

Ecological niche of coastal Beaufort Sea fishes defined by stable isotopes and fatty acids

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ABSTRACT: Little is known about the trophic ecology of freshwater, coastal and marine fish species that utilize coastal environments in the Beaufort Sea. In this study we use stable isotopes (SI) and fatty acid (FA) profiles to (1) characterize habitat and diet components of the ecological niche for 16 co-occurring fish species, (2) quantify niche overlap among these species and groups of species, and (3) identify resource partitioning and niche shift indicators for future monitoring. Ward's cluster analysis of SI ($\delta^{13}\text{C}$, $\delta^{15}\text{N}$) results identified 3 representative isotopic groups that were consistent with known life-history groups: marine, freshwater-rearing and coastal fishes. Correspondence and Ward's clustering analyses on FA profiles resulted in 5 FA groups that indicated feeding preferences and included: pelagic marine-feeding, benthic and pelagic brackish (both freshwater and marine)-feeding, benthic freshwater-feeding, benthic marine-feeding, and benthic brackish-feeding groups. Isotopic niche size and feeding preferences (FA) indicated generalist and specialist strategies that could be used as indicators for resource partitioning and niche shifts. Understanding the habitat use, diet, and trophic interactions among fish species is important in monitoring the Tarrum Niruyutait Marine Protected Area. Combining SI and FA tracers to quantify probability of niche overlap is a unique aspect of understanding species-specific niche interactions within the Beaufort Sea coastal environment, and our results contribute to understanding how these biotracers can contribute to current and future monitoring and management of this remote MPA.

KEY WORDS: Niche · Stable isotopes · Fatty acids · Marine protected areas · Fishes

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INTRODUCTION

Direct and indirect effects of climate variability and change on the marine environment and organisms of the Beaufort Sea are substantive and anticipated to continue (Cobb et al. 2008, Serreze & Barry 2011, Barber et al. 2012, Stroeve et al. 2012). Many climate-induced modifications of marine food webs will manifest through changes in the productivities and trophic structures of affected ecosystems (e.g. see

Wrona et al. 2006, Arrigo et al. 2008). Therefore, a baseline understanding of the feeding and habitat ecology of animals in the Beaufort Sea ecosystem is needed to understand and predict the full effects of future climate change. Coastal habitats of the southern Beaufort Sea are unique as they integrate the cooler marine water inputs of the Beaufort Sea and the warmer freshwater inputs from large rivers (Craig 1984, Wrona et al. 2006). The Mackenzie River and estuary serve as important transitional habitats

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between fresh and saltwater and, coupled with the stable buoyancy boundary current of brackish water along the Yukon coastal environments, serve as migration corridors for anadromous fishes in the summer months (Craig 1984, Carmack & Macdonald 2002). Summer freshwater inputs that mix with seawater also provide complex coastal habitats for eurythermal and euryhaline marine fishes. Accordingly, coastal habitat use by anadromous and marine fishes, and use of freshened marine waters by freshwater species, is complex (Carmack & Macdonald 2002). Documenting such usages through biological tracers (biotracers) such as stable carbon and nitrogen isotopes and fatty acid signatures can provide basic understanding of trophic structure and patterns in this important coastal fish community. Moreover, baselines established under present circumstances allow for follow-on studies monitoring changes and potentially documenting causation resulting from changes induced by climate shifts and other stressors.

Stable isotope (SI) ratios of carbon and nitrogen ($\delta^{13}\text{C}$ and $\delta^{15}\text{N}$) have successfully been used in many investigations of feeding ecology, trophic interactions, and habitat use in fish populations (e.g. Hobson et al. 2002, Cherel et al. 2011, Radabaugh et al. 2013). $\delta^{13}\text{C}$ values are often used to differentiate between benthic and pelagic, terrestrial and marine prey sources, whereas $\delta^{15}\text{N}$ values are widely used as indicators of trophic level (e.g. see Post 2002, Boecklen et al. 2011). Fatty acids (FAs) are also commonly used chemical tracers that reflect trophic interactions and predator diets (e.g. Iverson et al. 1997, 2004, Kolts et al. 2013). More recently, SI ratios and FA compositions have been used together to better characterize and understand long-term (3 to 4 mo; Post 2002, Iverson et al. 2004) feeding ecology and habitat use (Dahl et al. 2003, Wan et al. 2010, Connelly et al. 2014).

Recent advances in quantitative and statistical analyses of both SI and FA data (e.g. multi-dimensional plots and combined qualitative assessments) have enabled stronger analytical outcomes than those achieved through results of each individual marker type (Newsome et al. 2007, Swanson et al. 2015). A new approach in quantifying trophic (or other) niches beyond 2 dimensions has been developed in the statistical program 'nicheROVER' (Newsome et al. 2007, Swanson et al. 2015). This method can quantify niche region and the probabilities of overlap within or among species and may help better assess species-specific resource partitioning and plasticity.

Several locations along the Beaufort Sea coast have been designated as marine protected areas (MPAs).

The Tarium Niryuitait MPA consists of 3 regions, Niaqunnaq (including Shingle Point), Okeevik, and Kittigaryuit, and was established to protect Beaufort marine species and their supporting habitats (Government of Canada 2010). Efforts to conserve and protect the biota in this MPA require the establishment of effective monitoring. These monitoring programs must be founded on existing bodies of baseline research. This is particularly important for Shingle Point, where the ecology (diets/habitats) of the many fish species that use the area in summer months is poorly understood.

In this study, we used SI and FA data in conjunction with Bayesian and multivariate techniques to (1) characterize the niches of 16 co-occurring fish species from the coastal area of Shingle Point, (2) identify and quantify niche overlap among these species and group species based on their niche similarities, and (3) identify indicators for resource partitioning and niche shifts. Increased understanding of the Beaufort Sea coastal ecosystems can then be used to select key species and parameters relevant to the assessment of long-term ecosystem health of this MPA.

MATERIALS AND METHODS

Sample collection

Fish samples from 16 species (see Table 1) were collected under the auspices of the Arctic Coastal Ecosystem Study program (ACES, Department of Fisheries and Oceans) from coastal habitats at Shingle Point, Yukon Territory, Canada (Fig. 1), in each year between 2011 and 2013. The study species represent seasonally anadromous forms of salmonids that are important in subsistence fisheries as well as coastal (mixed low-salinity) and marine (high-salinity) species (Coad & Reist 2004).

Fish were collected in the brackish coastal environment of Shingle Point by local fisheries monitors and harvesters. Gill and seine nets allowed for the capture of a large range of fish sizes. The samples for this study were opportunistic, and collected in the months of July and August (2011 to 2013). Most fishes were vacuum-sealed and kept frozen (-18°C) on site before they were shipped to the Freshwater Institute (DFO, Winnipeg, Manitoba, Canada), for processing. Dolly varden char *Salvelinus malma* are an important traditional food for the Inuvialuit and Gwich'in peoples (Jarvela & Thorsteinson 1999). As such, the harvesters will normally prepare and con-

