New approaches to assess tissue concentrations and dietary accumulation of environmental contaminants in northern marine mammals

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LIST OF ABBREVIATIONS

Acronym	Definition
AA	Amino acids
AIC	Akaike's information criterion
AMAP	Arctic Monitoring and Assessment Programme
ANOVA	Analysis of variance
ASE	Accelerated solvent extraction
BFRs	Brominated flame retardants
BMF	Biomagnification factor
BPA	Bisphenol A
CEAC	Chemicals of emerging Arctic concern
CFR	Chlorinated flame retardants
CHL	Chlordane
ClBz	Chlorobenzenes
CS	Cumberland Sound
CSIA	Compound-specific isotope analysis
CSIA-FA	Compound-specific isotope analysis of fatty acids
CUP	Current-use pesticides
DANCEA	Danish Cooperation for Environment in the Arctic
DEHP	Di(2-ethylhexyl) phthalate
DEP	Diethyl phthalate
DPHP	Di(2-propylheptyl) phthalate
DCM	Dichloromethane
DDD	Dichlorodiphenyldichloroethane
DDE	Dichlorodiphenyldichloroethylene
DDT	Dichlorodiphenyltrichloroethane
EG	East Greenland
EMR	Enhanced matrix removal
ESI	Electrospray ionization
FA	Fatty acids
FAME	Fatty acid methyl esters
FDA	Food and Drug Administration
FID	Flame ionization detection
FRQNT	Fonds de recherche du Québec – Nature et Technologies
GC-MS	Gas chromatography mass spectrometry
GPC	Gel-permeation chromatography
HCB	Hexachlorobenzene
HBCDD	Hexabromocyclododecane
HCH	Hexachlorocyclohexane
HNP	Halogenated natural products
HPLC	High-performance liquid chromatography
HPV	High-production volume chemicals
HRMS	High-resolution mass spectrometry

ICH	International Conference on Harmonization
IRMS	Isotope-ratio mass spectrometer
ISO	International Organization for Standardization
IUPAC	International Union of Pure and Applied Chemistry
LC	Liquid chromatography
LM	Linear model
LoA	Limits of agreement
logK_{ow}	Octanol-water partition coefficient
lw	Lipid weight
MANOVA	Multivariate analysis of variance
MeHg	Methyl mercury
MEHP	Mono-(2-ethylhexyl) phthalate
MeO-PBDEs	Methoxylated polybrominated diphenyl ethers
MLOD	Method limits of detection
MLOQ	Method limits of quantification
MUFA	Monounsaturated fatty acids
NCP	Canadian Northern Contaminants Program
NIST	National Institute of Standards and Technology
NSERC	Natural Sciences and Engineering Research Council of Canada
OC	Organochlorine
OH-PBDEs	Hydroxylated polybrominated diphenyl ethers
OPE	Organophosphate-ester flame retardants
OPFRs	Organophosphate flame retardants
PAH	Polycyclic aromatic hydrocarbons
PBDE	Polybrominated diphenyl ethers
PBT	Persistent, bioaccumulative, toxic
PCA	Principal components analysis
PCB	Polychlorinated biphenyls
PCDD	Polychlorinated dibenzi-p-dioxins
PCDF	Polychlorinated dibenzofurans
PCDL	Personal compound database and library
PCN	Polychlorinated naphthalenes
PE	Polyethylene
PFAS	Per- and polyfluorinated alkyl substances
PFHxS	Perfluorohexane sulfonic acid
PFOA	Perfluorooctanoic sulfonic acid
PFOS	Perflurooctane sulfonic acid
PON1	Paraoxonase 1 gene
POP	Persistent organic pollutant
PP	Polypropylene
PPCP	Personal and pharmaceutical care products
PRC	Plastic-related compound
PSA	Primary secondary amine sorbent
PUFA	Polyunsaturated fatty acid
PVC	Polyvinyl chloride

