4.7).

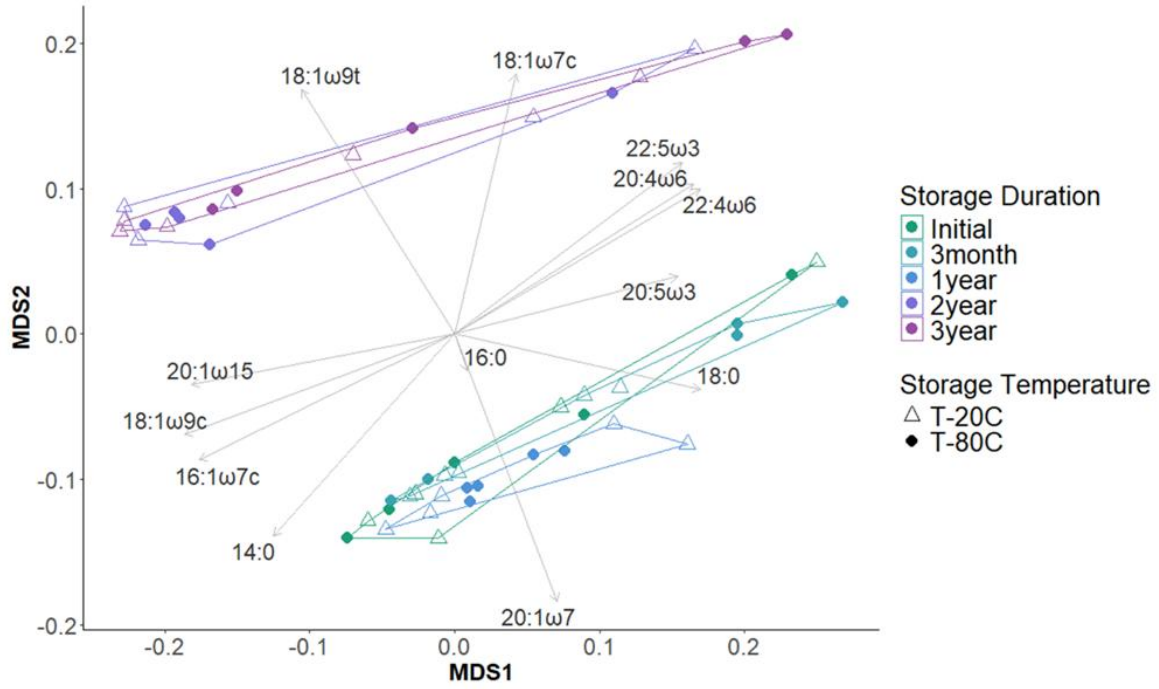


Figure 4.7. NMDS of gumboot FA proportions. Datapoints include all FAs measured in proportions, colored by storage duration and shaped by storage temperature. Vectors are drawn only for those FA that were identified by SIMPER analyses as the top 10 FA driving dissimilarity between any timepoint or temperature comparison for this taxon. Points are hulled per storage duration. NMDS stress = 0.044.

Increasing storage duration led to an increase in the number of individual FA that were statistically dissimilar between timepoint t0 and any other extraction timepoint, at either temperature and in either FA measure. Yet, overall, this significant finding was infrequent.

Across all timepoints, temperatures, and FAs, gumboot samples yielded a moderate range of change in FA proportions from t0: 18:1ω9c changed from -1.58% at T-80°C and timepoint 3months to +2.31% at T-80°C and timepoint 2years, giving a total change range of 3.89% (Fig. 4.4). Changes in FA proportions across time were more evenly spread across FAs as compared to fish or urchin samples. Temporal trends were much more consistent at T-20°C than at T-80°C. For example, at T-20°C, PUFAs 22:5ω3, 22:4ω6, 20:5ω3, 20:4ω6 all generally decreased with time, whereas at T-80°C, these same PUFAs all increased at t3month, then decreased at t1year

and t2year, then increased again at t3year. At T-20°C, MUFAs 18:1ω9c and 18:1ω9t mostly increased while SAFAs 16:0 and 18:0 mostly decreased, but all four FAs saw bidirectional change with time at T-80°C. MUFA 20:1ω7 decreased in both T-20°C and T-80°C.

Gumboot samples also did not change greatly in measure of FA concentrations with time (Fig. 4.5). The same FA that changed most proportionally changed most in measure of concentration: at T-80°C, 18:1ω9c decreased by -0.245 mg per g of dry wt at t3month, then this same FA increased by 0.562 mg per g dry wt at t2year, giving a total change range of 0.807 mg per g dry wt. Similar to patterns seen in proportional data, patterns in concentration data were variable, with some FA increasing with time and some decreasing. Concentration increases were larger than decreases, the same trend as seen for urchin and fish. In gumboot, PUFAs 22:5ω3, 22:4ω6, 20:5ω3, and 20:4ω6 all decreased in concentration with time at T-20°C but showed bidirectional change at T-80°C. PUFA 18:2ω6c decreased at both temperatures. MUFAs 18:1ω7c, 18:1ω9c, 18:1ω9t, and 16:1ω7c mostly increased in concentration with time with some variability. Same as with proportions, the concentration of MUFA 20:1ω7 decreased at both temperatures at later timepoints. Opposite to trends with proportions, SAFAs 16:0 and 18:0 generally increased at T-20°C and changed bidirectionally at T-80°C. At T-20°C, proportion or concentration increases were generally seen in SAFA and MUFA, while decreases were seen in almost all PUFA (Fig. 4.4, 4.5). At T-80°C, this trend still held but was more variable among FAs.

3.2.4. Taxon-Specific: Kelp

Of the four taxa tested, kelp was the most affected by storage duration. Compared to initial FA profiles, the profiles of kelp samples extracted at t2year and t3year were significantly different, at both temperatures and using both measures (proportions or concentrations) (Table

4.1, Fig. 4.8). The profiles at timepoints t3month and t1year were also significantly different for both measures at T-20°C. The only result that differed between measures was for FA profiles at t1year and T-80°C, which were significantly different for concentrations but not for proportions. kelp also exhibited some minor changes in total FA concentration with storage temperature. At each extraction timepoint, total FA concentration in kelp samples was higher in samples stored at T-80°C than at T-20°C by an average of +0.37±0.17 (mg total FA / g dry weight) (Fig. 4.2).

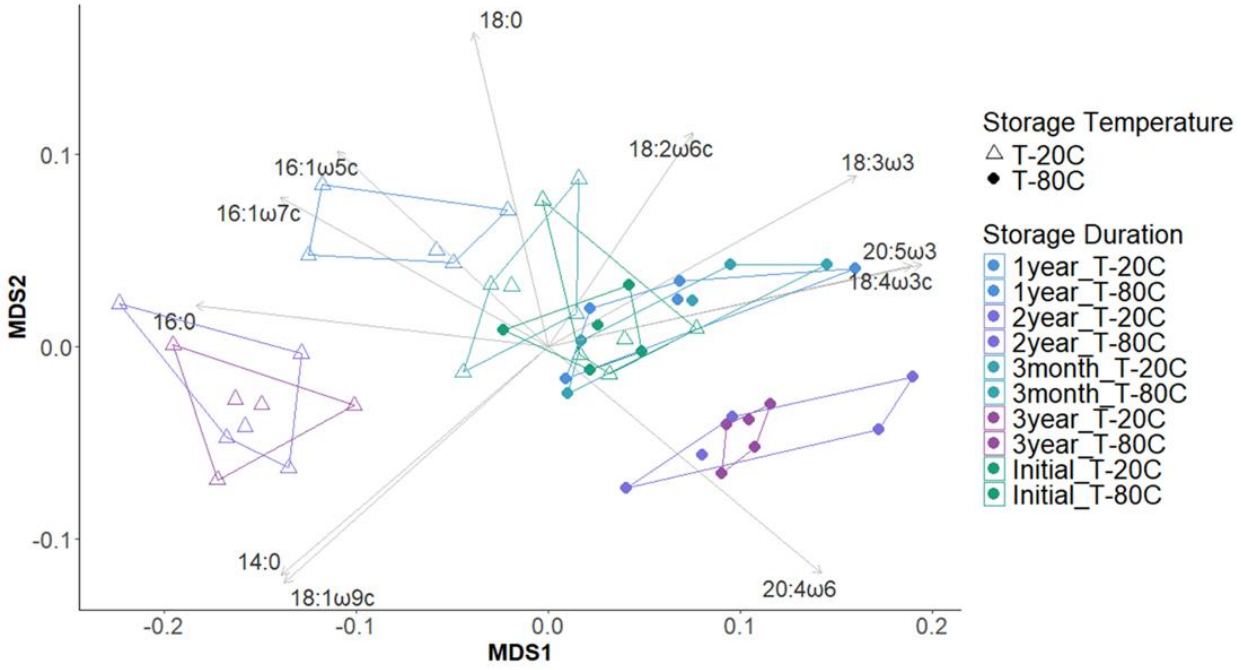


Figure 4.8. NMDS of kelp FA proportions. Datapoints include all FAs measured in proportions, colored by storage duration and shaped by storage temperature. Vectors are drawn only for those FA that were identified by SIMPER analyses as the top 10 FA driving dissimilarity between any timepoint or temperature comparison for this taxon. Points are hulled per storage duration/temperature combination. NMDS stress = 0.071.

Individual FA proportions changed the second most widely in kelp samples, after fish samples. Changes in FA proportions ranged from -3.78% in 20:4ω6 at T-20C & t3year to +4.06% in 16:0 at T-20°C & t2year, giving a total spread of proportional change of 7.84% (Fig. 4.4). At T-20°C, SAFAs and MUFAs mostly increased while PUFAs mostly decreased. At T-

80°C, MUFAs decreased while SAFAs and PUFAs changed variably. PUFAs 20:5ω3, 20:4ω6, 18:4ω3c, and 18:3ω3 all showed exact opposite trends based on storage temperature, with proportions increasing with time at T-80°C and decreasing with time at T-20°C, while also being largely significantly dissimilar from t0 at t2year and t3year at this higher storage temperature. Different from the other PUFA, 18:2ω6c decreased in proportion with time at both temperatures. MUFAs and SAFAs also showed opposite trends based on storage temperature, generally increasing with time at T-20°C and decreasing with time at T-80°C.

In measure of absolute change in concentrations and out of all taxa, kelp samples changed the least: 20:4ω6 decreased by -0.170 mg per g dry wt at T-20°C & t1year but this same FA then increased the most at +0.128 mg per g dry wt at T-80°C & t2year (Fig. 4.5). This gave a total concentration change range of 0.298 mg per g dry wt. This FA 20:4ω6 changed the most by far in measure of concentration, decreasing with time at T-20°C, and at T-80°C showing a trend of initial decrease then increase at timepoints t2year and t3year. Interestingly, 3 other PUFAs (20:5ω3, 18:4ω3c, and 18:3ω3) all showed exact opposite patterns according to storage temperature: these FAs all decreased in concentration at T-20°C, but all increased in concentration at T-80°C. PUFA 18:2ω6c decreased at both temperatures. MUFA 18:1ω9c and SAFAs 16:0 and 14:0 all showed the same pattern regardless of storage temperature: initial decrease in concentration at t3month/1year, then increase at t2year/3year. Many of the top drivers of dissimilarity between t0 and tX were significantly dissimilar at T-20°C (e.g., 20:4ω6 at t1year, or 20:5ω3 at t2year/3year) but not at T-80°C. Concentrations of PUFAs in kelp reliably decreased with time at T-20°C, but changed variably at T-80°C; concentrations of SAFAs and MUFAs changed bidirectionally at both temperatures.

3.2.5. Taxon-Specific: Urchin

Urchin FA profiles changed substantially with storage duration. At both temperatures and in both measures, FA profiles at t0 were significantly different than those at t2year and t3year (Table 4.1, Fig. 4.9).

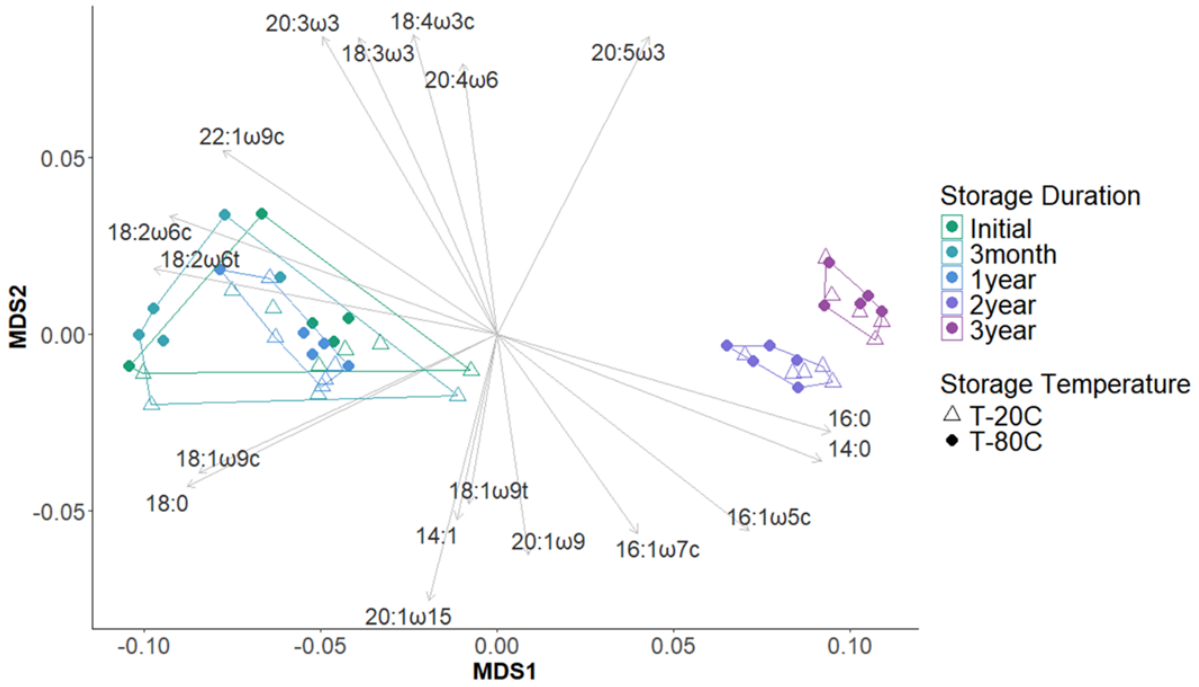


Figure 4.9. NMDS of urchin FA proportions. Datapoints include all FAs measured in proportions, colored by storage duration and shaped by storage temperature. Vectors are drawn only for those FA that were identified by SIMPER analyses as the top 10 FA driving dissimilarity between any timepoint or temperature comparison for this taxon. Points are hulled per storage duration/temperature combination. NMDS stress = 0.000086.

FA profiles were also significantly different at t1year and T-80°C in measure of concentrations, but, interestingly, not in measure of proportions and not at T-20°C. At both T-20°C and T-80°C, proportions of SAFAs changed bidirectionally while MUFAs and PUFAs mostly decreased with time, except notably 20:5ω3. In measure of concentrations, the trend was opposite to that seen using proportions: concentrations of MUFAs and PUFAs reliably increased with time, except for a few minor FAs (20:1ω7, 22:1ω9t, and 22:3ω6) which all initially

increased at t3month/1year but then decreased at t2year/3year. The combined effect of this notable increase in MUFA and PUFA concentrations translates to an impressive increase in total FA concentration over time (Fig. 4.2), which increased by over 50% over the course of 3 years at either storage temperature. This temporal increase in urchin total FA concentration was remarkably linear, fitting the following linear trendlines at either temperature. At T-20°C: *Total FA concentration in mg FA per g dry wt = 84.9 + 0.0416*(time in days);* R^2*=0.93*. At T-80°C: *Total FA concentration in mg FA per g dry wt = 81.2 + 0.0482*(time in days);* R^2*=0.98.* This extreme increase in total FA concentration over time was only seen in urchin samples and no other taxon. Proportional data also masked these effects. As individual FAs increased in concentration by varying degrees and because proportional data must always total to 100%, temporal changes in FA proportions are mixed, with some FAs increasing and some decreasing. At both temperatures, proportions of individual PUFAs decreased with time, except for 20:5ω3 which notably increased. The fact that this strong linear relationship between total FA concentration and time is essentially the same regardless of storage temperature again highlights how for this taxon, FA changes are overwhelmingly due to storage duration while temperature has very little effect.

Individual FAs also changed significantly in proportions and concentrations with time. Measured as proportions, urchin samples stored at either temp had less than 2 FAs that were significantly dissimilar between t0 and either t3month or t1year. Then a clear change occurred at both temperatures, where t2year or t3year samples had nearly all (>36/52) FA at proportions that were significantly dissimilar from those at t0. Measured as concentrations, urchin samples stored at T-20°C had less than 10 FAs significantly dissimilar until t3year, where this number jumped to 31 significantly dissimilar concentrations. For urchin samples stored at T-80°C, at t1year,

there were already 25 FAs significantly dissimilar in concentration from t0, and this number rose to 36 significantly dissimilar FAs at t3year.

3.3. Temperature: How did FA change with storage temperature?

3.3.1. Across all taxa

The effects of storage temperature on FA profiles were overall far less pronounced than the effects of storage duration, although the extent varied by taxon. The extent to which taxa were affected by storage temperature followed a trend that correlated negatively with total lipid content. Lipid-poor kelp samples were the most affected by temperature while lipid-rich urchin samples were the least affected. Fish and gumboot samples fell somewhere in between. It is possible the urchin samples were so unaffected by temperature due to any effect being drowned out by the overwhelmingly large effect of storage duration.

Generally across taxa, samples stored at T-80°C retained greater amounts of PUFA and lower amounts of MUFA and SAFA; this was true for data in proportions or concentrations (Fig. 4.4, 4.5) In PERMANOVA comparisons, only one taxon (kelp) showed significant differences in FA profiles with temperature, per any timepoint (Table 4.1).

Simper analyses comparing FA profiles between temperatures (across all taxa, FA measures, and timepoints) yielded 23 unique FAs within the list of top 10 FA driving dissimilarity in any one comparison. This list was again largely similar between measures of proportions and concentrations, with proportion data including 20:3ω3 and 22:1ω9c, while excluding 15:0. This list of 23 unique FAs was identical to the list of 25 unique FAs identified via SIMPER analyses of time comparisons, with the exception of excluding two FAs (18:2ω6t and 20:1ω7) which occurred infrequently and low within the list of top 10 FAs in temporal SIMPER analyses. Seeing the two lists of top 10 FAs that drive dissimilarity as essentially

identical between SIMPER comparisons of timepoints vs. that of temperatures suggests that FAs that are susceptible to degradation from storage duration are also susceptible to degradation from storage temperature.

3.3.2. Taxon-Specific: Fish

Temperature had only minor effects on fish FA profiles, with no significant differences between storage temperatures at any timepoint (Table 4.1; Fig. 4.6). In individual FA, few clear patterns emerged, except for 22:6ω3 which was consistently higher in proportion at T-80°C than at T-20°C for all extraction timepoints (Fig. 4.4, 4.5). Concentration of this same FA increased with time at a greater rate at T-80°C than at T-20°C. Other FAs were more likely to decrease in proportion and in concentration at T-80°C than at T-20°C, though this varied with FA and timepoint. Absolute changes in individual FA concentrations were overall less at T-80°C than at T-20°C.

Repeating the trend as observed for proportion data in time comparisons, DHA was again the number one driver of dissimilarity between temperatures at all timepoints, while EPA fell within the top five. In concentration data, DHA and EPA both fell within the top five FAs driving dissimilarity between temperatures. Notably, at t1year, although the FA profiles as a whole did not differ significantly between temperatures, almost all of the individual FA as measured in proportions (40/55) or concentrations (50/55) differed significantly, including DHA (in proportion but not in concentration), EPA, and the 8 other top 10 drivers of dissimilarity. All other timepoints had less than two individual FAs that differed significantly between temperatures.

3.3.3. Taxon-Specific: Gumboot

Temperature comparisons for the gumboot samples were highly variable and inconsistent, with no significant differences in overall FA profiles (Table 4.1). PUFAs were higher in proportions at T-80°C for timepoints t3month and t3year, but were mostly the same between temperatures at timepoints t1year and t2year, while others (e.g., 18:2ω6c) did not vary between temperatures (Fig. 4.4, 4.5). MUFAs and SAFAs were frequently lower in proportion at T-80°C than at T-20°C. Measured in concentrations, PUFAs were higher and SAFAs were lower at T-80°C than at T-20°C. MUFAs varied, except for 18:2ω6c and 20:1ω7 which both decreased with time equivalently across temperatures.

Individually, FA varied minimally between temperatures. At any timepoint, in measures of proportions, the two primary drivers of dissimilarity between temperatures were, in order, 18:1ω9c and 20:4ω6 (ARA). The number of individual FA that were significantly dissimilar in proportions between temperatures increased with storage duration and maxed out at 5 of the 43 FA by t3year, including ARA and EPA. Measured in concentrations, 18:1ω9c remained the number one driver of dissimilarity, while ARA became less important, falling within the top six drivers of dissimilarity. The highest number of significantly dissimilar FA concentrations occurred at t2year, at 11 of 43 FAs, and again including EPA and ARA.

3.3.4. Taxon-Specific: Kelp

Kelp samples were the most sensitive to changes in storage temperature, being the only taxon to have FA profiles significantly differ between temperatures (Table 4.1). FA profiles of kelp differed significantly between T-20°C and T-80°C at all timepoints and in both measures (proportions or concentrations) with only two exceptions at early timepoints: proportional data at t0 and concentration data at t3month (Table 4.1). With time, this effect of storage temperature

became exacerbated such that in multidimensional space, proportional data show a wide spread between temperatures at t2year and t3year that overwhelm differences between these timepoints (Fig. 4.7). Compared to T-20°C, FA profiles at T-80°C contained larger proportions of PUFAs and smaller proportions of MUFAs and SAFAs (Fig. 4.4, 4.5). In concentration data, PUFAs were again higher at T-80°C than at T-20°C for each timepoint. However, MUFAs and SAFAs were at very similar concentrations per timepoint regardless of temperature. Thus it is likely that the difference in kelp FA proportions between temperatures is driven primarily by the large changes in PUFA concentrations, not in MUFA or SAFA concentrations.

Individual FA varied significantly with temperature, more so at later timepoints than earlier, with nearly half (proportion data: 17/35, concentration data: 11/35) being significantly different by t3year. In either FA measure (proportion or concentration), 20:4ω6 (ARA) and 20:5ω3 (EPA) were within the top four drivers of dissimilarity between temperatures. These two PUFA became more influential with time such that by t2year, in drivers of dissimilarity between temperatures, ARA and EPA held the first and third positions (proportion data), and first and second positions (concentration data), respectively. At t2year and t3year, ARA and EPA were significantly dissimilar between temperatures in either FA measure.

3.3.5. Taxon-Specific: Urchin

Urchin samples were remarkably unaffected by storage temperature, with no significant differences found (Table 4.1). Unlike for all other taxa, FA proportions and concentrations were nearly identical between storage temperatures at any one timepoint (Fig. 4.4, 4.5). In multidimensional space, urchin FA data clearly separated out by timepoint, with no noticeable difference between temperatures within a timepoint (Fig. 4.9). What little differences there were between temperatures were primarily driven by MUFAs and SAFAs, although EPA and ARA

were within the top 11 drivers of dissimilarity at any timepoint. In proportional data, EPA moved up in importance with time to hold the position of primary driver of dissimilarity by t2year, but consistently held the second or third position at any timepoint in concentration data. Individual FA were rarely (≤3/52) significantly dissimilar between temperatures at any timepoint in either FA measure.

3.4. What characteristics make a particular FA more susceptible to degradation?

3.4.1. Saturation Level

Comparing concentrations of FAs at tX to those at t0 at either temperature showed no observable trend across taxa in regard to any saturation level changing more than another. In fact, this was highly taxon-dependent and sometimes temperature-dependent. Fish at T-20°C experienced the greatest changes in MUFA concentrations, while fish at T-80°C experienced large changes in PUFA concentrations, primarily a large increase in the concentration of 22:6ω3. Gumboot at either temperature saw mostly increases in concentrations of MUFA and SAFA, while PUFA changed relatively little. Kelp samples changed most in PUFA at both temperatures. Urchin samples experienced increased concentrations across all FA types at both temperatures, with the largest changes in MUFA and PUFA. Proportion patterns were different: fish samples changed the most in PUFA proportions at both temperatures, while gumboot proportions changed across all saturation levels at both temperatures. Kelp proportions changed in all saturation levels at T-20°C but most in PUFAs at T-80°C, and urchin proportions changed most in SAFAs and PUFAs. In comparing types of PUFAs, ω-3 LC-PUFAs generally changed more than other types (e.g., shorter chain or ω-6 PUFAs).

3.4.2. FA Amounts (proportions or concentrations)

FA abundance was perhaps the best determinant of which FA will change greatly in either proportion or concentration with time or temperature. Per taxon, the top 10 FAs that drove dissimilarity between temperatures or timepoints were consistently primarily those FAs that were highest in amount (proportion or concentration) for that taxon at timepoint t0 (Table S4.1). For kelp samples, this was exclusively true; the FA that made up the top 10 drivers of dissimilarity were the same top 10 highest proportionally and in concentrations. In fish, gumboot, and urchin samples, some FAs that were less concentrated were also included in the top 10 drivers of dissimilarity, including some SAFAs, MUFAs, and a few PUFAs (18:2ω6c/t and 20:3ω3).

In addition to observing this overarching trend of higher-amount FAs being more likely to be within the top 10 FAs contributing to dissimilarity, another trend was observed: for these influential FAs, as their initial amounts at t0 increased, so too did their average contribution to dissimilarity in time or temperature comparisons. This correlation was clearest in fish and gumboot samples, modest in urchin samples, and the least consistent in kelp samples. In gumboot, 16:0 was highly abundant but did not consistently drive dissimilarity, while 18:1ω9c and 20:4ω6 contributed more despite lower abundance. Kelp samples stored at T-80°C contained some abundant FAs (e.g., 20:4ω6) that contributed little or variably to dissimilarity, with no clear relationship to this FA's initial proportion or concentration. Across taxa, the variability in dissimilarity contributions was driven more by FA identity than by timepoint; for example in fish samples, 22:6ω3 contributed a similar amount of dissimilarity to differences between timepoints no matter the timepoint comparison. This suggests that the amount of degradation in FAs is related to some intrinsic properties of the FA such as structure or susceptibility to oxidation. In urchin samples, this positive correlation between initial FA amount and contribution to

dissimilarity was clearer when looking at concentration data rather than proportional data, while for fish samples the opposite was true. In fact, urchin proportional FA data showed almost no correlation while urchin concentration data showed a strong positive linear correlation. Gumboot and kelp samples exhibited weaker correlations in either FA measure. For example, in gumboot, 10 FAs within the list of top 10 drivers of dissimilarity in any time or temperature comparison, all had proportions ranging from 0-8%, yet each contributed approximately the same amount to dissimilarity (3-9%) with no correlation between FA proportion and contribution to dissimilarity.

4. DISCUSSION

4.1. FA profiles remain good indicator of taxonomic identity even after extended sample storage

The observation of distinct FA profiles per taxon was expected given the large taxonomic and trophic differences between taxa sampled (Dalsgaard *et al.*, 2003). Encouragingly, despite the wide variety in sample storage conditions per taxon, these FA profiles remained well separated taxonomically in multidimensional space, with no inter-taxonomic overlap. This suggests that FA composition remains a valuable trait for distinguishing taxa, even in samples stored for long periods of time or at sub-optimal temperatures. This interpretation is caveated by the fact that each taxon was sampled from just one individual and the four taxa were selected with the expectation of disparate FA profiles. Yet, a previous study in which samples of six individuals each of a different fish species were stored at these same temperatures (T-20°C and T-80°C) for up to 6 months still found FA profiles to be inter-taxonomically significantly different (Rudy *et al.*, 2016). Still, in FA studies where there is high individual variability in FA and/or taxa that are very closely related taxonomically, the ability to distinguish taxa by FA profiles may be less robust to storage-related FA degradation.

4.2. Storage duration affected FA more than temperature

Our results are aligned with previous studies suggesting FA degradation occurs progressively over time (reviewed in Couturier *et al.*, 2020), significant changes were observed in FA profiles and individual FAs (in both measures of proportions and concentrations) over time, especially after 2-3 years of storage. The number of individual FAs that were significantly dissimilar in amount from initially extracted samples also increased over time, indicating inter-FA variability in degradation rate with some FA changing quickly, some slowly, and some seemingly not at all. Both the extent and the direction of change depended on the taxon sampled, aligning with previous findings that FA degradation is taxon-specific (e.g., Rudy *et al.*, 2016). Interestingly, the taxon most sensitive to degradation was also our most lipid-poor taxon. Kelp samples stored at T-20°C changed in proportional FA profiles already after 3 months, while our most lipid-rich taxon (urchin) remained proportionally unchanged after 1 year at either temperature. Taxa of medium lipid content (fish and gumboot) remained unchanged after 3 years at either temperature. This is counter to previous findings (Rudy *et al.*, 2016; Sardenne *et al.*, 2019) where sensitivity to FA degradation was correlated with total lipid content. Kelp had a total lipid content of 2.03±0.59% dry weight and so falls well below the limit recommended by Sardenne *et al.* (2019), whereby samples with total lipid content <20% dry weight can be safely stored at T-20°C for up to 3 months without changing proportional FA content. Notably, the study by Sardenne *et al.* (2019) included fishes, crustaceans, and mollusks, but no primary producers, so it is possible this is why kelp was so heavily affected by degradation despite its low lipid content.

4.3. Temperature Effects were relatively small

Compared to the effects of storage duration, the effects of storage temperature on FA profiles was much less pronounced, with kelp being the only taxon significantly changed for any within-timepoint comparison between samples stored at T-20°C vs. T-80°C. Urchin samples were the least affected by temperature, thus repeating the trend observed in storage duration wherein susceptibility to FA degradation correlated negatively with total lipid content, counter to previous findings (Rudy *et al.*, 2016; Sardenne *et al.*, 2019). The more frequently observed effect of degradation due to temperature was the exacerbation of degradation due to time. For example, for any timepoint and taxon, the number of individual FAs that were significantly dissimilar in amount from initially extracted samples were generally higher for samples stored at T-20°C than at T-80°C. This further underscores the inter-FA variability in degradation susceptibility that was seen for temporal comparisons. A previous study (Schmid *et al.*, 2016) of FA degradation in another macroalgae, *Laminaria digitata*, from the same Phaeophyceae class found that dried powdered specimens of this species retained their PUFA content when stored at T-20°C for up to 22 months. This would suggest that the FA degradation seen here in the frozen minced samples of kelp may have been exacerbated by the water content of the samples, which can lead to increased lipid oxidation (Labuza *et al.*, 1972). Yet all samples were frozen as wet tissues, so this would still leave unanswered why kelp was more susceptible to degradation than the three other taxa. Variability in antioxidant content may explain this inter-taxonomic variability in susceptibility to FA degradation, but this was beyond the scope of this study.

4.4. Degradation susceptibility driven by FA identity and abundance

Two factors appeared to be the main determinants of which FAs were most susceptible to degradation: chemical structural features and abundance. Previous work (Lindsay, 1990; Koshio

et al., 1994) identified high levels of PUFAs, as opposed to MUFAs or SAFAs, as making lipids more susceptible to oxidation due to the methylene bridges between double bonds, in which the hydrogen atoms are particularly reactive to free radicals (Shahidi and Zhong, 2005; Shahidi and Zhong, 2010). Our results show some evidence of this; in temporal comparisons, kelp samples stored at T-80°C changed most in PUFA, while fish samples had 22:6ω3 (DHA) as the primary driver of proportional FA dissimilarity for every timepoint comparison at both temperatures. Two PUFAs in particular, 20:5ω3 (EPA) and 20:4ω6 (ARA), were frequently strong drivers of dissimilarity across taxa in SIMPER comparisons of time or temperature storage conditions. However, these PUFA that drove dissimilarity were also those that were most concentrated within the samples at initial extractions. Thus, it is unclear here if it is the structural nature of these FA that led to their high degree of degradation susceptibility or if it was due to their high initial abundance in the samples. Across all taxa, the SAFA 16:0 and MUFA 18:1ω9c were frequently the primary or secondary drivers of dissimilarity in FA profiles in time or temperature comparisons, with these also being the most concentrated SAFA and MUFA in all taxa. We hypothesize that the structural nature of a FA contributes less to its susceptibility to degradation than the abundance of that FA in the sample. Even in fish samples, where PUFA 22:6ω3 was consistently the number one driver of dissimilarity in proportional data, this finding is caveated by the fact that this PUFA was also the most abundant FA in fish, proportionally and in concentrations. This finding of the most abundant FAs also being those whose degradation drives dissimilarity is not surprising if we expect degradation is due to enzymatic activity (e.g., by lipases) that is able to persist in these storage conditions. Enzymatic activity would likely follow Michaelis-Menten kinetics in which the reaction rate increases with substrate concentration, up to a saturation point. Autoxidation is the most common method of lipid oxidation in tissue

samples (Shahidi and Zhong, 2010). In autoxidation too, higher concentrations of FA would be expected to correlate with greater rates of autoxidation due to more substrate available to react with free radicals. As with enzymatic oxidation, PUFA are also expected to be more vulnerable to autoxidation (Shahidi and Zhong, 2010). Thus our findings do not clarify which process is occurring more here, enzymatic oxidation or autoxidation; most likely, both processes are occurring to some extent.