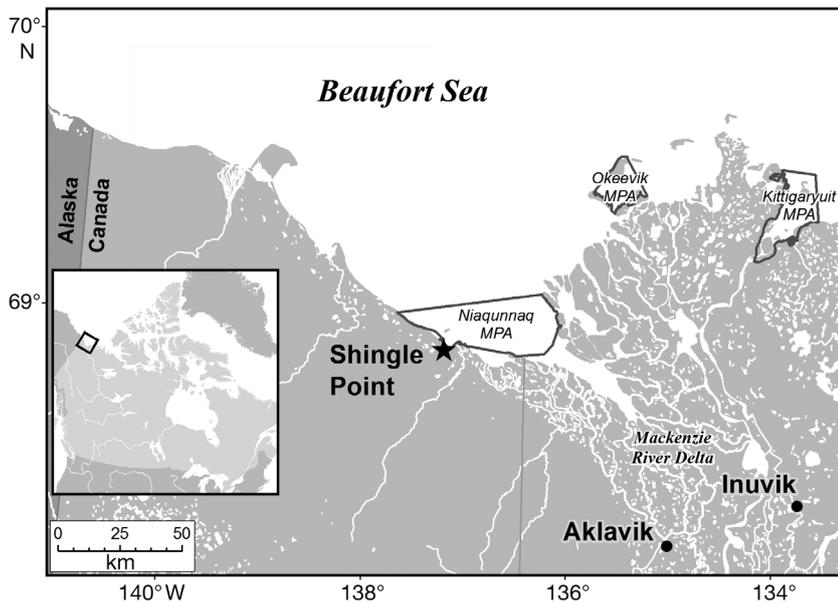


Fig. 1. Map of the Tarium Niryutait Marine Protected Area, Yukon Territory, Canada, including the Kittigaryuit, Niaqunnaq, and Okeevik regions. The study area Shingle Point is part of the Niaqunnaq area

sume the entire fish. Thus, muscle tissue for SI analysis was only taken from this species if local harvesters allowed us to sample their catches. FA analysis was not run for dolly varden char.

SI analysis

Dorsal muscle tissue was removed from individuals of the 16 species of fish to be processed for SI analyses. Each sample was freeze-dried and ground into fine powder using a mortar and pestle. Samples were sent to the Environment Isotope Laboratory at the University of Waterloo, Ontario, Canada, where standard isotopic methods analyzed each sample for carbon (C) and nitrogen (N) stable isotope ratios on a Thermo-Finnigan Delta Plus continuous flow isotope mass spectrometer (Thermo Finnigan) equipped with a Carlo Erba Elemental Analyzer (CHNS-O EA1108, Carlo Erba). Stable nitrogen ($\delta^{15}\text{N}/\delta^{14}\text{N}$) and carbon ($\delta^{13}\text{C}/\delta^{12}\text{C}$) isotopic ratios relative to the international standards of atmospheric nitrogen (Mariotti 1983) and Vienna Pee Dee Belemnite (Craig 1957) for N and C, respectively, were expressed in standard notation (δ) measured as per mil (‰). Internal laboratory standards included 1 standard of cellulose for $\delta^{13}\text{C}$ (-25.5‰) and 2 standards of $(\text{NH}_4)_2\text{SO}_4$ for $\delta^{15}\text{N}$ (0.77 and 20.2‰). Repeatability of sample material for $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ was 0.1 and 0.2‰, respectively, based on repeat analysis of duplicates (duplicates

run every $n = 10$). Repeat measurements of laboratory standards cross-calibrated against the International Atomic Energy Agency standards CH_6 for C and N1 and N2 for N validated the analytical precision since error did not exceed 0.2 and 0.3‰ for $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$, respectively.

FA analysis

FA samples comprised the lateral half of each fish cut lengthwise along the sagittal plane and excluded the gastrointestinal tract. Each sample was homogenized and stored in a -80°C freezer for a minimum of 24 h before being freeze-dried. The freeze-dried homogenate was sub-sampled and aliquots weighed (0.25 g), and a standard lipid extraction method using 2:1 chloroform-methanol containing 0.01% butylated hydroxytoluene (BHT) (v/v/w) was performed (Folch et al. 1957). The lipid phase of each sample was obtained by using anhydrous sodium sulphate to wash, collect and dry each sample, and then the sample was evaporated under N. The lipid phase was then weighed and recorded for lipid weight before being treated with Hilditch reagent (0.5 N H_2SO_4 in methanol) resulting in transesterification and FA methyl esters (FAMES) (Morrison & Smith 1964). Samples were heated at 100°C for 1 h. The techniques and processes in identifying FA peaks are outlined in more detail in Giraldo et al. (2015). Briefly, gas chromatography (on an Agilent Technologies 7890N GC equipped with a 30 m J&W DB-23 column) combined with a Flame Ionization Detector (FID) (running at 350°C) was used to identify FA compounds. Hydrogen was used as the carrier gas flowing at 1.25 ml min^{-1} for 14 min and ramped to 2.5 ml min^{-1} for 5 min. The split/splitless injector was heated to 260°C and run in splitless mode. The oven program was as follows: 60°C for 0.66 min, increase of $22.82^\circ\text{C min}^{-1}$ to 165°C with a 1.97 min hold, $4.56^\circ\text{C min}^{-1}$ to 174°C and $7.61^\circ\text{C min}^{-1}$ to 200°C with a 6 min hold (Giraldo et al. 2015). Percent FAs were used for statistical analysis. A total of 73 FAs were identified, 25 of which accounted for 90% or more of the total. These 25 FA profiles (FA signatures) are expressed using the notation A:BnX, reported as percent of total FA (%), and were used to identify the general diet of the fishes.

Study design and statistical analysis

Trophic level ($\delta^{15}\text{N}$) and habitat use/carbon source ($\delta^{13}\text{C}$) often vary with fish size and life stage (e.g. Peterson & Fry 1987, Bosley et al. 2002, Romanuk et al. 2011). As such, SI and FA analyses were thus limited to adult, non-spawning individuals. There was no significant relationship between $\delta^{13}\text{C}$ and fish size (fork length) observed ($r^2 < 0.3$, for all species) for adult, mature individuals (determined by visual inspection of gonads). In order to compare $\delta^{15}\text{N}$ among multiple fishes, $\delta^{15}\text{N}$ was normalized for each species separately. Species-specific residuals of the relationship between $\delta^{15}\text{N}$ and fork length for each individual were calculated and added to the mean $\delta^{15}\text{N}$ of the respective species, with analyses of $\delta^{15}\text{N}$ data performed on these size-corrected data (Swanson & Kidd 2010).

Lipid content can significantly affect $\delta^{13}\text{C}$ values and interpretation (Post et al. 2007). Since lipids were not chemically extracted from the dorsal muscle prior to SI analysis, a mathematical approach that incorporates the C to N ratio (C:N) within tissues was used (Post et al. 2007):

$$\delta^{13}\text{C}_{\text{normalized}} = \delta^{13}\text{C}_{\text{untreated}} - 3.32 + 0.99 \times \text{C:N} \quad (1)$$

All statistical analyses were performed in R v.3.1.0 (R Core Team 2012). Ward's hierarchical clustering analysis with Euclidean distance generated groups from mean $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values for each species using the package 'ade4'. Two-dimensional ($\delta^{13}\text{C}$ and $\delta^{15}\text{N}$) probabilistic (95%) regions for each of the groups identified from the Ward's clustering were developed using a Bayesian framework in the package 'nicheROVER' (Swanson et al. 2015). We also used nicheROVER to estimate probability of isotopic niche overlap (95% region) among species. Results for niche region size generated with the 40% probabilistic niche region are presented in Table S1 in the Supplement at www.int-res.com/articles/suppl/m559p159_supp.pdf. Here we define high niche overlap as a median overlap greater than 50% between 2 species. The default 'non-informative' prior was used in nicheROVER. Differences in niche centroid (defined by mean $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$) among species within the 3 isotopic groups (A, B, and C) were investigated using the residual permutation procedure (RPP) metric mean distance (MD). Variations in species-specific isotopic niche positions were identified if Euclidean distance between niche centroids was significantly greater than zero (Turner et al. 2010).