QA/QC	Quality assurance/quality control
QFASA	Quantitative fatty acid signature analysis
QTOF	Quadrupole time-of-flight
QuEChERS	Quick, easy, cheap, effective, rugged, and safe extractions
REACH	Registration, Evaluation, Authorization, and Restriction of Chemicals
RM	Reference material
RSD	Relative standard deviation
RT	Retention time
SAT	Saturated fatty acid
SCCP	Short chain chlorinated paraffins
SFA	Saturated fatty acid
SI	Stable isotopes
SIM	Selective ion monitoring
SPE	Solid-phase extraction
SRM	Standard reference material
TBBPA	Tetrabromobisphenol A
THg	Total mercury
TP	Trophic position
UNEP	United National Environmental Program
uPCB	Unintentionally produced polychlorinated biphenyls
USP	United States Pharmacopeia
UV	Ultraviolet
VIF	Variation inflation factor
ww	Weight wet

GENERAL ABSTRACT

Marine mammals in the Arctic show some of the highest concentrations of toxic "legacy" contaminants like persistent organic pollutants (POPs) and Hg globally. Established methods have been routinely used to assess POP accumulation from diet and detail concentrations in some marine mammal populations for several decades. However, these approaches have considerable drawbacks, and many are largely inaccessible to research groups. In particular, methods to measure POP concentrations are costly, time-intensive, and require large amounts of toxic solvents and expensive instrumentation. Replacement chemicals for globally banned POPs, including chemicals of emerging Arctic concern (CEACs), are also rarely, if at all, monitored using these approaches in any marine mammal species. In addition, current-use approaches to study dietary uptake of contaminants seldom employ novel techniques that may offer new insight into bioaccumulation and biomagnification. As such, the main objectives of this doctoral thesis are to develop and implement novel approaches to 1) improve contaminant monitoring for both "legacy" and "emerging" contaminants and 2) gain new insights into the dietary accumulation of contaminants in northern marine mammals using new, higher resolution bio(geo)chemical tracers.

To address objective one, Chapter Three develops a new, alternative chemical extraction method that reduces costs, time, instrumentation and solvent volumes, and provides accurate and reproducible results for POP analysis. Similarly, Chapter 4 presents a new approach, nontarget screening, to simultaneously screen for thousands of emerging contaminants, where I detail the presence of multiple, potentially toxic plastic-related compounds in marine mammals.

To address objective two, Chapters Five and Six use novel bio(geo)chemical tracer approaches to evaluate contaminant accumulation from diet in multiple marine mammal species

using fatty acid signatures and their stable carbon isotopes. Relative to current-use methods, FAs and their carbon isotopes may better explain wide differences in lipophilic POPs among marine mammal species. This doctoral thesis will provide future researchers with new and improved tools to better characterize the magnitude of legacy and emerging contaminant bioaccumulation and biomagnification in some of the world's most contaminated megafauna.

RESUME GENERAL

Les espèces prédatrices marines du Nord, comme les mammifères marins et les requins, présentent certaines des plus fortes concentrations de contaminants toxiques bien connus, comme les polluants organiques persistants (POP) et le mercure, à l'échelle mondiale. Depuis plusieurs décennies, des méthodes établies sont régulièrement utilisées pour surveiller l'accumulation des POP dans l'alimentation et détaillent les concentrations chez certaines populations de prédateurs marins. Toutefois, ces approches présentent des inconvénients considérables qui les rendent largement inaccessibles à de nombreux groupes de recherche. En particulier, les méthodes de mesure des concentrations de POP sont coûteuses, prennent beaucoup de temps et nécessitent de grandes quantités de solvants toxiques et des instruments coûteux. En outre, les produits chimiques de remplacement des POP interdits à l'échelle mondiale, y compris les produits chimiques qui suscitent de nouvelles inquiétudes dans l'Arctique, sont rarement, voire pas du tout, surveillés à l'aide de ces approches chez les espèces prédatrices marines. De même, les approches actuellement utilisées pour expliquer l'accumulation de contaminants chez les prédateurs marins n'offrent souvent qu'un aperçu limité du rôle de l'apport alimentaire. Ainsi, les principaux objectifs de cette thèse de doctorat sont de développer et de mettre en œuvre de nouvelles approches pour 1) améliorer la surveillance des contaminants "connus" et "émergents » et 2) obtenir de nouvelles informations sur l'accumulation des contaminants chez les prédateurs marins du Nord en utilisant de nouveaux traceurs alimentaires à plus haute résolution.