While it was generally true that the abundance of FA correlated with larger contributions to dissimilarity in SIMPER analyses, there were exceptions. MUFAs (16:1ω5c, 18:1ω9t, 20:1ω9, 20:1ω7, and 22:1ω9c/t) often contributed more to dissimilarity than would be expected given their abundances in initially extracted samples. Notably, in these cases, concentrations of PUFAs (e.g., fish: 20:4ω6; gumboot: 22:4ω6, 20:3ω9, 20:2ω6; urchin: 18:4ω3c, 18:3ω3, 18:2ω6c/t) exceeded those of these affected MUFAs, and yet these PUFAs contributed less to dissimilarity. This suggests that it may be MUFAs that are particularly susceptible to degradation, at least in these taxa in these storage conditions. This aligns with findings by Romotowska *et al.* (2017) in which lipid degradation in fishes correlated positively with MUFA content and not PUFA content. Overall, our findings suggest a nuanced understanding of degradation susceptibility in FA, where both chemical structure and relative abundance determine patterns.

Degradation patterns in urchin samples were unique in that nearly every FA increased in concentration with time, with little effect from storage temperature. This seems likely a result of substantial lipase hydrolysis taking place, in which fatty acids are freed from bound pools (e.g., from triacylglycerols (TAG)). The highly linear increase in total FA concentration of urchin samples with time hints again at Michaelis-Menten-like enzymatic activity and that concentrations of FAs are below the saturation point of this relationship.

4.5. FA as proportions vs. concentrations reveal differing degradation patterns

Patterns in FA proportions as compared to those in concentrations were similar on a wider scale, but differed in noticeable ways. Relatively minor differences, such as which FA drives dissimilarity between storage timepoints in fish samples or whether SAFA increased or decreased with time in kelp, were observed when comparing the two FA measures. However, major differences were also observed, such as at what timepoint kelp and urchin samples were significantly different in FA profiles from their original composition. Perhaps the largest difference observed was in the urchin data, where nearly every FA increased in concentration with time, yet proportional data would suggest some FA increased while others decreased. This finding underscores previous work (Mocking *et al.*, 2012) which advises caution in FA data handling, as measurement selection (proportion or concentration) can yield very differing results.

4.6. Implications for trophic studies using FA

Despite within-taxon differences caused by FA degradation, the inter-taxonomic differences in FA profiles held true even across the wide variety of storage conditions. This result suggests that FA data can still be meaningfully interpreted in ecological studies comparing taxa, even under suboptimal sample storage conditions. This is an encouraging finding for researchers who are limited in T-80°C freezer capacity or whose time constraints necessitate long-term storage prior to FA extraction. Given that storage duration drove much more degradation than storing at a moderate (T-20°C) temperature, sampling protocols should prioritize shorter storage periods over retaining samples at deep-freeze (T-80°C) temperatures. Future studies reporting FA measured from archived samples should report not only storage temperatures but also duration and use caution in interpreting FA results, especially for those FA

expected to be most susceptible to degradation, identified here as the most abundant FAs and to a lesser extent also the saturation level (i.e. PUFA and MUFA more than SAFA).

CHAPTER V

CONCLUSION

Commonly regarded as a homogenous and ecologically marginal group, gelatinous zooplankton are often dismissed as nutritionally poor and trophically insignificant components of pelagic food webs. The findings presented in this dissertation challenge that view. Through species-specific case studies, functional group comparisons, and methodological validation, this work highlights the diversity, dynamism, and ecological relevance of gelatinous taxa in a productive eastern boundary upwelling system. It also demonstrates the power and limitations of fatty acid biomarkers as tools for resolving trophic interactions in marine food webs.

In Chapter II, I explored the role of the cosmopolitan ctenophore *Pleurobrachia bachei* in the Northern California Current (NCC) as both predator and prey. Through paired gut content and fatty acid analyses, I discovered that *P. bachei* in the NCC primarily consume copepods, copepod eggs, and invertebrate eggs. This differs from previous studies that describe *P. bachei* as a consumer of primarily motile crustacean prey (Hirota, 1974; Larson, 1987; Purcell, 1990; Purcell and Sturdevant, 2001). Just as critical as its role as a predator, *P. bachei* also functions as an important prey resource in the NCC. I found that essential fatty acids (EFA) consistently comprised nearly half of its total fatty acid content, pointing to the importance of *P. bachei* as a quickly digestible source of concentrated EFA to potential predators. Finally, I demonstrated the seasonal and latitudinal variability in both *P. bachei*'s roles as predator and as prey, emphasizing how the dynamism of the NCC becomes translated into the complex trophic relationships present in this upwelling system.

In Chapter III, I broadened the scope of analysis to compare the trophic ecology of a diverse suite of co-occurring gelatinous zooplankton in the NCC. Using multivariate FA analyses, I first asked whether gelatinous zooplankton could be differentiated from non-gelatinous zooplankton based on FA composition. I found that, as a group, gelatinous zooplankton contained higher proportions of essential fatty acids (EFA) and polyunsaturated fatty acids (PUFA) compared to co-occurring crustaceans and larval fishes. Beyond this finding, categorizing zooplankton as "gelatinous" yielded a group that was highly heterogeneous in FA profiles, as well as in phylogeny and feeding patterns. This underscores the ineffectiveness of lumping all gelatinous zooplankton together as a single group in our characterizations of pelagic food webs (Pauly *et al.*, 2009). The strongest explanatory power for FA-based grouping came from using the lowest possible taxonomic resolution, supporting previous work in inter-taxonomic FA comparisons whereby each taxon exhibits a relatively distinct FA "signature" (Iverson 1993; Hiltunen *et al.*, 2022). I also noted intra-taxonomic seasonal variability in FA profiles across gelatinous taxa, mirroring my findings for *P. bachei* in Chapter II. At higher levels of categorization, I found that grouping gelatinous taxa by phyla, feeding style, and feeding guild all shed further light on the trophic heterogeneity of this diverse suite of organisms. One of the most compelling findings here was that among the gelatinous zooplankton, those taxa that consume primarily soft-bodied prey (i.e. other gelatinous zooplankton or eggs) are generally proportionally richer in PUFA, EFA, and arachidonic acid (ARA), as compared to gelatinous taxa that consume primarily hard-bodied prey. This result offers new insight into the "jelly web," the often-overlooked trophic interactions among gelatinous zooplankton. These findings suggest that gelatinous consumers of other gelatinous taxa may be especially important as prey due to their elevated nutritional quality. Taken together, these findings reinforce the need to include

gelatinous zooplankton in pelagic food web studies not as a single trophic dead end, but as a functionally diverse group of predators and prey with complex, dynamic roles.

Building on the demonstrated power of FA analysis for resolving the trophic roles of gelatinous zooplankton, I used Chapter IV to examine the limitations of this tool in ecological applications. The reliability of FA-based trophic inferences depends critically on sample storage protocols, yet the effect of storing samples in sub-ideal conditions remains unresolved. In Chapter IV, I sought to describe the FA degradation that occurs in organismal tissue based on storage temperature and duration. I discovered that the degree of FA degradation that occurs is highly taxon-specific and is determined more by storage duration than storage temperature. Effects among FA varied and I found that those FA that were most affected were those that were most concentrated upon initial extraction. I also found that PUFA and mono-unsaturated fatty acids were more likely to show degradation effects than saturated fatty acids, which tracks with expectations that higher levels of desaturation make FA more susceptible to oxidation (Couturier *et al.*, 2020). One encouraging result from this study was that even with the high intra-taxonomic variability in FA degradation, the inter-taxonomic differences in FA profiles held true despite the wide variety of storage conditions experienced by tissue aliquots. This suggests that FA data can still be meaningfully interpreted in ecological studies comparing taxa, even under suboptimal sample storage conditions. It provides key methodological validation for interpreting inter-taxonomic FA variation, including in my gelatinous zooplankton comparisons in Chapter III.

By integrating ecological and methodological perspectives, the studies in this dissertation offer new frameworks for understanding the multifaceted roles that gelatinous zooplankton occupy in pelagic ecosystems, as both predators and prey. This work supports recent calls to move beyond viewing gelatinous taxa solely through the lens of caloric content (e.g., Hays *et al.*,

2018), instead emphasizing their nutritional value and highlighting fatty acids as a particularly powerful tool for uncovering these dimensions. These findings are particularly relevant in the context of changing ocean conditions, which are expected to shift the abundance and distribution of gelatinous zooplankton globally (Purcell *et al.*, 2007). Whether as competitors, predators, or prey, gelatinous zooplankton will continue to shape pelagic food webs, and understanding their roles requires methodological rigor and a deeper appreciation of the ecological and functional diversity embodied by this remarkable group of organisms.

APPENDIX I:

SUPPLEMENTAL MATERIALS FOR CHAPTER II

Supplemental Table S2.1. Sampling locations within the Northern California Current. Two transects were sampled: Newport Hydrographic Line (NH) and Trinidad Head line (TR). Each transect was sampled with five stations running longitudinally, where increasing station numbers corresponded to increased distance offshore. Each transect was sampled on four separate 10-day cruises during winter and summer of 2018, and in the winter and summer of 2019.

Transect	**Station number**	**Latitude**	**Longitude**
NH	1	44.65207 N	-124.293611 W
NH	2	44.652324 N	-124.409746 W
NH	3	44.651767 N	-124.648379 W
NH	4	44.651895 N	-124.893101 W
NH	5	44.652247 N	-125.114874 W
TR	1	41.058344 N	-124.271976 W
TR	2	41.05798 N	-124.345573 W
TR	3	41.05867 N	-124.434449 W
TR	4	41.058304 N	-124.587974 W
TR	5	41.057841 N	-124.753291 W

Supplemental Table S2.2. Simper analyses of gut contents. Simper analyses comparing the gut contents of *P. bachei* between seasons (Wi=Winter vs. Su=Summer) and transects (TR vs. NH) yielded the results below. Gut contents were compared across *P. bachei* individuals as counts of each prey taxa per gut. Per group comparison, prey taxa are listed in order of decreasing contribution to the average between-group dissimilarity. Bolded p-values indicate prey taxa that were significantly dissimilar ($p<0.05$) in abundance between the two groups compared.

Simper Comparison		Simper Order	Prey Taxa	Avg Abundance (count/gut)		Contribution to Avg Between-Group Dissimilarity (Avg±Stdv)	Cumulative Contribution to Between-Group Dissimilarity (%, ordered)	p
Group A	Group B			Group A	Group B			
Su	Wi	1	*Egg - copepod*	5.21	4.39	0.302±0.316	37.00	0.230
Su	Wi	2	*Copepod adult*	2.32	2.16	0.205±0.223	62.13	0.135
Su	Wi	3	*Egg - invertebrate*	2.10	1.26	0.161±0.228	81.84	0.817
Su	Wi	4	*Unknown crustacean*	0.33	0.02	0.040±0.117	86.75	0.824
Su	Wi	5	*Chaetognath*	0.11	0.10	0.024±0.077	89.66	0.473
Su	Wi	6	*Copepod nauplius*	0.29	0.00	0.019±0.063	91.98	0.945
Su	Wi	7	*Barnacle larva*	0.03	0.11	0.013±0.055	93.63	0.152
Su	Wi	8	*Appendicularian*	0.02	0.03	0.011±0.062	94.94	0.333
Su	Wi	9	*Euphausiid*	0.09	0.03	0.010±0.046	96.22	0.773
Su	Wi	10	*Doliolid*	0.09	0.00	0.008±0.046	97.25	0.891
Su	Wi	11	*Unknown gelatinous*	0.05	0.00	0.007±0.041	98.11	0.853
Su	Wi	12	*Crab zoea*	0.00	0.03	0.005±0.039	98.73	0.125
Su	Wi	13	*Planula larva*	0.00	0.02	0.004±0.037	99.20	0.298
Su	Wi	14	*Cladoceran*	0.09	0.00	0.004±0.022	99.65	0.845
Su	Wi	15	*Gastropod*	0.00	0.02	0.003±0.026	100.00	0.313
NH	TR	1	*Egg - copepod*	5.57	3.22	0.270±0.304	32.31	0.997
NH	TR	2	*Copepod adult*	1.50	4.11	0.230±0.237	59.83	**0.002**
NH	TR	3	*Egg - invertebrate*	1.81	1.67	0.155±0.224	78.36	0.834
NH	TR	4	*Unknown crustacean*	0.08	0.51	0.058±0.129	85.24	**0.003**
NH	TR	5	*Copepod nauplius*	0.14	0.27	0.024±0.068	88.06	0.207
NH	TR	6	*Chaetognath*	0.12	0.07	0.023±0.077	90.86	0.525
NH	TR	7	*Euphausiid*	0.01	0.20	0.019±0.062	93.10	**0.002**
NH	TR	8	*Doliolid*	0.00	0.18	0.017±0.063	95.13	**0.003**
NH	TR	9	*Appendicularian*	0.02	0.04	0.011±0.063	96.40	0.272
NH	TR	10	*Barnacle larva*	0.09	0.00	0.009±0.045	97.45	0.979
NH	TR	11	*Cladoceran*	0.00	0.18	0.008±0.031	98.36	**0.011**
NH	TR	12	*Unknown gelatinous*	0.03	0.04	0.007±0.038	99.20	0.619
NH	TR	13	*Crab zoea*	0.02	0.00	0.003±0.030	99.55	0.781
NH	TR	14	*Planula larva*	0.01	0.00	0.002±0.029	99.81	0.677
NH	TR	15	*Gastropod*	0.01	0.00	0.002±0.020	100.00	0.695

Supplemental Table S2.3. Simper analyses of fatty acid proportions. Simper analyses comparing the fatty acid profiles of *P. bachei* between seasons (Wi=Winter vs. Su=Summer) and transects (TR vs. NH) yielded the results below. Fatty acids were compared across *P. bachei* samples as proportional contributions of each fatty acid to the total fatty acid concentration per sample. Per group comparison, fatty acids are listed in order of decreasing contribution to the average between-group dissimilarity. Bolded p-values indicate fatty acids that were significantly dissimilar ($p<0.05$) in proportion between the two groups compared.

Simper Comparison		Simper Order	FA	Avg Proportion (% of total FA)		Contribution to Avg Between-Group Dissimilarity (Avg±Stdv)	Cumulative Contribution to Between-Group Dissimiliarity (%, ordered)	p
Group A	Group B			Group A	Group B			
Su	Wi	1	22:6ω3	25.35	27.91	2.58±1.58	19.54	**0.024**
Su	Wi	2	20:5ω3	19.47	15.26	2.31±1.63	37.01	**0.024**
Su	Wi	3	16:0	16.69	18.76	1.10±0.78	45.36	**0.003**
Su	Wi	4	14:0	7.22	6.06	0.84±0.82	51.71	0.62
Su	Wi	5	18:1ω9c	4.26	4.87	0.77±0.56	57.5	0.525
Su	Wi	6	22:1ω9c	2.26	2.17	0.73±0.76	63.01	0.791
Su	Wi	7	16:1ω7c	2.7	1.99	0.67±0.57	68.1	0.5
Su	Wi	8	18:0	8.64	8.18	0.57±0.37	72.38	0.393
Su	Wi	9	18:4ω3c	1.3	1.69	0.37±0.32	75.15	0.696
Su	Wi	10	18:1ω7c	1.32	1.28	0.32±0.24	77.57	0.131
Su	Wi	11	22:1ω11	0.46	0.24	0.21±0.28	79.17	0.636
Su	Wi	12	20:4ω3	0.53	0.9	0.19±0.14	80.6	**0.015**
Su	Wi	13	20:1ω9c	1.05	1.05	0.18±0.17	81.95	0.681
Su	Wi	14	20:4ω6	0.78	0.51	0.18±0.16	83.28	0.553
Su	Wi	15	17:0	0.9	1.16	0.17±0.10	84.53	0.073
Su	Wi	16	22:5ω6	0.28	0.38	0.13±0.08	85.55	**0.041**
Su	Wi	17	18:2ω6c	0.92	1.01	0.13±0.11	86.56	0.548
Su	Wi	18	21:5ω3	0.06	0.24	0.13±0.18	87.55	0.065
Su	Wi	19	16:4ω1	0.05	0.23	0.13±0.20	88.51	0.156
Su	Wi	20	16:2ω4	0.22	0.34	0.12±0.11	89.42	0.237
Su	Wi	21	22:5ω3	0.81	0.77	0.12±0.08	90.3	0.576
Su	Wi	22	18:3ω3	0.81	0.77	0.11±0.07	91.11	0.911
Su	Wi	23	i-17:0	0.28	0.27	0.10±0.09	91.89	0.919
Su	Wi	24	24:1ω9c	0.26	0.36	0.09±0.08	92.58	**0.049**
Su	Wi	25	22:1ω7c	0.21	0.13	0.08±0.05	93.2	0.398
Su	Wi	26	18:2ω4	0.03	0.15	0.08±0.11	93.8	0.065

Su	Wi	27	a-17:0	0.11	0.14	0.07±0.08	94.33	0.47
Su	Wi	28	15:0	0.71	0.77	0.07±0.05	94.83	0.869
Su	Wi	29	20:1ω7	0.33	0.31	0.07±0.05	95.32	0.718
Su	Wi	30	16:1ω9	0.06	0.09	0.06±0.08	95.8	0.339
Su	Wi	31	12:0	0.1	0.18	0.05±0.04	96.21	0.061
Su	Wi	32	16:1ω7t	0.18	0.19	0.05±0.04	96.56	0.943
Su	Wi	33	10:0	0.01	0.09	0.04±0.04	96.88	**0.008**
Su	Wi	34	20:2ω6	0.33	0.28	0.04±0.04	97.2	0.868
Su	Wi	35	18:1ω5t	0.13	0.13	0.04±0.03	97.5	0.463
Su	Wi	36	i-18:0	0.08	0.06	0.03±0.02	97.74	0.302
Su	Wi	37	20:3ω3	0.11	0.09	0.03±0.03	97.98	0.463
Su	Wi	38	16:1ω5c	0.09	0.09	0.03±0.02	98.17	0.951
Su	Wi	39	17:1ω7c	0.03	0.04	0.03±0.03	98.36	0.405
Su	Wi	40	20:1ω11	0.06	0.06	0.03±0.02	98.56	0.541
Su	Wi	41	20:0	0.25	0.24	0.02±0.02	98.73	0.96
Su	Wi	42	20:3ω6	0.05	0.02	0.02±0.01	98.89	0.094
Su	Wi	43	18:1ω9t	0.11	0.11	0.02±0.02	99.04	0.968
Su	Wi	44	18:3ω6	0.05	0.03	0.02±0.01	99.18	0.183
Su	Wi	45	a-15:0	0.07	0.06	0.02±0.01	99.32	0.593
Su	Wi	46	24:1ω9t	0	0.03	0.02±0.03	99.44	**0.001**
Su	Wi	47	13:0	0.08	0.09	0.02±0.01	99.56	0.462
Su	Wi	48	22:0	0.1	0.09	0.01±0.01	99.67	0.981
Su	Wi	49	18:1ω5c	0.04	0.06	0.01±0.01	99.75	0.161
Su	Wi	50	8:0	0	0.02	0.01±0.02	99.81	**0.001**
Su	Wi	51	22:2ω6	0.02	0	0.01±0.02	99.87	0.647
Su	Wi	52	14:1	0.01	0.01	0.01±0.01	99.93	0.336
Su	Wi	53	i-14:0	0.03	0.03	0.01±0.01	99.98	0.933
Su	Wi	54	24:0	0	0	0.00±0.01	100	0.647
NH	TR	1	20:5ω3	16.28	20.74	2.45±1.58	18.87	**0.004**
NH	TR	2	22:6ω3	27.65	23.96	2.45±1.78	37.72	0.093
NH	TR	3	14:0	6.77	6.83	0.91±0.87	44.74	0.341
NH	TR	4	16:0	17.62	17.16	0.79±0.62	50.85	0.949
NH	TR	5	18:1ω9c	4.39	4.65	0.77±0.55	56.8	0.47
NH	TR	6	22:1ω9c	2.33	2.05	0.74±0.81	62.52	0.637
NH	TR	7	16:1ω7c	2.49	2.36	0.63±0.53	67.35	0.892
NH	TR	8	18:0	8.2	8.94	0.61±0.40	72.03	0.119
NH	TR	9	18:4ω3c	1.55	1.26	0.37±0.32	74.85	0.733
NH	TR	10	18:1ω7c	1.19	1.51	0.32±0.22	77.31	0.149
NH	TR	11	22:1ω11	0.53	0.12	0.22±0.30	79.01	0.45

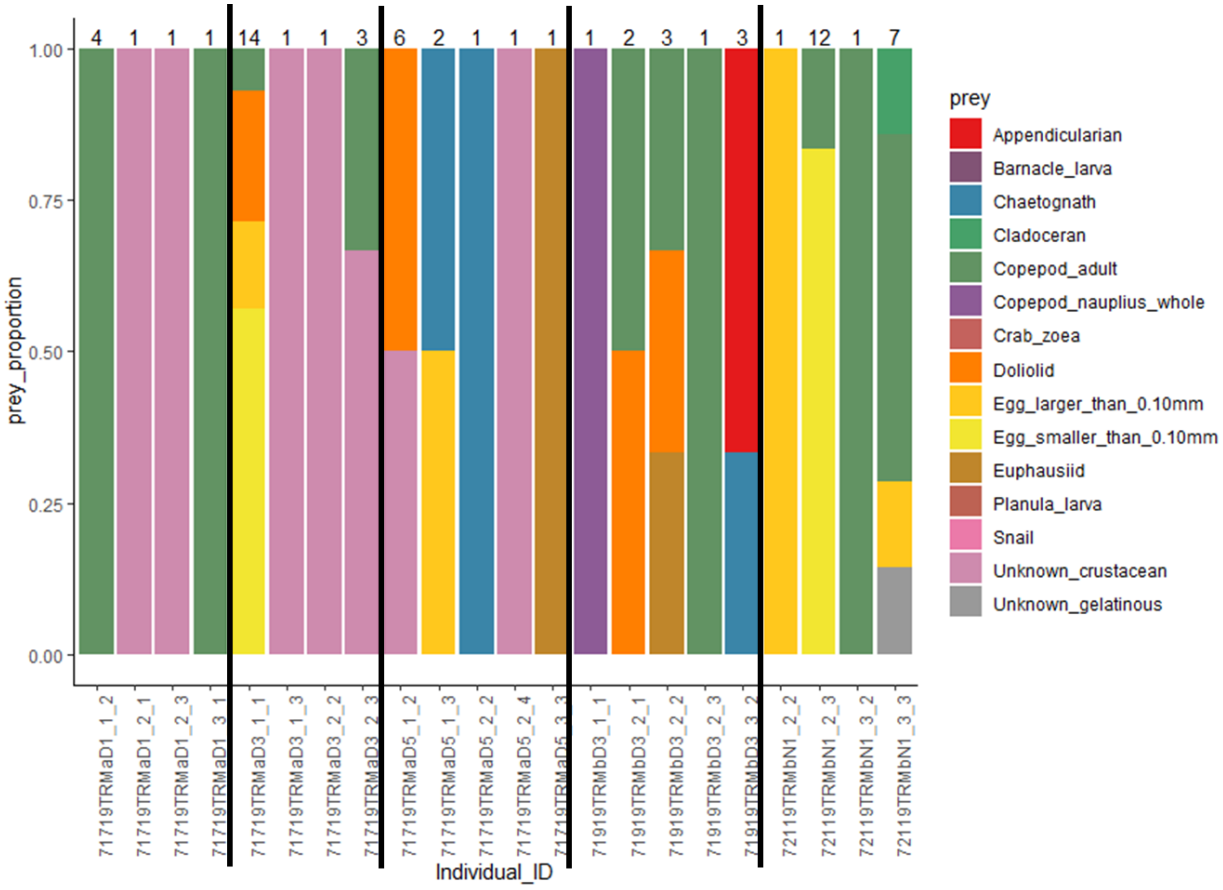
NH	TR	12	20:1ω9c	1.16	0.86	0.19±0.18	80.46	0.464
NH	TR	13	17:0	1.13	0.78	0.19±0.12	81.91	**0.004**
NH	TR	14	20:4ω6	0.68	0.68	0.17±0.13	83.21	0.797
NH	TR	15	18:2ω6c	0.87	1.09	0.16±0.13	84.43	0.062
NH	TR	16	20:4ω3	0.71	0.58	0.16±0.14	85.63	0.472
NH	TR	17	22:5ω3	0.74	0.9	0.13±0.07	86.61	0.083
NH	TR	18	22:5ω6	0.36	0.25	0.12±0.07	87.54	0.304
NH	TR	19	16:2ω4	0.26	0.28	0.12±0.10	88.46	0.323
NH	TR	20	16:4ω1	0.09	0.17	0.12±0.20	89.36	0.291
NH	TR	21	18:3ω3	0.8	0.78	0.11±0.08	90.21	0.688
NH	TR	22	21:5ω3	0.12	0.13	0.11±0.16	91.05	0.452
NH	TR	23	i-17:0	0.27	0.29	0.10±0.09	91.84	0.961
NH	TR	24	22:1ω7c	0.14	0.24	0.09±0.06	92.55	**0.04**
NH	TR	25	15:0	0.78	0.66	0.08±0.05	93.17	**0.023**
NH	TR	26	24:1ω9c	0.3	0.29	0.07±0.07	93.74	0.706
NH	TR	27	20:1ω7	0.3	0.36	0.07±0.06	94.31	0.152
NH	TR	28	a-17:0	0.15	0.08	0.07±0.08	94.82	0.902
NH	TR	29	18:2ω4	0.06	0.08	0.06±0.10	95.31	0.313
NH	TR	30	20:2ω6	0.27	0.38	0.06±0.04	95.79	**0.001**
NH	TR	31	16:1ω9	0.09	0.06	0.06±0.09	96.24	0.757
NH	TR	32	16:1ω7t	0.2	0.17	0.05±0.04	96.61	0.762
NH	TR	33	12:0	0.14	0.11	0.05±0.04	96.97	0.518
NH	TR	34	18:1ω5t	0.14	0.11	0.04±0.03	97.27	0.679
NH	TR	35	i-18:0	0.07	0.09	0.03±0.03	97.52	0.233
NH	TR	36	20:3ω3	0.09	0.12	0.03±0.02	97.76	0.319
NH	TR	37	10:0	0.06	0.01	0.03±0.04	97.97	0.892
NH	TR	38	16:1ω5c	0.1	0.07	0.03±0.02	98.18	0.65
NH	TR	39	20:1ω11	0.07	0.03	0.03±0.02	98.38	0.602
NH	TR	40	20:0	0.26	0.23	0.02±0.02	98.57	0.562
NH	TR	41	17:1ω7c	0.04	0.02	0.02±0.03	98.75	0.851
NH	TR	42	18:1ω9t	0.11	0.1	0.02±0.02	98.92	0.449
NH	TR	43	20:3ω6	0.03	0.05	0.02±0.01	99.08	0.246
NH	TR	44	a-15:0	0.07	0.06	0.02±0.01	99.21	0.633
NH	TR	45	18:3ω6	0.04	0.05	0.02±0.01	99.34	0.926
NH	TR	46	22:0	0.1	0.08	0.02±0.01	99.46	0.628
NH	TR	47	13:0	0.08	0.09	0.02±0.01	99.58	0.646
NH	TR	48	24:1ω9t	0.01	0.02	0.01±0.03	99.68	0.125
NH	TR	49	18:1ω5c	0.05	0.04	0.01±0.01	99.76	0.346
NH	TR	50	22:2ω6	0.01	0.01	0.01±0.02	99.83	0.384

NH	TR	51	i-14:0	0.03	0.02	0.01±0.01	99.89	0.521
NH	TR	52	14:1	0.01	0	0.01±0.01	99.94	0.83
NH	TR	53	8:0	0.01	0	0.00±0.02	99.98	0.385
NH	TR	54	24:0	0	0	0.00±0.01	100	0.384

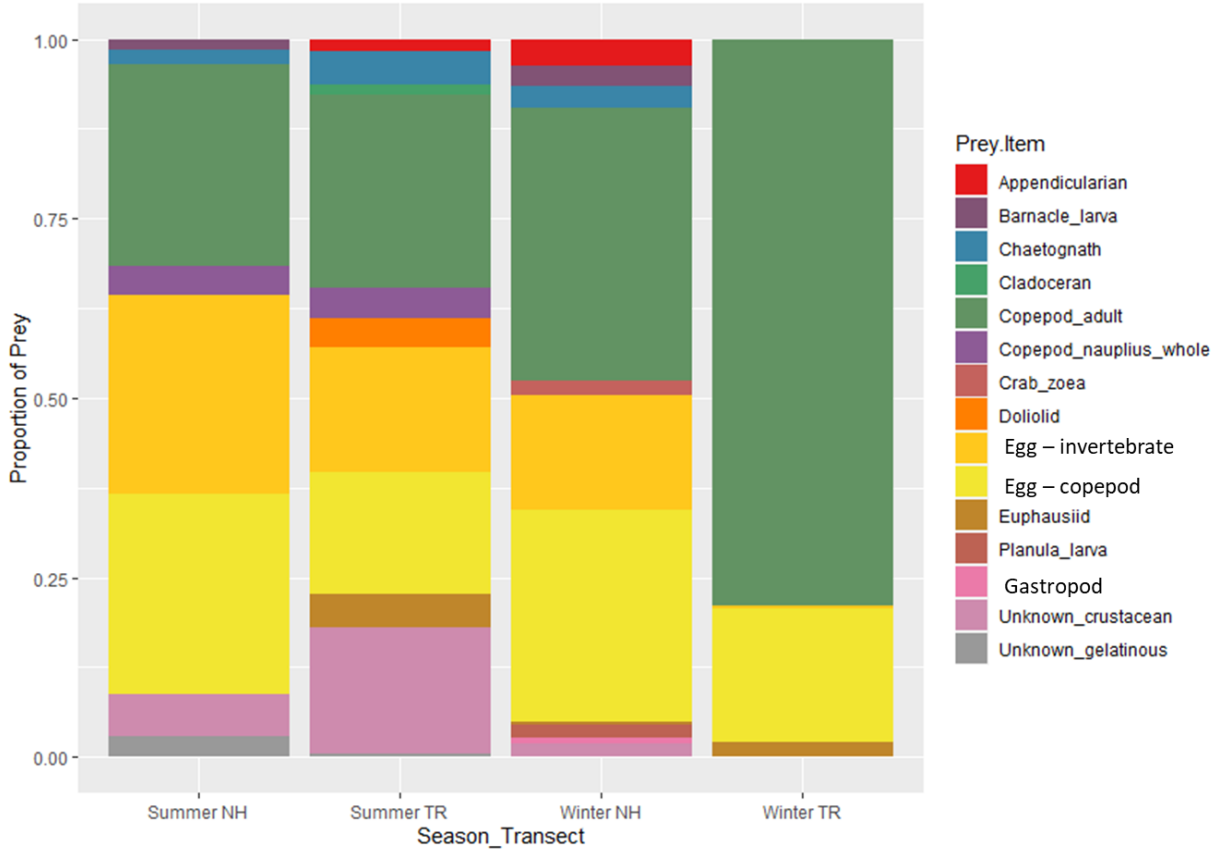
Supplemental Table S2.4. Carbon conversion rates used per prey category. Included are assumptions made in selecting these values as well as referenced sources: (a) King *et al.*, 1980, (b) Canino and Grant, 1984, (c) Larson, 1987, (d) Martinussen and Båmstedt, 1995, (e) Suchman *et al.*, 2008, and (f) Corrales-Ugalde *et al.*, 2021.

Prey Taxa	**µg C / ind**	**Sources**	**Assumptions**
Appendicularian	0.5	a	Same as *Oikopleura dioica* with trunk length 500 µm
Barnacle larva	0.5	c	
Chaetognath	6.64	b	Similar to *Sagitta tenuis*, size class 4.0-4.99 mm
Cladoceran	1	d	
Copepod adult	3	d	
Copepod nauplius	0.1	c	
Crab zoea	10	d	
Doliolid	1.86	d	Same as *Oikopleura* sp.
Egg - copepod	0.1	f	Assume eggs sized < 100 µm are copepod eggs
Egg - invertebrate	3.2	f	Assume eggs sized > 100 µm are invertebrate eggs with carbon content similar to euphausiid eggs
Euphausiid	10	d	Same as mysid shrimp sized 1.5 mm
Gastropod	0.2	d, e	
Planula larva	0.443	d	Same as unidentified medusa with diameter 1 mm
Unknown crustacean	3	d	Assume same as copepod adult (likely majority)
Unknown gelatinous	2	d, e	

Supplemental Figure S2.1. Gut contents of *P. bachei* individuals from summer 2019 sampling of TR transect. Each stacked bar represents the gut contents of one *P. bachei* individual. Sampling events are separated by vertical black lines. Numbers on top give the total number of prey items per individual's gut. In Individual_ID along the x-axis, the following designations are made: date sample was collected (e.g., 71719), transect sampled (TR), first or second sampling of transect (Ma/Mb), collected during the day or night (D/N), station number sampled (1/3/5), and preservation jar identifiers (e.g., 1_3).



Supplemental Figure S2.2. Proportional contribution of each prey taxa to *P. bachei* gut contents. Proportions are given in measure of counts of prey individuals per total number of prey items per gut. Data is split to compare *P. bachei* sampled from different transects in different seasons (Summer NH n=55; Summer TR n=39; Winter NH = n=55; Winter TR n=6).