The 25 FA signatures for all species studied, except dolly vaden char, were used to infer the general diet of each species (Table S2 in the Supplement). A

Kruskal-Wallis test was used to analyze differences in percent total lipid content (%TL) among species. The relationship between fork length (mm) with FA profiles and %TL for each species was assessed using linear regression analysis. For statistical and modeling analyses some FAs were combined. The FA markers for *Calanus* copepods 20:1n9, 20:1n11 and 22:1n9, 22:1n11 were combined as FA *Calanus* (e.g. Falk-Petersen et al. 2002). The 16PUFAs (polyunsaturated fatty acids) included: 16:2n6, 16:2n4, 16:3n4, 16:4n3, and 16:4n1. The 18PUFAs included: 18:2n7, 18:2n4, 18:3n6, 18:3n4, 18:3n1, 18:4n3, and 18:4n1. Essential FAs found in freshwater fish: 18:3n3 and 18:2n6 were separated from the 18PUFAs (Tocher 2010). Finally, non-methylene interrupted (NMI) FAs, indicative of bivalves or gastropods (Budge et al. 2006) included: 20:2n, 20:3n, 22:2n, and 22:3n.

Correspondence analysis (CA) was used to compare FA signatures among species using the packages 'Factoshiny' and 'FactoMineR'. Highest explained variance was indicated in the CA using the 25 FAs. To group individuals based on similar FA compositions, a Ward's cluster analysis was performed using mean FA signatures and 2 significant CA axes. This was done in the package 'hclust'. The FA groups generated from the Ward's cluster analysis were characterized by significant high and low proportions of FA signatures indicated by a v-test. The probability of niche overlap within groups (identified by the isotopic Ward's cluster analysis) was re-evaluated using both the mean SI signatures and mean dietary FA profiles identified by the v-test. The FA signatures included as variables in the probability of niche overlap calculation were: 20:3n6, 20:2n6, 21:5n3, 18:2n6, *Calanus* FA and 22:6n3.

RESULTS

SI analysis

Relatively wide variability in $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ was observed among the 16 species of fish ($n = 1048$) (Table 1). The $\delta^{13}\text{C}$ ranges among all species was (mean \pm SE; $4.6 \pm 0.22\%$). The species most depleted in ^{13}C was broad whitefish *Coregonus nasus* ($-27.47 \pm 0.25\%$), and the species most enriched in ^{13}C was saffron cod *Eleginus gracilis* ($-22.87 \pm 0.03\%$) (Table 1). Our results suggest a span of approximately 2 trophic levels identified among all species with a $\pm\delta^{15}\text{N}$ range of 6.37‰; the lowest values were observed in broad whitefish ($9.10 \pm 0.13\%$) and highest in saffron cod ($15.47 \pm 0.05\%$) (Table 1).

Table 1. Biological data of the 16 fish species captured at Shingle Point, Yukon Territory, Canada. Sample size (n), (mean \pm SE) fork length (FL), carbon to nitrogen ratio (C:N), % total lipid content (%TL), and stable isotopic signatures ($\delta^{13}\text{C}$ and $\delta^{15}\text{N}$) for each species are shown as well as $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ ranges. Species are grouped by family. N/A: information not available

Species common name (code), Scientific name	n	FL (mm)	C:N	%TL	$\delta^{13}\text{C}$ (‰)	$\delta^{13}\text{C}$ range (‰)	$\delta^{15}\text{N}$ (‰)	$\delta^{15}\text{N}$ range (‰)	Habitat
Catostomidae									
Longnose sucker (LNSK), <i>Catostomus catostomus</i>	11	160.09 \pm 22.60	3.33 \pm 0.039	16.12 \pm 2.21	-26.15 \pm 0.46	3.79	9.64 \pm 0.34	3.51	Freshwater/ brackish ^a
Clupeidae									
Pacific herring (PCHR), <i>Clupea pallasii</i>	18	277.50 \pm 3.70	4.63 \pm 0.30	37.42 \pm 3.00	-23.79 \pm 0.14	2.58	13.00 \pm 0.11	2.09	Marine/ brackish ^b
Cottidae									
Fourhorn sculpin (FHSC), <i>Myoxocephalus quadricornis</i>	105	247.64 \pm 5.27	3.42 \pm 0.02	16.43 \pm 1.00	-23.62 \pm 0.08	6.7	15.18 \pm 0.07	5.53	Marine ^b
Esocidae									
Northern pike (NRPK), <i>Esox Lucius</i>	9	426.33 \pm 53.19	3.18 \pm 0.06	9.94 \pm 1.63	-26.84 \pm 0.17	1.46	10.26 \pm 0.20	1.72	Freshwater/ brackish ^a
Gadidae									
Saffron cod (SFCD), <i>Eleginus gracilis</i>	129	442.26 \pm 2.38	3.33 \pm 0.02	11.94 \pm 0.56	-22.87 \pm 0.03	1.99	15.47 \pm 0.05	3.31	Brackish ^b
Burbot (BRBT), <i>Lota lota</i>	9	452.56 \pm 87.12	3.42 \pm 0.03	7.25 \pm 1.20	-25.95 \pm 0.51	4.39	10.26 \pm 0.36	3.45	Freshwater/ brackish ^c
Osmeridae									
Rainbow smelt (RBSM), <i>Osmerus mordax</i>	25	225.08 \pm 5.96	3.43 \pm 0.04	16.26 \pm 1.92	-24.15 \pm 0.09	1.85	13.96 \pm 0.07	1.27	Anadromous ^d
Pleuronectidae									
Arctic flounder (ARFL), <i>Liopsetta glacialis</i>	97	192.89 \pm 3.68	3.32 \pm 0.01	18.40 \pm 1.34	-24.01 \pm 0.12	9.84	11.55 \pm 0.07	4.45	Brackish/ marine/ freshwater ^b
Starry flounder (STFL) <i>Platichthys stellatus</i>	75	275.09 \pm 4.60	3.31 \pm 0.02	14.13 \pm 1.22	-24.85 \pm 0.13	5.94	12.42 \pm 0.09	4.06	Brackish/ marine/ freshwater ^b
Salmonidae									
Arctic cisco (ARCS), <i>Coregonus autumnalis</i>	74	327.82 \pm 7.33	3.65 \pm 0.06	28.68 \pm 2.38	-23.64 \pm 0.17	8.25	12.35 \pm 0.10	3.82	Anadromous ^d
Broad whitefish (BDWF), <i>C. nasus</i>	117	352.22 \pm 10.38	3.45 \pm 0.04	19.91 \pm 1.27	-27.47 \pm 0.25	13.57	9.10 \pm 0.13	8.79	Anadromous ^d
Lake whitefish (LKWF), <i>C. clupeaformis</i>	113	251.65 \pm 8.04	3.31 \pm 0.03	13.77 \pm 0.88	-25.94 \pm 0.17	9.06	10.90 \pm 0.10	5.47	Anadromous ^d
Least cisco (LSCS), <i>C. sardinella</i>	70	257.24 \pm 3.86	3.23 \pm 0.02	12.12 \pm 2.68	-26.13 \pm 0.11	10.96	11.84 \pm 0.06	4.87	Anadromous ^b
Inconnu (INCN), <i>Stenodus leucichthys</i>	86	497.23 \pm 10.65	3.28 \pm 0.03	10.71 \pm 0.88	-26.29 \pm 0.09	4.78	12.78 \pm 0.08	4.4	Anadromous ^d
Dolly varden char (DVCH), <i>Salvelinus malma</i>	37	448.62 \pm 14.05	6.17 \pm 0.31	N/A	-23.42 \pm 0.27	9.48	13.88 \pm 0.13	3.92	Anadromous ^d
Round whitefish (RDWF), <i>Prosopium cylindraceum</i>	73	131 \pm 594.73	321 \pm 0.02	11.04 \pm 0.57	-25.79 \pm 0.25	11.04	9.95 \pm 0.11	4.86	Freshwater/ ^d brackish