Pour répondre à l'objectif 1, le chapitre 3 présente une nouvelle méthode d'extraction chimique qui réduit considérablement les coûts, le temps, l'instrumentation nécessaires et l'exposition des chercheurs aux solvants toxiques, tout en fournissant des résultats précis et

reproductibles pour l'analyse des POP. De même, le chapitre 4 décrit une approche plus récente, le criblage non ciblé, utilisé pour rechercher simultanément des milliers de contaminants émergents. J'y détaille la présence de multiples composés potentiellement toxiques liés au plastique chez les mammifères marins.

Pour répondre à l'objectif 2, les chapitres 5 et 6 utilisent une nouvelle approche de suivi du régime alimentaire pour décrire l'accumulation de contaminants chez plusieurs espèces de prédateurs marins à l'aide de signatures d'acides gras et de leurs isotopes stables de carbone. Les résultats indiquent une meilleure résolution que les méthodes de suivi du régime alimentaire actuellement utilisées pour comprendre le rôle du régime alimentaire dans les grandes différences d'exposition aux contaminants dans les réseaux alimentaires marins et parmi les espèces de prédateurs. Cette thèse de doctorat fournira aux futurs chercheurs les outils nécessaires pour mieux caractériser l'ampleur de l'exposition aux contaminants connus et émergents chez certaines des espèces de mégafaune les plus charismatiques du monde, mais aussi les plus contaminées.

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CONTRIBUTION TO ORIGINAL KNOWLEDGE

This thesis provides details on significant methodological advancements for evaluating contaminant concentrations and bioaccumulation in northern marine mammals. Chapters Three and Four provide information on novel approaches to monitor legacy, new, and emerging contaminants, while Chapters Five and Six detail cutting-edge methods to assess the dietary accumulation of these contaminants in top marine mammals in the Arctic. This dissertation, overall, represents a significant milestone for the use and implementation of multiple new approaches to screen for legacy and emerging contaminants by marine mammal monitoring programs. Though enhancing our understanding of contaminants dynamics in top marine predators, these studies also promote the development of new and effective management strategies for assessing marine ecosystem pollution.

Chapter Three highlights the use of a new method for the analysis of legacy contaminants in marine mammal blubber and adipose tissues. Although existing methods have successfully monitored these contaminants for several decades, they are inaccessible for many research groups due to the costs, a need for very expensive and large laboratory instruments, and time required for analysis. Instead, we developed a QuEChERS (quick, easy, cheap, effective, rugged, and safe) method for the extraction of these same contaminants in the same tissues, but with significant decreases in cost, extraction time, and instruments required relative to current-use methods. In addition, far less hazardous solvents are used, decreasing the risks of human exposure. As such, our developed QuEChERS method is far more accessible than current-use methods for the analysis of legacy contaminants in marine mammal blubber and adipose samples, and one which future and routine contaminant monitoring programs can employ.

Chapter Four introduces a new method for screening new and emerging contaminants in marine mammal blubber and adipose tissues. Although legacy contaminants are routinely monitored in some marine mammal populations, new/emerging chemicals are rarely, if at all, monitored in any northern marine top predators. As such, we used a nontarget and suspect screening approach to simultaneously screen for thousands of different chemicals of potential concern. This study is the first to date to use a nontarget method to screen for contaminants in multiple cetacean species in the Arctic. I detail the presence of several never-before-screened chemicals in blubber/adipose including several plastic-related compounds (PRCs) including phthalates, antioxidants, UV stabilizers, synthetic dyes, and alkyl phenols. Future studies can use similar nontarget approaches to monitor new and emerging contaminants in different marine mammals sampled in other Arctic regions.