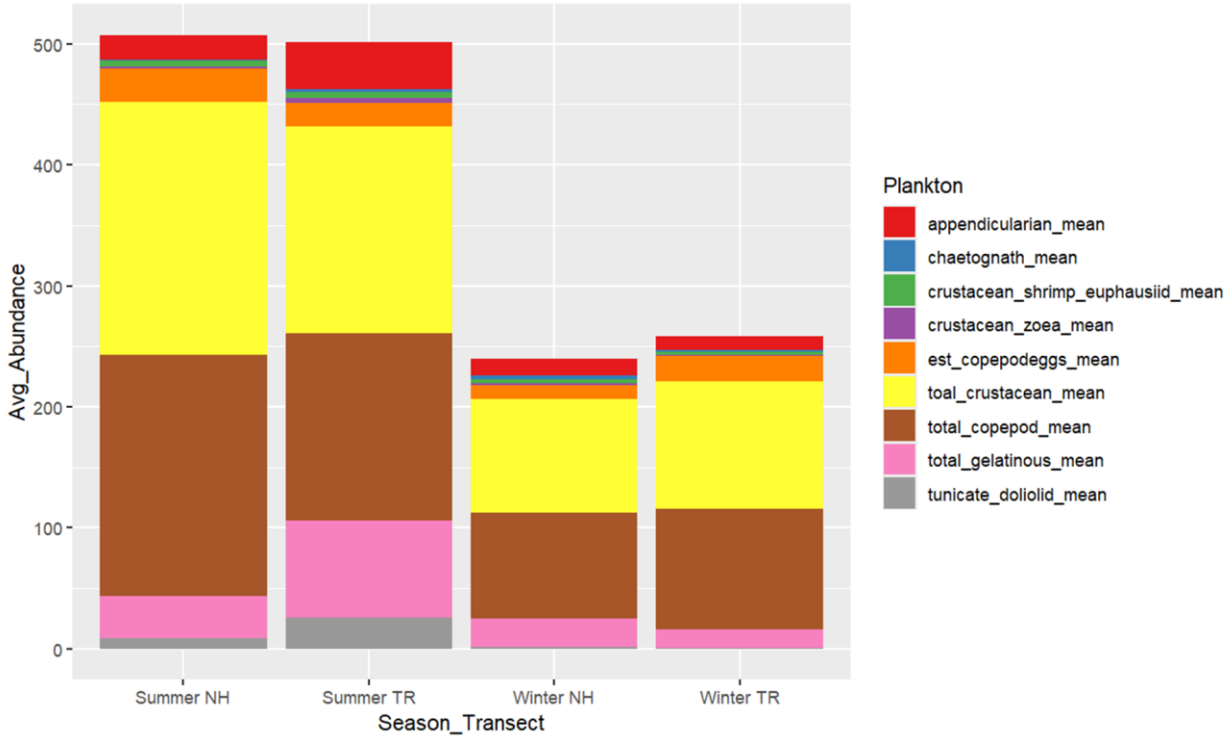


Supplemental Figure S2.3. Estimates of *P. bachei* prey abundance. Collected concurrently with our MOCNESS net sampling were plankton abundance estimates via underwater imaging using the In-situ Ichthyoplankton Imaging System (ISIIS). This system was run along the same transects during the same cruises with one notable difference being that ISIIS sampled depths 0-100m, while our MOCNESS system sampled only 0-25m. From the published ISIIS results (Supplementary Table 1 in Schmid *et al.*, 2023), we plotted the abundance of *P. bachei* and its prey through space and time, concurrent with our net collections. Schmid *et al.* (2023) combined all cydippid ctenophores imaged into one group, yet we may assume this group is dominated by *P. bachei*, based on personal observations and known relative abundances of cydippid ctenophores in the NCC. Copepod eggs were also not measured directly by Schmid *et al.* (2023), but the authors did record abundances of *Oithona* spp. carrying egg sacs; we used this to estimate the abundance of small eggs under the following assumptions: 1) each *Oithona* spp. female carries an average of 20 eggs (Ward and Hirst, 2007), 2) *Oithona* spp. are the primary contributors of copepod eggs during our cruises, and 3) the small (<100 μm diameter) eggs found in *P. bachei* guts are copepod eggs.

Of the observed prey of *P. bachei* found through our gut content analyses, the following nine taxa were estimated in abundance from Schmid *et al.* (2023): appendicularians, chaetognaths, euphausiids, crab zoea, doliolids, copepods, small eggs, total crustaceans, and total gelatinous zooplankton. Overall abundance of these potential prey items varied greatly between seasons, with summer exhibiting approximately double the total abundance of potential prey observed in winter (504±65 vs. 249±149 ind m^{-3}, respectively). This total prey abundance did not vary with transect (NH: 400±149 ind m^{-3}; TR: 404±184 ind m^{-3}). This observed double abundance in summer vs. winter and consistent abundance between transects held true even when comparing transects within each season or comparing seasons per transect.

Of the nine potential prey taxa measured in Schmid *et al.* (2023), all were found to be significantly (Asymptotic Wilcoxon-Mann-Whitney Test, $p<0.05$) more abundant in summer as compared to winter except chaetognaths and euphausiids which were both consistently abundant between seasons. In comparing transects with both seasons combined, no prey taxa were found to be significantly different in abundance between NH and TR transects. However, within summer samples, appendicularians, crab zoea, doliolids, and total gelatinous zooplankton were all significantly more abundant in the TR transect as compared to NH transect, while copepods

and small eggs were significantly more abundant in NH vs. TR. Within winter samples, potential prey abundances were more consistent between transects, with only chaetognaths and doliolids being significantly more abundant in NH vs. TR transects.



CHAPTER II: SUPPLEMENTAL MATERIAL REFERENCES

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APPENDIX II:

SUPPLEMENTAL MATERIALS FOR CHAPTER III

Supplemental Table S3.1. Averages of FA proportions per plankton category. Forty-six unique fatty acids (FA) found in zooplankton samples, listed in order of increasing desaturation and elongation, followed by FA summations: SAFA (saturated fatty acids), MUFA (monounsaturated fatty acids), PUFA (polyunsaturated fatty acids), SUM(EPA_DHA_ARA) (essential fatty acids), SUM(ALA_LA), SUM(Branched_OddC), and SUM(Calanoid_markers). Each result is the percent contribution of that FA to the overall FA content, averaged across samples with standard deviations. Samples are categorized according to plankton categories: Gelatinous, Crustacean, or Fish.

FA	Gelatinous	Crustacean	Fish
C8:0	0.02±0.12	0±0.01	0±0
C9:0	0.06±0.17	0.09±0.25	0.01±0.02
C10:0	0.03±0.06	0.02±0.03	0.02±0.02
C11:0	0.01±0.01	0±0.01	0.01±0.01
C12:0	0.28±0.4	0.15±0.2	0.41±0.58
C13:0	0.07±0.06	0.04±0.03	0.04±0.04
C14:0	5.83±2.72	4.95±3.58	2.79±1.25
C15:0	1.06±0.56	0.6±0.3	0.91±0.38
Ca-15:0	0.1±0.09	0.05±0.04	0.05±0.04
Ci-15:0	0.28±0.24	0.17±0.12	0.15±0.07
C16:0	16.84±3.2	20.43±4.62	25.18±8.4
C17:0	0.99±0.52	0.56±0.28	0.98±0.37
Ca-17:0	0.22±0.2	0.07±0.05	0.14±0.06
Ci-17:0	0.49±0.26	0.25±0.21	0.28±0.13
C18:0	6.15±2.83	3.71±2.47	10.44±4.81
C20:0	0.45±0.32	0.18±0.13	0.42±0.39
C22:0	0.23±0.24	0.11±0.04	0.26±0.32
C23:0	0.06±0.12	0.01±0.01	0.05±0.13
C24:0	0.14±0.2	0.05±0.04	0.18±0.25
C14:1ω5	0.05±0.05	0.05±0.05	0.03±0.04
C16:1ω7c	4.48±2.25	4.83±2.92	2.29±2.03
C17:1ω7c	0.04±0.04	0.04±0.04	0.03±0.02
C18:1ω7c	2.19±1.21	3.63±1.8	2.29±1.21
C18:1ω9c	5.73±3.83	10.22±6.41	9±6.47
C20:1ω9c	1.32±0.65	1.29±1.46	0.95±0.66
C20:1ω11	0.14±0.11	0.46±0.84	0.05±0.06
C22:1ω9c	3.14±2.81	2.06±2.72	5.3±7.65
C22:1ω11	0.29±0.62	1±1.99	0.06±0.08
C24:1ω9c	1.05±1.49	0.91±0.84	0.9±0.59

C16:4ω1	0.35±0.63	0.77±0.99	0.08±0.12
C18:2ω6c	1.65±0.96	1.82±0.77	1.77±0.5
C18:3ω3	1.42±1	1.35±0.92	0.88±0.33
C18:3ω6	0.11±0.1	0.11±0.06	0.06±0.05
C18:4ω3c	2.48±2.06	3.09±2.28	1.77±0.92
C20:2ω6	0.38±0.34	0.21±0.1	0.18±0.09
C20:3ω3	0.18±0.22	0.13±0.11	0.12±0.09
C20:3ω6	0.11±0.09	0.06±0.04	0.03±0.04
C20:4ω6	2.27±3.21	1.04±0.72	0.77±0.46
C20:5ω3	16.09±3.9	17.66±5.58	9.4±4.02
C21:5ω3	0.41±0.3	0.41±0.21	0.26±0.15
C22:2ω6	0.07±0.08	0.02±0.03	0.06±0.09
C22:3ω6	0.03±0.05	0.02±0.05	0.03±0.04
C22:4ω6	0.1±0.21	0.01±0.01	0.03±0.04
C22:5ω3	0.85±0.38	0.66±0.34	0.9±0.56
C22:5ω6	0.84±1.14	0.22±0.21	0.25±0.14
C22:6ω3	20.95±5.67	16.5±6.14	20.16±7.37
SAFA	33.31±5.08	31.43±7.56	42.34±14.52
MUFA	18.42±6.7	24.49±8.23	20.91±10.89
PUFA	48.26±7.06	44.08±11.22	36.75±12.45
SUM(EPA_DHA_ARA)	39.3±6.36	35.21±10.07	30.33±11.06
SUM(ALA_LA)	3.06±1.75	3.17±1.53	2.65±0.71
SUM(Branched_OddC)	3.79±1.3	2.27±0.94	2.92±0.9
SUM(Calanoid_markers)	4.89±3.01	4.81±5.14	6.36±7.96

Supplemental Table S3.2. SIMPER analyses of fatty acid profiles of all zooplankton separated by plankton categories. SIMPER analyses compared the fatty acid (FA) profiles of all zooplankton, including gelatinous and non-gelatinous, between the following plankton categories: gelatinous (G), crustacean (C), and fish (F). FA profiles were compared across samples as proportional contributions of each FA to the total FA concentration per sample. Per group comparison, the top 10 FAs contributing to dissimilarity are listed in order of decreasing contribution to the average between-group dissimilarity. Bolded p-values indicate FAs that were significantly dissimilar ($p<0.05$) in proportion between the two groups compared.

Plankton Category		SIMPER Order	FA	Avg Proportion (% of total FA)		Contribution to Avg Between-Group Dissimilarity (Avg±Stdv)	Cumulative Contribution to Between-Group Dissimiliarity (%, ordered)	p
Group A	Group B			Group A	Group B			
C	F	1	C20:5ω3	17.66	9.4	4.51±2.88	14.31	**0.001**
C	F	2	C22:6ω3	16.5	20.16	4.2±2.86	27.63	**0.001**
C	F	3	C16:0	20.43	25.18	3.87±3.63	39.88	**0.001**
C	F	4	C18:0	3.71	10.44	3.53±2.45	51.06	**0.001**
C	F	5	C18:1ω9c	10.22	9	2.65±3.69	59.47	0.249
C	F	6	C22:1ω9c	2.06	5.3	2.48±3.55	67.32	**0.002**
C	F	7	C16:1ω7c	4.83	2.29	1.65±1.41	72.55	**0.001**
C	F	8	C14:0	4.95	2.79	1.45±1.61	77.15	0.915
C	F	9	C18:1ω7c	3.63	2.29	1.05±0.71	80.47	**0.001**
C	F	10	C18:4ω3c	3.09	1.77	1.01±0.95	83.67	0.264
C	G	1	C22:6ω3	16.5	20.95	3.86±2.7	13.86	**0.021**
C	G	2	C18:1ω9c	10.22	5.73	3.09±3.03	24.96	**0.001**
C	G	3	C20:5ω3	17.66	16.09	2.82±2.02	35.08	0.761
C	G	4	C16:0	20.43	16.84	2.68±1.95	44.69	0.965
C	G	5	C18:0	3.71	6.15	1.82±1.29	51.22	0.996
C	G	6	C14:0	4.95	5.83	1.79±1.4	57.64	**0.007**
C	G	7	C16:1ω7c	4.83	4.48	1.41±1.18	62.7	0.417
C	G	8	C22:1ω9c	2.06	3.14	1.38±1.47	67.64	0.991
C	G	9	C18:4ω3c	3.09	2.48	1.13±1.06	71.71	**0.003**
C	G	10	C18:1ω7c	3.63	2.19	1.07±0.72	75.56	**0.001**
F	G	1	C16:0	25.18	16.84	4.71±3.87	15.79	**0.001**
F	G	2	C22:6ω3	20.16	20.95	3.68±2.81	28.1	0.323
F	G	3	C20:5ω3	9.4	16.09	3.62±2.41	40.22	**0.001**
F	G	4	C18:0	10.44	6.15	2.61±2.33	48.97	**0.001**
F	G	5	C18:1ω9c	9	5.73	2.46±3.23	57.21	0.397
F	G	6	C22:1ω9c	5.3	3.14	2.37±3.43	65.17	**0.001**
F	G	7	C14:0	2.79	5.83	1.73±1.24	70.96	0.071
F	G	8	C16:1ω7c	2.29	4.48	1.5±1.1	75.97	0.054
F	G	9	C20:4ω6	0.77	2.27	0.89±1.54	78.95	0.735
F	G	10	C18:4ω3c	1.77	2.48	0.76±0.9	81.48	0.998

Supplemental Table S3.3 – part 1. Averages of FA proportions per gelatinous taxon. Forty-six unique fatty acids (FA) found in gelatinous zooplankton samples, listed in order of increasing desaturation and elongation, followed by FA summations: SAFA (saturated fatty acids), MUFA (monounsaturated fatty acids), PUFA (polyunsaturated fatty acids), SUM(EPA_DHA_ARA) (essential fatty acids), SUM(ALA_LA), SUM(Branched_OddC), and SUM(Calanoid_markers). Each result is the percent contribution of that FA to the overall FA content, averaged across samples with standard deviations. Samples are categorized according to taxon (lowest level of taxonomic identification possible).

FA	***Aequorea* sp.**	**Appendicularia**	***Beroe* sp.**	**Chaetognatha**	***Clytia* sp.**	**Doliolida**	***Eutonina* sp.**	***Mitrocoma* sp.**
Sample size (n)	**4**	**6**	**7**	**36**	**9**	**9**	**2**	**4**
C8:0	0±0	0.02±0.05	0±0.01	0.05±0.23	0±0	0.01±0.01	0±0	0.01±0.02
C9:0	0.08±0.07	0.06±0.07	0.02±0.03	0.08±0.13	0.01±0.01	0.07±0.04	0.04±0.03	0.03±0.06
C10:0	0.01±0.01	0.09±0.09	0.01±0.01	0.03±0.05	0.02±0.01	0.04±0.03	0.06±0.05	0.02±0.01
C11:0	0.01±0	0.02±0.02	0±0	0.01±0.01	0.01±0.01	0.03±0.01	0.04±0.02	0.01±0
C12:0	0.07±0.03	0.78±0.6	0.2±0.08	0.19±0.23	0.25±0.21	0.29±0.3	0.49±0.33	0.12±0.02
C13:0	0.04±0.01	0.16±0.07	0.08±0.07	0.02±0.01	0.06±0.02	0.11±0.03	0.07±0.02	0.1±0.07
C14:0	6.3±1.22	7.72±1.09	7.24±1.52	3.26±1.43	5.88±0.84	11.67±2.16	6.68±0.64	6.6±0.38
C15:0	1.03±0.21	1.21±0.31	0.63±0.45	0.74±0.26	1.84±0.67	2.04±0.36	1.37±0.11	1.69±0.72
Ca-15:0	0.03±0.01	0.17±0.08	0.05±0.02	0.07±0.03	0.08±0.03	0.34±0.08	0.07±0	0.09±0.01
Ci-15:0	0.41±0.17	0.46±0.16	0.12±0.03	0.2±0.09	0.35±0.09	0.9±0.13	0.47±0.02	0.63±0.08
C16:0	11.32±1.13	20.06±4.71	12.34±1.34	17.63±2.23	17.24±3.46	16.29±2.36	11.26±0.17	11.76±1.35
C17:0	0.51±0.05	0.39±0.09	1.03±0.85	1.37±0.37	0.6±0.15	0.73±0.13	0.72±0.06	0.64±0.21
Ca-17:0	0.39±0.12	0.05±0.03	0.06±0.05	0.16±0.06	0.38±0.15	0.12±0.01	0.43±0.03	0.46±0.12
Ci-17:0	0.69±0.18	0.14±0.05	0.35±0.18	0.52±0.15	0.72±0.23	0.52±0.05	0.52±0	0.65±0.09
C18:0	9.49±1.52	2.79±2.7	6.99±2.84	5.79±1.23	7.5±2.03	2.42±0.91	10.4±0.34	6.77±0.7
C20:0	0.79±0.37	0.32±0.38	0.33±0.42	0.6±0.33	0.76±0.35	0.34±0.11	0.57±0.26	0.69±0.16
C22:0	0.11±0.06	0.24±0.31	0.07±0.06	0.47±0.3	0.17±0.06	0.23±0.06	0.14±0.01	0.23±0.06
C23:0	0±0	0±0	0±0	0.15±0.2	0.09±0.11	0.03±0.01	0±0.01	0.03±0.03
C24:0	0.03±0.01	0.12±0.2	0.03±0.03	0.27±0.25	0.11±0.1	0.08±0.04	0.09±0.03	0.08±0.03
C14:1ω5	0.01±0.01	0.05±0.05	0.05±0.02	0.08±0.05	0.03±0.02	0.05±0.03	0±0	0.04±0.01
C16:1ω7c	2.47±0.22	3.97±0.63	5.92±3.4	6.22±1.27	4.69±2.19	5.24±1.56	2.37±0.24	2.96±0.51
C17:1ω7c	0.02±0	0.07±0.04	0.02±0.01	0.03±0.01	0.05±0.02	0.04±0.02	0.04±0.01	0.04±0.01
C18:1ω7c	1.78±0.08	2.37±0.58	1.32±0.15	2.04±0.54	3.61±0.93	5.04±1.7	1.65±0.09	1.97±0.3
C18:1ω9c	5.18±0.22	4.12±2.34	8.94±2.6	7.09±2.63	3.96±1.08	3.83±0.6	2.8±0.05	3.3±0.97
C20:1ω9c	2.26±0.18	0.68±0.48	2.57±0.86	1.38±0.45	0.97±0.29	0.9±0.27	1.32±0.12	2.67±0.45
C20:1ω11	0.19±0.04	0.05±0.08	0.22±0.11	0.14±0.07	0.15±0.04	0.08±0.02	0.07±0	0.13±0.02
C22:1ω9c	2.87±0.3	8.93±7.52	2.22±0.96	2.73±1.42	3.12±1.37	2.56±1.72	2.41±0.04	2.25±0.72
C22:1ω11	0.57±0.52	0.14±0.2	2.09±1.66	0.14±0.14	0.23±0.17	0.09±0.05	0.24±0.01	0.53±0.31
C24:1ω9c	0.17±0.08	0.24±0.2	0.14±0.04	3.18±1.42	0.39±0.13	0.11±0.04	0.2±0.04	0.57±0.22

C16:4ω1	0.19±0.13	0.09±0.04	1.17±1.12	0.07±0.08	0.56±0.48	0.1±0.15	0±0	0±0
C18:2ω6c	0.52±0.18	2.84±0.62	1.04±0.4	1.64±0.45	1.08±0.23	4.15±0.74	0.93±0.14	0.86±0.22
C18:3ω3	0.36±0.14	4.51±2.04	1.04±0.58	1.41±0.47	1.01±0.55	2.01±0.35	1.04±0.08	0.96±0.23
C18:3ω6	0.04±0.01	0.13±0.07	0.11±0.05	0.07±0.04	0.1±0.04	0.38±0.13	0.07±0	0.07±0.01
C18:4ω3c	0.63±0.31	6.47±3.13	1.54±0.55	1.53±0.67	2.3±1.3	2.59±0.78	2.66±0.48	2.09±0.49
C20:2ω6	0.28±0.08	0.07±0.04	0.45±0.36	0.24±0.06	0.31±0.08	0.28±0.07	0.47±0.02	0.58±0.32
C20:3ω3	0.06±0.02	0.04±0.02	0.16±0.15	0.17±0.08	0.12±0.05	0.1±0.02	0.17±0.03	0.25±0.18
C20:3ω6	0.14±0.01	0.02±0.02	0.11±0.03	0.06±0.04	0.16±0.07	0.34±0.12	0.16±0.01	0.18±0.13
C20:4ω6	11.21±0.63	0.4±0.11	1.23±0.35	0.76±0.24	6.06±2.17	2.38±0.87	11.1±1.71	13.46±0.64
C20:5ω3	16.47±0.74	13.27±5.55	20.66±4.12	14.23±2.46	17.58±2.3	14.2±1.54	14.78±1.39	14.49±2.08
C21:5ω3	0.3±0.1	0.18±0.07	0.56±0.1	0.36±0.11	0.3±0.08	0.71±0.32	0.23±0.03	0.24±0.04
C22:2ω6	0.04±0.01	0.12±0.1	0.05±0.05	0.08±0.02	0.06±0.02	0.04±0.02	0.07±0.01	0.09±0.05
C22:3ω6	0.02±0.02	0.02±0.02	0.01±0.01	0.06±0.04	0.01±0.01	0.02±0.01	0±0	0±0
C22:4ω6	0.43±0.09	0±0.01	0.04±0.01	0.02±0.02	0.22±0.09	0.04±0.03	0.67±0.11	0.73±0.07
C22:5ω3	1.47±0.46	0.31±0.09	0.81±0.13	0.63±0.14	1.12±0.37	1±0.27	1.14±0.12	1.75±0.17
C22:5ω6	3.53±0.37	0.33±0.16	0.36±0.22	0.42±0.15	2.18±0.66	0.21±0.05	4.46±0.41	4.92±0.87
C22:6ω3	17.48±2.78	15.79±7.43	17.63±4.32	23.62±2.12	13.57±2.11	17.28±2.03	17.51±2.76	14.25±1.8
SAFA	31.31±3.11	34.8±10.13	29.55±4.63	31.6±4.62	36.05±1.88	36.24±4.72	33.43±1.39	30.61±0.81
MUFA	15.52±0.64	20.61±10.83	23.47±6.06	23.04±4.33	17.2±3.95	17.94±1.81	11.1±0.06	14.46±2.64
PUFA	53.17±3.03	44.59±18.38	46.97±3.47	45.36±3.4	46.74±4.48	45.81±4.3	55.46±1.33	54.93±3.02
SUM (EPA +DHA +ARA)	45.17±3.45	29.46±12.9	39.52±3.72	38.61±2.96	37.21±2.93	33.87±2.47	43.39±2.44	42.2±0.98
SUM (ALA +LA)	0.87±0.32	7.35±2.33	2.08±0.95	3.05±0.85	2.09±0.74	6.16±1.04	1.97±0.22	1.82±0.45
SUM (Branched +OddC)	3.52±0.73	2.91±0.75	2.91±1.51	3.7±0.8	4.48±1.12	5.62±0.5	4.01±0.12	4.61±1.25
SUM (Calanoid markers)	5.88±0.53	9.79±8.03	7.09±2.34	4.39±1.67	4.48±1.6	3.63±1.89	4.04±0.18	5.59±0.98

Supplemental Table S3.3 – part 2. Averages of FA proportions per gelatinous taxon. Forty-six unique fatty acids (FA) found in gelatinous zooplankton samples, listed in order of increasing desaturation and elongation, followed by FA summations: SAFA (saturated fatty acids), MUFA (monounsaturated fatty acids), PUFA (polyunsaturated fatty acids), SUM(EPA_DHA_ARA) (essential fatty acids), SUM(ALA_LA), SUM(Branched_OddC), and SUM(Calanoid_markers). Each result is the percent contribution of that FA to the overall FA content, averaged across samples with standard deviations. Samples are categorized according to taxon (lowest level of taxonomic identification possible).

FA	***Pleurobrachia bachei***	**Pteropod Gymnosomata**	**Pteropod Thecosomata**	***Pyrosoma atlanticum***	**Salpidae**	**Siphonophorae Calycophorae**	**Siphonophorae Physonectae**	***Tomopteris* sp.**
Sample size (n)	**19**	**2**	**7**	**3**	**8**	**11**	**3**	**5**
C8:0	0.01±0.03	0±0	0±0.01	0.01±0.02	0.01±0.02	0.01±0.04	0±0	0.01±0.02
C9:0	0±0	0.01±0.01	0.05±0.06	0.14±0.13	0.08±0.12	0.17±0.5	0.05±0.06	0.14±0.12
C10:0	0.04±0.07	0.01±0.01	0.01±0.01	0.13±0.16	0.03±0.02	0.04±0.09	0.02±0.02	0.02±0.01
C11:0	0±0	0±0	0±0	0.04±0.04	0.01±0	0.01±0.01	0.01±0.01	0.02±0.01
C12:0	0.14±0.09	0.1±0.04	0.19±0.03	0.98±1.19	0.18±0.11	0.23±0.27	0.17±0.15	1.44±0.58
C13:0	0.09±0.03	0.04±0	0.08±0.01	0.14±0.11	0.06±0.02	0.04±0.02	0.04±0.02	0.18±0.09
C14:0	6.94±1.66	3.25±0.22	7.91±1.55	7.56±0.67	5.17±1.77	5.34±1.71	6.95±1.7	2.47±0.24
C15:0	0.75±0.13	1.67±0.02	0.95±0.12	1.7±0.39	1.62±0.36	0.69±0.31	0.77±0.2	0.9±0.2
Ca-15:0	0.07±0.03	0.04±0	0.07±0.01	0.2±0.09	0.17±0.11	0.09±0.03	0.06±0.03	0.04±0.02
Ci-15:0	0±0	0.24±0.03	0.27±0.06	0.41±0.03	0.28±0.16	0.29±0.1	0.41±0.07	0.14±0.04
C16:0	17.85±1.58	17.59±2.62	19.45±1.8	18.39±1.64	17.69±3.06	15.82±3.47	15.79±2.26	17.4±3.1
C17:0	1.02±0.27	2.41±0.24	0.52±0.08	0.69±0.1	0.95±0.2	0.65±0.32	0.81±0.1	1.97±0.61
Ca-17:0	0.13±0.16	1.01±0.13	0.64±0.1	0.11±0.02	0.16±0.05	0.21±0.12	0.16±0.04	0.21±0.11
Ci-17:0	0.29±0.21	0.61±0.11	0.65±0.16	0.9±0.05	0.87±0.26	0.13±0.04	0.29±0.02	0.62±0.24
C18:0	8.67±0.99	4.61±0.52	2.8±0.32	2.02±0.42	2.96±0.99	9.27±3	7.6±2.27	6.54±1.63
C20:0	0.25±0.05	0.11±0.01	0.11±0.02	0.47±0.11	0.46±0.33	0.41±0.31	0.29±0.04	0.29±0.06
C22:0	0.1±0.03	0.07±0	0.09±0.04	0.15±0.04	0.14±0.09	0.2±0.24	0.09±0.05	0.14±0.04
C23:0	0±0	0.04±0.04	0.01±0.01	0.03±0.01	0.02±0.01	0.01±0.01	0.02±0.01	0.05±0.06
C24:0	0±0.01	0.24±0.31	0.08±0.1	0.09±0.01	0.31±0.25	0.12±0.2	0.04±0.02	0.16±0.26
C14:1ω5	0.01±0.02	0.06±0	0.04±0.01	0.14±0.16	0.03±0.02	0.05±0.03	0.02±0.01	0.02±0.02

C16:1ω7c	2.5±1.29	2.82±0.03	5.87±3.05	4.36±2.03	4.35±1.05	3.84±2.57	1.68±1.09	1.95±0.82
C17:1ω7c	0.03±0.06	0.03±0.01	0.05±0.02	0.04±0.01	0.11±0.03	0.01±0.01	0.03±0.02	0.04±0.02
C18:1ω7c	1.34±0.56	1.75±0.09	2.5±0.74	2.15±0.41	2.03±1	1.07±0.44	2.68±0.49	2.64±1.02
C18:1ω9c	4.59±1.38	1.51±0.01	1.46±0.47	5.77±0.29	3.71±0.76	12.86±7.25	3.9±1.46	4.25±1.64
C20:1ω9c	1.08±0.38	2.6±0.31	1.24±0.28	0.87±0.51	0.59±0.27	1.46±0.32	1.64±0.25	1.06±0.17
C20:1ω11	0.06±0.05	0.63±0.12	0.37±0.08	0.12±0.02	0.06±0.06	0.16±0.08	0.09±0.02	0.07±0.03
C22:1ω9c	2.27±1.69	0.71±0.64	1.69±1.42	8.13±7.59	1.93±0.98	5.52±2.4	1.99±1.1	3.47±0.57
C22:1ω11	0.39±0.56	0±0	0.06±0.06	0.13±0.11	0.06±0.1	0.12±0.1	0.08±0.01	0.05±0.04
C24:1ω9c	0.3±0.15	0.02±0.03	0.15±0.11	0.37±0.06	0.23±0.18	0.51±0.17	0.4±0.18	0.13±0.08
C16:4ω1	0.12±0.31	0.14±0.05	1.49±1.1	0.7±0.57	0.9±0.59	0.5±0.83	0.26±0.33	0.09±0.11
C18:2ω6c	0.97±0.27	1.15±0.07	1.37±0.26	2.17±0.3	2.74±0.58	1.39±0.38	0.96±0.24	1.51±0.48
C18:3ω3	0.81±0.2	1.97±0.06	1.71±0.81	1.07±0.33	2.33±0.91	0.92±0.22	0.75±0.19	1.18±0.27
C18:3ω6	0.04±0.03	0.09±0.01	0.17±0.03	0.13±0.01	0.21±0.04	0.09±0.04	0.04±0.02	0.15±0.07
C18:4ω3c	1.48±0.72	3.48±0.32	3.82±0.95	3.13±0.99	7.11±3.56	2.32±0.8	0.86±0.76	2.65±0.92
C20:2ω6	0.32±0.09	1.57±0.08	1.46±0.29	0.15±0.02	0.22±0.05	0.21±0.1	0.59±0.11	0.63±0.17
C20:3ω3	0.1±0.06	0.62±0.05	0.5±0.18	0.06±0.01	0.09±0.02	0.05±0.02	0.25±0.08	1.01±0.29
C20:3ω6	0.04±0.03	0.09±0	0.18±0.05	0.08±0.02	0.09±0.05	0.06±0.03	0.09±0.05	0.14±0.08
C20:4ω6	0.7±0.35	1.18±0.07	0.75±0.1	1.81±0.45	1.45±0.42	1.15±0.55	4.23±1.37	1.46±0.43
C20:5ω3	18.34±3.62	18.09±1.1	22.19±2.33	10.93±3.49	14.18±2.54	14.91±4.72	19.34±0.85	17.5±2.03
C21:5ω3	0.13±0.28	0.91±0.04	1.08±0.12	0.4±0.11	0.78±0.23	0.32±0.19	0.32±0.16	0.5±0.12
C22:2ω6	0.01±0.03	0.03±0	0.04±0.02	0.12±0.1	0.04±0.01	0.05±0.05	0.04±0.02	0.41±0.06
C22:3ω6	0±0	0.01±0.01	0.01±0.01	0.07±0.01	0.02±0.02	0±0	0.01±0.02	0.18±0.08
C22:4ω6	0±0	0.06±0	0.05±0.01	0.01±0.01	0.02±0.01	0±0	0.85±0.44	0.04±0.02
C22:5ω3	0.82±0.21	0.92±0.03	0.95±0.17	0.73±0.25	0.75±0.14	0.66±0.31	1.92±0.47	0.92±0.19
C22:5ω6	0.32±0.21	0.58±0.09	0.31±0.12	0.22±0.08	0.48±0.14	0.86±0.31	1.43±0.83	0.49±0.24
C22:6ω3	26.89±3.98	26.92±2.42	16.61±5.88	21.96±6.14	24.32±5.26	17.17±5.34	22±3.39	24.74±2.58
SAFA	36.33±2.65	32.07±4.19	33.88±3.08	34.16±4.81	31.16±2.98	33.73±8.99	33.57±2.23	32.73±4
MUFA	12.56±3.46	10.12±0.98	13.42±3.78	22.08±6.32	13.09±2.76	25.6±8.18	12.52±3.19	13.67±3.19
PUFA	51.11±3.09	57.81±3.21	52.69±6.04	43.76±11.12	55.74±4.23	40.67±7.6	53.92±4.62	53.6±3.33
SUM(EPA_DHA_ARA)	45.93±3.33	46.19±3.58	39.55±4.89	34.71±9.44	39.94±3.32	33.24±7.88	45.56±5.09	43.7±2.93

SUM(ALA_LA)	1.78±0.41	3.12±0.13	3.08±1.02	3.25±0.56	5.07±1.16	2.31±0.55	1.71±0.39	2.69±0.49
SUM(Branched_OddC)	2.5±0.61	7.02±0.53	4.37±0.29	4.8±0.59	5.1±0.54	2.62±0.97	2.95±0.56	4.8±1.3
SUM(Calanoid_markers)	3.79±1.84	3.93±1.07	3.36±1.46	9.24±8.21	2.64±1.11	7.26±2.61	3.81±1.02	4.65±0.57

Supplemental Table S3.4. Averages of FA proportions per crustacean taxon. Forty-six unique fatty acids (FA) found in crustacean zooplankton samples, listed in order of increasing desaturation and elongation, followed by FA summations: SAFA (saturated fatty acids), MUFA (monounsaturated fatty acids), PUFA (polyunsaturated fatty acids), SUM(EPA_DHA_ARA) (essential fatty acids), SUM(ALA_LA), SUM(Branched_OddC), and SUM(Calanoid_markers). Each result is the percent contribution of that FA to the overall FA content, averaged across samples with standard deviations. Samples are categorized according to taxon (lowest level of taxonomic identification possible).