^aScott & Crossman (1973); ^bCoad & Reist (2004); ^cKottelat & Freyhof (2007); ^dRiede (2004)

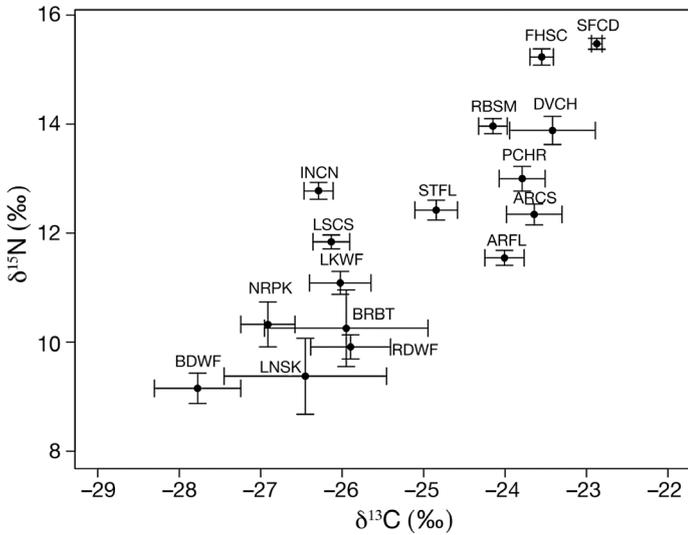


Fig. 2. Stable isotope biplot indicating the mean $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ positions of the 16 fish species captured at Shingle Point. See Table 1 for species names and codes. SE is indicated by error bars

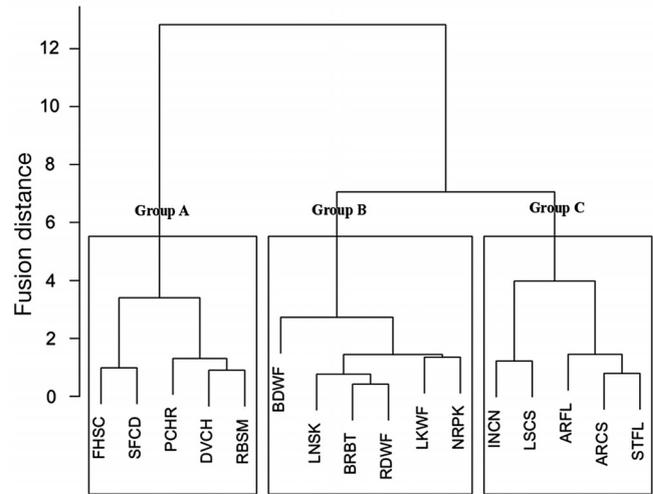


Fig. 3. Dendrogram of the 16 fish species captured at Shingle Point, produced from Ward's cluster analysis using the mean isotopic signatures ($\delta^{13}\text{C}$ and $\delta^{15}\text{N}$) as variables. See Table 1 for species names and codes

SI-determined groups

Based on the SI values (Fig. 2), Ward's cluster analysis identified 3 'isotopic groups' within among the 16 species (Table 1, Fig. 3). The species in Group A were characterized by more enriched ^{13}C and ^{15}N , and included: fourhorn sculpin *Myoxocephalus quadricornis*, saffron cod, Pacific herring *Clupea pallasii*, dolly varden char, and rainbow smelt *Osmerus mordax*. Group B was characterized by depleted ^{13}C and

lower $\delta^{15}\text{N}$ ratios and included: broad whitefish, longnose sucker *Catostomus catostomus*, burbot *Lota lota*, round whitefish *Prosopium cylindraceum*, lake whitefish *Coregonus clupeaformis*, and northern pike *Esox lucius*. The species in Group C had intermediate $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ compared to the other groups, and included: inconnu *Stenodus leucichthys*, least cisco *Coregonus sardinella*, Arctic flounder *Liopsetta glacialis*, Arctic cisco *Coregonus autumnalis* and starry flounder *Platichthys stellatus* (Fig. 4).

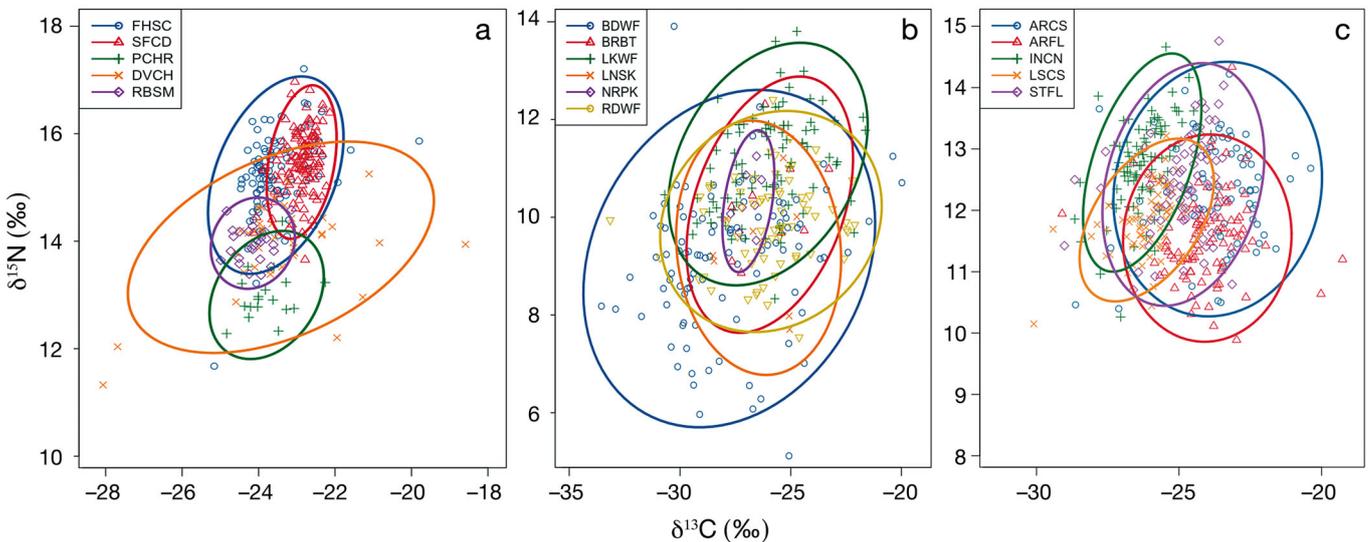


Fig. 4. The 95 % isotopic ellipses of the 16 species of fish captured at Shingle Point, separated into 3 groups (generated from the Ward's cluster analysis, see Fig. 3). (a) Group A; (b) Group B; (c) Group C. See Table 1 for species names and codes

Isotopic niche assessment

Among the 3 isotopically defined groups (Fig. 3), the highest niche overlap was observed between Groups B and C (Table 2, Fig. 4). Probabilistic niche regions (95% level of inclusion) ranged from the narrow niche of rainbow smelt (2.93) to the broad niche of broad whitefish (73.04), (Table 2). The species with the broadest probabilistic 2-dimensional niches were dolly varden char, broad whitefish, and Arctic cisco (Fig. 4).

