Seasonal fatty acid profiles of marine algae and invertebrates from Sitka Sound, Alaska in 2019

Website: https://www.bco-dmo.org/dataset/947067
Data Type: Other Field Results
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Project
» CAREER: Energy fluxes and community stability in a dynamic, high-latitude kelp ecosystem (High latitude kelp dynamics)

Contributors	Affiliation	Role
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Abstract
These data include fatty acid compositions of select marine macroalgae and macroinvertebrate grazers collected in Sitka Sound, Alaska in January 2019 and July 2019. Samples were collected using SCUBA at three sites, all within 6 km of each other in Sitka Sound: Harris Island (N 57.03165, W 135.27754), Breast Island (N 57.03896, W 135.33309), and Samsing Pinnacle (N 56.98750, W 135.35718). Sampled species included six seaweeds, including three Laminarian kelps (Ochrophyta) and three red algae from the Gigartinales and Ceramiales, that are present in both seasons in these sites: Neoagarum fimbriatum, Macrocystis pyrifera, Hedophyllum nigripes, Cryptopleura ruprechtiana, Opuntiella californica, and Osmundia spectabilis. They also include six macro-invertebrates (two each of gastropods, crustaceans, echinoderms) that are present and dominant herbivores in these sites: Haliotis kamtschatkana, Tegula pulligo, Pentidotea resecata, Pugettia producta, Mesocentrotus franciscanus, and Strongylocentrotus droebachiensis. Understanding seasonal variation in fatty acid trophic biomarkers between dominant macrophyte resources and their benthic herbivores can help reveal how producers and their primary consumers may respond to future environmental change. These unique data from a high latitude kelp forest ecosystem were collected by a collaborative team of marine ecologists: Dr. Reyn Yoshioka, Dr. Aaron Galloway, Dr. Julie Schram, Dr. Kristy Kroeker, and Dr. Lauren Bell.

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Coverage

Location: Sitka Sound, Alaska
Spatial Extent: **N**:57.03165 **E**:-135.27754 **S**:56.9875 **W**:-135.35718
Temporal Extent: 2019-01-11 - 2019-07-14

Methods & Sampling

We collected samples using SCUBA at three sites in Sitka Sound, all within 6 km of each other: Harris Island (N 57.03165, W 135.27754), Breast Island (N 57.03896, W 135.33309), and Samsing Pinnacle (N 56.98750, W 135.35718). Samples were collected during one week in two seasons: winter (January 2019) and summer (July 2019). Generally, we collected ~4 replicate samples for each species at each of the three sites in each season for fatty acids analysis. For seaweeds, this resulted in 4 replicates from one site in each season, and for invertebrates, this resulted in ~12 replicates (across 3 sites) for each season, with the exception of the isopod Pentidotea resecata in the summer, for which only one sample was collected due to a paucity of isopods residing in the seaweeds across our 3 sampling sites.

We sampled six seaweeds, including three Laminarian kelps (Ochrophyta, urn:lsid:marinespecies.org:taxname:345465) and three red algae from the Gigartinales (urn:lsid:marinespecies.org:taxname:871) and Ceramiales (urn:lsid:marinespecies.org:taxname:860), that are present in both seasons in these sites: *Neoagarum fimbriatum, Macrocystis pyrifera, Hedophyllum nigripes, Cryptopleura ruprechtiana, Opuntiella californica,* and *Osmundia spectabilis* (See supplemental species_list.csv for identifiers).
Note: "*Neoagarum fimbriatum*" appears as the unaccepted synonym "*Agarum fimbriatum*" used in this dataset.

We sampled six macro-invertebrates (two each of gastropods, crustaceans, echinoderms) that are present and dominant herbivores in these sites: *Haliotis kamtschatkana, Tegula pulligo, Pentidotea resecata, Pugettia producta, Mesocentrotus franciscanus, and Strongylocentrotus droebachiensis* (See supplemental species_list.csv for identifiers).

M. pyrifera blades were collected from the distal ends of the thallus near the scimitar area from a boat at the surface, but other collections were made by SCUBA divers between 5-8 m depth. In general, all seaweeds were sampled in a consistent way within each species, targeting the same general tissues, avoiding proximal and distal areas of blades, avoiding sori, holdfasts, and stipes. All seaweeds were wiped clean with a paper towel and inspected to ensure they were not contaminated by epiphytes or endophytes. Invertebrates were sacrificed by freezing (-20°) for ~30 minutes before subsequent dissection. Invertebrate tissues were sampled in a consistent way for each taxon: Haliotis were sampled by snipping the foot muscle; Tegula were crushed with a hammer and the foot muscle was snipped; whole P. resecata individuals were sampled owing to their small size; for Pugettia, muscle tissue was removed from the legs; for Mesocentrotus and Strongylocentrotus, the test was cut open and gonadal tissue sampled. Sampling equipment was wiped clean with kimwipes and ethanol between samples. All samples were placed into 1.5 ml Eppendorf tubes, which were immediately frozen in a -20°C freezer. No solvents were introduced to samples in plastic storage vials.Within 3 days, all samples were moved to a -80°C freezer where they were stored until shipment to the -80°C freezer at the Oregon Institute of Marine Biology, where all fatty acid extractions were performed.