FA	**Amphipoda Hyperiidea**	**Copepoda**	**Euphausiidae**
SampleSize_n	**5**	**21**	**22**
C8:0	0.01±0.01	0±0.01	0±0
C9:0	0.07±0.06	0.15±0.37	0.04±0.06
C10:0	0.01±0.01	0.03±0.04	0.01±0.01
C11:0	0±0	0.01±0.01	0±0
C12:0	0.45±0.44	0.14±0.12	0.09±0.12
C13:0	0.05±0.02	0.05±0.04	0.02±0.01
C14:0	4.93±1.53	6.77±4.69	3.22±0.92
C15:0	0.85±0.62	0.59±0.31	0.54±0.16
Ca-15:0	0.04±0.01	0.07±0.05	0.03±0.01
Ci-15:0	0.13±0.05	0.23±0.15	0.12±0.05
C16:0	15.74±2.63	21.72±6.18	20.26±1.75
C17:0	0.96±0.59	0.47±0.18	0.55±0.16
Ca-17:0	0.14±0.12	0.05±0.03	0.07±0.02
Ci-17:0	0.58±0.42	0.13±0.1	0.28±0.1
C18:0	4.38±0.97	5.48±2.62	1.88±0.42
C20:0	0.17±0.04	0.29±0.13	0.09±0.04
C22:0	0.06±0.04	0.13±0.05	0.1±0.03
C23:0	0.01±0.01	0.01±0.01	0.02±0.01
C24:0	0.02±0	0.06±0.05	0.05±0.03
C14:1ω5	0.04±0.02	0.08±0.06	0.03±0.01
C16:1ω7c	4.68±1.01	5.99±3.57	3.77±2.07
C17:1ω7c	0.03±0.02	0.02±0.03	0.05±0.04
C18:1ω7c	2.57±0.32	2.5±1.77	4.95±0.91
C18:1ω9c	16.17±4.07	10.88±8.79	8.24±1.56

C20:1ω9c	2.59±1.76	1.83±1.7	0.46±0.18
C20:1ω11	0.39±0.3	0.9±1.13	0.05±0.03
C22:1ω9c	2.24±1.73	3.54±3.37	0.62±0.88
C22:1ω11	1.82±1.67	1.75±2.67	0.11±0.13
C24:1ω9c	0.5±0.27	1.64±0.75	0.3±0.24
C16:4ω1	0.18±0.22	0.81±1.24	0.86±0.8
C18:2ω6c	1.49±0.85	1.67±0.75	2.04±0.75
C18:3ω3	0.85±0.54	0.97±0.43	1.81±1.12
C18:3ω6	0.13±0.03	0.1±0.08	0.12±0.03
C18:4ω3c	1.99±1.67	3.44±2.36	3±2.33
C20:2ω6	0.23±0.08	0.13±0.07	0.28±0.08
C20:3ω3	0.18±0.13	0.07±0.1	0.17±0.09
C20:3ω6	0.08±0.02	0.04±0.05	0.07±0.03
C20:4ω6	1.32±0.44	0.33±0.24	1.66±0.41
C20:5ω3	15.32±2.38	13.74±4.67	21.94±3.45
C21:5ω3	0.45±0.15	0.26±0.13	0.55±0.19
C22:2ω6	0.03±0.01	0.03±0.04	0.01±0.01
C22:3ω6	0.11±0.12	0±0	0.02±0.01
C22:4ω6	0.01±0.01	0.01±0.01	0.02±0.01
C22:5ω3	0.66±0.08	0.69±0.5	0.63±0.14
C22:5ω6	0.16±0.01	0.19±0.29	0.26±0.1
C22:6ω3	17.18±7.59	12.04±3.76	20.6±4.73
SAFA	28.62±2.55	36.35±8.98	27.37±2.54
MUFA	31.02±10.29	29.12±7.51	18.58±3.06
PUFA	40.36±8.62	34.52±6.8	54.05±4.98
SUM(EPA_DHA_ARA)	33.82±5.81	26.12±6.24	44.2±3.96
SUM(ALA_LA)	2.33±1.38	2.64±0.84	3.86±1.82
SUM(Branched_OddC)	3.31±1.99	2.02±0.79	2.28±0.55
SUM(Calanoid_markers)	7.04±5.32	8.01±5.41	1.25±1.02

Supplemental Table S3.5. Averages of FA proportions per fish taxon. Forty-six unique fatty acids (FA) found in fish larvae samples, listed in order of increasing desaturation and elongation, followed by FA summations: SAFA (saturated fatty acids), MUFA (monounsaturated fatty acids), PUFA (polyunsaturated fatty acids), SUM(EPA_DHA_ARA) (essential fatty acids), SUM(ALA_LA), SUM(Branched_OddC), and SUM(Calanoid_markers). Each result is the percent contribution of that FA to the overall FA content, averaged across samples with standard deviations. Samples are categorized according to taxon (lowest level of taxonomic identification possible).

FA	***Sebastes* sp.**	***Stenobrachius leucopsarus***
SampleSize_n	**24**	**19**
C8:0	0±0	0±0
C9:0	0.02±0.03	0±0.01
C10:0	0.02±0.02	0.02±0.02
C11:0	0.01±0.01	0.01±0.01
C12:0	0.33±0.5	0.51±0.67
C13:0	0.03±0.03	0.06±0.05
C14:0	2.42±0.88	3.26±1.51
C15:0	0.75±0.22	1.12±0.44
Ca-15:0	0.04±0.03	0.07±0.04
Ci-15:0	0.14±0.06	0.16±0.07
C16:0	24.3±6.73	26.3±10.21
C17:0	1.02±0.34	0.93±0.42
Ca-17:0	0.14±0.06	0.14±0.07
Ci-17:0	0.3±0.13	0.26±0.13
C18:0	11.05±4.3	9.67±5.41
C20:0	0.42±0.35	0.43±0.46
C22:0	0.27±0.26	0.25±0.38
C23:0	0.03±0.04	0.07±0.18
C24:0	0.17±0.21	0.19±0.31
C14:1ω5	0.02±0.02	0.04±0.06
C16:1ω7c	1.9±0.81	2.78±2.88
C17:1ω7c	0.04±0.02	0.02±0.02
C18:1ω7c	2.64±0.84	1.84±1.47
C18:1ω9c	7.96±1.85	10.31±9.48
C20:1ω9c	1.19±0.63	0.65±0.59
C20:1ω11	0.04±0.04	0.06±0.07
C22:1ω9c	4.49±4.65	6.34±10.34
C22:1ω11	0.06±0.08	0.06±0.09
C24:1ω9c	1.1±0.5	0.65±0.61
C16:4ω1	0.07±0.09	0.09±0.16

C18:2ω6c	1.63±0.46	1.94±0.5
C18:3ω3	0.77±0.32	1.01±0.31
C18:3ω6	0.05±0.04	0.07±0.06
C18:4ω3c	1.43±0.86	2.2±0.84
C20:2ω6	0.23±0.07	0.11±0.07
C20:3ω3	0.16±0.09	0.07±0.04
C20:3ω6	0.04±0.03	0.03±0.04
C20:4ω6	0.89±0.45	0.62±0.43
C20:5ω3	9.88±3.65	8.79±4.47
C21:5ω3	0.28±0.13	0.24±0.17
C22:2ω6	0.06±0.04	0.07±0.12
C22:3ω6	0.03±0.03	0.03±0.05
C22:4ω6	0.04±0.05	0.01±0.02
C22:5ω3	1.21±0.47	0.5±0.39
C22:5ω6	0.26±0.12	0.25±0.16
C22:6ω3	22.05±6.97	17.78±7.33
SAFA	41.47±11.51	43.44±17.9
MUFA	19.45±5.22	22.75±15.34
PUFA	39.09±11.74	33.8±13
SUM(EPA_DHA_ARA)	32.82±10.22	27.18±11.54
SUM(ALA_LA)	2.4±0.69	2.96±0.62
SUM(Branched_OddC)	2.8±0.67	3.08±1.14
SUM(Calanoid_markers)	5.78±4.76	7.1±10.86

Supplemental Table S3.6. PERMANOVA and Permutest comparisons based on taxon. PERMANOVA and permutests were run to compare the FA profiles of all gelatinous zooplankton samples to each other categorized by taxon (lowest identification level possible). FA profiles were compared across samples as proportional contributions of each FA to the total FA concentration per sample. Bolded values indicate significance ($p<0.05$). Highlighted in grey are those comparisons which had a significnat PERMANOVA and non-significant Permutest result.

Comparison: Taxon		**Sample sizes**		**PERMANOVA**			**Permutest**	
Group A	**Group B**	**A**	**B**	**Pseudo-F**	**R^2**	**p**	**F**	**p**
Aequorea sp.	*Mitrocoma sp.*	4	4	5.4	0.474	**0.042**	0.05	0.864
Appendicularia	*Beroe sp.*	7	6	7.91	0.418	**0.002**	1.45	0.252
Appendicularia	*Clytia sp.*	9	6	7.72	0.373	**0.001**	4.43	0.072
Appendicularia	Salpidae	6	8	3.81	0.241	**0.014**	3.76	0.069
Appendicularia	Siphonophorae Calycophorae	11	6	5.61	0.272	**0.001**	0.16	0.709
Appendicularia	Siphonophorae Physonectae	3	6	4.26	0.378	**0.042**	2.9	0.153
Beroe sp.	Pteropod Thecosomata	7	7	9.38	0.439	**0.001**	1.75	0.222
Chaetognatha	*Clytia sp.*	36	9	34.4	0.444	**0.001**	1.84	0.162

Chaetognatha	Doliolida	36	9	40.04	0.482	**0.001**	1.32	0.26
Chaetognatha	*Pleurobrachia bachei*	36	19	31.8	0.375	**0.001**	0.71	0.403
Chaetognatha	Pteropod Thecosomata	36	7	35.47	0.464	**0.001**	0.33	0.577
Chaetognatha	*Pyrosoma atlanticum*	36	3	9.42	0.203	**0.001**	1.73	0.197
Chaetognatha	Siphonophorae Physonectae	36	3	10.69	0.224	**0.001**	0.48	0.477
Clytia sp.	*Beroe sp.*	7	9	9.41	0.402	**0.002**	1.02	0.347
Clytia sp.	*Pleurobrachia bachei*	19	9	25.27	0.493	**0.001**	3	0.093
Clytia sp.	Pteropod Thecosomata	7	9	12.63	0.474	**0.001**	0.25	0.643
Clytia sp.	Siphonophorae Physonectae	9	3	3.64	0.267	**0.023**	1.49	0.251
Doliolida	*Clytia sp.*	9	9	15.65	0.494	**0.001**	3.63	0.095
Doliolida	*Mitrocoma sp.*	4	9	28.85	0.724	**0.004**	3.63	0.1
Doliolida	*Pleurobrachia bachei*	19	9	42.68	0.621	**0.001**	0.2	0.639
Doliolida	Pteropod Thecosomata	7	9	16.94	0.548	**0.001**	2.01	0.165
Doliolida	*Pyrosoma atlanticum*	9	3	6.05	0.377	**0.004**	3.06	0.101
Doliolida	Siphonophorae Physonectae	3	9	13.63	0.577	**0.005**	0	0.99
Mitrocoma sp.	Siphonophorae Physonectae	4	3	10.63	0.68	**0.031**	1.99	0.173
Pleurobrachia bachei	Pteropod Thecosomata	7	19	25.25	0.513	**0.001**	1.11	0.296
Pyrosoma atlanticum	*Beroe sp.*	7	3	6.24	0.438	**0.01**	0.15	0.744
Pyrosoma atlanticum	*Clytia sp.*	9	3	7.28	0.421	**0.004**	0.11	0.759
Pyrosoma atlanticum	*Mitrocoma sp.*	4	3	13.79	0.734	**0.035**	4.44	0.125
Pyrosoma atlanticum	*Pleurobrachia bachei*	19	3	10.8	0.351	**0.001**	2.37	0.132
Pyrosoma atlanticum	Pteropod Thecosomata	7	3	7.13	0.471	**0.005**	0.47	0.531
Pyrosoma atlanticum	Salpidae	3	8	3.09	0.256	**0.01**	0.02	0.911
Pyrosoma atlanticum	Siphonophorae Calycophorae	11	3	3.32	0.217	**0.032**	1.28	0.26
Salpidae	*Beroe sp.*	7	8	12.83	0.497	**0.001**	0.66	0.424
Salpidae	*Clytia sp.*	9	8	14.82	0.497	**0.001**	0.17	0.678
Salpidae	Pteropod Thecosomata	7	8	10.8	0.454	**0.001**	1.2	0.328
Salpidae	Siphonophorae Calycophorae	11	8	10.05	0.371	**0.001**	4.11	0.052
Siphonophorae Calycophorae	*Beroe sp.*	7	11	4.02	0.201	**0.02**	1.3	0.297
Siphonophorae Physonectae	*Beroe sp.*	7	3	3.71	0.317	**0.046**	2.23	0.19
Siphonophorae Physonectae	*Pleurobrachia bachei*	19	3	4.37	0.179	**0.003**	0.07	0.789

Siphonophorae Physonectae	Pteropod Thecosomata	7	3	8.16	0.505	**0.011**	0.96	0.374
Tomopteris sp.	*Beroe sp.*	5	7	9.4	0.485	**0.005**	4.03	0.067
Tomopteris sp.	Chaetognatha	5	36	9.66	0.199	**0.001**	1.11	0.302
Tomopteris sp.	*Clytia sp.*	5	9	11.5	0.489	**0.002**	2.77	0.106
Tomopteris sp.	Doliolida	5	9	22.41	0.651	**0.001**	0.03	0.865
Tomopteris sp.	*Eutonina sp.*	5	2	12.72	0.718	**0.034**	11.23	0.053
Tomopteris sp.	*Mitrocoma sp.*	5	4	27.6	0.798	**0.014**	2.47	0.173
Tomopteris sp.	*Pleurobrachia bachei*	5	19	8.34	0.275	**0.001**	0.25	0.627
Tomopteris sp.	Pteropod Thecosomata	5	7	13.69	0.578	**0.003**	1.83	0.222
Tomopteris sp.	*Pyrosoma atlanticum*	5	3	5.89	0.495	**0.011**	2.4	0.181
Tomopteris sp.	Siphonophorae Physonectae	5	3	4.72	0.44	**0.018**	0.03	0.934
Aequorea sp.	*Beroe sp.*	7	4	7.58	0.457	**0.01**	8.85	**0.001**
Aequorea sp.	*Clytia sp.*	4	9	6.94	0.387	**0.004**	10.83	**0.004**
Aequorea sp.	*Eutonina sp.*	4	2	2.9	0.42	0.133333	12.39	**0.001389**
Aequorea sp.	*Pleurobrachia bachei*	19	4	22.84	0.521	**0.001**	6.57	**0.019**
Aequorea sp.	Pteropod Gymnosomata	2	4	34.6	0.896	0.066667	12.89	**0.001389**
Aequorea sp.	Pteropod Thecosomata	7	4	28.45	0.76	**0.002**	11.54	**0.003**
Aequorea sp.	Siphonophorae Calycophorae	4	11	6.44	0.331	**0.003**	10.77	**0.009**
Aequorea sp.	Siphonophorae Physonectae	4	3	7.15	0.588	**0.027**	11.82	**0.001**
Appendicularia	*Aequorea sp.*	4	6	9.66	0.547	**0.006**	7.14	**0.017**
Appendicularia	Doliolida	6	9	5.77	0.307	**0.002**	9.09	**0.006**
Appendicularia	*Eutonina sp.*	2	6	4.18	0.411	0.083	4.36	0.081
Appendicularia	*Mitrocoma sp.*	4	6	9.18	0.534	**0.005**	6.36	**0.027**
Appendicularia	*Pleurobrachia bachei*	19	6	15.89	0.409	**0.001**	15.24	**0.001**
Appendicularia	Pteropod Gymnosomata	2	6	3.22	0.349	0.073	4.38	0.076
Appendicularia	Pteropod Thecosomata	7	6	5.55	0.335	**0.001**	4.52	**0.048**
Appendicularia	*Pyrosoma atlanticum*	6	3	1.04	0.129	0.379	1.14	0.311
Beroe sp.	*Pleurobrachia bachei*	7	19	15.48	0.392	**0.001**	7.37	**0.008**
Beroe sp.	Pteropod Gymnosomata	2	7	5.23	0.428	**0.029**	6.44	**0.03**
Chaetognatha	*Aequorea sp.*	36	4	30.46	0.445	**0.001**	9.9	**0.006**
Chaetognatha	Appendicularia	36	6	20.78	0.342	**0.001**	21.54	**0.001**
Chaetognatha	*Beroe sp.*	36	7	20.75	0.336	**0.001**	7.46	**0.011**
Chaetognatha	*Eutonina sp.*	36	2	17.2	0.323	**0.003**	9.95	**0.008**
Chaetognatha	*Mitrocoma sp.*	36	4	36.27	0.488	**0.001**	7.52	**0.008**
Chaetognatha	Pteropod Gymnosomata	36	2	7.23	0.167	**0.003**	10.07	**0.005**

Chaetognatha	Salpidae	36	8	17.03	0.289	**0.001**	3.91	**0.04**
Chaetognatha	Siphonophorae Calycophorae	36	11	16.13	0.264	**0.001**	26.26	**0.001**
Clytia sp.	*Eutonina sp.*	9	2	3.99	0.307	0.051	9.15	**0.015**
Clytia sp.	*Mitrocoma sp.*	9	4	7.15	0.394	**0.01**	7.35	**0.023**
Clytia sp.	Pteropod Gymnosomata	2	9	8.45	0.484	**0.017**	9.24	**0.021**
Clytia sp.	Siphonophorae Calycophorae	9	11	7.18	0.285	**0.001**	5.07	**0.034**
Doliolida	*Aequorea sp.*	4	9	33.36	0.752	**0.003**	7.79	**0.016**
Doliolida	*Beroe sp.*	7	9	16.28	0.538	**0.001**	6.17	**0.019**
Doliolida	*Eutonina sp.*	2	9	15.61	0.634	**0.021**	9.52	**0.001**
Doliolida	Pteropod Gymnosomata	2	9	15.14	0.627	**0.014**	9.66	**0.001**
Doliolida	Salpidae	9	8	10.78	0.418	**0.001**	9.55	**0.01**
Doliolida	Siphonophorae Calycophorae	11	9	14.54	0.447	**0.001**	11.99	**0.001**
Eutonina sp.	*Beroe sp.*	7	2	5.27	0.43	**0.027**	6.39	**0.029**
Eutonina sp.	*Mitrocoma sp.*	2	4	2.64	0.397	0.066667	0.85	0.401389
Eutonina sp.	*Pleurobrachia bachei*	19	2	12.74	0.401	**0.006**	7.3	**0.027**
Eutonina sp.	Pteropod Gymnosomata	2	2	32.33	0.942	0.333333	7.26E+26	**0.041667**
Eutonina sp.	Pteropod Thecosomata	7	2	13.81	0.664	**0.022**	10.46	**0.001**
Eutonina sp.	Siphonophorae Calycophorae	2	11	3.45	0.239	**0.023**	7.08	**0.016**
Eutonina sp.	Siphonophorae Physonectae	2	3	5.34	0.64	0.1	14.82	**0.008333**
Mitrocoma sp.	*Beroe sp.*	7	4	10.69	0.543	**0.004**	6.9	**0.027**
Mitrocoma sp.	*Pleurobrachia bachei*	19	4	33.75	0.616	**0.001**	4.48	**0.041**
Mitrocoma sp.	Pteropod Gymnosomata	2	4	28.91	0.878	0.066667	0.88	0.401389
Mitrocoma sp.	Pteropod Thecosomata	7	4	26.03	0.743	**0.004**	6.35	**0.035**
Mitrocoma sp.	Siphonophorae Calycophorae	4	11	8.75	0.402	**0.002**	9.52	**0.011**
Pleurobrachia bachei	Pteropod Gymnosomata	2	19	6.33	0.25	**0.005**	7.4	**0.029**
Pteropod Gymnosomata	Pteropod Thecosomata	2	7	5.21	0.427	**0.033**	10.57	**0.001**
Pyrosoma atlanticum	*Aequorea sp.*	4	3	14.16	0.739	**0.035**	7.88	**0.001**
Pyrosoma atlanticum	*Eutonina sp.*	2	3	6.8	0.694	0.1	5.52	**0.008333**
Pyrosoma atlanticum	Pteropod Gymnosomata	2	3	4.8	0.615	0.1	5.57	**0.008333**
Pyrosoma atlanticum	Siphonophorae Physonectae	3	3	5.03	0.557	0.1	1.31	0.301389
Salpidae	*Aequorea sp.*	4	8	21.2	0.679	**0.002**	38.14	**0.001**
Salpidae	*Eutonina sp.*	2	8	9.74	0.549	**0.019**	31.77	**0.001**
Salpidae	*Mitrocoma sp.*	4	8	21.69	0.684	**0.005**	17.07	**0.003**

Salpidae	*Pleurobrachia bachei*	19	8	18.01	0.419	**0.001**	5.96	**0.02**
Salpidae	Pteropod Gymnosomata	2	8	3.46	0.302	**0.018**	32.05	**0.001**
Salpidae	Siphonophorae Physonectae	3	8	7.35	0.45	**0.011**	5.81	**0.028**
Siphonophorae Calycophorae	*Pleurobrachia bachei*	19	11	13.16	0.32	**0.001**	19.3	**0.001**
Siphonophorae Calycophorae	Pteropod Gymnosomata	2	11	4.05	0.269	**0.014**	7.12	**0.011**
Siphonophorae Calycophorae	Pteropod Thecosomata	7	11	11.48	0.418	**0.001**	5.53	**0.035**
Siphonophorae Calycophorae	Siphonophorae Physonectae	11	3	3.14	0.207	**0.044**	4.06	**0.041**
Siphonophorae Physonectae	Pteropod Gymnosomata	2	3	5.48	0.646	0.1	15.03	**0.008333**
Tomopteris sp.	*Aequorea sp.*	5	4	22.58	0.763	**0.006**	8.71	**0.012**
Tomopteris sp.	Appendicularia	5	6	5.89	0.396	**0.007**	5.23	**0.049**
Tomopteris sp.	Pteropod Gymnosomata	5	2	3.41	0.406	0.096	11.4	**0.044**
Tomopteris sp.	Salpidae	5	8	7.04	0.39	**0.001**	9.13	**0.008**
Tomopteris sp.	Siphonophorae Calycophorae	5	11	5.35	0.276	**0.004**	7.15	**0.017**

Supplemental Table S3.7. SIMPER analyses of fatty acid profiles of all gelatinous zooplankton separated by phylum. SIMPER analyses compared the fatty acid (FA) profiles of all gelatinous zooplankton, categorized by phylum. FA profiles were compared across samples as proportional contributions of each FA to the total FA concentration per sample. Per group comparison, the top 10 FAs contributing to dissimilarity are listed in order of decreasing contribution to the average between-group dissimilarity. Bolded p-values indicate FAs that were significantly dissimilar ($p<0.05$) in proportion between the two groups compared.

Phylum		**SIMPER Order**	**FA**	**Avg Proportion (% of total FA)**		**Contribution to Avg Between-Group Dissimilarity (Avg±Stdv)**	**Cumulative Contribution to Between-Group Dissimiliarity (%, ordered)**	**p**
Group A	**Group B**			**Group A**	**Group B**			
Annelida	Chaetognatha	1	C16:1ω7c	1.95	6.22	2.14±0.73	11.82	**0.001**
Annelida	Chaetognatha	2	C20:5ω3	17.5	14.23	1.87±1.22	22.14	0.732
Annelida	Chaetognatha	3	C18:1ω9c	4.25	7.09	1.67±1.21	31.35	0.575
Annelida	Chaetognatha	4	C24:1ω9c	0.13	3.18	1.53±0.7	39.8	**0.001**
Annelida	Chaetognatha	5	C16:0	17.4	17.63	1.49±0.96	48.03	0.863
Annelida	Chaetognatha	6	C22:6ω3	24.74	23.62	1.37±0.93	55.63	1
Annelida	Chaetognatha	7	C18:0	6.54	5.79	0.84±0.58	60.26	1
Annelida	Chaetognatha	8	C14:0	2.47	3.26	0.75±0.33	64.4	1
Annelida	Chaetognatha	9	C22:1ω9c	3.47	2.73	0.71±0.43	68.36	0.967
Annelida	Chaetognatha	10	C12:0	1.44	0.19	0.63±0.28	71.83	**0.001**
Annelida	Chordata	1	C22:6ω3	24.74	19.64	3.36±2.31	13.71	0.372

Annelida	Chordata	2	C14:0	2.47	8.29	2.91±1.56	25.6	**0.001**
Annelida	Chordata	3	C20:5ω3	17.5	13.6	2.04±1.75	33.93	0.556
Annelida	Chordata	4	C18:0	6.54	2.63	2.02±0.89	42.16	0.051
Annelida	Chordata	5	C16:0	17.4	17.83	1.68±1.35	49.03	0.629
Annelida	Chordata	6	C22:1ω9 c	3.47	4.48	1.63±2.04	55.68	0.148
Annelida	Chordata	7	C18:4ω3 c	2.65	4.94	1.37±1.44	61.29	0.098
Annelida	Chordata	8	C16:1ω7 c	1.95	4.57	1.32±0.74	66.68	0.371
Annelida	Chordata	9	C18:2ω6 c	1.51	3.19	0.84±0.51	70.1	**0.01**
Annelida	Chordata	10	C18:1ω9 c	4.25	4.08	0.81±0.57	73.4	1
Annelida	Cnidaria	1	C22:6ω3	24.74	16.33	4.28±2.26	17.4	**0.028**
Annelida	Cnidaria	2	C20:4ω6	1.46	6.08	2.46±2.16	27.38	**0.036**
Annelida	Cnidaria	3	C16:0	17.4	14.89	2.15±1.43	36.1	0.133
Annelida	Cnidaria	4	C18:1ω9 c	4.25	6.92	1.97±2.66	44.08	0.299
Annelida	Cnidaria	5	C14:0	2.47	5.98	1.76±0.66	51.22	0.154
Annelida	Cnidaria	6	C20:5ω3	17.5	16.17	1.47±1.36	57.21	0.967
Annelida	Cnidaria	7	C18:0	6.54	8.43	1.35±0.99	62.7	0.879
Annelida	Cnidaria	8	C16:1ω7 c	1.95	3.51	0.96±0.94	66.61	0.973
Annelida	Cnidaria	9	C22:5ω6	0.49	2.31	0.92±0.76	70.35	**0.026**
Annelida	Cnidaria	10	C22:1ω9 c	3.47	3.64	0.83±0.66	73.72	0.88
Annelida	Ctenophora	1	C22:6ω3	24.74	24.4	2.46±1.83	12.88	0.936
Annelida	Ctenophora	2	C14:0	2.47	7.02	2.28±0.8	24.78	**0.021**
Annelida	Ctenophora	3	C20:5ω3	17.5	18.96	1.77±1.33	34.02	0.814
Annelida	Ctenophora	4	C16:0	17.4	16.37	1.71±1.15	42.95	0.597
Annelida	Ctenophora	5	C18:1ω9 c	4.25	5.76	1.24±1.11	49.42	0.909
Annelida	Ctenophora	6	C18:0	6.54	8.22	1.17±0.8	55.53	0.988
Annelida	Ctenophora	7	C16:1ω7 c	1.95	3.42	0.99±1.11	60.71	0.954
Annelida	Ctenophora	8	C22:1ω9 c	3.47	2.26	0.83±0.54	65.06	0.852
Annelida	Ctenophora	9	C18:1ω7 c	2.64	1.33	0.69±0.46	68.69	0.239
Annelida	Ctenophora	10	C12:0	1.44	0.15	0.64±0.27	72.05	**0.001**
Annelida	Mollusca	1	C22:6ω3	24.74	18.91	3.63±2.71	16.41	0.234
Annelida	Mollusca	2	C14:0	2.47	6.88	2.2±1.18	26.39	**0.042**
Annelida	Mollusca	3	C20:5ω3	17.5	21.27	2.08±1.33	35.8	0.518
Annelida	Mollusca	4	C18:0	6.54	3.2	1.68±0.82	43.41	0.421
Annelida	Mollusca	5	C16:1ω7 c	1.95	5.19	1.65±1.42	50.89	0.054
Annelida	Mollusca	6	C16:0	17.4	19.04	1.49±1.13	57.64	0.794
Annelida	Mollusca	7	C18:1ω9 c	4.25	1.47	1.39±0.76	63.91	0.734

Annelida	Mollusca	8	C22:1ω9c	3.47	1.47	1.07±0.57	68.74	0.499
Annelida	Mollusca	9	C18:4ω3c	2.65	3.75	0.66±0.44	71.74	0.734
Annelida	Mollusca	10	C17:0	1.97	0.94	0.64±0.31	74.62	**0.001**
Chaetognatha	Chordata	1	C22:6ω3	23.62	19.64	3.02±2.17	12.45	0.802
Chaetognatha	Chordata	2	C14:0	3.26	8.29	2.58±1.6	23.1	**0.001**
Chaetognatha	Chordata	3	C18:4ω3c	1.53	4.94	1.73±1.58	30.25	**0.001**
Chaetognatha	Chordata	4	C18:1ω9c	7.09	4.08	1.68±1.25	37.18	0.754
Chaetognatha	Chordata	5	C18:0	5.79	2.63	1.67±0.76	44.09	0.316
Chaetognatha	Chordata	6	C22:1ω9c	2.73	4.48	1.66±2.23	50.95	**0.016**
Chaetognatha	Chordata	7	C20:5ω3	14.23	13.6	1.57±1.3	57.45	0.998
Chaetognatha	Chordata	8	C16:0	17.63	17.83	1.53±1.25	63.75	0.979
Chaetognatha	Chordata	9	C24:1ω9c	3.18	0.21	1.49±0.7	69.9	**0.001**
Chaetognatha	Chordata	10	C16:1ω7c	6.22	4.57	1.01±0.69	74.07	0.999
Chaetognatha	Cnidaria	1	C22:6ω3	23.62	16.33	3.76±2.15	14.79	**0.003**
Chaetognatha	Cnidaria	2	C20:4ω6	0.76	6.08	2.69±2.27	25.35	**0.001**
Chaetognatha	Cnidaria	3	C18:1ω9c	7.09	6.92	2.32±2.21	34.49	**0.011**
Chaetognatha	Cnidaria	4	C16:0	17.63	14.89	2.09±1.36	42.71	**0.003**
Chaetognatha	Cnidaria	5	C20:5ω3	14.23	16.17	1.83±1.35	49.9	0.976
Chaetognatha	Cnidaria	6	C16:1ω7c	6.22	3.51	1.58±0.88	56.12	**0.001**
Chaetognatha	Cnidaria	7	C18:0	5.79	8.43	1.52±1.1	62.07	0.891
Chaetognatha	Cnidaria	8	C14:0	3.26	5.98	1.41±0.89	67.62	0.8
Chaetognatha	Cnidaria	9	C24:1ω9c	3.18	0.41	1.38±0.71	73.06	**0.001**
Chaetognatha	Cnidaria	10	C22:1ω9c	2.73	3.64	1±0.87	76.99	0.891
Chaetognatha	Ctenophora	1	C20:5ω3	14.23	18.96	2.68±1.85	13.16	**0.002**
Chaetognatha	Ctenophora	2	C22:6ω3	23.62	24.4	2.5±1.75	25.42	0.999
Chaetognatha	Ctenophora	3	C14:0	3.26	7.02	1.88±1.06	34.66	**0.001**
Chaetognatha	Ctenophora	4	C16:1ω7c	6.22	3.42	1.76±0.88	43.31	**0.001**
Chaetognatha	Ctenophora	5	C18:1ω9c	7.09	5.76	1.56±1.16	50.97	0.854
Chaetognatha	Ctenophora	6	C16:0	17.63	16.37	1.49±1.2	58.27	0.99
Chaetognatha	Ctenophora	7	C24:1ω9c	3.18	0.26	1.46±0.7	65.45	**0.001**
Chaetognatha	Ctenophora	8	C18:0	5.79	8.22	1.4±0.81	72.33	0.988
Chaetognatha	Ctenophora	9	C22:1ω9c	2.73	2.26	0.78±0.69	76.18	0.995
Chaetognatha	Ctenophora	10	C18:1ω7c	2.04	1.33	0.42±0.28	78.23	0.999
Chaetognatha	Mollusca	1	C20:5ω3	14.23	21.27	3.57±1.68	14.27	**0.001**
Chaetognatha	Mollusca	2	C22:6ω3	23.62	18.91	3.38±2.4	27.79	0.307