We expected that probability of overlap would be high among all species within each group; however, considerable overlap (i.e. > 50%) was only observed within Group A. All species in Group A overlapped with the large niche region of dolly varden char (24.86), whereas rainbow smelt and saffron cod overlapped considerably with fourhorn sculpin (Table 2, Fig. 4a). The niche region size of Pacific herring (5.61; Table 2) was similar to saffron cod (4.11) and rainbow smelt (2.93). The lower probability of isotopic niche overlap of other Group A species onto the isotopic niches of Pacific herring, rainbow smelt, and saffron cod can be attributed to the narrow $\delta^{13}\text{C}$ range and $\delta^{15}\text{N}$ range that was observed for each of these species (Tables 1 & 2). Additionally, the lower $\delta^{15}\text{N}$ of Pacific herring separated this species from others in Group A (Fig. 4a). The narrow $\delta^{13}\text{C}$ range for saffron cod and rainbow smelt fell within the larger niche of fourhorn sculpin, which resulted in a 98.48 and 92.02% probability of overlap of saffron cod and rainbow smelt onto fourhorn sculpin, respectively (Table 2). Niche centroids differed among all species (MD > 0.74, $p < 0.03$ for all).

Within a group, the highest probabilities of niche overlap (>50%)

Table 2. Results of the probabilities of niche overlap among the fishes in Groups A, B and C (see Fig. 2 for the corresponding species and Table 1 for abbreviations). The mean probability indicates the probability of Species A niche being found within the niche of Species B. The probability of overlap is indicated by mean and credible intervals (2.5%, 97.5%). The niche overlaps were calculated using $\alpha = 0.95$. 95% isotopic ellipses or niche region size ($\alpha = 0.95$) of each species were calculated using isotopic signatures ($\delta^{13}\text{C}$ and $\delta^{15}\text{N}$) and recorded (‰). SI: stable isotope; FA: fatty acid. N/A: information not available

Species B (95% niche region size)	Species A	SI mean probability [credible interval]	FA and SI mean probability [credible interval]
Group A			
DVCH (24.86)	FHSC	67.49 [45.15, 88.89]	N/A
	PCHR	95.36 [80.75, 99.97]	N/A
	RBSM	99.93 [99.36, 100.00]	N/A
	SFCD	64.42 [37.05, 91.02]	N/A
FHSC (11.45)	DVCH	41.05 [26.87, 56.45]	N/A
	PCHR	15.08 [2.47, 37.33]	16.53 [2.80, 39.00]
	RBSM	92.02 [75.68, 99.39]	92.13 [76.19, 99.60]
	SFCD	98.48 [95.86, 99.76]	98.82 [96.00, 100.00]
PCHR (5.61)	DVCH	32.29 [18.12, 51.22]	N/A
	FHSC	5.43 [1.21, 15.86]	6.11 [1.29, 17.40]
	RBSM	45.05 [12.37, 87.65]	47.68 [13.30, 90.70]
	SFCD	1.45 [0.08, 7.20]	0.95 [0.00, 5.50]
RBSM (2.93)	DVCH	26.68 [16.83, 39.12]	N/A
	FHSC	20.32 [11.74, 32.57]	20.36 [12.10, 32.40]
	PCHR	22.33 [6.45, 47.37]	23.70 [6.90, 46.32]
	SFCD	3.63 [0.65, 11.29]	3.23 [0.40, 9.90]
SFCD (4.11)	DVCH	12.72 [7.07, 19.77]	N/A
	FHSC	46.73 [38.03, 55.88]	48.19 [37.79, 58.30]
	PCHR	0.88 [0.01, 4.38]	0.52 [0.00, 2.91]
	RBSM	5.40 [0.68, 15.55]	4.71 [0.40, 16.31]
Group B			
BDWF (73.04)	BRBT	95.94 [81.95, 99.94]	41.04 [21.48, 61.50]
	LKWF	90.84 [80.97, 97.25]	46.42 [33.76, 59.01]
	LNSK	98.06 [89.92, 99.99]	71.77 [42.38, 93.94]
	NRPK	99.86 [98.66, 100.00]	37.32 [18.37, 58.59]
	RDWF	97.15 [92.44, 99.50]	68.61 [56.19, 80.06]
	BRBT (31.23)	BDWF	48.51 [28.46, 73.80]
LKWF		77.06 [55.81, 94.38]	0.08 [0.01, 0.20]
LNSK		79.29 [51.44, 98.04]	0.00 [0.00, 0.00]
NRPK		98.06 [85.56, 100.00]	0.56 [0.00, 2.06]
RDWF		77.26 [57.45, 94.52]	0.08 [0.01, 0.21]
LKWF (35.49)		BDWF	51.34 [40.80, 62.67]
	BRBT	91.59 [72.15, 99.49]	69.71 [40.67, 90.66]
	LNSK	82.07 [59.27, 96.51]	81.07 [52.93, 96.99]
	NRPK	99.50 [95.62, 100.00]	77.44 [52.31, 96.06]
	RDWF	85.75 [75.78, 93.43]	80.45 [69.74, 89.19]
	LNSK (31.97)	BDWF	58.46 [39.06, 80.42]
BRBT		85.00 [57.30, 99.25]	0.00 [0.00, 0.00]
LKWF		72.20 [47.08, 93.54]	0.02 [0.00, 0.07]
NRPK		97.77 [83.31, 100.00]	0.00 [0.00, 0.02]
RDWF		81.47 [63.27, 95.88]	0.06 [0.00, 0.15]
NRPK (5.57)		BDWF	13.34 [6.98, 24.30]
	BRBT	31.70 [13.23, 58.29]	0.03 [0.00, 0.19]
	LKWF	25.65 [14.43, 43.05]	0.01 [0.00, 0.04]
	LNSK	27.69 [11.39, 51.88]	0.00 [0.00, 0.01]
	RDWF	24.68 [14.17, 40.65]	0.01 [0.00, 0.04]

Table continued on next page

Table 2 (continued)

Species B (95% niche region size)	Species A	SI mean probability [credible interval]	FA and SI mean probability [credible interval]
Group B			
RDWF (36.30)	BDWF	65.58 [54.37, 76.99]	38.51 [28.11, 49.39]
	BRBT	91.88 [72.90, 99.56]	46.69 [24.01, 69.84]
	LKWF	83.36 [72.23, 92.63]	55.66 [43.87, 67.40]
	LNSK	90.67 [72.44, 99.19]	90.78 [68.74, 99.48]
	NRPK	99.26 [94.01, 100.00]	43.01 [21.82, 67.40]
Group C			
ARCS (23.89)	ARFL	92.74 [83.69, 98.20]	93.64 [85.69, 98.60]
	INCN	72.82 [47.99, 92.10]	73.81 [50.09, 92.60]
	LSCS	80.39 [60.10, 94.40]	80.28 [61.69, 95.50]
	STFL	93.25 [85.60, 98.30]	94.94 [87.60, 99.20]
ARFL (15.71)	ARCS	73.43 [61.50, 84.30]	67.01 [55.40, 79.30]
	INCN	27.87 [11.19, 50.91]	23.52 [8.90, 44.10]
	LSCS	72.63 [52.80, 88.40]	70.99 [51.89, 88.01]
	STFL	73.18 [60.00, 84.71]	72.34 [56.80, 85.60]
INCN (11.62)	ARCS	19.00 [10.80, 29.00]	19.17 [11.40, 28.80]
	ARFL	10.57 [5.20, 18.00]	10.19 [4.80, 17.80]
	LSCS	72.20 [56.70, 86.21]	72.23 [55.39, 85.20]
	STFL	45.54 [32.70, 58.70]	50.06 [36.19, 64.00]
LSCS (9.82)	ARCS	30.10 [19.30, 43.30]	29.71 [19.09, 42.71]
	ARFL	32.67 [21.10, 45.50]	33.16 [21.90, 46.40]
	INCN	55.24 [40.39, 71.00]	54.68 [40.40, 70.50]
	STFL	58.08 [43.08, 71.21]	63.45 [47.60, 77.41]
STFL (17.62)	ARCS	76.34 [63.40, 87.40]	70.14 [57.20, 83.71]
	ARFL	75.56 [61.00, 87.90]	71.61 [53.70, 87.50]
	INCN	85.07 [69.40, 95.30]	81.76 [65.50, 93.90]
	LSCS	89.77 [78.30, 97.80]	81.37 [66.00, 94.20]