Tissue samples were kept at -80°C until extraction; all samples for both collection efforts were extracted within 9 months of collection. Samples were lyophilized to dryness for 48 hours. Once tissues were dried they were ground to fine, homogeneous powder with a stainless-steel mortar and pestle. Homogenized tissues were then immediately digested in chloroform for ~12 hrs sealed under nitrogen at -20°C. Total lipid extraction and subsequent derivatization of fatty acid methyl esters (FAME) was performed using a modification of the method described by (Taipale et al. 2016) and briefly summarized here. All sample extractions were performed in pre-combusted glassware.

Following initial tissue digestion in chloroform, 70 ul of unmethylated nonadecanoic acid (C19) was added as an internal standard. Total lipids were extracted using a 2:1:0.75 solution of chloroform: methanol: 0.9% NaCl solution, which was subsequently sonicated, vortexed, and centrifuged so that the more dense organic layer could be removed and evaporated to dryness under a steady stream of nitrogen gas. The organic phase was immediately resuspended in toluene and 1% sulfuric acid-methanol solution for 90 minutes at 90°C to transesterify FAME. Following transesterification, solutions were cooled to room temperature and KHCO3, to neutralize the acidic solution, and hexane was added. The combined solution was then vortexed and centrifuged to separate FAME in the hexane solution, which was concentrated to 1.5 ml in glass vials for gas chromatography.

FAME were analyzed with a gas chromatograph mass spectrometer (GC-MS, Shimadzu, Model QP2020), fitted with a DB-23 column (30 x 0.25mm x 0.15 µm, Agilent, Santa Clara, CA, USA), using helium as the carrier gas. To ensure sufficient separation between fatty acid peaks we utilized a heating program modified from Taipale et

al. (2016) and described by Thomas et al. (2020). Individual fatty acids were identified using relative retention times of a FAME standard (GLC 566C, Nu-Chek Prep, Elysian, MN, USA) and specific ions. Fatty acids were quantified using integration of the major ion peaks (Taipale et al. 2016) with Shimadzu Lab Solutions software. Following identification and quantification, individual peak areas for all fatty acids identified were converted to proportions, representing the % contribution of all fatty acids identified in each sample.

Data Processing Description

Shimadzu Lab Solutions software.

Note [2024-12-30] The spCode (species codes) column was not changed in the data and subsequent analysis. However, the genus and species associated with the codes were updated as follows:

* spCode "AGFIM" was originally associated with the scientific name "Agarum fimbriatum" (LSID urn:lsid:marinespecies.org:taxname:372699). The genus and species were updated in the data and metadata to use the currently accepted name for the organism "Neoagarum fimbriatum" (LSID urn:lsid:marinespecies.org:taxname:1313053).
* The scientific name associated with the code "SACCH" was updated from "Saccharina sp." to "Hedophyllum nigripes." Organisms originally identified as "Saccharina sp." were later reclassified as "Hedophyllum nigripes" (LSID urn:lsid:marinespecies.org:taxname:1356699).
* spCode "OSMUNDIA" "Osmundia spectabalis" and "Osmundia spectabilis" corrected to: OSMUNDIA "Osmundea spectabilis" (LSID urn:lsid:marinespecies.org:taxname:372624)

BCO-DMO Processing Description

* Data table within submitted file "pHAKFA_FA_conc_pub.csv" was imported into the BCO-DMO data system for this dataset. Values "NA" imported as missing data values. The missing data identifiers were described as NA = not applicable.
** In the BCO-DMO data system missing data identifiers are displayed according to the format of data you access. For example, in csv files it will be blank (null) values. In Matlab .mat files it will be NaN values. When viewing data online at BCO-DMO, the missing value will be shown as blank (null) values.

* Year_Month column added.

* lengthDia_comment column added to hold string notes that were in the lengthDia column ("partial blade").