Chaetognatha	Mollusca	3	C18:1ω9c	7.09	1.47	2.81±1.31	39.01	**0.033**
Chaetognatha	Mollusca	4	C14:0	3.26	6.88	1.94±1.16	46.77	**0.026**
Chaetognatha	Mollusca	5	C24:1ω9c	3.18	0.12	1.53±0.7	52.88	**0.001**
Chaetognatha	Mollusca	6	C16:1ω7c	6.22	5.19	1.46±0.7	58.7	0.12
Chaetognatha	Mollusca	7	C16:0	17.63	19.04	1.33±0.9	64.03	0.992
Chaetognatha	Mollusca	8	C18:0	5.79	3.2	1.31±0.7	69.27	0.978
Chaetognatha	Mollusca	9	C18:4ω3c	1.53	3.75	1.12±0.5	73.75	0.225
Chaetognatha	Mollusca	10	C22:1ω9c	2.73	1.47	0.91±0.66	77.4	0.848
Chordata	Cnidaria	1	C22:6ω3	19.64	16.33	3.16±2.43	11.11	0.57
Chordata	Cnidaria	2	C18:0	2.63	8.43	2.93±1.3	21.43	**0.001**
Chordata	Cnidaria	3	C20:4ω6	1.57	6.08	2.48±2.12	30.15	**0.001**
Chordata	Cnidaria	4	C16:0	17.83	14.89	2.28±1.66	38.18	**0.002**
Chordata	Cnidaria	5	C20:5ω3	13.6	16.17	2.04±1.69	45.36	0.687
Chordata	Cnidaria	6	C18:1ω9c	4.08	6.92	1.93±2.71	52.14	0.38
Chordata	Cnidaria	7	C22:1ω9c	4.48	3.64	1.8±2.11	58.47	**0.003**
Chordata	Cnidaria	8	C18:4ω3c	4.94	1.97	1.61±1.53	64.14	**0.001**
Chordata	Cnidaria	9	C14:0	8.29	5.98	1.59±1.27	69.75	0.241
Chordata	Cnidaria	10	C16:1ω7c	4.57	3.51	1.11±0.73	73.66	0.99
Chordata	Ctenophora	1	C22:6ω3	19.64	24.4	3.88±2.72	14.84	**0.003**
Chordata	Ctenophora	2	C20:5ω3	13.6	18.96	2.92±2.18	26.02	**0.001**
Chordata	Ctenophora	3	C18:0	2.63	8.22	2.82±1.07	36.8	**0.001**
Chordata	Ctenophora	4	C16:0	17.83	16.37	1.77±1.46	43.57	0.536
Chordata	Ctenophora	5	C18:4ω3c	4.94	1.5	1.74±1.58	50.23	**0.001**
Chordata	Ctenophora	6	C22:1ω9c	4.48	2.26	1.66±2.34	56.58	**0.033**
Chordata	Ctenophora	7	C14:0	8.29	7.02	1.45±1.16	62.11	0.654
Chordata	Ctenophora	8	C16:1ω7c	4.57	3.42	1.24±0.86	66.87	0.681
Chordata	Ctenophora	9	C18:1ω9c	4.08	5.76	1.23±1.13	71.58	0.991
Chordata	Ctenophora	10	C18:2ω6c	3.19	0.99	1.1±0.49	75.77	**0.001**
Chordata	Mollusca	1	C20:5ω3	13.6	21.27	3.84±2.05	15.65	**0.001**
Chordata	Mollusca	2	C22:6ω3	19.64	18.91	3.64±2.48	30.48	0.124
Chordata	Mollusca	3	C22:1ω9c	4.48	1.47	1.8±2.43	37.82	0.081
Chordata	Mollusca	4	C14:0	8.29	6.88	1.63±1.26	44.47	0.28
Chordata	Mollusca	5	C16:0	17.83	19.04	1.57±1.21	50.85	0.838
Chordata	Mollusca	6	C16:1ω7c	4.57	5.19	1.36±0.8	56.37	0.312
Chordata	Mollusca	7	C18:1ω9c	4.08	1.47	1.31±0.68	61.69	0.918

Chordata	Mollusca	8	C18:4ω3c	4.94	3.75	1.26±1.18	66.83	0.106
Chordata	Mollusca	9	C18:2ω6c	3.19	1.32	0.93±0.48	70.63	**0.001**
Chordata	Mollusca	10	C18:1ω7c	3.17	2.33	0.74±0.72	73.65	0.168
Cnidaria	Ctenophora	1	C22:6ω3	16.33	24.4	4.56±2.82	19.04	**0.001**
Cnidaria	Ctenophora	2	C20:4ω6	6.08	0.84	2.67±2.26	30.18	**0.001**
Cnidaria	Ctenophora	3	C20:5ω3	16.17	18.96	2.2±1.83	39.39	0.417
Cnidaria	Ctenophora	4	C18:1ω9c	6.92	5.76	2.13±2.46	48.27	0.14
Cnidaria	Ctenophora	5	C16:0	14.89	16.37	1.98±1.33	56.55	0.089
Cnidaria	Ctenophora	6	C18:0	8.43	8.22	1.21±0.83	61.63	1
Cnidaria	Ctenophora	7	C16:1ω7c	3.51	3.42	1.19±1.08	66.61	0.843
Cnidaria	Ctenophora	8	C22:1ω9c	3.64	2.26	1.07±0.97	71.07	0.782
Cnidaria	Ctenophora	9	C22:5ω6	2.31	0.33	0.99±0.77	75.2	**0.001**
Cnidaria	Ctenophora	10	C14:0	5.98	7.02	0.86±0.76	78.78	1
Cnidaria	Mollusca	1	C22:6ω3	16.33	18.91	3.37±2.29	11.98	0.332
Cnidaria	Mollusca	2	C18:1ω9c	6.92	1.47	2.73±2.94	21.66	**0.044**
Cnidaria	Mollusca	3	C20:5ω3	16.17	21.27	2.7±1.91	31.24	0.055
Cnidaria	Mollusca	4	C20:4ω6	6.08	0.84	2.66±2.27	40.67	**0.007**
Cnidaria	Mollusca	5	C18:0	8.43	3.2	2.62±1.24	49.97	**0.001**
Cnidaria	Mollusca	6	C16:0	14.89	19.04	2.47±1.49	58.74	**0.006**
Cnidaria	Mollusca	7	C16:1ω7c	3.51	5.19	1.51±1.2	64.11	**0.046**
Cnidaria	Mollusca	8	C22:1ω9c	3.64	1.47	1.27±1	68.63	0.371
Cnidaria	Mollusca	9	C14:0	5.98	6.88	1.2±0.73	72.88	0.926
Cnidaria	Mollusca	10	C22:5ω6	2.31	0.37	0.97±0.76	76.33	**0.006**
Ctenophora	Mollusca	1	C22:6ω3	24.4	18.91	4.17±2.96	17.78	**0.007**
Ctenophora	Mollusca	2	C18:0	8.22	3.2	2.51±0.96	28.5	**0.001**
Ctenophora	Mollusca	3	C18:1ω9c	5.76	1.47	2.15±1.3	37.66	0.213
Ctenophora	Mollusca	4	C20:5ω3	18.96	21.27	2.1±1.46	46.61	0.557
Ctenophora	Mollusca	5	C16:0	16.37	19.04	1.72±1.32	53.97	0.587
Ctenophora	Mollusca	6	C16:1ω7c	3.42	5.19	1.63±1.27	60.92	**0.014**
Ctenophora	Mollusca	7	C14:0	7.02	6.88	1.16±0.79	65.87	0.947
Ctenophora	Mollusca	8	C18:4ω3c	1.5	3.75	1.13±0.5	70.71	0.21
Ctenophora	Mollusca	9	C22:1ω9c	2.26	1.47	0.78±0.7	74.04	0.934
Ctenophora	Mollusca	10	C16:4ω1	0.41	1.19	0.58±0.49	76.51	**0.001**

Supplemental Table S3.8. Averages of FA proportions per phylum. Forty-six unique fatty acids (FA) found in gelatinous zooplankton samples, listed in order of increasing desaturation and elongation, followed by FA summations: SAFA (saturated fatty acids), MUFA (monounsaturated fatty acids), PUFA (polyunsaturated fatty acids), SUM(EPA_DHA_ARA) (essential fatty acids), SUM(ALA_LA), SUM(Branched_OddC), and SUM(Calanoid_markers). Each result is the percent contribution of that FA to the overall FA content, averaged across samples with standard deviations. Samples are categorized according to phylum.

FA	Annelida	Chaetognatha	Mollusca	Ctenophora	Cnidaria	Chordata
C8:0	0.01±0.02	0.05±0.23	0±0.01	0.01±0.02	0.01±0.02	0.01±0.03
C9:0	0.14±0.12	0.08±0.13	0.04±0.05	0.01±0.02	0.08±0.29	0.08±0.09
C10:0	0.02±0.01	0.03±0.05	0.01±0.01	0.03±0.06	0.03±0.05	0.06±0.07
C11:0	0.02±0.01	0.01±0.01	0±0	0±0	0.01±0.01	0.02±0.02
C12:0	1.44±0.58	0.19±0.23	0.17±0.05	0.15±0.09	0.21±0.22	0.45±0.56
C13:0	0.18±0.09	0.02±0.01	0.07±0.02	0.08±0.04	0.05±0.03	0.11±0.07
C14:0	2.47±0.24	3.26±1.43	6.88±2.46	7.02±1.6	5.98±1.32	8.29±3.17
C15:0	0.9±0.2	0.74±0.26	1.11±0.33	0.72±0.25	1.22±0.67	1.68±0.46
Ca-15:0	0.04±0.02	0.07±0.03	0.06±0.02	0.06±0.03	0.08±0.03	0.23±0.12
Ci-15:0	0.14±0.04	0.2±0.09	0.26±0.05	0.03±0.06	0.38±0.14	0.55±0.3
C16:0	17.4±3.1	17.63±2.23	19.04±1.99	16.37±2.91	14.89±3.6	17.83±3.34
C17:0	1.97±0.61	1.37±0.37	0.94±0.84	1.02±0.47	0.64±0.22	0.72±0.25
Ca-17:0	0.21±0.11	0.16±0.06	0.72±0.19	0.11±0.14	0.32±0.15	0.11±0.05
Ci-17:0	0.62±0.24	0.52±0.15	0.64±0.15	0.3±0.2	0.46±0.3	0.58±0.33
C18:0	6.54±1.63	5.79±1.23	3.2±0.87	8.22±1.8	8.43±2.39	2.63±1.45
C20:0	0.29±0.06	0.6±0.33	0.11±0.02	0.27±0.21	0.58±0.34	0.39±0.26
C22:0	0.14±0.04	0.47±0.3	0.08±0.03	0.09±0.04	0.17±0.15	0.19±0.16
C23:0	0.05±0.06	0.15±0.2	0.01±0.02	0±0	0.03±0.06	0.02±0.01
C24:0	0.16±0.26	0.27±0.25	0.12±0.15	0.01±0.02	0.09±0.13	0.16±0.19
C14:1ω5	0.02±0.02	0.08±0.05	0.04±0.01	0.02±0.02	0.03±0.02	0.05±0.06
C16:1ω7c	1.95±0.82	6.22±1.27	5.19±2.96	3.42±2.52	3.51±2.09	4.57±1.33
C17:1ω7c	0.04±0.02	0.03±0.01	0.04±0.02	0.03±0.05	0.03±0.02	0.07±0.04
C18:1ω7c	2.64±1.02	2.04±0.54	2.33±0.72	1.33±0.48	2.14±1.17	3.17±1.8
C18:1ω9c	4.25±1.64	7.09±2.63	1.47±0.41	5.76±2.62	6.92±5.96	4.08±1.34
C20:1ω9c	1.06±0.17	1.38±0.45	1.54±0.66	1.48±0.86	1.58±0.63	0.75±0.36
C20:1ω11	0.07±0.03	0.14±0.07	0.43±0.14	0.1±0.1	0.15±0.06	0.07±0.05
C22:1ω9c	3.47±0.57	2.73±1.42	1.47±1.32	2.26±1.51	3.64±2.09	4.48±5.18
C22:1ω11	0.05±0.04	0.14±0.14	0.04±0.06	0.84±1.21	0.26±0.27	0.1±0.12
C24:1ω9c	0.13±0.08	3.18±1.42	0.12±0.11	0.26±0.15	0.41±0.19	0.21±0.16
C16:4ω1	0.09±0.11	0.07±0.08	1.19±1.12	0.41±0.77	0.37±0.57	0.41±0.53
C18:2ω6c	1.51±0.48	1.64±0.45	1.32±0.25	0.99±0.3	1.07±0.39	3.19±0.95
C18:3ω3	1.18±0.27	1.41±0.47	1.77±0.71	0.87±0.35	0.87±0.38	2.58±1.55
C18:3ω6	0.15±0.07	0.07±0.04	0.15±0.04	0.06±0.05	0.08±0.04	0.24±0.14
C18:4ω3c	2.65±0.92	1.53±0.67	3.75±0.84	1.5±0.67	1.97±1.07	4.94±3.2

C20:2ω6	0.63±0.17	0.24±0.06	1.48±0.25	0.36±0.2	0.34±0.19	0.2±0.1
C20:3ω3	1.01±0.29	0.17±0.08	0.52±0.17	0.12±0.09	0.12±0.1	0.08±0.03
C20:3ω6	0.14±0.08	0.06±0.04	0.16±0.06	0.06±0.05	0.12±0.07	0.16±0.16
C20:4ω6	1.46±0.43	0.76±0.24	0.84±0.21	0.84±0.42	6.08±4.68	1.57±0.94
C20:5ω3	17.5±2.03	14.23±2.46	21.27±2.73	18.96±3.82	16.17±3.37	13.6±3.29
C21:5ω3	0.5±0.12	0.36±0.11	1.04±0.13	0.25±0.31	0.3±0.13	0.57±0.33
C22:2ω6	0.41±0.06	0.08±0.02	0.04±0.02	0.02±0.04	0.06±0.04	0.07±0.06
C22:3ω6	0.18±0.08	0.06±0.04	0.01±0.01	0±0.01	0.01±0.01	0.03±0.03
C22:4ω6	0.04±0.02	0.02±0.02	0.05±0.01	0.01±0.02	0.32±0.33	0.02±0.02
C22:5ω3	0.92±0.19	0.63±0.14	0.94±0.15	0.82±0.19	1.16±0.54	0.73±0.32
C22:5ω6	0.49±0.24	0.42±0.15	0.37±0.16	0.33±0.21	2.31±1.55	0.32±0.16
C22:6ω3	24.74±2.58	23.62±2.12	18.91±6.88	24.4±5.78	16.33±4.27	19.64±6.03
SAFA	32.73±4	31.6±4.62	33.48±3.15	34.51±4.43	33.66±5.57	34.11±6.05
MUFA	13.67±3.19	23.04±4.33	12.69±3.6	15.5±6.46	18.67±7.34	17.54±6.4
PUFA	53.6±3.33	45.36±3.4	53.83±5.81	49.99±3.64	47.67±7.82	48.35±10.68
SUM(EPA_DHA_ARA)	43.7±2.93	38.61±2.96	41.02±5.3	44.2±4.44	38.59±6.93	34.81±7.82
SUM(ALA_LA)	2.69±0.49	3.05±0.85	3.09±0.89	1.86±0.6	1.94±0.69	5.77±1.85
SUM(Branched_OddC)	4.8±1.3	3.7±0.8	4.96±1.21	2.61±0.92	3.59±1.25	4.74±1.19
SUM(Calanoid markers)	4.65±0.57	4.39±1.67	3.48±1.34	4.68±2.45	5.62±2.17	5.39±5.45

Supplemental Table S3.9. SIMPER analyses of fatty acid profiles of all gelatinous zooplankton separated by feeding style. SIMPER analyses compared the fatty acid (FA) profiles of all gelatinous zooplankton, categorized by feeding style (predator vs. grazer). FA profiles were compared across samples as proportional contributions of each FA to the total FA concentration per sample. Per group comparison, the top 10 FAs contributing to dissimilarity are listed in order of decreasing contribution to the average between-group dissimilarity. Bolded p-values indicate FAs that were significantly dissimilar ($p<0.05$) in proportion between the two groups compared.

Feeding Style		**SIMPER Order**	**FA**	**Avg Proportion (% of total FA)**		**Contribution to Avg Between-Group Dissimilarity (Avg±Stdv)**	**Cumulative Contribution to Between-Group Dissimiliarity (%, ordered)**	**p**
Group A	**Group B**			**Group A**	**Group B**			
predator	grazer	1	C22:6ω3	21.58	19	3.41±2.48	13.06	0.057
predator	grazer	2	C18:0	7.27	2.66	2.35±1.19	22.05	**0.001**
predator	grazer	3	C20:5ω3	16.3	15.42	2.32±1.84	30.94	**0.047**
predator	grazer	4	C14:0	5.06	8.21	1.91±1.42	38.25	**0.001**
predator	grazer	5	C16:0	16.41	18.18	1.85±1.46	45.33	0.242
predator	grazer	6	C18:1ω9c	6.45	3.53	1.79±1.92	52.16	0.661
predator	grazer	7	C22:1ω9c	2.9	3.89	1.55±2.03	58.1	**0.005**
predator	grazer	8	C18:4ω3c	1.76	4.7	1.54±1.42	64	**0.001**
predator	grazer	9	C16:1ω7c	4.36	4.85	1.23±0.87	68.7	0.916
predator	grazer	10	C20:4ω6	2.55	1.4	1.09±1.6	72.89	0.992

Supplemental Table S3.10. Averages of FA proportions per feeding style. Forty-six unique fatty acids (FA) found in gelatinous zooplankton samples, listed in order of increasing desaturation and elongation, followed by FA summations: SAFA (saturated fatty acids), MUFA (monounsaturated fatty acids), PUFA (polyunsaturated fatty acids), SUM(EPA_DHA_ARA) (essential fatty acids), SUM(ALA_LA), SUM(Branched_OddC), and SUM(Calanoid_markers). Each result is the percent contribution of that FA to the overall FA content, averaged across samples with standard deviations. Samples are categorized according to feeding style (predator vs. grazer).

FA	grazer	predator
C8:0	0.01±0.02	0.02±0.14
C9:0	0.07±0.08	0.06±0.18
C10:0	0.05±0.07	0.03±0.05
C11:0	0.02±0.02	0.01±0.01
C12:0	0.39±0.5	0.25±0.35
C13:0	0.1±0.06	0.06±0.05
C14:0	8.21±2.88	5.06±2.17
C15:0	1.53±0.51	0.91±0.5
Ca-15:0	0.2±0.12	0.07±0.03
Ci-15:0	0.49±0.29	0.21±0.17
C16:0	18.18±3.12	16.41±3.12
C17:0	0.68±0.24	1.09±0.55
Ca-17:0	0.23±0.23	0.22±0.18
Ci-17:0	0.6±0.3	0.45±0.24
C18:0	2.66±1.29	7.27±2.2
C20:0	0.33±0.26	0.49±0.33
C22:0	0.17±0.15	0.25±0.25
C23:0	0.02±0.01	0.07±0.14
C24:0	0.14±0.18	0.14±0.2
C14:1ω5	0.05±0.06	0.05±0.04
C16:1ω7c	4.85±1.85	4.36±2.36
C17:1ω7c	0.06±0.04	0.03±0.03
C18:1ω7c	3.02±1.65	1.92±0.88
C18:1ω9c	3.53±1.62	6.45±4.06
C20:1ω9c	0.85±0.4	1.48±0.65
C20:1ω11	0.13±0.14	0.14±0.1
C22:1ω9c	3.89±4.77	2.9±1.75
C22:1ω11	0.09±0.11	0.35±0.69
C24:1ω9c	0.19±0.15	1.33±1.62
C16:4ω1	0.64±0.8	0.25±0.53
C18:2ω6c	2.8±1.14	1.27±0.48
C18:3ω3	2.4±1.46	1.1±0.48
C18:3ω6	0.23±0.13	0.08±0.04

C18:4ω3c	4.7±2.9	1.76±0.9
C20:2ω6	0.47±0.54	0.35±0.25
C20:3ω3	0.17±0.19	0.19±0.22
C20:3ω6	0.17±0.14	0.09±0.06
C20:4ω6	1.4±0.9	2.55±3.62
C20:5ω3	15.42±4.71	16.3±3.6
C21:5ω3	0.68±0.37	0.33±0.21
C22:2ω6	0.06±0.06	0.07±0.09
C22:3ω6	0.02±0.02	0.03±0.05
C22:4ω6	0.03±0.02	0.12±0.23
C22:5ω3	0.78±0.31	0.87±0.4
C22:5ω6	0.32±0.15	1.01±1.26
C22:6ω3	19±6.04	21.58±5.43
SAFA	34.06±5.51	33.07±4.93
MUFA	16.67±6.13	18.99±6.8
PUFA	49.27±9.96	47.94±5.85
SUM(EPA_DHA_ARA)	35.82±7.49	40.43±5.54
SUM(ALA_LA)	5.2±2.03	2.37±0.9
SUM(Branched_OddC)	4.66±1.07	3.5±1.24
SUM(Calanoid_markers)	4.96±4.93	4.86±2.07

Supplemental Table S3.11. SIMPER analyses of fatty acid profiles of all gelatinous zooplankton separated by feeding guild. SIMPER analyses compared the fatty acid (FA) profiles of all gelatinous zooplankton, categorized by feeding guild: HB consumer (H_BC), MB consumer (M_BC), SB consumer (S_BC), or grazer. FA profiles were compared across samples as proportional contributions of each FA to the total FA concentration per sample. Per group comparison, the top 10 FAs contributing to dissimilarity are listed in order of decreasing contribution to the average between-group dissimilarity. Bolded p-values indicate FAs that were significantly dissimilar ($p<0.05$) in proportion between the two groups compared.

Feeding Guild		**SIMPER Order**	**FA**	**Avg Proportion (% of total FA)**		**Contribution to Avg Between-Group Dissimilarity (Avg±Stdv)**	**Cumulative Contribution to Between-Group Dissimiliarity (%, ordered)**	**p**
Group A	**Group B**			**Group A**	**Group B**			
S_BC	H_BC	1	C22:6ω3	17.73	23.49	3.47±1.97	14.18	0.085
S_BC	H_BC	2	C20:4ω6	5.87	1.03	2.53±2.3	24.52	**0.001**
S_BC	H_BC	3	C16:0	14.5	17.49	2.21±1.32	33.56	**0.001**
S_BC	H_BC	4	C20:5ω3	17.58	14.62	2.01±1.52	41.76	0.845
S_BC	H_BC	5	C18:1ω9c	4.91	6.84	1.7±1.25	48.7	0.767
S_BC	H_BC	6	C16:1ω7c	3.8	5.87	1.57±0.87	55.11	**0.001**
S_BC	H_BC	7	C14:0	5.68	3.55	1.4±0.89	60.82	0.849
S_BC	H_BC	8	C24:1ω9c	0.26	2.97	1.36±0.77	66.38	**0.001**

S_BC	H_BC	9	C18:0	7.4	5.93	1.18±0.9	71.21	1
S_BC	H_BC	10	C22:5ω6	2.08	0.49	0.86±0.8	74.75	**0.001**
S_BC	grazer	1	C22:6ω3	17.73	19	3.17±2.35	11.55	0.558
S_BC	grazer	2	C16:0	14.5	18.18	2.47±1.67	20.54	**0.001**
S_BC	grazer	3	C20:4ω6	5.87	1.4	2.42±2.22	29.33	**0.001**
S_BC	grazer	4	C18:0	7.4	2.66	2.41±1.19	38.1	**0.001**
S_BC	grazer	5	C20:5ω3	17.58	15.42	2.33±1.85	46.57	0.122
S_BC	grazer	6	C14:0	5.68	8.21	1.65±1.32	52.58	0.103
S_BC	grazer	7	C18:4ω3c	2.06	4.7	1.46±1.39	57.88	**0.001**
S_BC	grazer	8	C22:1ω9c	2.66	3.89	1.44±2.02	63.13	0.112
S_BC	grazer	9	C16:1ω7c	3.8	4.85	1.26±0.95	67.7	0.657
S_BC	grazer	10	C18:1ω9c	4.91	3.53	1.24±1.15	72.22	0.999
S_BC	M_BC	1	C22:6ω3	17.73	23.33	4.14±2.7	17.22	**0.001**
S_BC	M_BC	2	C20:4ω6	5.87	0.86	2.54±2.33	27.77	**0.001**
S_BC	M_BC	3	C18:1ω9c	4.91	7.63	2.27±2.66	37.22	**0.027**
S_BC	M_BC	4	C16:0	14.5	17.11	2.17±1.32	46.23	**0.001**
S_BC	M_BC	5	C20:5ω3	17.58	17.08	2±1.69	54.56	0.808
S_BC	M_BC	6	C18:0	7.4	8.89	1.34±0.94	60.13	1
S_BC	M_BC	7	C16:1ω7c	3.8	2.99	1.15±1.06	64.93	0.956
S_BC	M_BC	8	C22:1ω9c	2.66	3.46	1.06±0.92	69.35	0.796
S_BC	M_BC	9	C14:0	5.68	6.35	1.02±0.85	73.6	1
S_BC	M_BC	10	C22:5ω6	2.08	0.52	0.87±0.79	77.21	**0.001**
H_BC	grazer	1	C22:6ω3	23.49	19	3.17±2.25	12.81	0.609
H_BC	grazer	2	C14:0	3.55	8.21	2.43±1.51	22.65	**0.001**
H_BC	grazer	3	C20:5ω3	14.62	15.42	2.13±1.69	31.26	0.553
H_BC	grazer	4	C18:1ω9c	6.84	3.53	1.83±1.34	38.68	0.547
H_BC	grazer	5	C18:0	5.93	2.66	1.7±0.8	45.56	0.181
H_BC	grazer	6	C18:4ω3c	1.48	4.7	1.63±1.44	52.18	**0.001**
H_BC	grazer	7	C16:0	17.49	18.18	1.51±1.2	58.29	0.99
H_BC	grazer	8	C22:1ω9c	2.67	3.89	1.49±2.03	64.32	0.054
H_BC	grazer	9	C24:1ω9c	2.97	0.19	1.39±0.77	69.94	**0.001**
H_BC	grazer	10	C16:1ω7c	5.87	4.85	1.13±0.75	74.51	0.982
H_BC	M_BC	1	C22:6ω3	23.49	23.33	2.67±2.08	13.05	0.996
H_BC	M_BC	2	C18:1ω9c	6.84	7.63	2.27±2.32	24.17	**0.019**
H_BC	M_BC	3	C20:5ω3	14.62	17.08	2.24±1.68	35.13	0.286
H_BC	M_BC	4	C16:1ω7c	5.87	2.99	1.69±0.93	43.4	**0.001**
H_BC	M_BC	5	C18:0	5.93	8.89	1.61±0.99	51.28	0.55
H_BC	M_BC	6	C14:0	3.55	6.35	1.55±1.06	58.84	0.337
H_BC	M_BC	7	C16:0	17.49	17.11	1.32±1.07	65.3	1
H_BC	M_BC	8	C24:1ω9c	2.97	0.38	1.3±0.76	71.67	**0.001**
H_BC	M_BC	9	C22:1ω9c	2.67	3.46	1.11±0.96	77.12	0.745
H_BC	M_BC	10	C18:1ω7c	2.09	1.24	0.48±0.3	79.49	0.974

grazer	M_BC	1	C22:6ω3	19	23.33	3.99±2.8	15.09	**0.002**
grazer	M_BC	2	C18:0	2.66	8.89	3.12±1.12	26.9	**0.001**
grazer	M_BC	3	C20:5ω3	15.42	17.08	2.57±1.98	36.62	**0.015**
grazer	M_BC	4	C18:1ω9c	3.53	7.63	2.32±2.84	45.4	**0.017**
grazer	M_BC	5	C22:1ω9c	3.89	3.46	1.75±2.01	52	**0.001**
grazer	M_BC	6	C16:0	18.18	17.11	1.61±1.3	58.06	0.933
grazer	M_BC	7	C18:4ω3c	4.7	1.79	1.51±1.43	63.79	**0.001**
grazer	M_BC	8	C14:0	8.21	6.35	1.51±1.19	69.49	0.498
grazer	M_BC	9	C16:1ω7c	4.85	2.99	1.33±0.91	74.51	0.259
grazer	M_BC	10	C18:1ω7c	3.02	1.24	0.94±0.8	78.06	**0.001**

Supplemental Table S3.12. Averages of FA proportions per feeding guild. Forty-six unique fatty acids (FA) found in gelatinous zooplankton samples, listed in order of increasing desaturation and elongation, followed by FA summations: SAFA (saturated fatty acids), MUFA (monounsaturated fatty acids), PUFA (polyunsaturated fatty acids), SUM(EPA_DHA_ARA) (essential fatty acids), SUM(ALA_LA), SUM(Branched_OddC), and SUM(Calanoid_markers). Each result is the percent contribution of that FA to the overall FA content, averaged across samples with standard deviations. Samples are categorized according to feeding guild: HB consumer (H_BC), MB consumer (M_BC), SB consumer (S_BC), or grazer.

FA	H_BC	M_BC	S_BC	grazer
C8:0	0.04±0.22	0.01±0.03	0±0.01	0.01±0.02
C9:0	0.08±0.13	0.06±0.3	0.04±0.07	0.07±0.08
C10:0	0.03±0.05	0.04±0.07	0.02±0.02	0.05±0.07
C11:0	0.01±0.01	0±0.01	0.01±0.01	0.02±0.02
C12:0	0.19±0.22	0.17±0.18	0.39±0.52	0.39±0.5
C13:0	0.03±0.02	0.07±0.04	0.08±0.07	0.1±0.06
C14:0	3.55±1.74	6.35±1.83	5.68±1.88	8.21±2.88
C15:0	0.74±0.25	0.73±0.21	1.29±0.67	1.53±0.51
Ca-15:0	0.07±0.03	0.08±0.03	0.06±0.03	0.2±0.12
Ci-15:0	0.21±0.1	0.11±0.15	0.31±0.18	0.49±0.29
C16:0	17.49±2.25	17.11±2.59	14.5±3.6	18.18±3.12
C17:0	1.32±0.38	0.89±0.34	1.01±0.75	0.68±0.24
Ca-17:0	0.16±0.06	0.16±0.15	0.34±0.25	0.23±0.23
Ci-17:0	0.5±0.15	0.23±0.18	0.6±0.22	0.6±0.3
C18:0	5.93±1.38	8.89±1.95	7.4±2.23	2.66±1.29
C20:0	0.58±0.33	0.31±0.2	0.54±0.37	0.33±0.26
C22:0	0.44±0.3	0.13±0.15	0.14±0.07	0.17±0.15
C23:0	0.14±0.19	0±0.01	0.04±0.07	0.02±0.01
C24:0	0.25±0.25	0.05±0.13	0.09±0.13	0.14±0.18
C14:1ω5	0.08±0.05	0.02±0.03	0.03±0.02	0.05±0.06
C16:1ω7c	5.87±1.75	2.99±1.93	3.8±2.39	4.85±1.85
C17:1ω7c	0.03±0.01	0.02±0.05	0.03±0.02	0.06±0.04
C18:1ω7c	2.09±0.56	1.24±0.53	2.33±1.08	3.02±1.65

C18:1ω9c	6.84±2.69	7.63±5.98	4.91±2.68	3.53±1.62
C20:1ω9c	1.4±0.44	1.22±0.4	1.81±0.88	0.85±0.4
C20:1ω11	0.13±0.07	0.09±0.08	0.18±0.14	0.13±0.14
C22:1ω9c	2.67±1.4	3.46±2.51	2.66±1.11	3.89±4.77
C22:1ω11	0.14±0.13	0.29±0.46	0.66±1.07	0.09±0.11
C24:1ω9c	2.97±1.55	0.38±0.19	0.26±0.2	0.19±0.15
C16:4ω1	0.08±0.12	0.26±0.57	0.45±0.7	0.64±0.8
C18:2ω6c	1.59±0.47	1.13±0.37	1.04±0.39	2.8±1.14
C18:3ω3	1.36±0.49	0.85±0.21	1.02±0.52	2.4±1.46
C18:3ω6	0.07±0.04	0.06±0.04	0.1±0.05	0.23±0.13
C18:4ω3c	1.48±0.69	1.79±0.84	2.06±1.08	4.7±2.9
C20:2ω6	0.27±0.11	0.28±0.11	0.5±0.36	0.47±0.54
C20:3ω3	0.17±0.08	0.09±0.05	0.31±0.35	0.17±0.19
C20:3ω6	0.07±0.04	0.05±0.03	0.14±0.07	0.17±0.14
C20:4ω6	1.03±1.01	0.86±0.48	5.87±4.8	1.4±0.9
C20:5ω3	14.62±2.74	17.08±4.31	17.58±3.08	15.42±4.71
C21:5ω3	0.35±0.11	0.2±0.27	0.41±0.2	0.68±0.37
C22:2ω6	0.08±0.03	0.03±0.04	0.11±0.13	0.06±0.06
C22:3ω6	0.05±0.04	0±0	0.03±0.07	0.02±0.02
C22:4ω6	0.09±0.25	0±0	0.26±0.26	0.03±0.02
C22:5ω3	0.73±0.39	0.76±0.26	1.13±0.4	0.78±0.31
C22:5ω6	0.49±0.36	0.52±0.36	2.08±1.74	0.32±0.15
C22:6ω3	23.49±2.22	23.33±6.51	17.73±5.12	19±6.04
SAFA	31.75±4.5	35.38±5.82	32.53±3.82	34.06±5.51
MUFA	22.23±5.08	17.34±8.45	16.66±5.46	16.67±6.13
PUFA	46.02±4.13	47.28±7.21	50.8±5.2	49.27±9.96
SUM(EPA_DHA_ARA)	39.14±3.6	41.27±8.18	41.17±4.2	35.82±7.49
SUM(ALA_LA)	2.95±0.89	1.98±0.53	2.05±0.83	5.2±2.03
SUM(Branched_OddC)	3.64±0.8	2.54±0.75	4.22±1.48	4.66±1.07
SUM(Calanoid_markers)	4.34±1.63	5.06±2.71	5.3±1.76	4.96±4.93

Supplemental Table S3.13. Conversion factors from the literature. Listed are values used to convert experimental FA data from measurements of "ng FA per mg dry weight" to measurements of "ng FA per mg wet weight" and "ng FA per mg carbon content." Listed also are the references used and assumptions made in using these referenced values. References include: (1) Kiørboe, T. (2013) Zooplankton body composition. *Limnol. Oceanogr*. **58**, 1843–1850. and (2) Ikeda, T. (1996) Metabolism, body composition, and energy budget of the mesopelagic fish *Maurolicus muelleri* in the Sea of Japan. *Fish. Bull*., **94**, 49–58.