were observed among Group B fishes; this was due to similar mean isotopic ratios and similar niche region sizes (Table 2). Probabilistic niche region sizes were similar among burbot (31.23), lake whitefish (35.49), longnose sucker (31.97), and round whitefish (36.30). Broad whitefish and northern pike had the largest and smallest niche region size 73.04 and 5.57, respectively (Table 2). Although the isotopic niche for northern pike is located at the center of all species in Group B, the small isotopic niche of northern pike (5.57) resulted in relatively low probability of other Group B species overlapping onto the northern pike niche (Fig. 4b, Table 2). Differences among Group B niche centroids only existed between broad whitefish and both lake whitefish (MD = 2.49, $p = 0.00$) and round whitefish (MD = 1.70, $p = 0.00$), and between lake whitefish and longnose sucker (MD = 1.66, $p = 0.00$), northern pike (MD = 1.32, $p < 0.01$), and round whitefish (MD = 1.01, $p = 0.00$).

High probability of niche overlap was observed among most fishes in Group C with the exception of inconnu (see Group C in Table 2). Inconnu were char-

acterized by a relatively small niche region size (11.62), narrow $\delta^{13}\text{C}$ range and depleted ^{13}C (Table 1), and higher $\delta^{15}\text{N}$ relative to other fishes in this group (Fig. 3c). Arctic cisco (23.89), starry flounder (17.62), and Arctic flounder (15.71) had the largest niche regions compared to other Group C species and showed similar $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ ranges (Table 2, Fig. 3c). In turn, this resulted in high probability of finding other Group C species within these isotopic niches. Niche centroids differed among all species (MD < 0.71, $p > 0.02$ for all).

FA analysis

Differences in %TL existed among species (Kruskal-Wallis chi-squared = 189.21, $df = 14$, $p < 0.05$), and ranged from (mean \pm SE) 7.25 \pm 1.20% for burbot to 37.42 \pm 3.00% for Pacific herring (Table 1). Within-species no significant relationship was observed between fork length and %TL ($r^2 < 0.48$, $p < 0.97$ for all) and between fork length and most FA profiles. North-

ern pike did indicate some relationship between fork length and 20:4n6 ($r^2 = 0.54$, $p = 0.02$); however, this relationship was not strong.

To assess how FAs defined species groups, a CA was performed on 15 species of fish ($n = 1011$) processed for FAs. The total variance of the first and second dimensions of the CA was 57.45%, where the first dimension explained 38.67% of the variance and the second dimension explained 18.78% of the variance. Dimension 1 illustrated a marine pelagic-freshwater gradient, with the greatest influence on the positive side (+) for *Calanus*-markers (pelagic), and docosahexaenoic acid (DHA, 22:6n3) and palmitoleic acid (16:1n7) on the negative side (-) (Fig. 5a). Pacific herring and Arctic cisco were most associated with the positive dimension 1. This was consistent with the high content of *Calanus*-markers in these species (~12–23% of total FAs for Arctic cisco and Pacific herring, respectively). *Calanus*-markers were also found in inconnu, least cisco, and round whitefish tissues, but to a lesser extent (~1–7%, Table S2 in the Supplement) (Fig. 5b).

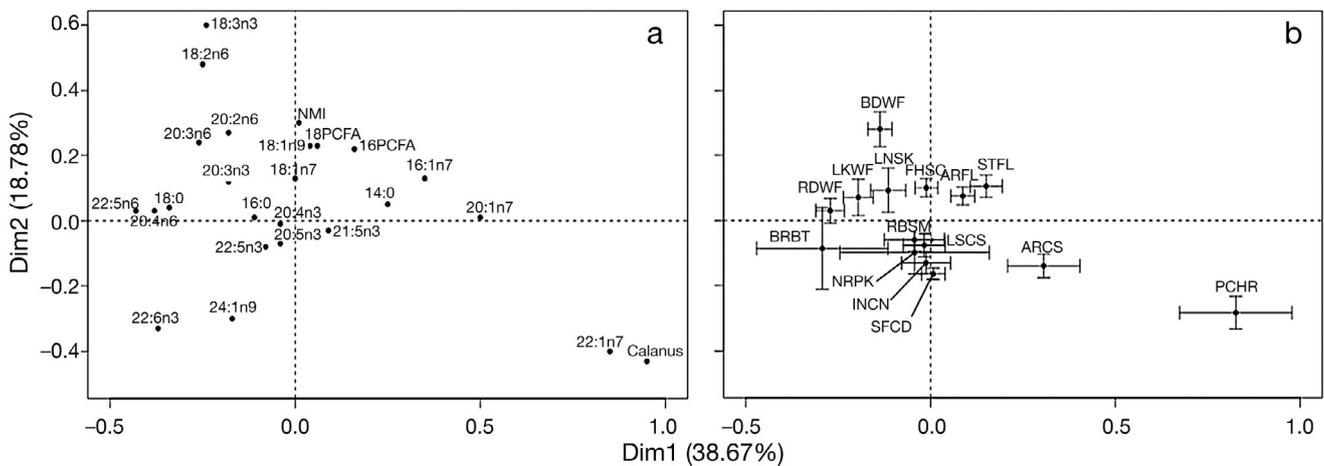


Fig. 5. Correspondence analysis on the (a) 25 fatty acid signatures of (b) 15 species of fish captured at Shingle Point. Bars represent SE for each species and were included to represent the spread of individuals within each species. See Table 1 for species names and codes

The second dimension of the CA was characterized by DHA, *Calanus*-markers, oleic acid (18:1n9), linoleic acid (18:2n6), and alpha-linolenic acid (18:3n3) (Fig. 5a). Lake whitefish, followed by least cisco and Arctic cisco, were most associated with the second dimension (5b). Results indicate that (1) Arctic flounder and starry flounder were highly associated with the benthic marker NMI (2) burbot was highly associated with the FA arachidonic acid (20:4n6) (3) broad whitefish, lake whitefish, and round whitefish had relatively higher proportions of 18:2n6 and 18:3n3 (Table S2 in the Supplement, Fig. 5a), and (4) Pacific herring and starry flounder had the highest proportions of 16:1n7 (Table S2) and Pacific herring had the lowest proportions of DHA.

Groups inferred from FA analysis

A hierarchical analysis on the first 2 dimensions of the CA identified groups of species based on similarities of FA signatures. Five groups were identified (Fig. 6) using the 25 FA profiles described earlier for each species. The FA composition of the one fish species (Pacific herring) in Group 1 was characterized by high proportions of *Calanus*-markers and low proportions of the essential FA DHA (Table 3). Group 2 (also 1 species; burbot) was characterized by high proportions of 20:3n6 and 20:2n6, followed by 20:4n6, and low proportions of 16:1n7 (Table 3). The proportions of FA were not distinct enough to describe diets of fish within Group 5 (rainbow smelt, northern pike, least cisco, inconnu, saffron cod, and Arctic cisco); however, higher levels of *Calanus*-markers (compared to Groups 2, 3, and 4) and combined benthic markers

found in these fishes (Table 3) suggest feeding in both pelagic and benthic zones. Fish species in Group 3 (broad whitefish, round whitefish, lake whitefish, and longnose sucker) were characterized by high proportions of heneicosapentaenoic acid (21:5n3) and 18:2n6 and low proportions of *Calanus*-markers (Table 3). High proportions of 21:5n3 and low proportions of DHA characterized the FA composition of Group 4 (fourhorn sculpin, Arctic flounder, starry flounder; Table 3).