* Taxnomomic name checking and dataset update: World Register of Marine Species taxa match tool used to find misspellings and match names to identifier "Life Science Identifier" (LSID) on 2024-12-27.
* Changes were made to the genus and species columns in the dataset after a discussion with data submitter. Name spelling matches the currently accepted names for the organisms as of the time of this dataset's publication. A note in the "Data Processing Description" metadata section was added to clarify why the codes may not all look like a representation of the genus and species names in the dataset. And to clarify a re-classification of one of the codes.
* Species list with the species codes, scientific names, LSID, taxon status and match quality were added as a supplemental file.

* Supplemental site list table extracted from provided metadata and added as a supplemental file.

* lengthDia and height columns contained variable units described in additional column lengthHeightUnits as either "mm" or "cm". Columns with consistent units in mm added for lengthDia_mm and height_mm instead.

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Related Publications

Nu-Check Prep, Inc. (n.d.) Standards: A LOOK AT NU-CHEK GLC & TLC STANDARDS. http://www.nu-chekprep.com/s.htm Accessed 2024-12-27
Methods

Shimadzu Scientific Instruments (n.d.) LabSolutions CS: Analysis Data System. https://www.ssi.shimadzu.com/products/software-informatics/labsolutions-series/labsolutions-cs/index.html *Software*

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Parameters

Parameter	Description	Units
sampleID	sample identifier, based on raw file created by the gas chromatographer-mass spectrometer	unitless
season	season of sampling, either winter or summer	unitless
site	site of specimen collection (BREAST = Breast Island, HARRIS = Harris Island, SAMSING = Samsing Pinnacle, SANDYCOVE = Sandy Cove)	unitless
Year_Month	Year and month of sampling	unitless
lat	site latitude	decimal degrees
lon	site longitude	decimal degrees
spCode	species shorthand code for specimen, primarily for recording and coding convenience, based on the genus name or a combination of genus name and species epithet. Note that SACCH is corrected to current name Hedophyllum nigripes in analysis and manuscript. See more information in the supplemental species_list.csv	unitless
type	guild of the specimen, Invert = intertebrates or herbivores, Algae = algae or producers	unitless
genus	Genus name of sampled specimen	unitless
species	Species epithet of sampled specimen	unitless
LSID	Life Science Identifier (LSID) for the taxonomic name used in the genus + species columns. See more information in the supplemental species_list.csv	unitless
lengthDia_comment	Comment explaining blanks in the lengthDia column (e.g. partial blade).	unitless
lengthDia	length or diameter of specimen, relevant size measure dependent on taxon.	millimeters (mm)

height	height of specimen, relevant size measure dependent on taxon	millimeters (mm)
wetWeightG	specimen wet weight	grams (g)
C12_0	fatty acid quantity of sample determined via GC-MS for 12:0, lauric acid	micrograms (mg)
C14_0	fatty acid quantity of sample determined via GC-MS for 14:0, myristic acid	micrograms (mg)
C14_1nX_1	fatty acid quantity of sample determined via GC-MS for 14:1, unknown omega double bond location	micrograms (mg)
C14_1nX_2	fatty acid quantity of sample determined via GC-MS for 14:1, unknown omega double bond location	micrograms (mg)
C14_1n5	fatty acid quantity of sample determined via GC-MS for 14:1 omega-5	micrograms (mg)
i15_0	fatty acid quantity of sample determined via GC-MS for iso 15:0, branched	micrograms (mg)
a15_0	fatty acid quantity of sample determined via GC-MS for anteiso 15:0, branched	micrograms (mg)
C15_0	fatty acid quantity of sample determined via GC-MS for 15:0	micrograms (mg)
i16_0	fatty acid quantity of sample determined via GC-MS for iso 16:0, branched	micrograms (mg)
C16_0	fatty acid quantity of sample determined via GC-MS for 16:0, palmitic acid	micrograms (mg)
C16_1nX_1	fatty acid quantity of sample determined via GC-MS for 16:1, unknown omega double bond location	micrograms (mg)
C16_1nX_2	fatty acid quantity of sample determined via GC-MS for 16:1, unknown omega double bond location	micrograms (mg)
C16_1n7	fatty acid quantity of sample determined via GC-MS for 16:1 omega-7, palmitoleic acid	micrograms (mg)
C16_1nX_3	fatty acid quantity of sample determined via GC-MS for 16:1, unknown omega double bond location	micrograms (mg)
C16_1nX_4	fatty acid quantity of sample determined via GC-MS for 16:1, unknown omega double bond location	micrograms (mg)