Taxon	**Dry (% wet)**	**C (% dry)**	**Reference**	**Assume same as:**
Tomopteris sp.	13.4	37	Kiørboe (2013)	Polychaetes
Chaetognatha	9.3	36.7	Kiørboe (2013)	Chaetognaths
Appendicularia	5.4	10.3	Kiørboe (2013)	Tunicates
Doliolida	5.4	10.3	Kiørboe (2013)	Tunicates
Pyrosoma atlanticum	5.4	10.3	Kiørboe (2013)	Tunicates
Salpidae	5.4	10.3	Kiørboe (2013)	Tunicates
Aequorea sp.	4.1	13.2	Kiørboe (2013)	Cnidarians
Clytia sp.	4.1	13.2	Kiørboe (2013)	Cnidarians
Eutonina sp.	4.1	13.2	Kiørboe (2013)	Cnidarians
Mitrocoma sp.	4.1	13.2	Kiørboe (2013)	Cnidarians
Siphonophorae Calycophorae	4.1	13.2	Kiørboe (2013)	Cnidarians
Siphonophorae Physonectae	4.1	13.2	Kiørboe (2013)	Cnidarians
Beroe sp.	4	5.1	Kiørboe (2013)	Ctenophores
Pleurobrachia bachei	4	5.1	Kiørboe (2013)	Ctenophores
Pteropod Gymnosomata	23	28.9	Kiørboe (2013)	Pteropods
Pteropod Thecosomata	23	28.9	Kiørboe (2013)	Pteropods
Amphipoda Hyperiidea	23.9	34.5	Kiørboe (2013)	Amphipods
Copepoda	16.2	48	Kiørboe (2013)	Copepods
Euphausiidae	22.8	41.9	Kiørboe (2013)	Euphausids
Sebastes spp.	23	42.3	Ikeda (1996)	Larval *Maurolicus muelleri* with total length <15mm
Stenobrachius leucopsarus	23	42.3	Ikeda (1996)	Larval *Maurolicus muelleri* with total length <15mm

Supplemental Table S3.14. Averages of FA concentrations per gelatinous taxon (*1 of 4*). Forty-six unique fatty acids (FA) were found in samples, listed in order of increasing desaturation and elongation, followed by FA summations: SAFA (saturated fatty acids), MUFA (monounsaturated fatty acids), PUFA (polyunsaturated fatty acids), SUM(EPA+DHA+ARA) (essential fatty acids), SUM(ALA+LA), SUM(15:0+17:0), SUM(Branched+OddC), SUM(Calanoid_markers), and Total FA concentration. For each taxon, sample size is given by (n) and FA concentrations are presented in two units: "ng FA per mg dry weight" and "ng FA per mg wet weight." Each result is the average across samples with standard deviations. Samples are categorized according to taxon (lowest level of taxonomic identification possible).

Taxon:	***Aequorea* sp. (n=4)**		**Appendicularia (n=6)**		***Beroe* sp. (n=7)**		**Chaetognatha (n=36)**	
FA	*ng FA / mg dry wt*	*ng FA / mg wet wt*	*ng FA / mg dry wt*	*ng FA / mg wet wt*	*ng FA / mg dry wt*	*ng FA / mg wet wt*	*ng FA / mg dry wt*	*ng FA / mg wet wt*
C8:0	0.21 ±0.19	0.01 ±0.01	0.3 ±0.73	0.02 ±0.04	0.81 ±1.26	0.03 ±0.05	1.84 ±5.74	0.17 ±0.53
C9:0	3.06 ±2.25	0.13 ±0.09	0.78 ±1.19	0.04 ±0.06	3.23 ±4.87	0.13 ±0.19	11.85 ±42.91	1.1 ±3.99
C10:0	0.3 ±0.21	0.01 ±0.01	1.24 ±1.5	0.07 ±0.08	1.86 ±1.31	0.07 ±0.05	1.58 ±2.59	0.15 ±0.24
C11:0	0.23 ±0.09	0.01 ±0	0.32 ±0.26	0.02 ±0.01	0.67 ±0.32	0.03 ±0.01	0.42 ±0.59	0.04 ±0.06
C12:0	3.2 ±2.52	0.13 ±0.1	11.62 ±8.45	0.63 ±0.46	35.88 ±19.91	1.44 ±0.8	8.66 ±9.31	0.81 ±0.87
C13:0	2.02 ±0.82	0.08 ±0.03	3.94 ±3.39	0.21 ±0.18	11.6 ±7.39	0.46 ±0.3	1.64 ±2.3	0.15 ±0.21
C14:0	306.84 ±186.7	12.58 ±7.65	248.97 ±302.61	13.44 ±16.34	1303.3 ±752.11	52.13 ±30.08	255.04 ±335.49	23.72 ±31.2
C15:0	46.92 ±18.61	1.92 ±0.76	32.91 ±33.35	1.78 ±1.8	89.61 ±42.85	3.58 ±1.71	58.03 ±77.7	5.4 ±7.23
Ca-15:0	1.48 ±0.79	0.06 ±0.03	3.52 ±2.69	0.19 ±0.15	7.48 ±2.86	0.3 ±0.11	4.86 ±5.83	0.45 ±0.54
Ci-15:0	17.91 ±8.39	0.73 ±0.34	11.89 ±11.25	0.64 ±0.61	20.39 ±8.73	0.82 ±0.35	15.12 ±19.49	1.41 ±1.81
C16:0	525.47 ±223.16	21.54 ±9.15	601.89 ±733.68	32.5 ±39.62	2029.73 ±699.88	81.19 ±28	1634.9 ±2958.18	152.05 ±275.11
C17:0	24.93 ±13.33	1.02 ±0.55	11.1 ±12.11	0.6 ±0.65	130.13 ±65.86	5.21 ±2.63	111.36 ±184.26	10.36 ±17.14
Ca-17:0	17.68 ±8.58	0.72 ±0.35	0.87 ±0.54	0.05 ±0.03	8.27 ±4.42	0.33 ±0.18	13.3 ±16.24	1.24 ±1.51
Ci-17:0	31.5 ±13.64	1.29 ±0.56	3.68 ±3.91	0.2 ±0.21	49.12 ±12.05	1.96 ±0.48	41.9 ±54.03	3.9 ±5.02
C18:0	433.24 ±171.67	17.76 ±7.04	42.86 ±33.59	2.31 ±1.81	1021.23 ±154.54	40.85 ±6.18	464.56 ±732.19	43.2 ±68.09
C20:0	33.05 ±12.47	1.36 ±0.51	4.34 ±3.73	0.23 ±0.2	41.69 ±43.07	1.67 ±1.72	46.1 ±79.02	4.29 ±7.35
C22:0	4.64 ±2.02	0.19 ±0.08	2.49 ±1.95	0.13 ±0.11	9.21 ±3	0.37 ±0.12	35.52 ±61.79	3.3 ±5.75
C23:0	0.04 ±0.08	0 ±0	0.03 ±0.07	0 ±0	0.13 ±0.27	0.01 ±0.01	7.75 ±12.32	0.72 ±1.15
C24:0	1.17 ±0.52	0.05 ±0.02	0.6 ±0.48	0.03 ±0.03	3.29 ±1.51	0.13 ±0.06	25.14 ±64.15	2.34 ±5.97
C14:1ω5	0.59 ±0.4	0.02 ±0.02	1.37 ±1.75	0.07 ±0.09	9.18 ±6.03	0.37 ±0.24	6.77 ±8.49	0.63 ±0.79
C16:1ω7c	122.11 ±71.74	5.01 ±2.94	136.46 ±168.45	7.37 ±9.1	1184.65 ±998.65	47.39 ±39.95	571.5 ±770.08	53.15 ±71.62
C17:1ω7c	1.01 ±0.49	0.04 ±0.02	2.77 ±3.56	0.15 ±0.19	2.26 ±0.57	0.09 ±0.02	2.44 ±4.28	0.23 ±0.4
C18:1ω7c	86.85 ±46.65	3.56 ±1.91	71.37 ±76.99	3.85 ±4.16	225.06 ±96.46	9 ±3.86	203.38 ±313.75	18.91 ±29.18

C18:1ω9c	245.53 ±117.54	10.07 ±4.82	97.85 ±101.38	5.28 ±5.47	1607.14 ±858.72	64.29 ±34.35	683.45 ±1216.02	63.56 ±113.09
C20:1ω9c	109.14 ±60.02	4.47 ±2.46	10.72 ±7.63	0.58 ±0.41	449.61 ±285.59	17.98 ±11.42	104.2 ±140.42	9.69 ±13.06
C20:1ω11	9.58 ±6.38	0.39 ±0.26	0.21 ±0.24	0.01 ±0.01	41.83 ±31.22	1.67 ±1.25	12.59 ±22.65	1.17 ±2.11
C22:1ω9c	133.48 ±58.73	5.47 ±2.41	125.27 ±90.33	6.76 ±4.88	324.25 ±65.85	12.97 ±2.63	157.55 ±144.39	14.65 ±13.43
C22:1ω11	33.74 ±41.48	1.38 ±1.7	2.16 ±3.79	0.12 ±0.2	416.98 ±431.69	16.68 ±17.27	16.09 ±38.13	1.5 ±3.55
C24:1ω9c	7.65 ±4.54	0.31 ±0.19	3.42 ±2.48	0.18 ±0.13	24.1 ±11.19	0.96 ±0.45	322.95 ±696.94	30.03 ±64.82
C16:4ω1	9.56 ±10.61	0.39 ±0.44	2.05 ±1.62	0.11 ±0.09	256.72 ±272.83	10.27 ±10.91	12.1 ±35.38	1.13 ±3.29
C18:2ω6c	23.87 ±12.55	0.98 ±0.51	107.76 ±145.08	5.82 ±7.83	155.29 ±36.39	6.21 ±1.46	136.96 ±192.46	12.74 ±17.9
C18:3ω3	16.35 ±8.89	0.67 ±0.36	223.71 ±336.09	12.08 ±18.15	145.1 ±56.33	5.8 ±2.25	112.38 ±131.43	10.45 ±12.22
C18:3ω6	2.16 ±1.21	0.09 ±0.05	5.87 ±7.79	0.32 ±0.42	20.75 ±15.48	0.83 ±0.62	7.21 ±10.45	0.67 ±0.97
C18:4ω3c	29.16 ±18.34	1.2 ±0.75	315.96 ±460.26	17.06 ±24.85	270.1 ±151.05	10.8 ±6.04	130.06 ±173.15	12.1 ±16.1
C20:2ω6	13.3 ±6.8	0.55 ±0.28	2.65 ±3	0.14 ±0.16	59.79 ±30.82	2.39 ±1.23	20.21 ±27.69	1.88 ±2.58
C20:3ω3	2.75 ±1.44	0.11 ±0.06	1.69 ±2.2	0.09 ±0.12	20.89 ±14.14	0.84 ±0.57	13.42 ±16.24	1.25 ±1.51
C20:3ω6	6.72 ±3.47	0.28 ±0.14	1.19 ±1.94	0.06 ±0.11	19.56 ±11.16	0.78 ±0.45	6.94 ±10.02	0.65 ±0.93
C20:4ω6	535.61 ±253.58	21.96 ±10.4	15.61 ±20.1	0.84 ±1.09	193.84 ±72.27	7.75 ±2.89	69.62 ±97.55	6.47 ±9.07
C20:5ω3	801.86 ±433.84	32.88 ±17.79	589.91 ±793.68	31.86 ±42.86	3639.16 ±1849.06	145.57 ±73.96	1337.55 ±2007.94	124.39 ±186.74
C21:5ω3	14.18 ±7.78	0.58 ±0.32	8.03 ±10.68	0.43 ±0.58	96.19 ±45.94	3.85 ±1.84	35.15 ±56.14	3.27 ±5.22
C22:2ω6	2.17 ±1.24	0.09 ±0.05	1.63 ±1.27	0.09 ±0.07	5.45 ±4.28	0.22 ±0.17	6.04 ±7.31	0.56 ±0.68
C22:3ω6	1.03 ±1.46	0.04 ±0.06	0.5 ±0.45	0.03 ±0.02	0.77 ±1.5	0.03 ±0.06	5.32 ±8.08	0.49 ±0.75
C22:4ω6	21.86 ±13.21	0.9 ±0.54	0.1 ±0.24	0.01 ±0.01	6.13 ±3.01	0.25 ±0.12	2.52 ±4.25	0.23 ±0.4
C22:5ω3	68.3 ±35.12	2.8 ±1.44	12.94 ±17.56	0.7 ±0.95	142.74 ±74.03	5.71 ±2.96	56.74 ±75.57	5.28 ±7.03
C22:5ω6	171.79 ±89.09	7.04 ±3.65	15.29 ±23.09	0.83 ±1.25	48.31 ±12.71	1.93 ±0.51	33.07 ±50.35	3.08 ±4.68
C22:6ω3	865.22 ±495.43	35.47 ±20.31	763.82 ±1096.59	41.25 ±59.22	2751.95 ±684.38	110.08 ±27.38	2103.72 ±3321.69	195.65 ±308.92
SAFA	1453.89 ±630.32	59.61 ±25.84	983.35 ±1140.41	53.1 ±61.58	4767.61 ±1534.39	190.7 ±61.38	2739.56 ±4572.98	254.78 ±425.29
MUFA	749.69 ±398.79	30.74 ±16.35	451.59 ±435.09	24.39 ±23.49	4285.05 ±2556.79	171.4 ±102.27	2080.94 ±3250.96	193.53 ±302.34
PUFA	2585.9 ±1352.54	106.02 ±55.45	2068.71 ±2919.1	111.71 ±157.63	7832.74 ±2954.64	313.31 ±118.19	4088.98 ±6133.59	380.28 ±570.42
SUM (EPA+DHA+ ARA)	2202.69 ±1176.71	90.31 ±48.25	1369.34 ±1910.06	73.94 ±103.14	6584.95 ±2493.4	263.4 ±99.74	3510.88 ±5385.96	326.51 ±500.89
SUM (ALA+LA)	40.23 ±21.41	1.65 ±0.88	331.47 ±480.84	17.9 ±25.97	300.39 ±83.2	12.02 ±3.33	249.34 ±318.12	23.19 ±29.59
SUM (15:0+17:0)	140.42 ±59.06	5.76 ±2.42	63.97 ±63.37	3.45 ±3.42	305 ±120.9	12.2 ±4.84	244.56 ±346.42	22.74 ±32.22

SUM (Branched+ OddC)	160.96 ±67.72	6.6 ±2.78	79.85 ±80.58	4.31 ±4.35	419.08 ±117.83	16.76 ±4.71	303.8 ±456.7	28.25 ±42.47
SUM (Calanoid markers)	285.94 ±161.66	11.72 ±6.63	138.35 ±97.38	7.47 ±5.26	1232.67 ±785.43	49.31 ±31.42	290.44 ±337.89	27.01 ±31.42
Total FA	4789.48 ±2377.97	196.37 ±97.5	3503.66 ±4481.42	189.2 ±242	16885.4 ±6876.69	675.42 ±275.07	8909.49 ±13920.43	828.58 ±1294.6

Supplemental Table S3.15. Averages of FA concentrations per gelatinous taxon (*2 of 4*). Forty-six unique fatty acids (FA) were found in samples, listed in order of increasing desaturation and elongation, followed by FA summations: SAFA (saturated fatty acids), MUFA (monounsaturated fatty acids), PUFA (polyunsaturated fatty acids), SUM(EPA+DHA+ARA) (essential fatty acids), SUM(ALA+LA), SUM(15:0+17:0), SUM(Branched+OddC), SUM(Calanoid_markers), and Total FA concentration. For each taxon, sample size is given by (n) and FA concentrations are presented in two units: "ng FA per mg dry weight" and "ng FA per mg wet weight." Each result is the average across samples with standard deviations. Samples are categorized according to taxon (lowest level of taxonomic identification possible).

Taxon:	***Clytia* sp. (n=9)**		**Doliolida (n=9)**		***Eutonina* sp. (n=2)**		***Mitrocoma* sp. (n=4)**	
FA	*ng FA / mg dry wt*	*ng FA / mg wet wt*	*ng FA / mg dry wt*	*ng FA / mg wet wt*	*ng FA / mg dry wt*	*ng FA / mg wet wt*	*ng FA / mg dry wt*	*ng FA / mg wet wt*
C8:0	0.02 ±0.07	0 ±0	0.73 ±0.6	0.04 ±0.03	0 ±0	0 ±0	0.29 ±0.57	0.01 ±0.02
C9:0	0.41 ±0.68	0.02 ±0.03	3.56 ±2.62	0.19 ±0.14	1.02 ±0.78	0.04 ±0.03	1.14 ±1.97	0.05 ±0.08
C10:0	0.66 ±0.75	0.03 ±0.03	2.08 ±1.69	0.11 ±0.09	1.81 ±1.2	0.07 ±0.05	0.48 ±0.49	0.02 ±0.02
C11:0	0.34 ±0.2	0.01 ±0.01	1.28 ±0.81	0.07 ±0.04	1.32 ±0.2	0.05 ±0.01	0.28 ±0.18	0.01 ±0.01
C12:0	9.24 ±6.59	0.38 ±0.27	10.73 ±5.36	0.58 ±0.29	14.11 ±6.93	0.58 ±0.28	3.41 ±0.58	0.14 ±0.02
C13:0	2.56 ±0.9	0.1 ±0.04	5.19 ±2.66	0.28 ±0.14	2.19 ±0.04	0.09 ±0	2.74 ±1.34	0.11 ±0.05
C14:0	272.34 ±135.96	11.17 ±5.57	620.52 ±394.7	33.51 ±21.31	204.4 ±25.55	8.38 ±1.05	194.54 ±37.5	7.98 ±1.54
C15:0	82.93 ±58.57	3.4 ±2.4	102.72 ±53.23	5.55 ±2.87	41.95 ±5.94	1.72 ±0.24	47.68 ±12.46	1.95 ±0.51
Ca-15:0	3.54 ±2.04	0.15 ±0.08	17.17 ±9.76	0.93 ±0.53	2.08 ±0.39	0.09 ±0.02	2.56 ±0.45	0.11 ±0.02
Ci-15:0	15.38 ±6.41	0.63 ±0.26	48.38 ±31.37	2.61 ±1.69	14.5 ±2.64	0.59 ±0.11	18.48 ±4.38	0.76 ±0.18
C16:0	805.45 ±410.53	33.02 ±16.83	858.66 ±518.19	46.37 ±27.98	347.42 ±70.9	14.24 ±2.91	350.39 ±91.05	14.37 ±3.73
C17:0	27.93 ±17.42	1.15 ±0.71	37.61 ±18.33	2.03 ±0.99	22.44 ±6.8	0.92 ±0.28	18.03 ±2.94	0.74 ±0.12
Ca-17:0	16.44 ±9.26	0.67 ±0.38	6.35 ±3.96	0.34 ±0.21	13.24 ±2.04	0.54 ±0.08	13.31 ±2.3	0.55 ±0.09
Ci-17:0	31.28 ±14.03	1.28 ±0.58	27.46 ±15.37	1.48 ±0.83	16.08 ±3.4	0.66 ±0.14	19.06 ±3.44	0.78 ±0.14
C18:0	338.74 ±192.04	13.89 ±7.87	107.66 ±36.73	5.81 ±1.98	320.36 ±59.91	13.13 ±2.46	202.52 ±58.16	8.3 ±2.38
C20:0	35.34 ±29.25	1.45 ±1.2	15.74 ±7.47	0.85 ±0.4	18.54 ±11.88	0.76 ±0.49	19.85 ±2.71	0.81 ±0.11
C22:0	7.69 ±5.07	0.32 ±0.21	11.5 ±6.8	0.62 ±0.37	4.27 ±1.2	0.17 ±0.05	6.9 ±2.03	0.28 ±0.08
C23:0	2.59 ±2.62	0.11 ±0.11	1.6 ±0.76	0.09 ±0.04	0.14 ±0.2	0.01 ±0.01	0.69 ±0.52	0.03 ±0.02

C24:0	5.29 ±4.58	0.22 ±0.19	3.64 ±2.58	0.2 ±0.14	2.9 ±1.54	0.12 ±0.06	2.31 ±0.97	0.09 ±0.04
C14:1ω5	1.71 ±1.37	0.07 ±0.06	2.25 ±1.42	0.12 ±0.08	0 ±0	0 ±0	1.2 ±0.25	0.05 ±0.01
C16:1ω7c	248.28 ±191.3	10.18 ±7.84	311.7 ±262.32	16.83 ±14.17	74.1 ±23.55	3.04 ±0.97	88.52 ±27.22	3.63 ±1.12
C17:1ω7c	2.1 ±1.02	0.09 ±0.04	2.16 ±1.54	0.12 ±0.08	1.21 ±0.47	0.05 ±0.02	1.05 ±0.35	0.04 ±0.01
C18:1ω7c	178.1 ±106.91	7.3 ±4.38	289.88 ±193.36	15.65 ±10.44	50.73 ±8.4	2.08 ±0.34	58.82 ±17.24	2.41 ±0.71
C18:1ω9c	193.52 ±118.2	7.93 ±4.85	190.99 ±83.88	10.31 ±4.53	86.8 ±20.44	3.56 ±0.84	100.77 ±42.76	4.13 ±1.75
C20:1ω9c	43.58 ±21.84	1.79 ±0.9	41.81 ±15.43	2.26 ±0.83	40.54 ±5.17	1.66 ±0.21	79.66 ±21.93	3.27 ±0.9
C20:1ω11	7.04 ±3.3	0.29 ±0.14	4.35 ±3.23	0.24 ±0.17	2.22 ±0.37	0.09 ±0.01	4.02 ±1.27	0.16 ±0.05
C22:1ω9c	135.02 ±72.77	5.54 ±2.98	101.16 ±27.32	5.46 ±1.48	74.22 ±14.91	3.04 ±0.61	68.46 ±33.4	2.81 ±1.37
C22:1ω11	11.95 ±12.25	0.49 ±0.5	5.53 ±4.41	0.3 ±0.24	7.32 ±1.27	0.3 ±0.05	16.22 ±9.58	0.67 ±0.39
C24:1ω9c	17.08 ±7.85	0.7 ±0.32	5.7 ±3.24	0.31 ±0.18	6.33 ±2.55	0.26 ±0.1	17.29 ±7.53	0.71 ±0.31
C16:4ω1	28.65 ±29.67	1.17 ±1.22	5.7 ±8.07	0.31 ±0.44	0 ±0	0 ±0	0 ±0	0 ±0
C18:2ω6c	51.38 ±29.06	2.11 ±1.19	208.22 ±93.29	11.24 ±5.04	28.12 ±1.95	1.15 ±0.08	24.48 ±1.98	1 ±0.08
C18:3ω3	48.87 ±44.32	2 ±1.82	104.9 ±51.9	5.66 ±2.8	31.96 ±4.58	1.31 ±0.19	27.37 ±2.63	1.12 ±0.11
C18:3ω6	4.97 ±3.33	0.2 ±0.14	21.43 ±13.53	1.16 ±0.73	2.23 ±0.57	0.09 ±0.02	2 ±0.39	0.08 ±0.02
C18:4ω3c	111.79 ±98	4.58 ±4.02	142.45 ±81.24	7.69 ±4.39	80.66 ±3.04	3.31 ±0.12	59.79 ±4.4	2.45 ±0.18
C20:2ω6	14.17 ±8.47	0.58 ±0.35	13.61 ±5.89	0.73 ±0.32	14.43 ±2.65	0.59 ±0.11	15.86 ±5.66	0.65 ±0.23
C20:3ω3	5.7 ±4.6	0.23 ±0.19	5.17 ±2.92	0.28 ±0.16	5.15 ±0.34	0.21 ±0.01	6.87 ±3.48	0.28 ±0.14
C20:3ω6	7.92 ±5.61	0.32 ±0.23	18.45 ±11.01	1 ±0.59	4.81 ±0.65	0.2 ±0.03	5.01 ±2.53	0.21 ±0.1
C20:4ω6	256.92 ±115.04	10.53 ±4.72	134.13 ±112.75	7.24 ±6.09	337.43 ±22.27	13.83 ±0.91	396.21 ±72.29	16.24 ±2.96
C20:5ω3	820.33 ±375.14	33.63 ±15.38	766.59 ±426.43	41.4 ±23.03	461.72 ±143.16	18.93 ±5.87	434.78 ±134.26	17.83 ±5.5
C21:5ω3	14.29 ±7.27	0.59 ±0.3	39.81 ±26.19	2.15 ±1.41	7.27 ±2.59	0.3 ±0.11	7.13 ±1.89	0.29 ±0.08
C22:2ω6	2.61 ±1	0.11 ±0.04	1.93 ±0.93	0.1 ±0.05	2.33 ±0.67	0.1 ±0.03	2.46 ±0.92	0.1 ±0.04
C22:3ω6	0.31 ±0.43	0.01 ±0.02	1.16 ±1.61	0.06 ±0.09	0 ±0	0 ±0	0 ±0	0 ±0
C22:4ω6	9.4 ±3.74	0.39 ±0.15	2.38 ±2.62	0.13 ±0.14	20.34 ±1.09	0.83 ±0.04	21.72 ±5.42	0.89 ±0.22
C22:5ω3	51 ±25.35	2.09 ±1.04	53.14 ±29.53	2.87 ±1.59	35.57 ±11.54	1.46 ±0.47	52.34 ±14.89	2.15 ±0.61
C22:5ω6	92.58 ±39.56	3.8 ±1.62	11.62 ±8.41	0.63 ±0.45	136.54 ±17.65	5.6 ±0.72	142.65 ±18.54	5.85 ±0.76
C22:6ω3	606.51 ±254.11	24.87 ±10.42	908.28 ±498.74	49.05 ±26.93	550.48 ±203.69	22.57 ±8.35	413.74 ±41.23	16.96 ±1.69
SAFA	1658.16 ±748.01	67.98 ±30.67	1882.59 ±1075.46	101.66 ±58.07	1028.79 ±183.22	42.18 ±7.51	904.65 ±184.34	37.09 ±7.56
MUFA	838.38 ±500.35	34.37 ±20.51	955.52 ±539.57	51.6 ±29.14	343.45 ±77.11	14.08 ±3.16	436.01 ±144.28	17.88 ±5.92
PUFA	2127.4 ±902.91	87.22 ±37.02	2438.96 ±1308.86	131.7 ±70.68	1719.05 ±416.44	70.48 ±17.07	1612.39 ±261.57	66.11 ±10.72

SUM (EPA+DHA+ ARA)	1683.77 ±675.48	69.03 ±27.69	1809.01 ±1008.76	97.69 ±54.47	1349.63 ±369.12	55.33 ±15.13	1244.72 ±235.92	51.03 ±9.67
SUM (ALA+LA)	100.24 ±69.88	4.11 ±2.86	313.12 ±144.47	16.91 ±7.8	60.08 ±6.54	2.46 ±0.27	51.85 ±3.93	2.13 ±0.16
SUM (15:0+17:0)	177.5 ±102.66	7.28 ±4.21	239.69 ±130.44	12.94 ±7.04	110.3 ±21.2	4.52 ±0.87	119.13 ±21.03	4.88 ±0.86
SUM (Branched+ OddC)	199.78 ±105.52	8.19 ±4.33	293.28 ±153.9	15.84 ±8.31	123.45 ±23.42	5.06 ±0.96	132.16 ±23.01	5.42 ±0.94
SUM (Calanoid markers)	197.59 ±100.87	8.1 ±4.14	152.85 ±39.45	8.25 ±2.13	124.29 ±21.71	5.1 ±0.89	168.37 ±55.95	6.9 ±2.29
Total FA	4623.94 ±2069.1	189.58 ±84.83	5277.07 ±2879.6	284.96 ±155.5	3091.29 ±676.77	126.74 ±27.75	2953.05 ±578.83	121.07 ±23.73

Supplemental Table S3.16. Averages of FA concentrations per gelatinous taxon (*3 of 4*). Forty-six unique fatty acids (FA) were found in samples, listed in order of increasing desaturation and elongation, followed by FA summations: SAFA (saturated fatty acids), MUFA (monounsaturated fatty acids), PUFA (polyunsaturated fatty acids), SUM(EPA+DHA+ARA) (essential fatty acids), SUM(ALA+LA), SUM(15:0+17:0), SUM(Branched+OddC), SUM(Calanoid_markers), and Total FA concentration. For each taxon, sample size is given by (n) and FA concentrations are presented in two units: "ng FA per mg dry weight" and "ng FA per mg wet weight." Each result is the average across samples with standard deviations. Samples are categorized according to taxon (lowest level of taxonomic identification possible).

Taxon:	***Pleurobrachia bachei* (n=19)**		**Pteropod Gymnosomata (n=2)**		**Pteropod Thecosomata (n=7)**		***Pyrosoma atlanticum* (n=3)**	
FA	*ng FA / mg dry wt*	*ng FA / mg wet wt*	*ng FA / mg dry wt*	*ng FA / mg wet wt*	*ng FA / mg dry wt*	*ng FA / mg wet wt*	*ng FA / mg dry wt*	*ng FA / mg wet wt*
C8:0	0.74 ±3.2	0.03 ±0.13	0 ±0	0 ±0	0.72 ±0.95	0.17 ±0.22	0.37 ±0.6	0.02 ±0.03
C9:0	0 ±0	0 ±0	3.3 ±1.59	0.76 ±0.37	8.76 ±10.78	2.02 ±2.48	3.62 ±5.1	0.2 ±0.28
C10:0	2.32 ±6.24	0.09 ±0.25	1.89 ±0.13	0.43 ±0.03	1.96 ±2.09	0.45 ±0.48	1.76 ±0.4	0.1 ±0.02
C11:0	0 ±0	0 ±0	1.05 ±0.32	0.24 ±0.07	0.64 ±0.48	0.15 ±0.11	0.63 ±0.06	0.03 ±0
C12:0	6.28 ±7.08	0.25 ±0.28	24.77 ±11.44	5.7 ±2.63	23.31 ±13.72	5.36 ±3.16	14.81 ±7.73	0.8 ±0.42
C13:0	3.82 ±2.27	0.15 ±0.09	12.64 ±9.77	2.91 ±2.25	10.58 ±6.97	2.43 ±1.6	2.92 ±1.46	0.16 ±0.08
C14:0	311.08 ±185.16	12.44 ±7.41	983.73 ±822.58	226.26 ±189.19	1022.35 ±604.08	235.14 ±138.94	237.91 ±171.65	12.85 ±9.27
C15:0	34.74 ±24.27	1.39 ±0.97	495.3 ±396.03	113.92 ±91.09	119.18 ±73.17	27.41 ±16.83	49.68 ±32.81	2.68 ±1.77
Ca-15:0	3.36 ±3.04	0.13 ±0.12	11.09 ±9.53	2.55 ±2.19	8.13 ±4.02	1.87 ±0.93	5.75 ±4.72	0.31 ±0.25
Ci-15:0	0 ±0	0 ±0	74.8 ±65.66	17.2 ±15.1	31.89 ±18.16	7.33 ±4.18	13.39 ±10.16	0.72 ±0.55
C16:0	809.44 ±485.95	32.38 ±19.44	5488.84 ±4876.38	1262.43 ±1121.57	2465.97 ±1428.89	567.17 ±328.64	574.55 ±403.29	31.03 ±21.78
C17:0	46.9 ±35.03	1.88 ±1.4	737.5 ±631.65	169.62 ±145.28	64.63 ±40.27	14.86 ±9.26	21.22 ±14.08	1.15 ±0.76