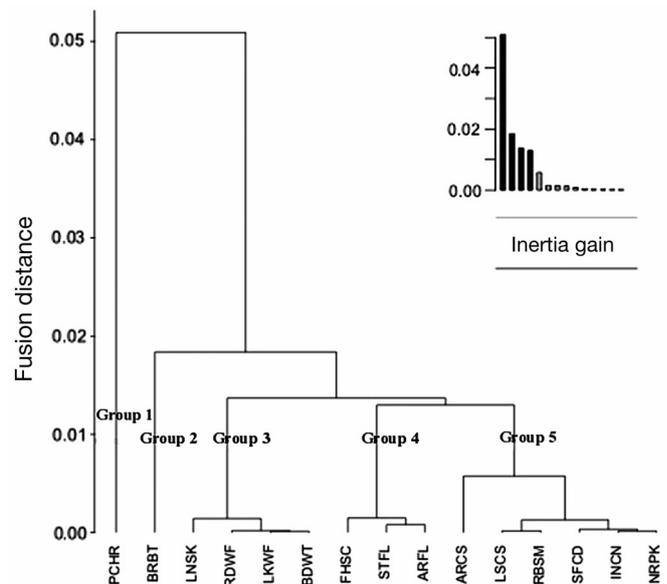


Fig. 6. Hierarchical Ward's cluster analysis performed on a correspondence analysis of 25 fatty acid profiles. The 15 species of fish were grouped based on similarities using the mean fatty acid compositions. The 5 groups were characterized by high fatty acid (+) and low fatty acid (-) proportions indicated by the v-test (Table 3). See Table 1 for species names and codes

Table 3. Results from the Ward's cluster and correspondence analysis on fatty acid (FA) profiles. The 15 species of fish were used and grouped based on similar FA signatures. Groups 1, 2, 3, 4, and 5 are characterized by the highest to lowest proportions of FA, indicated by the highest to lowest (–) v-test values, respectively. Inf: infinite values

FA cluster group	Species	FA	v-test	p
Group 1	Pacific herring	<i>Calanus</i>	5.86	0
		22:6n3	–2.81	0
Group 2	Burbot	20:3n6	Inf	0
		20:2n6	Inf	0
		20:4n6	3.19	0
		16:1n7	–2.44	0.01
Group 3	Broad whitefish, round whitefish, lake whitefish, longnose sucker	21:5n3	Inf	0
		18:2n6	2.05	0
		<i>Calanus</i>	–4.71	0
Group 4	Fourhorn sculpin, Arctic flounder, starry flounder	21:5n3	Inf	0
		22:6n3	–2.40	0.02
Group 5	Rainbow smelt, northern pike, least cisco, inconnu, saffron cod, Arctic cisco	Null	Null	Null

FA and SI group niche assessment

Probabilities of niche overlap within the 3 isotopic groups previously identified by the cluster analysis (Fig. 3) were re-analyzed with SI and FA data combined. The dietary FA signatures that characterized the 5 FA groups: 20:3n6, 20:2n6, 18:2n6, 21:5n3, 22:6n3, and *Calanus*-markers (Table 3) were combined with the isotopic data, and probabilities of niche overlap were re-calculated using a total of 8 dimensions of data. The probabilities of niche overlap using SI and FA data together only marginally differed from the results of the overlap in Groups A and C previously determined using only SI data (Table 2). For Group B, the probability of niche overlap decreased considerably when key dietary FA profiles were combined with SI data (Table 2). SI data alone indicated that Group B had the highest niche overlap among species, but when FA data were included, high (>50%) niche overlap was restricted to various combinations of longnose sucker, burbot, northern pike, and the 3 species of whitefish (Table 2).

DISCUSSION

Characterizing diet and habitat ecology of co-occurring freshwater, coastal, and anadromous fishes in summer Beaufort Sea coastal environments will further our understanding of prey sources and partitioning of resources in the study species and environ-

ment (Post 2003, Layman et al. 2007, Swanson et al. 2015). These results may be used to indicate future shifts in species-specific niches, understand implications of climate change on important habitat features (Carmack & Macdonald 2002, Kelly & Scheibling 2012), develop monitoring programs, and inform testable hypotheses for competitive interactions among species.

Habitat and diet niche overlap

Three distinct isotopic groups and 5 FA-based dietary groups identified the general habitat and feeding ecologies of the 16 fish species studied. The $\delta^{13}\text{C}$ ranges and $\delta^{15}\text{N}$ ranges found here suggest that these species are feeding across a range of salinities, in both pelagic and benthic habitats, and that the species assemblage examined represents approximately 2 trophic levels (Post 2002, Hill et al. 2006, Cherel et al. 2011). FA analyses further demonstrated the importance and heavy reliance on benthic prey sources. We recognize potential problems when interpreting dietary FAs from species with low %TL (<10%); however, since FA interpretations are supported by SI results and previous literature-based stomach analyses, and samples were limited to adult non-spawning individuals, we are confident FA interpretations are representative of the species diet.

Group A had enriched isotopic ratios and was isotopically delineated as marine fishes. High variability among species in $\delta^{15}\text{N}$ along with narrow species niches resulted in the lowest niche overlap among species. The relatively ^{13}C -enriched muscle tissue in dolly varden char compared to other species reinforces the fact that, although dolly varden char move to freshwater habitats for spawning and overwintering (Reist 1989, Reist & Sawatzky 2010), the majority of feeding is occurring in the marine environment (Morita et al. 2009, Courtney et al. 2016). Some consumption of fresh- or brackish-water prey by dolly varden char likely explains the larger $\delta^{13}\text{C}$ range observed for this species relative to other Group A species. The small isotopic niche region and pelagic marine feeding ecology with a diet likely comprised primarily of *Calanus*, or *Calanus* consumers (Group 1) is consistent with previous

findings (Dahl et al. 2000, Coad & Reist 2004), and resulted in Pacific herring having lower overlap with other Group A species. The isotopic niche of rainbow smelt was narrow, indicating low within-species diet variability. It is likely that fish and crustaceans are a resource shared among rainbow smelt, fourhorn sculpin, and saffron cod (Lacho 1991, Coad & Reist 2004), as indicated by benthic feeding inferred from FAs for Group 5 species.

Group B species were characterized as freshwater-rearing fish, and had depleted ^{13}C and benthic and nearshore FA indicators. Similar $\delta^{13}\text{C}$ ranges and $\delta^{15}\text{N}$ ranges among species within Group B indicate shared habitat use and foraging strategies (Hesslein et al. 1991, Coad & Reist, 2004, Gallagher & Dick 2015) and resulted in high isotopic overlap. A large $\delta^{13}\text{C}$ range and the most depleted ^{13}C suggest that broad whitefish is feeding upon a variety of prey in multiple habitats.