Chapter Five uses fatty acid (FA) signatures as a newer approach to assess contaminant accumulation in marine mammals. Fatty acids in blubber are commonly used to assess feeding patterns in marine mammals; however, they have been used rarely to assess the dietary accumulation of contaminants. Here, I compared dietary patterns among polar bear, killer whale, narwhal, and long-finned pilot whale blubber via FA signatures. I then used our previously developed QuEChERS method to measure legacy contaminant concentrations in these same samples. Results demonstrate that FAs explain more variation in contaminants among these species than bulk stable isotopes (the most commonly used diet tracing approach in marine mammals). Future studies should seek to use FA signatures to interpret intra- and interspecific variation in contaminants in other marine mammal species sampled elsewhere using similar modelling-based approaches.

Chapter Six uses stable carbon isotopes of FAs to assess legacy contaminant accumulation among marine mammals and biomagnification through a marine food web. Carbon isotope values of some "dietary" FAs (i.e., those acquired nearly exclusively from diet) have been shown previously to be useful dietary tracers, similar to FA proportions (e.g., as shown in Chapter Five) and bulk stable isotopes; however, thus far studies have only involved lower trophic level consumers, mostly zooplankton. To date, FA carbon isotopes have not been used to assess contaminant accumulation in any marine mammals. As such, we investigated carbon isotope values of numerous FAs in the same marine mammals from Chapter Five. To further investigate this approach, we determined FA isotope values throughout a full Arctic marine food web. Our results indicate that carbon isotopes of certain dietary FAs are useful in assessing contaminant biomagnification across food webs and variation among marine mammals, especially for lipophilic (i.e., fat-soluble) contaminants in fatty tissues like blubber. Due to the novelty of this analysis, future studies should test how FA carbon isotopes vary among other species, regions, and time periods.

CONTRIBUTION OF AUTHORS

This thesis is structured as four data-based manuscripts (Chapters Three, Four, Five and Six), with each manuscript adhering to the formatting guidelines of the respective journal in which it is currently published or was submitted for publication. I am the sole first author of each manuscript.

For Chapter Three, Melissa A. McKinney and I developed the method, and I performed all contaminant analysis, performed all data analysis, and wrote and edited the original draft of the manuscript with input from Melissa A. McKinney. Rune Dietz, Christian Sonne, and Aqqulu Rosving-Asvid provided all killer whale samples. Lan Liu assisted with training and the development of the analytical method on the instrument. Melissa A. McKinney, Christian Sonne, and Rune Dietz led the funding acquisition. All authors reviewed and edited the subsequent version of the manuscript.

For Chapter Four, I performed the contaminant analysis, conducted data analysis, and wrote and edited the original draft of the manuscript with input from Melissa A. McKinney. Stéphane Bayen and Melissa A. McKinney conceptualized the project and conducted funding acquisition. Lan Liu conducted the instrumental analysis. Rune Dietz, Christian Sonne, and Aqqulu Rosving-Asvid provided most of the killer whale, narwhal, long-finned pilot whale, and polar bear samples. Steven H. Ferguson provided some additional killer whale samples. All authors reviewed and edited the subsequent version of the manuscript.

For Chapter Five, I performed all contaminant and FA analysis and data analysis and wrote and edited the original draft of the manuscript with input from Melissa A. McKinney. Melissa A. McKinney and I also conceptualized the project. Robert J. Letcher and his research group provided some of the polar bear contaminant data. Rune Dietz, Christian Sonne, and

Aqqulu Rosving-Asvid provided most of the killer whale, narwhal, long-finned pilot whale, and polar bear samples, Steven H. Ferguson provided some additional killer whale samples, and Anna M. Roos and Malene Simon provided some additional pilot whale samples. Rune Dietz and Christian Sonne also provided relevant biological information for many of the individual samples. Melissa A. McKinney, Christian Sonne, and Rune Dietz assisted with funding acquisition. All authors reviewed and edited the subsequent versions of the manuscript.

For Chapter Six, I performed the contaminant, FA isotope, and bulk stable isotope analyses for all marine mammal samples, while Aaron T. Fisk and his research group including Bailey McMeans provided bulk stable isotope and contaminant data for all of the Cumberland Sound food web dataset. Melissa A. McKinney, along with Anna Hussey and Amy Tanner carried out FA isotope analysis for the Cumberland Sound food web. I performed the data analysis and edited the original draft of the manuscript with input from Melissa A. McKinney. McKinney A. McKinney and I also conceptualized the project, with input from Aaron Fisk and Bailey McMeans. Rune Dietz, Christian Sonne, and Aqqulu Rosving-Asvid provided most of the killer whale, narwhal, long-finned pilot whale, and polar bear samples, while Steven H. Ferguson provided some additional killer whale. Melissa A. McKinney, Christian Sonne, and Rune Dietz conducted funding acquisition. All authors reviewed and edited the subsequent versions of the manuscript.