Ca-17:0	7.34 ±12.49	0.29 ±0.5	313.44 ±275.16	72.09 ±63.29	80.23 ±45.46	18.45 ±10.46	3.74 ±3.25	0.2 ±0.18
Ci-17:0	11.94 ±10.62	0.48 ±0.42	191.21 ±173.24	43.98 ±39.84	74.66 ±43.05	17.17 ±9.9	29.98 ±22.34	1.62 ±1.21
C18:0	388.05 ±206.09	15.52 ±8.24	1418.93 ±1229.14	326.35 ±282.7	351.69 ±216.27	80.89 ±49.74	59.11 ±37.63	3.19 ±2.03
C20:0	11.35 ±7.01	0.45 ±0.28	33.4 ±27.99	7.68 ±6.44	12.06 ±5.71	2.77 ±1.31	13.64 ±8.51	0.74 ±0.46
C22:0	4.37 ±3.17	0.17 ±0.13	21.22 ±17.82	4.88 ±4.1	9.74 ±5.94	2.24 ±1.37	4.17 ±2.54	0.23 ±0.14
C23:0	0 ±0	0 ±0	17.37 ±21.88	4 ±5.03	0.5 ±0.72	0.11 ±0.17	0.8 ±0.49	0.04 ±0.03
C24:0	0.07 ±0.21	0 ±0.01	106.65 ±146.87	24.53 ±33.78	8.99 ±6.82	2.07 ±1.57	2.87 ±2.05	0.15 ±0.11
C14:1ω5	0.73 ±1.68	0.03 ±0.07	16.4 ±12.56	3.77 ±2.89	4.55 ±2.96	1.05 ±0.68	2.28 ±1.26	0.12 ±0.07
C16:1ω7c	137.47 ±155.63	5.5 ±6.23	834.45 ±666.1	191.92 ±153.2	798.09 ±571.23	183.56 ±131.38	171.64 ±173.94	9.27 ±9.39
C17:1ω7c	2.1 ±4.68	0.08 ±0.19	10.06 ±9.36	2.31 ±2.15	5.53 ±3.79	1.27 ±0.87	1.17 ±0.79	0.06 ±0.04
C18:1ω7c	66.5 ±55.97	2.66 ±2.24	526.67 ±435.41	121.13 ±100.14	332.75 ±215.78	76.53 ±49.63	76.89 ±63.21	4.15 ±3.41
C18:1ω9c	230.07 ±199.65	9.2 ±7.99	443.33 ±349.81	101.97 ±80.46	186.29 ±131.92	42.85 ±30.34	191.81 ±147.12	10.36 ±7.94
C20:1ω9c	52.78 ±52.6	2.11 ±2.1	729.48 ±515.81	167.78 ±118.64	144.37 ±84.87	33.2 ±19.52	20.15 ±9.24	1.09 ±0.5
C20:1ω11	3.25 ±4.99	0.13 ±0.2	171.68 ±112.28	39.49 ±25.82	48.51 ±30.71	11.16 ±7.06	4.11 ±2.92	0.22 ±0.16
C22:1ω9c	82.06 ±38.46	3.28 ±1.54	133.55 ±24.62	30.72 ±5.66	140.92 ±80.73	32.41 ±18.57	144.43 ±58.39	7.8 ±3.15
C22:1ω11	25.46 ±60.82	1.02 ±2.43	0 ±0	0 ±0	8.4 ±9.78	1.93 ±2.25	2.51 ±1.34	0.14 ±0.07
C24:1ω9c	15.45 ±15.14	0.62 ±0.61	2.38 ±3.37	0.55 ±0.77	19.76 ±21.16	4.55 ±4.87	11.02 ±7.49	0.6 ±0.4
C16:4ω1	9.27 ±24.55	0.37 ±0.98	47.88 ±48.6	11.01 ±11.18	210.65 ±185.54	48.45 ±42.68	29.04 ±38.32	1.57 ±2.07
C18:2ω6c	44.78 ±31.23	1.79 ±1.25	346.81 ±289.53	79.77 ±66.59	159.86 ±89.44	36.77 ±20.57	75.04 ±57.2	4.05 ±3.09
C18:3ω3	38.87 ±32.14	1.55 ±1.29	586.69 ±475.93	134.94 ±109.46	185.4 ±107.53	42.64 ±24.73	35.64 ±25.84	1.92 ±1.4
C18:3ω6	2.44 ±3.12	0.1 ±0.12	26.92 ±23.31	6.19 ±5.36	21.98 ±13.13	5.06 ±3.02	4.23 ±3.1	0.23 ±0.17
C18:4ω3c	80.89 ±84.62	3.24 ±3.38	1063.45 ±906.74	244.59 ±208.55	457.73 ±254.64	105.28 ±58.57	110.17 ±82.4	5.95 ±4.45
C20:2ω6	13.87 ±7.16	0.55 ±0.29	452.1 ±340.99	103.98 ±78.43	176.43 ±112.58	40.58 ±25.89	4.67 ±3.15	0.25 ±0.17
C20:3ω3	4.87 ±4.09	0.19 ±0.16	175.81 ±128.31	40.44 ±29.51	57.61 ±38.58	13.25 ±8.87	1.87 ±1.33	0.1 ±0.07
C20:3ω6	2.24 ±2.59	0.09 ±0.1	27.64 ±21.27	6.36 ±4.89	23.4 ±13.92	5.38 ±3.2	2.98 ±2.68	0.16 ±0.14
C20:4ω6	35.14 ±34.29	1.41 ±1.37	339.12 ±255.36	78 ±58.73	91.36 ±53.54	21.01 ±12.31	65.36 ±50.99	3.53 ±2.75
C20:5ω3	851.54 ±497.58	34.06 ±19.9	5200.54 ±3896.52	1196.12 ±896.2	2750.89 ±1546.22	632.7 ±355.63	411.14 ±369.78	22.2 ±19.97
C21:5ω3	8.52 ±19.59	0.34 ±0.78	263.22 ±200.82	60.54 ±46.19	138.74 ±86.32	31.91 ±19.85	14.48 ±11.15	0.78 ±0.6
C22:2ω6	0.21 ±0.64	0.01 ±0.03	9.35 ±6.71	2.15 ±1.54	4.55 ±1.72	1.05 ±0.4	2.49 ±0.98	0.13 ±0.05
C22:3ω6	0 ±0	0 ±0	2.6 ±0.84	0.6 ±0.19	1.81 ±1.58	0.42 ±0.36	2.28 ±1.55	0.12 ±0.08

C22:4ω6	0 ±0	0 ±0	16.44 ±12.23	3.78 ±2.81	6.74 ±3.97	1.55 ±0.91	0.39 ±0.67	0.02 ±0.04
C22:5ω3	40.46 ±32.15	1.62 ±1.29	266.54 ±204.12	61.31 ±46.95	117.36 ±73.03	26.99 ±16.8	27.91 ±23.87	1.51 ±1.29
C22:5ω6	14.14 ±17.12	0.57 ±0.68	182.23 ±163.09	41.91 ±37.51	35.09 ±21.55	8.07 ±4.96	7.3 ±5.43	0.39 ±0.29
C22:6ω3	1193 ±686.81	47.72 ±27.47	7650.23 ±5569.69	1759.55 ±1281.03	1909.35 ±1195.3	439.15 ±274.92	802.91 ±633.98	43.36 ±34.23
SAFA	1641.79 ±953.12	65.67 ±38.12	9937.14 ±8717.18	2285.54 ±2004.95	4296.01 ±2490.84	988.08 ±572.89	1040.91 ±714.98	56.21 ±38.61
MUFA	615.87 ±513.2	24.63 ±20.53	2868 ±2073.36	659.64 ±476.87	1689.17 ±989.49	388.51 ±227.58	626.01 ±402.81	33.8 ±21.75
PUFA	2340.25 ±1376.58	93.61 ±55.06	16657.57 ±12542.38	3831.24 ±2884.75	6348.96 ±3534.93	1460.26 ±813.03	1597.9 ±1286.84	86.29 ±69.49
SUM (EPA+DHA+ ARA)	2079.69 ±1164.99	83.19 ±46.6	13189.89 ±9721.56	3033.67 ±2235.96	4751.61 ±2655.82	1092.87 ±610.84	1279.4 ±1045.12	69.09 ±56.44
SUM (ALA+LA)	83.65 ±61.91	3.35 ±2.48	933.5 ±765.46	214.7 ±176.06	345.25 ±194.09	79.41 ±44.64	110.67 ±81.27	5.98 ±4.39
SUM (15:0+17:0)	104.27 ±72.61	4.17 ±2.9	1823.34 ±1551.26	419.37 ±356.79	378.73 ±214.89	87.11 ±49.42	123.76 ±86.5	6.68 ±4.67
SUM (Branched+ OddC)	118.72 ±89.74	4.75 ±3.59	2130.99 ±1795.02	490.13 ±412.85	543.49 ±318.26	125 ±73.2	147.38 ±100.74	7.96 ±5.44
SUM (Calanoid markers)	163.55 ±125.86	6.54 ±5.03	1034.71 ±603.48	237.98 ±138.8	342.2 ±110.04	78.71 ±25.31	171.2 ±65.44	9.24 ±3.53
Total FA	4597.91 ±2806.3	183.92 ±112.25	29462.71 ±23332.92	6776.42 ±5366.57	12334.14 ±6793.63	2836.85 ±1562.54	3264.82 ±2404.36	176.3 ±129.84

Supplemental Table S3.17. Averages of FA concentrations per gelatinous taxon (*4 of 4*). Forty-six unique fatty acids (FA) were found in samples, listed in order of increasing desaturation and elongation, followed by FA summations: SAFA (saturated fatty acids), MUFA (monounsaturated fatty acids), PUFA (polyunsaturated fatty acids), SUM(EPA+DHA+ARA) (essential fatty acids), SUM(ALA+LA), SUM(15:0+17:0), SUM(Branched+OddC), SUM(Calanoid_markers), and Total FA concentration. For each taxon, sample size is given by (n) and FA concentrations are presented in two units: "ng FA per mg dry weight" and "ng FA per mg wet weight." Each result is the average across samples with standard deviations. Samples are categorized according to taxon (lowest level of taxonomic identification possible).

Taxon:	**Salpidae (n=8)**		**Siphonophorae Calycophorae (n=11)**		**Siphonophorae Physonectae (n=3)**		***Tomopteris* sp. (n=5)**	
FA	*ng FA / mg dry wt*	*ng FA / mg wet wt*	*ng FA / mg dry wt*	*ng FA / mg wet wt*	*ng FA / mg dry wt*	*ng FA / mg wet wt*	*ng FA / mg dry wt*	*ng FA / mg wet wt*
C8:0	0.74 ±1.66	0.04 ±0.09	0.08 ±0.18	0 ±0.01	0.08 ±0.14	0 ±0.01	6.44 ±6.91	0.86 ±0.93
C9:0	4.97 ±8.26	0.27 ±0.45	0.99 ±2.16	0.04 ±0.09	1.94 ±1.95	0.08 ±0.08	91.16 ±143.08	12.22 ±19.17
C10:0	1.88 ±1.76	0.1 ±0.1	0.48 ±0.76	0.02 ±0.03	0.92 ±0.7	0.04 ±0.03	5.92 ±4.37	0.79 ±0.59
C11:0	0.56 ±0.3	0.03 ±0.02	0.1 ±0.1	0 ±0	0.33 ±0.19	0.01 ±0.01	5.92 ±4.23	0.79 ±0.57
C12:0	10.26 ±8.28	0.55 ±0.45	4.03 ±3.95	0.17 ±0.16	8.9 ±5.52	0.37 ±0.23	551.86 ±285.56	73.95 ±38.27

C13:0	3.03 ±1.09	0.16 ±0.06	0.64 ±0.53	0.03 ±0.02	2.64 ±0.89	0.11 ±0.04	71.05 ±40.13	9.52 ±5.38
C14:0	272.8 ±84.13	14.73 ±4.54	100.62 ±71.74	4.13 ±2.94	459.91 ±234.56	18.86 ±9.62	1151.94 ±1042.46	154.36 ±139.69
C15:0	92.91 ±45.18	5.02 ±2.44	12.37 ±9.28	0.51 ±0.38	50.62 ±25.29	2.08 ±1.04	391.41 ±266.35	52.45 ±35.69
Ca-15:0	8.28 ±4.59	0.45 ±0.25	1.74 ±1.42	0.07 ±0.06	3.57 ±0.9	0.15 ±0.04	13.54 ±6.9	1.81 ±0.92
Ci-15:0	14 ±6.19	0.76 ±0.33	5.62 ±4.89	0.23 ±0.2	27.8 ±16.38	1.14 ±0.67	55.11 ±27.65	7.39 ±3.71
C16:0	1000.03 ±414.56	54 ±22.39	289.63 ±174.76	11.87 ±7.17	1177.84 ±898.23	48.29 ±36.83	7875.72 ±7149.95	1055.35 ±958.09
C17:0	52.11 ±16.55	2.81 ±0.89	10.97 ±6.39	0.45 ±0.26	56.37 ±36.3	2.31 ±1.49	852.73 ±575.32	114.27 ±77.09
Ca-17:0	8.8 ±3.76	0.48 ±0.2	3.69 ±2.56	0.15 ±0.11	10.62 ±6.51	0.44 ±0.27	81.76 ±43.33	10.96 ±5.81
Ci-17:0	48.31 ±18.22	2.61 ±0.98	2.9 ±2.95	0.12 ±0.12	20.56 ±14.46	0.84 ±0.59	247.41 ±130.44	33.15 ±17.48
C18:0	161.03 ±62.39	8.7 ±3.37	161.12 ±89.04	6.61 ±3.65	564.19 ±455.42	23.13 ±18.67	3251.39 ±3428.8	435.69 ±459.46
C20:0	26.32 ±19.08	1.42 ±1.03	6.1 ±3.74	0.25 ±0.15	23.11 ±20.78	0.95 ±0.85	131.88 ±116.43	17.67 ±15.6
C22:0	8.04 ±5.64	0.43 ±0.3	2.69 ±1.75	0.11 ±0.07	5.88 ±2.96	0.24 ±0.12	68.88 ±69.83	9.23 ±9.36
C23:0	0.99 ±0.8	0.05 ±0.04	0.19 ±0.23	0.01 ±0.01	1.59 ±1.04	0.07 ±0.04	12.26 ±6.7	1.64 ±0.9
C24:0	15.62 ±14.88	0.84 ±0.8	1.45 ±1.45	0.06 ±0.06	2.34 ±0.6	0.1 ±0.02	44.9 ±45.75	6.02 ±6.13
C14:1ω5	1.76 ±0.7	0.09 ±0.04	1.08 ±1.16	0.04 ±0.05	0.95 ±0.29	0.04 ±0.01	6.1 ±7.51	0.82 ±1.01
C16:1ω7c	231.31 ±70.02	12.49 ±3.78	110.37 ±138.69	4.53 ±5.69	101.93 ±49.36	4.18 ±2.02	728.64 ±335.15	97.64 ±44.91
C17:1ω7c	6.34 ±2.62	0.34 ±0.14	0.21 ±0.38	0.01 ±0.02	2.44 ±1.65	0.1 ±0.07	21.24 ±29.21	2.85 ±3.91
C18:1ω7c	122.27 ±86.3	6.6 ±4.66	26.97 ±34.23	1.11 ±1.4	187.26 ±117.75	7.68 ±4.83	1047.66 ±558.69	140.39 ±74.86
C18:1ω9c	204.63 ±77.91	11.05 ±4.21	313.03 ±353.86	12.83 ±14.51	333.34 ±338.66	13.67 ±13.89	1752.8 ±1032.73	234.87 ±138.39
C20:1ω9c	31.47 ±14.93	1.7 ±0.81	26.94 ±16.84	1.1 ±0.69	130.18 ±115.87	5.34 ±4.75	469.71 ±349.59	62.94 ±46.85
C20:1ω11	3.7 ±4.36	0.2 ±0.24	4.21 ±4.99	0.17 ±0.2	7.04 ±5.73	0.29 ±0.24	25.24 ±13.27	3.38 ±1.78
C22:1ω9c	117.09 ±87.92	6.32 ±4.75	84.95 ±30.76	3.48 ±1.26	117.5 ±43.13	4.82 ±1.77	1564.23 ±1376.75	209.61 ±184.48
C22:1ω11	4.36 ±7.62	0.24 ±0.41	2.37 ±1.99	0.1 ±0.08	6.46 ±5.36	0.26 ±0.22	14.95 ±11.76	2 ±1.58
C24:1ω9c	12.87 ±11.73	0.7 ±0.63	11.28 ±12.74	0.46 ±0.52	35.28 ±37.5	1.45 ±1.54	72.08 ±105.03	9.66 ±14.07
C16:4ω1	47.1 ±30.16	2.54 ±1.63	17.75 ±41.78	0.73 ±1.71	12.88 ±14.01	0.53 ±0.57	26.41 ±39.14	3.54 ±5.25
C18:2ω6c	149.9 ±47.02	8.09 ±2.54	27.19 ±20.35	1.11 ±0.83	62.23 ±28.94	2.55 ±1.19	601.66 ±311.39	80.62 ±41.73
C18:3ω3	116.31 ±27.79	6.28 ±1.5	18.79 ±15.85	0.77 ±0.65	50.65 ±28.98	2.08 ±1.19	535.78 ±498.54	71.79 ±66.8
C18:3ω6	11.57 ±3.22	0.62 ±0.17	2.39 ±2.81	0.1 ±0.12	2.08 ±0.56	0.09 ±0.02	56.68 ±30.68	7.6 ±4.11
C18:4ω3c	350.68 ±110.01	18.94 ±5.94	52.52 ±55.37	2.15 ±2.27	48.92 ±30.06	2.01 ±1.23	1067.35 ±728.81	143.02 ±97.66
C20:2ω6	11.8 ±2.89	0.64 ±0.16	4.28 ±3.44	0.18 ±0.14	39.58 ±22.04	1.62 ±0.9	270.59 ±182.29	36.26 ±24.43

C20:3ω3	5.08 ±1.72	0.27 ±0.09	1.13 ±0.84	0.05 ±0.03	16.65 ±9.32	0.68 ±0.38	505.99 ±555.83	67.8 ±74.48
C20:3ω6	5.34 ±2.98	0.29 ±0.16	1.55 ±1.61	0.06 ±0.07	5.45 ±1.5	0.22 ±0.06	59.07 ±37.26	7.92 ±4.99
C20:4ω6	81.51 ±37.11	4.4 ±2	23.24 ±18.01	0.95 ±0.74	313.72 ±254.43	12.86 ±10.43	710.3 ±633.41	95.18 ±84.88
C20:5ω3	787.83 ±297.66	42.54 ±16.07	354.19 ±324.18	14.52 ±13.29	1458.82 ±1164.4	59.81 ±47.74	7861.15 ±6342.87	1053.39 ±849.94
C21:5ω3	42.12 ±16.74	2.27 ±0.9	8.98 ±11.49	0.37 ±0.47	21.14 ±12.21	0.87 ±0.5	210.86 ±138.58	28.26 ±18.57
C22:2ω6	2.57 ±1.43	0.14 ±0.08	1.02 ±1.22	0.04 ±0.05	2.2 ±0.79	0.09 ±0.03	188.22 ±158.66	25.22 ±21.26
C22:3ω6	1.14 ±1.35	0.06 ±0.07	0 ±0	0 ±0	1.13 ±1.03	0.05 ±0.04	101.41 ±132.22	13.59 ±17.72
C22:4ω6	1.1 ±0.77	0.06 ±0.04	0 ±0	0 ±0	58.2 ±41.48	2.39 ±1.7	24.18 ±32.74	3.24 ±4.39
C22:5ω3	41.73 ±15.32	2.25 ±0.83	17.08 ±20.91	0.7 ±0.86	134.16 ±89.94	5.5 ±3.69	442.96 ±417.5	59.36 ±55.94
C22:5ω6	24.6 ±3.82	1.33 ±0.21	17.14 ±10.24	0.7 ±0.42	125.17 ±142.42	5.13 ±5.84	265.14 ±358.83	35.53 ±48.08
C22:6ω3	1336.68 ±460.6	72.18 ±24.87	334.71 ±209.08	13.72 ±8.57	1748.34 ±1582.36	71.68 ±64.88	11636.51 ±11012.8	1559.29 ±1475.71
SAFA	1730.67 ±577.52	93.46 ±31.19	605.39 ±361.03	24.82 ±14.8	2419.21 ±1690.54	99.19 ±69.31	14911.28 ±13093.04	1998.11 ±1754.47
MUFA	735.8 ±329.8	39.73 ±17.81	581.42 ±554.06	23.84 ±22.72	922.38 ±680.82	37.82 ±27.91	5702.64 ±3446.85	764.15 ±461.88
PUFA	3017.05 ±701.71	162.92 ±37.89	881.97 ±702.06	36.16 ±28.78	4101.31 ±3359.58	168.15 ±137.74	24564.26 ±21346.46	3291.61 ±2860.43
SUM (EPA+DHA+ ARA)	2206.02 ±682.37	119.13 ±36.85	712.15 ±535.48	29.2 ±21.95	3520.87 ±2996.98	144.36 ±122.88	20207.96 ±17925.04	2707.87 ±2401.96
SUM (ALA+LA)	266.21 ±50.38	14.38 ±2.72	45.98 ±35.76	1.89 ±1.47	112.88 ±57.6	4.63 ±2.36	1137.44 ±769.28	152.42 ±103.08
SUM (15:0+17:0)	224.41 ±74.95	12.12 ±4.05	37.28 ±26.53	1.53 ±1.09	169.53 ±98.88	6.95 ±4.05	1641.97 ±1024.56	220.02 ±137.29
SUM (Branched+ OddC)	282.42 ±93.87	15.25 ±5.07	48.39 ±35.37	1.98 ±1.45	199.61 ±111.36	8.18 ±4.57	2054.45 ±1345.85	275.3 ±180.34
SUM (Calanoid markers)	156.61 ±105.06	8.46 ±5.67	118.47 ±49.54	4.86 ±2.03	261.18 ±154.59	10.71 ±6.34	2074.13 ±1717.33	277.93 ±230.12
Total FA	5483.52 ±1535.35	296.11 ±82.91	2068.79 ±1580.65	84.82 ±64.81	7442.9 ±5711.49	305.16 ±234.17	45178.18 ±37574.08	6053.88 ±5034.93

Supplemental Table S3.18. Averages of FA concentrations per crustacean taxon. Forty-six unique fatty acids (FA) were found in samples, listed in order of increasing desaturation and elongation, followed by FA summations: SAFA (saturated fatty acids), MUFA (monounsaturated fatty acids), PUFA (polyunsaturated fatty acids), SUM(EPA+DHA+ARA) (essential fatty acids), SUM(ALA+LA), SUM(15:0+17:0), SUM(Branched+OddC), SUM(Calanoid_markers), and Total FA concentration. For each taxon, sample size is given by (n) and FA concentrations are presented in two units: "ng FA per mg dry weight" and "ng FA per mg wet weight." Each result is the average across samples with standard deviations. Samples are categorized according to taxon (lowest level of taxonomic identification possible).

Taxon:	**Amphipoda Hyperiidea (n=5)**		**Copepoda (n=21)**		**Euphausiidae (n=22)**	
FA	*ng FA / mg dry wt*	*ng FA / mg wet wt*	*ng FA / mg dry wt*	*ng FA / mg wet wt*	*ng FA / mg dry wt*	*ng FA / mg wet wt*
C8:0	3.06 ±2.85	0.73 ±0.68	0.91 ±2.58	0.15 ±0.42	0.55 ±0.78	0.13 ±0.18
C9:0	33.74 ±33.12	8.06 ±7.92	7.8 ±18.06	1.26 ±2.93	7.83 ±8.15	1.79 ±1.86
C10:0	3.93 ±1.68	0.94 ±0.4	2.83 ±5.94	0.46 ±0.96	1.84 ±1.46	0.42 ±0.33
C11:0	1.46 ±0.55	0.35 ±0.13	0.61 ±1.06	0.1 ±0.17	0.6 ±0.32	0.14 ±0.07
C12:0	208.21 ±296.9	49.76 ±70.96	11.4 ±24.74	1.85 ±4.01	19.41 ±15.54	4.43 ±3.54
C13:0	23.34 ±15.61	5.58 ±3.73	4.88 ±11.63	0.79 ±1.88	5.79 ±3.72	1.32 ±0.85
C14:0	2506.49 ±2105.71	599.05 ±503.27	676.28 ±1744.95	109.56 ±282.68	969.78 ±738.78	221.11 ±168.44
C15:0	431.33 ±389.53	103.09 ±93.1	60.59 ±105.69	9.82 ±17.12	151.25 ±84.01	34.49 ±19.16
Ca-15:0	16.84 ±8.38	4.03 ±2	8 ±17.22	1.3 ±2.79	6.68 ±3.69	1.52 ±0.84
Ci-15:0	59.68 ±28.31	14.26 ±6.77	27.17 ±56.24	4.4 ±9.11	30.62 ±17.94	6.98 ±4.09
C16:0	7788.7 ±4280.25	1861.5 ±1022.98	2369.27 ±3984.99	383.82 ±645.57	5968.93 ±3552.65	1360.91 ±810.01
C17:0	479.98 ±386.5	114.72 ±92.37	51.79 ±88.34	8.39 ±14.31	155.6 ±80.34	35.48 ±18.32
Ca-17:0	73.21 ±73.44	17.5 ±17.55	7.14 ±13.37	1.16 ±2.17	17.81 ±9.59	4.06 ±2.19
Ci-17:0	294.52 ±264.22	70.39 ±63.15	21.06 ±44.9	3.41 ±7.27	74.39 ±40.83	16.96 ±9.31
C18:0	2005.82 ±1028.74	479.39 ±245.87	518.86 ±917.63	84.05 ±148.66	573.42 ±425.12	130.74 ±96.93
C20:0	76.26 ±35.24	18.22 ±8.42	24.14 ±36.56	3.91 ±5.92	21.5 ±11.1	4.9 ±2.53
C22:0	23.46 ±9.78	5.61 ±2.34	11.81 ±20.04	1.91 ±3.25	24.58 ±11	5.6 ±2.51
C23:0	3.65 ±3.35	0.87 ±0.8	0.58 ±1.33	0.09 ±0.22	5.24 ±2.81	1.19 ±0.64
C24:0	8.12 ±3.52	1.94 ±0.84	3.95 ±5.99	0.64 ±0.97	12.59 ±12.96	2.87 ±2.96
C14:1ω5	17.56 ±11.35	4.2 ±2.71	13.11 ±28.55	2.12 ±4.63	8.07 ±6.51	1.84 ±1.48
C16:1ω7c	2395.5 ±1918.13	572.52 ±458.43	1121.23 ±2485.47	181.64 ±402.65	1173.3 ±1116.13	267.51 ±254.48
C17:1ω7c	12.87 ±11.31	3.08 ±2.7	3.52 ±6.84	0.57 ±1.11	14.86 ±12	3.39 ±2.74
C18:1ω7c	1283.11 ±771.57	306.66 ±184.41	271.44 ±392.93	43.97 ±63.65	1512.46 ±992.61	344.84 ±226.32
C18:1ω9c	8164.97 ±6606.07	1951.43 ±1578.85	2342.59 ±5230.51	379.5 ±847.34	2492.11 ±1394.51	568.2 ±317.95
C20:1ω9c	1283.45 ±1556.59	306.75 ±372.02	469.83 ±1143.21	76.11 ±185.2	121.72 ±67.1	27.75 ±15.3
C20:1ω11	200.92 ±273.34	48.02 ±65.33	71.73 ±123.23	11.62 ±19.96	17.44 ±16.15	3.98 ±3.68

C22:1ω9c	954.78 ±1038.85	228.19 ±248.28	163.59 ±206.55	26.5 ±33.46	77.07 ±32.72	17.57 ±7.46
C22:1ω11	871.52 ±1293.04	208.29 ±309.04	383.73 ±1452.96	62.16 ±235.38	39.93 ±70.1	9.1 ±15.98
C24:1ω9c	223.65 ±175.08	53.45 ±41.84	239.41 ±428.8	38.78 ±69.47	77.51 ±57.33	17.67 ±13.07
C16:4ω1	111.15 ±172.48	26.56 ±41.22	119.08 ±338.95	19.29 ±54.91	334.99 ±459.93	76.38 ±104.86
C18:2ω6c	728.22 ±564.87	174.05 ±135	156.18 ±205.59	25.3 ±33.31	557.65 ±311.49	127.15 ±71.02
C18:3ω3	399.06 ±333.96	95.37 ±79.82	127.34 ±222.25	20.63 ±36	511.53 ±368.05	116.63 ±83.91
C18:3ω6	62.16 ±35.57	14.86 ±8.5	16.79 ±42.12	2.72 ±6.82	37.36 ±26.48	8.52 ±6.04
C18:4ω3c	1038.26 ±1063.6	248.15 ±254.2	381.3 ±608.37	61.77 ±98.56	877.39 ±782.5	200.05 ±178.41
C20:2ω6	103.43 ±54.97	24.72 ±13.14	18.57 ±31.69	3.01 ±5.13	82.19 ±43.36	18.74 ±9.89
C20:3ω3	87.07 ±82.65	20.81 ±19.75	10.31 ±18.55	1.67 ±3.01	50.15 ±32	11.44 ±7.3
C20:3ω6	41.56 ±30.48	9.93 ±7.29	7.64 ±22.63	1.24 ±3.67	19.2 ±14.25	4.38 ±3.25
C20:4ω6	685.99 ±438.85	163.95 ±104.89	62.74 ±162.75	10.16 ±26.37	484.64 ±246.55	110.5 ±56.21
C20:5ω3	7682.17 ±5442.3	1836.04 ±1300.71	1595.68 ±2418.4	258.5 ±391.78	6564.36 ±4315.56	1496.67 ±983.95
C21:5ω3	222.92 ±137.18	53.28 ±32.79	37.31 ±61.1	6.04 ±9.9	175.95 ±126.96	40.12 ±28.95
C22:2ω6	12.35 ±4.49	2.95 ±1.07	1.47 ±3.81	0.24 ±0.62	2.22 ±1.93	0.51 ±0.44
C22:3ω6	64.82 ±95.57	15.49 ±22.84	0.06 ±0.29	0.01 ±0.05	4.96 ±3.15	1.13 ±0.72
C22:4ω6	1.87 ±2.71	0.45 ±0.65	2.09 ±7.03	0.34 ±1.14	5.38 ±4.69	1.23 ±1.07
C22:5ω3	331.33 ±222.41	79.19 ±53.16	82.96 ±130.7	13.44 ±21.17	173.63 ±94.03	39.59 ±21.44
C22:5ω6	78.58 ±44.47	18.78 ±10.63	28.62 ±51.11	4.64 ±8.28	78.37 ±40.96	17.87 ±9.34
C22:6ω3	8809.86 ±5991.76	2105.56 ±1432.03	1677.07 ±2820.69	271.69 ±456.95	5857.6 ±2789.13	1335.53 ±635.92
SAFA	14041.81 ±7764	3355.99 ±1855.6	3809.07 ±6024.06	617.07 ±975.9	8048.4 ±4886.86	1835.03 ±1114.2
MUFA	15408.33 ±13199.31	3682.59 ±3154.64	5080.18 ±8978	822.99 ±1454.44	5534.47 ±3533.46	1261.86 ±805.63
PUFA	20460.8 ±12229.03	4890.13 ±2922.74	4325.21 ±6639.05	700.68 ±1075.53	15817.59 ±8363.84	3606.41 ±1906.96
SUM (EPA+DHA+ ARA)	17178.02 ±10230.19	4105.55 ±2445.01	3335.49 ±5146.75	540.35 ±833.77	12906.6 ±6919.67	2942.7 ±1577.69
SUM (ALA+LA)	1127.28 ±895.43	269.42 ±214.01	283.52 ±420.71	45.93 ±68.15	1069.19 ±668.52	243.77 ±152.42
SUM (15:0+17:0)	1355.56 ±1137.26	323.98 ±271.81	175.76 ±300.82	28.47 ±48.73	436.35 ±228.65	99.49 ±52.13
SUM (Branched+OddC)	1653.54 ±1319.16	395.2 ±315.28	230.46 ±378.83	37.33 ±61.37	646.61 ±354	147.43 ±80.71
SUM (Calanoid markers)	3310.67 ±4137.21	791.25 ±988.79	1088.88 ±2709.41	176.4 ±438.92	256.16 ±157.9	58.4 ±36
Total FA	49910.94 ±30543.28	11928.72 ±7299.84	13214.47 ±20976.36	2140.74 ±3398.17	29400.45 ±16471.26	6703.3 ±3755.45

Supplemental Table S3.19. Averages of FA concentrations per fish taxon. Forty-six unique fatty acids (FA) were found in samples, listed in order of increasing desaturation and elongation, followed by FA summations: SAFA (saturated fatty acids), MUFA (monounsaturated fatty acids), PUFA (polyunsaturated fatty acids), SUM(EPA+DHA+ARA) (essential fatty acids), SUM(ALA+LA), SUM(15:0+17:0), SUM(Branched+OddC), SUM(Calanoid_markers), and Total FA concentration. For each taxon, sample size is given by (n) and FA concentrations are presented in two units: "ng FA per mg dry weight" and "ng FA per mg wet weight." Each result is the average across samples with standard deviations. Samples are categorized according to taxon (lowest level of taxonomic identification possible).