i17_0	fatty acid quantity of sample determined via GC-MS for iso 17:0, branched	micrograms (mg)
a17_0	fatty acid quantity of sample determined via GC-MS for anteiso 17:0, branched	micrograms (mg)
C16_2nX_1	fatty acid quantity of sample determined via GC-MS for 16:2, uknown omega double bond location	micrograms (mg)
C16_2nX_2	fatty acid quantity of sample determined via GC-MS for 16:2, uknown omega double bond location	micrograms (mg)
C17_0	fatty acid quantity of sample determined via GC-MS for 17:0	micrograms (mg)
C16_3n4	fatty acid quantity of sample determined via GC-MS for 16:3 omega-4	micrograms (mg)
C17_1	fatty acid quantity of sample determined via GC-MS for 17:1, uknown omega double bond location	micrograms (mg)
C16_4n1	fatty acid quantity of sample determined via GC-MS for 16:4 omega-1	micrograms (mg)
i18_0	fatty acid quantity of sample determined via GC-MS for iso 18:0, branched	micrograms (mg)
C18_0	fatty acid quantity of sample determined via GC-MS for 18:0, stearic acid	micrograms (mg)
C18_1nX_1	fatty acid quantity of sample determined via GC-MS for 17:1, uknown omega double bond location	micrograms (mg)
C18_1n9	fatty acid quantity of sample determined via GC-MS for 18:1 omega-9, oleic acid	micrograms (mg)
C18_1n7c	fatty acid quantity of sample determined via GC-MS for 18:1 omega-7, cis, cis vaccenic acid	micrograms (mg)
C18_1nX_2	fatty acid quantity of sample determined via GC-MS for 18:1, uknown omega double bond location	micrograms (mg)
C18_2n6t	fatty acid quantity of sample determined via GC-MS for 18:2 omega-6, trans	micrograms (mg)
C18_2n6c	fatty acid quantity of sample determined via GC-MS for 18:2 omega-6, cis, linoleic acid	micrograms (mg)

i19_0	fatty acid quantity of sample determined via GC-MS for iso 19:0, branched	micrograms (mg)
C18_2	fatty acid quantity of sample determined via GC-MS for 18:2, uknown omega double bond location	micrograms (mg)
C18_3n6	fatty acid quantity of sample determined via GC-MS for 18:3 omega-6	micrograms (mg)
C19_0	fatty acid quantity of sample determined via GC-MS for 19:0	micrograms (mg)
C18_3n3	fatty acid quantity of sample determined via GC-MS for 18:3 omega-3, alpha-linolenic acid	micrograms (mg)
C19_1	fatty acid quantity of sample determined via GC-MS for 19:1, uknown omega double bond location	micrograms (mg)
C18_4n3	fatty acid quantity of sample determined via GC-MS for 18:4 omega-3, stearidonic acid	micrograms (mg)
C20_0	fatty acid quantity of sample determined via GC-MS for 20:0, arachidic acid	micrograms (mg)
C20_1nX_1	fatty acid quantity of sample determined via GC-MS for 20:1, uknown omega double bond location	micrograms (mg)
C20_1n9	fatty acid quantity of sample determined via GC-MS for 20:1 omega-9	micrograms (mg)
C20_1nX_2	fatty acid quantity of sample determined via GC-MS for 20:1, uknown omega double bond location	micrograms (mg)
C20_2nX_1	fatty acid quantity of sample determined via GC-MS for 20:2, uknown omega double bond location	micrograms (mg)
C20_1nX_3	fatty acid quantity of sample determined via GC-MS for 20:1, uknown omega double bond location	micrograms (mg)
C20_2nX_2	fatty acid quantity of sample determined via GC-MS for 20:2, uknown omega double bond location	micrograms (mg)
C20_2nX_3	fatty acid quantity of sample determined via GC-MS for 20:2, uknown omega double bond location	micrograms (mg)
C20_2n6	fatty acid quantity of sample determined via GC-MS for 20:2 omega-6	micrograms (mg)