The freshwater input of the Mackenzie River introduces terrestrial carbon into the Mackenzie estuary and coastal environments (Saupe et al. 1989, Schell et al. 1989, Dunton et al. 2012); thus, the nearshore and benthic FA signatures 18:2n6 and 18:3n3 (found in green algae and vascular plants, Kelly & Scheibling 2012) are reflected in FA in tissues of Group 3 species (broad whitefish, round whitefish, lake whitefish, and longnose sucker) (Steffens 1997, Carmack & Macdonald 2002). These freshwater influences and benthic feeding strategies are consistent with known diets for these fishes, i.e. amphipods, crustaceans and bivalves (Ackman 1967, Graeve et al. 1997, Kharlamenko et al. 2008, Legezynska et al. 2014). Low proportions of *Calanus*-markers (Falk-Petersen et al. 2002, Hill et al. 2006) in Group 3 fishes further supports benthic feeding for this group.

Group C isotopically defined species were characterized as 'coastal' fish, and were characterized further as benthic feeders as indicated by Group 4 (i.e. Arctic flounder and starry flounder) and both pelagic and benthic feeders by Group 5 (i.e. inconnu, least cisco, Arctic cisco). These species are known benthic and shallow-water foraging fish that feed at higher trophic levels on fishes and crustaceans (Hesslein et al. 1991, Jarvela & Thorsteinson 1999, Coad & Reist 2004, Logerwell et al. 2015); similar feeding strategies coincide with the large overlap among Group C fishes. Arctic cisco had the broadest niche region in this group, and had high proportions of benthic and pelagic FAs and high $\delta^{13}\text{C}$ ranges, indicating feeding both in the benthic and pelagic zones. Arctic cisco also appeared to feed at both higher (i.e. crustaceans and small fishes), and lower (i.e. *Calanus*) trophic

levels (Coad & Reist 2004, Dunton et al. 2006, Von Biela et al. 2013). This is in contrast to starry flounder, a species that shares a similar isotopic niche size but narrow feeding strategy observed in Group 4 species. Group 4 species characterized as benthic feeders had high proportions of 21:5n3 and FA profiles with an origin linked to marine algae and also the diatom species *Skeletonema costatum* (Mayzaud & Ackman 1978). These FA profiles, along with higher NMI markers (indicative of feeding on bivalves and gastropods, Budge et al. 2006), suggest feeding on the benthos.

Partitioning of resources

The ability to partition resources through habitat and trophic segregation is an important feature in ecologically similar species and serves as a measure of interspecific competition and plasticity (Schoener 1974). Variation in $\delta^{13}\text{C}$ observed across species likely indicates variation in habitat use of benthic vs. pelagic prey and differences in use of marine, brackish, and freshwater environments over the last several months (e.g. Fry & Sherr 1984, Peterson & Fry 1987, Cherel et al. 2011), since at the time of collection (July–August) these species shared the same coastal environment. This variation also reflects known differences in life history among species that are known to be anadromous (i.e. dolly varden char, Arctic cisco, Coad & Reist 2004, Morita et al. 2009), those that obviously migrated to the coastal environment but are usually characterized as freshwater species (i.e. northern pike, broad whitefish), and those that are coastal residents species (i.e. saffron cod, flounders) (Hesslein et al. 1993, Coad & Reist 2004).

Estuarine and coastal environments at higher latitudes remain relatively unstudied in regard to understanding structure of the benthic communities, importance of terrestrial carbon and how it is assimilated, overall trophic structure, and resource partitioning among co-occurring freshwater, anadromous and marine fish species (Reist et al. 2006, Dunton et al. 2006, 2012). The high probability of overlap and large reliance on benthic resources within FA groupings (excluding Pacific herring [Group 1] and Arctic cisco [Group 5]) likely indicates that benthic prey are more abundant/available than pelagic prey, as indicated by previous studies (Kharlamenko et al. 2008, Dunton et al. 2012, Kelly & Scheibling 2012).

Known generalist feeding strategies of some Beaufort Sea fishes (e.g. broad whitefish, Arctic cisco) is optimal in Arctic marine ecosystems where produc-

tivity is generally low (Hesslein et al. 1993, McLaughlin & Carmack 2010, Varela et al. 2013). Similar isotopic ratios and large niche regions within Group B were observed for burbot, longnose sucker, lake whitefish, and round whitefish. Broad niche regions observed in both Group B and C species (e.g. broad whitefish, Arctic cisco) can act as an indicator for plasticity in habitat and diet resource partitioning (Layman et al. 2007, Svanbäck & Bolnick 2007).

We expected to find a smaller probability of niche overlap when combining both SI and key dietary FAs (identified by the CA). Results indicated that the addition of FAs did not alter the probabilities of niche overlap for Groups A and C, but that these data did in general lower probabilities of niche overlap among species in Group B. This likely indicates that, although species in Group B may share habitat and trophic levels, specific prey sources differ. For all groups, FAs better defined the diets of each species and highlighted the importance of benthic prey resources for the fish populations at Shingle Point.

Use of niche metrics in monitoring (MPAs and elsewhere)

Studies of the direct effects of climate change on Arctic marine ecosystems (e.g. warming temperatures and change in productivity) can inform our understanding of the resilience and resistance in different Arctic fish species, and these investigations can be relatively straightforward. The secondary effects of climate change, such as changes in larger ecosystem structure and drivers (i.e. top-down and bottom-up control) are less known and more intractable to strong inference studies (Reist et al. 2006, Barber et al. 2012), making it difficult to predict species responses. Further understanding of basic habitat and diet ecology, and inter- and intra-specific competition and resource partitioning will aid in developing effective and efficient monitoring programs for fish populations in MPAs. Presently, whether benthic prey will be a limiting factor is unknown; however, shifts in primary production to pelagic sources are expected to have an effect on primary consumers in Beaufort Sea shelf habitats (Carmack et al. 2004, Arigo et al. 2008). Species with more narrow niches may be more susceptible to environmental changes (Layman et al. 2007, Svanbäck & Bolnick 2007, Turner et al. 2010). The susceptibility of species with narrow niches to environmental changes (e.g. reduced prey availability) has been observed in species including European perch *Perca fluviatilis* (Svanbäck

& Persson 2004) and sea birds (e.g. *Calonectris diomedea*, Ceia et al. 2014). Narrow niches can also reflect specialist feeding strategies in piscivores (e.g. northern pike). Since the signatures of prey are reflected in consumer's tissues, the high habitat and diet overlap observed for these predatory fish with other co-occurring fish species can reflect significant changes in prey species (McCann et al. 2005, Guzzo et al. 2016), and act as potential indicators to niche shifts in prey availability and/or predator choice.

CONCLUSION AND FUTURE DIRECTIONS

Identifying and understanding how fish species partition resources in the coastal Canadian Beaufort Sea is important for understanding trophic interactions in this highly dynamic and sensitive environment. Both marine and anadromous fishes in the Beaufort Sea are culturally important and serve as a direct food source to the Inuvialuit people (Papik et al. 2003); they also play an important role as the main prey of beluga whales *Delphinapterus leucas* and seal species (Loseto et al. 2008, Harwood et al. 2014). Knowledge gaps remain, however, regarding trophic interactions, habitat use, and ecological niches occupied by marine and anadromous fishes (Reist & Bond 1988, Chipperzak et al. 2003, Coad & Reist 2004) in the nearshore Beaufort Sea. This makes it difficult to predict effects of climate variability and change. Delineating trophic groups of fishes using SIs and FAs will inform development of management and monitoring indicators. Together with parallel monitoring of both drivers (e.g. oceanographic parameters) and stressors (e.g. climate change driven shifts in habitats, species complements, functional relationships), the findings outlined herein will inform our continuing assessment of the integrity and health of this northern coastal ecosystem.

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