Taxon:	***Sebastes* spp. (n=24)**		***Stenobrachius leucopsarus (n=19)***	
FA	*ng FA / mg dry wt*	*ng FA / mg wet wt*	*ng FA / mg dry wt*	*ng FA / mg wet wt*
C8:0	0.17 ±0.43	0.04 ±0.1	0.29 ±0.66	0.07 ±0.15
C9:0	1.49 ±2.74	0.34 ±0.63	1.94 ±3.86	0.45 ±0.89
C10:0	1.11 ±1.45	0.26 ±0.33	1.51 ±3.08	0.35 ±0.71
C11:0	0.44 ±0.51	0.1 ±0.12	0.94 ±1.58	0.22 ±0.36
C12:0	10.99 ±8.43	2.53 ±1.94	15.28 ±25.44	3.51 ±5.85
C13:0	1.91 ±2.01	0.44 ±0.46	4.34 ±5.9	1 ±1.36
C14:0	260.34 ±380.59	59.88 ±87.54	519.55 ±793.75	119.5 ±182.56
C15:0	83.22 ±116.13	19.14 ±26.71	164.65 ±258.69	37.87 ±59.5
Ca-15:0	3.86 ±5.33	0.89 ±1.23	12.31 ±19.54	2.83 ±4.49
Ci-15:0	18.55 ±26.88	4.27 ±6.18	43.18 ±79.61	9.93 ±18.31
C16:0	3143.57 ±4769.65	723.02 ±1097.02	4220.18 ±6036.87	970.64 ±1388.48
C17:0	133.16 ±202.58	30.63 ±46.59	130.21 ±192.29	29.95 ±44.23
Ca-17:0	20.02 ±30.75	4.6 ±7.07	31.4 ±57.4	7.22 ±13.2
Ci-17:0	45.76 ±69.4	10.52 ±15.96	68.17 ±131.57	15.68 ±30.26
C18:0	1257.01 ±1887.14	289.11 ±434.04	1240.03 ±1657.87	285.21 ±381.31
C20:0	43.86 ±76.62	10.09 ±17.62	37.14 ±57.36	8.54 ±13.19
C22:0	31.25 ±55.47	7.19 ±12.76	23.42 ±32.95	5.39 ±7.58
C23:0	2.8 ±4.93	0.64 ±1.13	3.57 ±4.93	0.82 ±1.13
C24:0	23.39 ±44.93	5.38 ±10.33	25.01 ±52.37	5.75 ±12.05
C14:1ω5	2.49 ±4.65	0.57 ±1.07	34.35 ±133.85	7.9 ±30.79
C16:1ω7c	255.31 ±400.24	58.72 ±92.05	2292.85 ±6294.67	527.36 ±1447.77
C17:1ω7c	5.45 ±8.11	1.25 ±1.87	5.64 ±8.89	1.3 ±2.05
C18:1ω7c	350.93 ±537.8	80.71 ±123.69	966.05 ±1818.89	222.19 ±418.35
C18:1ω9c	937.54 ±1401.35	215.63 ±322.31	7712.21 ±26773.15	1773.81 ±6157.82
C20:1ω9c	167.62 ±336.2	38.55 ±77.33	197.45 ±553.74	45.41 ±127.36
C20:1ω11	2.01 ±3.69	0.46 ±0.85	40.3 ±133.26	9.27 ±30.65
C22:1ω9c	146.62 ±130.67	33.72 ±30.05	124.54 ±111.69	28.64 ±25.69
C22:1ω11	4.83 ±8.51	1.11 ±1.96	51.4 ±140.24	11.82 ±32.25
C24:1ω9c	179.11 ±289.92	41.2 ±66.68	264.78 ±620.29	60.9 ±142.67
C16:4ω1	11.88 ±27.86	2.73 ±6.41	63.6 ±143.11	14.63 ±32.92
C18:2ω6c	178.7 ±241.79	41.1 ±55.61	474.7 ±957.52	109.18 ±220.23

C18:3ω3	92.84 ±133.55	21.35 ±30.72	363 ±836	83.49 ±192.28
C18:3ω6	6.84 ±11.08	1.57 ±2.55	35.82 ±68.01	8.24 ±15.64
C18:4ω3c	182.57 ±284.04	41.99 ±65.33	832.76 ±1977.91	191.53 ±454.92
C20:2ω6	33.32 ±51.36	7.66 ±11.81	50.67 ±140.33	11.65 ±32.28
C20:3ω3	23.06 ±35.35	5.3 ±8.13	29.98 ±82.43	6.9 ±18.96
C20:3ω6	4.88 ±8.77	1.12 ±2.02	20.68 ±39.12	4.76 ±9
C20:4ω6	94.99 ±141.33	21.85 ±32.51	271.81 ±490.15	62.52 ±112.73
C20:5ω3	1514.39 ±2492.91	348.31 ±573.37	3169.25 ±5497.63	728.93 ±1264.46
C21:5ω3	39.77 ±63.22	9.15 ±14.54	109.47 ±229.07	25.18 ±52.69
C22:2ω6	4.06 ±4.98	0.93 ±1.14	4.53 ±9.57	1.04 ±2.2
C22:3ω6	4.45 ±7.61	1.02 ±1.75	4.03 ±7.85	0.93 ±1.81
C22:4ω6	5.29 ±9.34	1.22 ±2.15	11.55 ±24.26	2.66 ±5.58
C22:5ω3	177.96 ±291.42	40.93 ±67.03	224.01 ±431.61	51.52 ±99.27
C22:5ω6	30.07 ±47.74	6.92 ±10.98	87.73 ±175.15	20.18 ±40.29
C22:6ω3	3194.08 ±5501.46	734.64 ±1265.34	4899.96 ±8220.6	1126.99 ±1890.74
SAFA	5082.92 ±7608.01	1169.07 ±1749.84	6543.1 ±9213.48	1504.91 ±2119.1
MUFA	2051.92 ±2922.21	471.94 ±672.11	11689.58 ±36124.27	2688.6 ±8308.58
PUFA	5599.13 ±9212.59	1287.8 ±2118.9	10653.54 ±18854.03	2450.31 ±4336.43
SUM (EPA+DHA+ARA)	4803.46 ±8088.1	1104.8 ±1860.26	8341.01 ±14089.13	1918.43 ±3240.5
SUM (ALA+LA)	271.53 ±374.16	62.45 ±86.06	837.71 ±1790.26	192.67 ±411.76
SUM (15:0+17:0)	304.58 ±445.61	70.05 ±102.49	449.91 ±717.74	103.48 ±165.08
SUM (Branched+OddC)	356.43 ±519.71	81.98 ±119.53	575.81 ±898.56	132.44 ±206.67
SUM (Calanoid markers)	321.09 ±378.61	73.85 ±87.08	413.69 ±916.06	95.15 ±210.69
Total FA	12733.97 ±19051.97	2928.81 ±4381.95	28886.23 ±58603.07	6643.83 ±13478.71

Supplemental Table S3.20. Average concentrations of select FAs per plankton category. Averages are given for a subset of individual FAs and FA summations that are of ecological interest. FA concentrations are given in three different units: "mg FA per g dry weight,", "mg FA per g wet weight," and "mg FA per g carbon content." For each group, sample size is given by (n). Each result is the average across samples with standard deviations. Samples are categorized according to "plankton categories" (gelatinous zooplankton, crustaceans, fishes).

	FA	**Gelatinous zooplankton (n=135)**	**Crustacean zooplankton (n=48)**	**Fishes (n=43)**
FA per dry weight (mg FA / g DW)	*LA (18:2ω6)*	0.12±0.17	0.4±0.37	0.31±0.67
	ALA (18:3ω3)	0.11±0.18	0.33±0.35	0.21±0.57
	ARA (20:4ω6)	0.14±0.22	0.32±0.33	0.17±0.35
	EPA (20:5ω3)	1.47±2.28	4.51±4.49	2.25±4.13
	DHA (22:6ω3)	1.86±3.43	4.34±4.04	3.95±6.8
	ALA+LA	0.24±0.33	0.73±0.71	0.52±1.24
	EPA+DHA+ARA	3.47±5.79	9.16±8.37	6.37±11.14
	SAFA	2.72±4.43	6.82±6.45	5.73±8.28
	MUFA	1.51±2.28	6.36±8.03	6.31±24.24
	PUFA	4.24±6.93	11.27±10.15	7.83±14.33
	Total FA	8.47±13.31	24.46±22.91	19.87±41.67
FA per wet weight (mg FA / g WW)	*LA (18:2ω6)*	0.01±0.02	0.09±0.09	0.07±0.15
	ALA (18:3ω3)	0.01±0.03	0.07±0.08	0.05±0.13
	ARA (20:4ω6)	0.01±0.03	0.07±0.08	0.04±0.08
	EPA (20:5ω3)	0.15±0.33	0.99±1.04	0.52±0.95
	DHA (22:6ω3)	0.19±0.48	0.95±0.93	0.91±1.56
	ALA+LA	0.02±0.05	0.16±0.16	0.12±0.28
	EPA+DHA+ARA	0.35±0.83	2.01±1.94	1.46±2.56
	SAFA	0.27±0.64	1.46±1.42	1.32±1.91
	MUFA	0.14±0.25	1.32±1.66	1.45±5.57
	PUFA	0.43±1.01	2.47±2.34	1.8±3.3
	Total FA	0.84±1.88	5.25±5.08	4.57±9.58
FA per carbon weight (mg FA / g C)	*LA (18:2ω6)*	0.84±0.93	0.97±0.97	0.73±1.58
	ALA (18:3ω3)	0.75±1.07	0.8±0.86	0.5±1.35
	ARA (20:4ω6)	1.05±1.35	0.79±0.87	0.41±0.83
	EPA (20:5ω3)	11.07±18.05	10.95±11.38	5.31±9.76
	DHA (22:6ω3)	12.53±15.83	10.6±10.57	9.33±16.08
	ALA+LA	1.59±1.91	1.77±1.78	1.23±2.93
	EPA+DHA+ARA	24.65±33.57	22.34±21.57	15.05±26.33
	SAFA	19.27±24.5	16.52±16.41	13.54±19.58
	MUFA	11.2±21.38	15.34±20.22	14.92±57.3
	PUFA	29.84±39.78	27.42±26	18.52±33.87
	Total FA	60.31±83.73	59.27±58.75	46.98±98.51

Supplemental Table S3.21. Gelatinous zooplankton: average concentrations of select FAs per phylum. Averages are given for a subset of individual FAs and FA summations that are of ecological interest. FA concentrations are given in three different units: "mg FA per g dry weight,", "mg FA per g wet weight," and "mg FA per g carbon content." For each group, sample size is given by (n). Each result is the average across samples with standard deviations. Samples are gelatinous zooplankton categorized according to phylum.

	FA	**Annelida (n=5)**	**Chaetognatha (n=36)**	**Chordata (n=26)**	**Cnidaria (n=33)**	**Ctenophora (n=26)**	**Mollusca (n=9)**
FA per dry weight (mg FA / g DW)	*LA (18:2ω6)*	0.6±0.31	0.14±0.19	0.15±0.1	0.04±0.02	0.07±0.06	0.2±0.15
	ALA (18:3ω3)	0.54±0.5	0.11±0.13	0.13±0.16	0.03±0.03	0.07±0.06	0.27±0.26
	ARA (20:4ω6)	0.71±0.63	0.07±0.1	0.08±0.08	0.24±0.21	0.08±0.09	0.15±0.15
	EPA (20:5ω3)	7.86±6.34	1.34±2.01	0.69±0.49	0.65±0.53	1.6±1.61	3.3±2.2
	DHA (22:6ω3)	11.64±11.01	2.1±3.32	0.99±0.68	0.62±0.61	1.61±0.97	3.19±3.37
	ALA+LA	1.14±0.77	0.25±0.32	0.28±0.24	0.07±0.05	0.14±0.12	0.48±0.41
	EPA+DHA+ ARA	20.21±17.93	3.51±5.39	1.77±1.18	1.52±1.26	3.29±2.57	6.63±5.56
	SAFA	14.91±13.09	2.74±4.57	1.53±0.96	1.22±0.86	2.48±1.79	5.55±4.51
	MUFA	5.7±3.45	2.08±3.25	0.73±0.46	0.67±0.49	1.6±2.12	1.95±1.24
	PUFA	24.56±21.35	4.09±6.13	2.43±1.66	1.86±1.46	3.82±3.1	8.64±7.05
	Total FA	45.18±37.57	8.91±13.92	4.7±2.95	3.75±2.68	7.91±6.92	16.14±12.64
FA per wet weight (mg FA / g WW)	*LA (18:2ω6)*	0.08±0.04	0.01±0.02	0.01±0.01	<0.01	<0.01	0.05±0.04
	ALA (18:3ω3)	0.07±0.07	0.01±0.01	0.01±0.01	<0.01	<0.01	0.06±0.06
	ARA (20:4ω6)	0.1±0.08	0.01±0.01	<0.01	0.01±0.01	<0.01	0.03±0.03
	EPA (20:5ω3)	1.05±0.85	0.12±0.19	0.04±0.03	0.03±0.02	0.06±0.06	0.76±0.51
	DHA (22:6ω3)	1.56±1.48	0.2±0.31	0.05±0.04	0.03±0.02	0.06±0.04	0.73±0.78
	ALA+LA	0.15±0.1	0.02±0.03	0.02±0.01	<0.01	0.01±0	0.11±0.09
	EPA+DHA+ ARA	2.71±2.4	0.33±0.5	0.1±0.06	0.06±0.05	0.13±0.1	1.52±1.28
	SAFA	2±1.75	0.25±0.43	0.08±0.05	0.05±0.04	0.1±0.07	1.28±1.04
	MUFA	0.76±0.46	0.19±0.3	0.04±0.02	0.03±0.02	0.06±0.08	0.45±0.29
	PUFA	3.29±2.86	0.38±0.57	0.13±0.09	0.08±0.06	0.15±0.12	1.99±1.62
	Total FA	6.05±5.03	0.83±1.29	0.25±0.16	0.15±0.11	0.32±0.28	3.71±2.91
FA per carbon weight (mg FA / g C)	*LA (18:2ω6)*	1.63±0.84	0.37±0.52	1.47±0.98	0.27±0.19	1.46±1.16	0.7±0.53
	ALA (18:3ω3)	1.45±1.35	0.31±0.36	1.24±1.6	0.24±0.22	1.32±1.21	0.95±0.9
	ARA (20:4ω6)	1.92±1.71	0.19±0.27	0.8±0.8	1.82±1.61	1.53±1.67	0.51±0.52
	EPA (20:5ω3)	21.25±17.14	3.64±5.47	6.71±4.72	4.94±4.03	31.41±31.55	11.4±7.63
	DHA (22:6ω3)	31.45±29.76	5.73±9.05	9.66±6.65	4.73±4.62	31.62±19.1	11.02±11.66
	ALA+LA	3.07±2.08	0.68±0.87	2.71±2.35	0.51±0.39	2.78±2.32	1.65±1.42
	EPA+DHA+ ARA	54.62±48.45	9.57±14.68	17.17±11.5	11.49±9.53	64.56±50.46	22.93±19.25
	SAFA	40.3±35.39	7.46±12.46	14.87±9.33	9.26±6.52	48.69±35.18	19.2±15.61
	MUFA	15.41±9.32	5.67±8.86	7.12±4.48	5.08±3.68	31.45±41.66	6.75±4.3
	PUFA	66.39±57.69	11.14±16.71	23.63±16.09	14.09±11.09	74.88±60.85	29.9±24.39
	Total FA	122.1±101.55	24.28±37.93	45.62±28.64	28.43±20.29	155.02±135.72	55.85±43.73

Supplemental Table S3.22. Gelatinous zooplankton: average concentrations of select FAs per feeding style/guild. Avgs are given for a subset of individual FAs and FA summations that are of ecological interest. FA concentrations are given in three different units: "mg FA / g dry weight,", "mg FA / g wet weight," and "mg FA / g carbon content." For each group, n gives sample size. Each result is the average across samples with standard deviations. Samples are categorized according to "feeding style" (predator or grazer) and "feeding guild" [grazer, hard-body consumer (H_BC), mixed-body consumer (M_BC), or soft-body consumer (S_BC)].

	FA		Feeding Guild			
		Feeding Style				
		Predator (n=102)	**Grazer (n=33)**	**H_BC (n=39)**	**M_BC (n=30)**	**S_BC (n=33)**
FA per dry weight (mg FA / g DW)	*LA (18:2ω6)*	0.12±0.18	0.15±0.1	0.13±0.19	0.04±0.03	0.17±0.24
	ALA (18:3ω3)	0.1±0.19	0.14±0.15	0.11±0.13	0.03±0.03	0.17±0.29
	ARA (20:4ω6)	0.16±0.24	0.08±0.08	0.09±0.13	0.03±0.03	0.37±0.31
	EPA (20:5ω3)	1.58±2.53	1.13±1.17	1.35±1.95	0.67±0.5	2.68±3.65
	DHA (22:6ω3)	2.08±3.89	1.19±0.88	2.08±3.21	0.88±0.7	3.16±5.71
	ALA+LA	0.22±0.36	0.29±0.23	0.24±0.31	0.07±0.06	0.33±0.51
	EPA+DHA+ARA	3.82±6.54	2.4±1.99	3.51±5.21	1.58±1.18	6.22±9.52
	SAFA	2.92±4.99	2.12±1.79	2.71±4.41	1.26±0.93	4.67±7
	MUFA	1.7±2.57	0.94±0.71	1.99±3.14	0.6±0.52	2.34±2.68
	PUFA	4.55±7.81	3.26±2.67	4.09±5.94	1.81±1.36	7.59±11.5
	Total FA	9.17±15	6.32±5.05	8.8±13.43	3.67±2.7	14.6±20.74
FA per wet weight (mg FA / g WW)	*LA (18:2ω6)*	0.01±0.02	0.01±0.02	0.01±0.02	<0.01	0.02±0.04
	ALA (18:3ω3)	0.01±0.03	0.01±0.02	0.01±0.01	<0.01	0.02±0.05
	ARA (20:4ω6)	0.01±0.03	0.01±0.01	0.01±0.01	<0.01	0.03±0.05
	EPA (20:5ω3)	0.14±0.34	0.16±0.29	0.12±0.18	0.03±0.02	0.28±0.55
	DHA (22:6ω3)	0.2±0.54	0.14±0.2	0.19±0.3	0.04±0.03	0.38±0.87
	ALA+LA	0.02±0.05	0.03±0.03	0.02±0.03	<0.01	0.04±0.08
	EPA+DHA+ARA	0.36±0.91	0.31±0.49	0.31±0.48	0.06±0.05	0.69±1.46
	SAFA	0.27±0.69	0.27±0.45	0.24±0.41	0.05±0.04	0.51±1.09
	MUFA	0.14±0.27	0.11±0.18	0.18±0.29	0.02±0.02	0.21±0.34
	PUFA	0.43±1.1	0.41±0.66	0.36±0.55	0.07±0.05	0.85±1.78
	Total FA	0.85±2.04	0.8±1.28	0.79±1.25	0.15±0.11	1.57±3.2
FA per carbon weight (mg FA / g C)	*LA (18:2ω6)*	0.7±0.88	1.28±0.96	0.38±0.51	0.63±0.59	1.13±1.22
	ALA (18:3ω3)	0.63±0.9	1.11±1.45	0.31±0.35	0.53±0.59	1.1±1.31
	ARA (20:4ω6)	1.16±1.48	0.7±0.74	0.36±0.78	0.5±0.59	2.71±1.5
	EPA (20:5ω3)	12.29±20.45	7.31±4.92	4.21±5.97	11.56±10.41	22.49±31.51
	DHA (22:6ω3)	13.67±17.74	9.01±6.27	6.31±9.33	15.74±14.76	20.5±23.96
	ALA+LA	1.33±1.74	2.39±2.19	0.69±0.84	1.17±1.16	2.23±2.48
	EPA+DHA+ARA	27.12±37.85	17.02±10.92	10.88±15.71	27.8±25.11	45.69±54.59
	SAFA	20.69±27.6	14.87±9.05	8.3±12.66	22.07±20.06	34.08±38.41
	MUFA	12.61±24.34	6.85±4.26	5.77±8.59	9.26±9.11	23.74±38.88
	PUFA	31.96±44.81	23.28±15.19	12.67±17.9	31.51±28.83	55.17±64.76
	Total FA	65.27±94.68	45±27.31	26.75±38.71	62.84±57.11	112.99±139.26

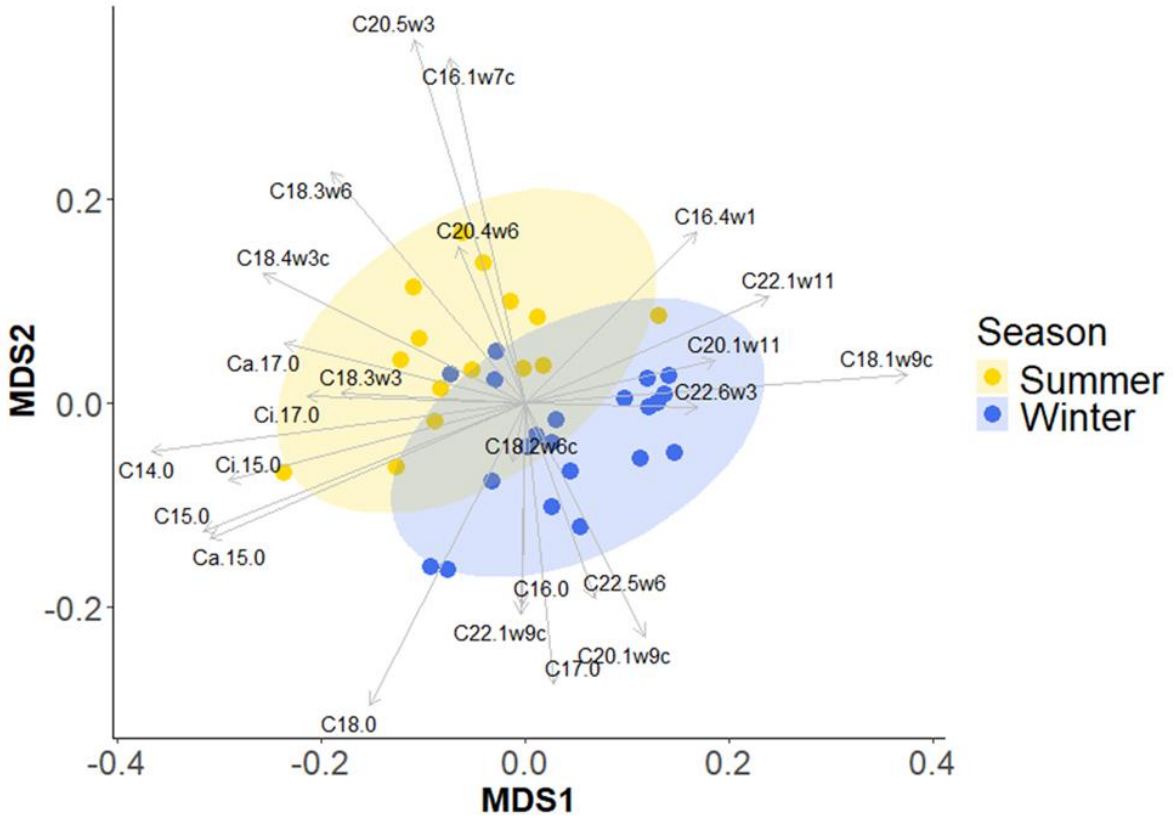

Figure S3.1. NMDS plot of FA profiles of Chaetognatha comparing seasons. Datapoints are colored denoting if the Chaetognatha sample was collected in summer (yellow) or winter (blue) and ellipses indicate 95% confidence intervals. FA vectors displayed are a subset of FA that were found to frequently drive dissimilarity across comparisons throughout this study, as well as FA that are of ecological importance.

APPENDIX III:

SUPPLEMENTAL MATERIALS FOR CHAPTER IV

Table S4.1. Table of average FA concentrations and proportions per taxon at extraction timepoint t0 and storage temperature T-80°C. Concentrations are given in units of "mg FA / g dry wt" and proportions are given in units %. All values are given with standard deviations. FA summations are also given for saturated fatty acids (SAFA), mono-unsaturated fatty acids (MUFA), poly-unsaturated fatty acids (PUFA), and total fatty acids (Total FA). Individual FA are listed in order of decreasing saturation and increasing carbon chain length.

FA	**Fish**		**Gumboot**		**Kelp**		**Urchin**	
	Conc.	*Prop.*	*Conc.*	*Prop.*	*Conc.*	*Prop.*	*Conc.*	*Prop.*
C10:0	0 ±0	0.001 ±0	0 ±0	0 ±0	0 ±0	0.002 ±0.001	0.006 ±0.001	0.007 ±0.001
C12:0	0.008 ±0.008	0.021 ±0.009	0.003 ±0.001	0.026 ±0.005	0.002 ±0	0.055 ±0.006	0.068 ±0.005	0.081 ±0.004
C13:0	0.003 ±0.004	0.009 ±0.005	0.002 ±0.001	0.019 ±0.005	0.001 ±0	0.032 ±0.003	0.056 ±0.004	0.066 ±0.006
C14:0	0.648 ±0.676	1.848 ±0.762	0.548 ±0.18	4.185 ±0.827	0.294 ±0.009	9.419 ±0.268	9.432 ±0.437	11.184 ±0.168
Ci-14:0	0.003 ±0.004	0.008 ±0.005	0 ±0	0 ±0	0 ±0	0 ±0	0.019 ±0.001	0.023 ±0.001
C15:0	0.09 ±0.078	0.277 ±0.063	0.238 ±0.07	1.826 ±0.294	0.011 ±0.001	0.348 ±0.032	0.575 ±0.016	0.682 ±0.032
Ca-15:0	0.007 ±0.009	0.02 ±0.011	0.002 ±0.001	0.017 ±0.003	0 ±0	0.009 ±0.001	0.042 ±0.001	0.049 ±0.003
Ci-15:0	0.032 ±0.039	0.087 ±0.049	0.011 ±0.003	0.083 ±0.013	0 ±0	0.009 ±0.003	0.088 ±0.003	0.105 ±0.006
C16:0	5.379 ±2.042	19.37 ±2.687	2.639 ±0.418	20.63 ±0.316	0.691 ±0.019	22.149 ±0.785	13.106 ±0.497	15.545 ±0.116
C17:0	0.076 ±0.05	0.252 ±0.015	0.145 ±0.015	1.148 ±0.14	0.004 ±0	0.142 ±0.01	0.155 ±0.005	0.184 ±0.01

Ca-17:0	0.019 ±0.02	0.055 ±0.021	0.01 ±0.003	0.081 ±0.014	0 ±0	0 ±0	0 ±0	0 ±0
C18:0	1.494 ±0.597	5.361 ±0.734	0.566 ±0.064	4.47 ±0.532	0.08 ±0.011	2.546 ±0.342	2.709 ±0.054	3.215 ±0.081
C20:0	0.036 ±0.034	0.108 ±0.033	0.022 ±0.005	0.176 ±0.063	0.026 ±0.001	0.844 ±0.025	0 ±0	0 ±0
C22:0	0.014 ±0.013	0.044 ±0.011	0.009 ±0.001	0.069 ±0.014	0.002 ±0	0.051 ±0.005	0.026 ±0.001	0.031 ±0.001
C23:0	0 ±0	0 ±0	0 ±0	0 ±0	0 ±0	0 ±0	0.011 ±0.001	0.014 ±0.001
C24:0	0.022 ±0.013	0.091 ±0.053	0.003 ±0.001	0.024 ±0.004	0.003 ±0	0.089 ±0.006	0.03 ±0.001	0.035 ±0.002
C14:1	0.016 ±0.021	0.04 ±0.029	0 ±0	0 ±0	0.002 ±0	0.074 ±0.007	2.273 ±0.093	2.696 ±0.045
C16:1ω5c	0.075 ±0.054	0.242 ±0.025	0.017 ±0.003	0.131 ±0.007	0.082 ±0.006	2.628 ±0.199	4.46 ±0.174	5.29 ±0.081
C16:1ω7c	1.181 ±1.2	3.402 ±1.31	0.388 ±0.123	2.965 ±0.566	0.141 ±0.008	4.52 ±0.286	4.015 ±0.143	4.763 ±0.035
C16:1ω7t	0.077 ±0.068	0.234 ±0.059	0.041 ±0.011	0.313 ±0.044	0.005 ±0	0.16 ±0.005	0.281 ±0.005	0.334 ±0.013
C16:1ω9	0.157 ±0.123	0.495 ±0.08	0 ±0	0 ±0	0 ±0	0 ±0	0 ±0	0 ±0
C17:1ω7c	0.005 ±0.004	0.016 ±0.003	0 ±0	0 ±0	0 ±0	0 ±0	0 ±0	0 ±0
C18:1ω5c	0.099 ±0.085	0.304 ±0.066	0.013 ±0.002	0.099 ±0.007	0.005 ±0	0.144 ±0.016	0.396 ±0.007	0.47 ±0.013
C18:1ω7c	1.216 ±0.886	3.899 ±0.453	1.002 ±0.117	7.883 ±0.393	0.006 ±0.001	0.19 ±0.018	3.834 ±0.14	4.547 ±0.043
C18:1ω9c	3.883 ±3.641	11.52 ±3.571	1.885 ±0.639	14.375 ±3.093	0.597 ±0.009	19.108 ±0.356	4.96 ±0.167	5.883 ±0.047

C18:1ω9t	0.144 ±0.063	0.512 ±0.127	0 ±0	0 ±0	0 ±0	0 ±0	1.187 ±0.196	1.403 ±0.193
C20:1ω15	0.269 ±0.343	0.701 ±0.451	0.46 ±0.131	3.533 ±0.514	0.009 ±0.001	0.293 ±0.03	2.747 ±0.37	3.263 ±0.482
C20:1ω7	0.051 ±0.064	0.135 ±0.083	0.146 ±0.025	1.14 ±0.032	0 ±0	0 ±0	0.238 ±0.009	0.283 ±0.017
C20:1ω9	0.626 ±0.682	1.756 ±0.784	0.252 ±0.038	1.973 ±0.054	0 ±0	0 ±0	2.976 ±0.406	3.522 ±0.381
C22:1ω7c	0.033 ±0.028	0.1 ±0.031	0 ±0	0 ±0	0 ±0	0 ±0	0 ±0	0 ±0
C22:1ω9c	0.119 ±0.133	0.33 ±0.167	0.025 ±0.006	0.196 ±0.017	0.007 ±0.003	0.226 ±0.105	2.582 ±0.103	3.062 ±0.041
C22:1ω9t	0.528 ±0.688	1.362 ±0.92	0.017 ±0.001	0.131 ±0.012	0.003 ±0.001	0.086 ±0.02	0.1 ±0.004	0.119 ±0.007
C24:1ω9	0.342 ±0.153	1.199 ±0.125	0.023 ±0.004	0.181 ±0.006	0 ±0	0 ±0	0.038 ±0.001	0.045 ±0.002
C16:2ω4	0.177 ±0.221	0.465 ±0.284	0.005 ±0.002	0.035 ±0.01	0.004 ±0	0.141 ±0.004	0.296 ±0.009	0.352 ±0.02
C16:2ω6	0.01 ±0.014	0.026 ±0.018	0 ±0	0 ±0	0.002 ±0	0.078 ±0.002	0.023 ±0.001	0.027 ±0.002
C16:3ω4	0 ±0	0 ±0	0 ±0	0 ±0	0 ±0	0 ±0	0.35 ±0.007	0.416 ±0.019
C16:4ω1	0.07 ±0.094	0.178 ±0.128	0 ±0	0 ±0	0 ±0	0 ±0	0.257 ±0.009	0.305 ±0.018
C16:4ω3	0 ±0	0 ±0	0 ±0	0 ±0	0 ±0	0 ±0	0.271 ±0.01	0.322 ±0.02
C18:2ω3	0.057 ±0.049	0.175 ±0.037	0.04 ±0.012	0.307 ±0.052	0 ±0	0 ±0	0.185 ±0.003	0.22 ±0.01
C18:2ω6c	0.512 ±0.462	1.544 ±0.4	0.101 ±0.008	0.801 ±0.082	0.194 ±0.008	6.201 ±0.26	1.373 ±0.028	1.629 ±0.05

C18:2ω6t	0.013 ±0.014	0.037 ±0.014	0.009 ±0.003	0.072 ±0.014	0.002 ±0	0.058 ±0.005	1.488 ±0.022	1.766 ±0.035
C18:3ω3	0.169 ±0.164	0.497 ±0.157	0.015 ±0.003	0.12 ±0.004	0.065 ±0.003	2.069 ±0.099	1.588 ±0.04	1.884 ±0.048
C18:3ω6	0.028 ±0.032	0.079 ±0.036	0.004 ±0.001	0.033 ±0.003	0.011 ±0.001	0.365 ±0.035	0.238 ±0.006	0.283 ±0.013
C18:4ω3c	0.174 ±0.213	0.462 ±0.27	0 ±0	0 ±0	0.061 ±0.006	1.948 ±0.189	1.91 ±0.047	2.266 ±0.05
C20:2ω6	0.076 ±0.064	0.235 ±0.048	0.169 ±0.013	1.345 ±0.217	0.004 ±0	0.114 ±0.006	0.715 ±0.017	0.849 ±0.043
C20:2ω7	0.006 ±0.007	0.018 ±0.008	0.023 ±0.008	0.171 ±0.043	0 ±0	0 ±0	0.947 ±0.019	1.125 ±0.053
C20:3ω3	0.029 ±0.03	0.082 ±0.032	0.017 ±0.002	0.134 ±0.01	0 ±0	0 ±0	1.037 ±0.03	1.231 ±0.069
C20:3ω6	0.032 ±0.026	0.099 ±0.018	0.017 ±0.003	0.136 ±0.003	0.013 ±0.002	0.416 ±0.067	0.648 ±0.022	0.769 ±0.048
C20:3ω9	0 ±0	0 ±0	0.176 ±0.051	1.352 ±0.212	0 ±0	0 ±0	0.875 ±0.017	1.039 ±0.047
C20:4ω3	0.095 ±0.09	0.282 ±0.081	0.004 ±0.001	0.03 ±0.003	0.01 ±0.001	0.311 ±0.03	0.769 ±0.031	0.914 ±0.062
C20:4ω6	0.676 ±0.258	2.432 ±0.343	1.59 ±0.114	12.652 ±1.998	0.604 ±0.025	19.352 ±0.598	4.684 ±0.162	5.557 ±0.102
C20:5ω3	3.264 ±1.468	11.488 ±1.109	0.895 ±0.087	7.06 ±0.609	0.182 ±0.016	5.822 ±0.457	9.178 ±0.409	10.886 ±0.266
C21:5ω3	0.084 ±0.095	0.231 ±0.111	0 ±0	0 ±0	0 ±0	0 ±0	0 ±0	0 ±0
C22:2ω6	0.006 ±0.006	0.018 ±0.006	0.014 ±0.003	0.107 ±0.007	0 ±0	0 ±0	0 ±0	0 ±0
C22:3ω6	0.003 ±0.001	0.009 ±0.002	0 ±0	0 ±0	0 ±0	0 ±0	0.103 ±0.004	0.122 ±0.007

C22:4ω6	0.036 ±0.035	0.105 ±0.034	0.545 ±0.052	4.356 ±0.856	0 ±0	0 ±0	0.203 ±0.008	0.241 ±0.012
C22:5ω3	0.512 ±0.447	1.565 ±0.352	0.702 ±0.062	5.615 ±1.164	0 ±0	0 ±0	0.488 ±0.018	0.579 ±0.014
C22:5ω6	0.108 ±0.05	0.381 ±0.044	0 ±0	0 ±0	0 ±0	0 ±0	0.018 ±0.003	0.021 ±0.003
C22:6ω3	6.839 ±1.62	25.793 ±6.161	0 ±0	0 ±0	0 ±0	0 ±0	0.25 ±0.009	0.297 ±0.013
SAFA	7.834 ±3.565	27.553 ±2.542	4.198 ±0.727	32.753 ±0.973	1.114 ±0.022	35.694 ±0.813	26.322 ±0.959	31.22 ±0.154
MUFA	8.822 ±8.221	26.248 ±7.886	4.268 ±1.089	32.92 ±3.798	0.856 ±0.024	27.43 ±0.821	30.087 ±1.321	35.68 ±0.524
PUFA	12.973 ±5.435	46.199 ±5.662	4.326 ±0.326	34.328 ±4.568	1.152 ±0.053	36.876 ±1.318	27.894 ±0.576	33.1 ±0.615
Total FA	29.629 ±17.198	100	12.793 ±2.02	100	3.123 ±0.048	100	84.303 ±2.728	100

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Chapter V

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