C20_3n6	fatty acid quantity of sample determined via GC-MS for 20:3 omega-6	micrograms (mg)
C20_4n6	fatty acid quantity of sample determined via GC-MS for 20:4 omega-6, arachidonic acid	micrograms (mg)
C20_3n3	fatty acid quantity of sample determined via GC-MS for 20:3 omega-3	micrograms (mg)
C20_4n3	fatty acid quantity of sample determined via GC-MS for 20:4 omega-3	micrograms (mg)
C20_5n3	fatty acid quantity of sample determined via GC-MS for 20:5 omega-3, eicosapentaenoic acid or EPA	micrograms (mg)
C22_0	fatty acid quantity of sample determined via GC-MS for 22:0, behenic acid	micrograms (mg)
C22_1n9c	fatty acid quantity of sample determined via GC-MS for 22:1 omega-9	micrograms (mg)
C22_2n6	fatty acid quantity of sample determined via GC-MS for 22:2 omega-6	micrograms (mg)
C22_2nX	fatty acid quantity of sample determined via GC-MS for 22:2, uknown omega double bond location	micrograms (mg)
C22_4n6	fatty acid quantity of sample determined via GC-MS for 22:4 omega-6	micrograms (mg)
C22_3n6	fatty acid quantity of sample determined via GC-MS for 22:3 omega-6	micrograms (mg)
C22_4n3	fatty acid quantity of sample determined via GC-MS for 22:4 omega-3	micrograms (mg)
C22_5n3	fatty acid quantity of sample determined via GC-MS for 22:5 omega-3, docosapentaenoic acid or DPA	micrograms (mg)
C22_6n3	fatty acid quantity of sample determined via GC-MS for 22:6 omega-3, docosahexaenoic acid or DHA	micrograms (mg)
C24_1n9	fatty acid quantity of sample determined via GC-MS for 24:1 omega-9	micrograms (mg)

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Instruments

Dataset-specific Instrument Name	Gas chromatograph mass spectrometer (GC-MS, Shimadzu, Model QP2020)
Generic Instrument Name	Gas Chromatograph Mass Spectrometer
Dataset-specific Description	Gas chromatograph mass spectrometer (GC-MS, Shimadzu, Model QP2020), fitted with a DB-23 column (30 x 0.25mm x 0.15 µm, Agilent, Santa Clara, CA, USA), using helium as the carrier gas.
Generic Instrument Description	Instruments separating gases, volatile substances or substances dissolved in a volatile solvent by transporting an inert gas through a column packed with a sorbent to a detector for assay by a mass spectrometer.

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Project Information

CAREER: Energy fluxes and community stability in a dynamic, high-latitude kelp ecosystem (High latitude kelp dynamics)

Coverage: SE Alaskan coastal waters

NSF Award Abstract:
High latitude kelp forests support a wealth of ecologically and economically important species, buffer coastlines from high-energy storms, and play a critical role in the marine carbon cycle by sequestering and storing large amounts of carbon. Understanding how energy fluxes and consumer-resource interactions vary in these kelp communities is critical for defining robust management strategies that help maintain these valuable ecosystem services. In this integrated research and education program, the project team will investigate how consumer populations respond to variability in temperature, carbonate chemistry and resource quality to influence the food webs and ecosystem stability of kelp forests. A comprehensive suite of studies conducted at the northern range limit for giant kelp (Macrocystis pyrifera) in SE Alaska will examine how kelp communities respond to variable environmental conditions arising from seasonal variability and changing ocean temperature and acidification conditions. As part of this project, undergraduate and high school students will receive comprehensive training through (1) an immersive field-based class in Sitka Sound, Alaska, (2) intensive, mentored research internships, and (3) experiential training in science communication and public outreach that will include a variety of opportunities to disseminate research findings through podcasts, public lectures and radio broadcasts.

Consumer-resource interactions structure food webs and govern ecosystem stability, yet our understanding of how these important interactions may change under future climatic conditions is hampered by the complexity of direct and indirect effects of multiple stressors within and between trophic levels. For example, environmentally mediated changes in nutritional quality and chemical deterrence of primary producers have the potential to alter herbivory rates and energy fluxes between primary producers and consumers, with implications for ecosystem stability. Moreover, the effects of global change on primary producers are likely to depend on other limiting resources, such as light and nutrients, which vary seasonally in dynamic, temperate and high latitude ecosystems. In marine ecosystems at high latitude, climate models predict that ocean acidification will be most pronounced during the winter months, when primary production is limited by light. This project is built around the hypothesis that there could be a mismatch in the energetic demands of primary consumers caused by warming and ocean acidification and resource availability and quality during winter months, with cascading effects on trophic structure and ecosystem stability in the future. Through complementary lab and field experiments, the project team will determine 1) how temperature and carbonate chemistry combine to affect primary consumer bioenergetics across a diversity of species and 2) the indirect effects of ocean acidification and warming on primary consumers via environmentally mediated changes in the availability, nutritional quality and palatability of primary producers across seasons. Using the data from the laboratory and field experiments, the project team will 3) construct a model of the emergent effects of warming and ocean acidification on trophic structure and ecosystem stability in seasonally dynamic, high

latitude environments.

This award reflects NSF's statutory mission and has been deemed worthy of support through evaluation using the Foundation's intellectual merit and broader impacts review criteria.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1752600

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