CHAPTER 1: GENERAL INTRODUCTION

Chemical pollution is currently regarded as one of the main current and future threats to human and wildlife health in the Anthropocene (Tong et al., 2022), with an estimated 350,000 chemicals currently registered for production and use (Wang et al., 2020a). Some chemicals, such as persistent organic pollutants (POPs), have received extensive scientific interest due to their high environmental persistence (i.e., resistance to degradation), tendency to accumulate in biological tissues over time, toxicity, and long-range transport potential (Alharbi et al., 2018). As such, in 2004, the United Nations Stockholm Convention on Persistent Organic Pollutants came into effect initially listing twelve "legacy" POPs (referred to as the "Dirty Dozen"), for which signatory countries agreed to substantially reduce or eliminate their production (The Stockholm Convention on Persistent Organic Pollutants, 2001). However, even today, POPs are ubiquitous in the environment in soil, air, fresh- and marine water, and in food (Harrad, 2010; Guo et al., 2019). Similarly, the heavy metal, mercury (Hg) is also a toxic, persistent and globally-distributed contaminant with large anthropogenic sources, including coal combustion, mining, and waste incineration, and is now regulated under the United Nations Minamata Convention on Mercury in 2017 (The Minamata Convention on Mercury, 2017).

Despite long distances from major source regions, the Arctic is a global environmental sink for contaminants such as POPs and Hg (Muir et al., 1992a). Current levels of most POPs and Hg are not related to known use or release from sources in the Arctic, and instead originate through long-range transport from lower latitude environments (Burkow et al., 2000). In particular, for semi-volatile POPs, air transport and subsequent deposition into the Arctic is a significant and relatively rapid pathway to the Arctic (Burkow et al., 2000). However, ocean currents are also a dominant pathway for some chemicals, with a previously estimated 60% of all

POPs present in the oceans (Tanabe, 1988). Hg is similarly transported by air currents (Jackson, 1997) and through rivers (Schartup et al., 2015) and deposits in the Arctic in high quantities, with a previously estimated 325 tonnes of Hg in the region (Ariya et al., 2004). As such, the Arctic currently remains one of the largest global sinks for contaminants like POPs and Hg, where some of the highest concentrations globally in biota have been reported (Lohmann et al., 2007).

Although POPs and Hg are ubiquitously distributed in the environment and in marine food webs (Alharbi et al., 2018), it is their concentrations in marine predators that are often of particular concern. Top marine predators, including marine mammals, often feed at high trophic positions as tertiary or even quaternary consumers within marine food webs. Consequently, relative to other marine organisms, they tend to show very high concentrations of biomagnifying POPs and Hg (Dietz et al., 2019). At these high concentrations, POPs and Hg are also associated with a wide variety of health risks, including endocrine disruption and cancer for POPs (Dietz et al., 2019), while Hg is a known neurotoxin (Mergler et al., 2007). As such, these species are considered important sentinels used in national (e.g., the Canadian Northern Contaminants Program) and international monitoring programs (e.g., the Arctic Monitoring and Assessment Programme) for assessing biota exposures and effects of POPs and Hg (Muir et al., 2007; Dietz et al., 2019).

Given these elevated concentrations, some populations of marine predators are routinely monitored for concentrations, mostly for legacy POPs and Hg, using establish analytical and sample preparation methods. Hg is proteinophilic, and generally higher in protein-rich tissues like skin, muscle, and liver, while POPs are more lipophilic, showing higher concentrations in fatty tissues like blubber in cetaceans and adipose tissue in polar bear (*Ursus maritimus*) (Dietz

et al., 2013; McKinney et al., 2017). As such, fatty tissues like blubber and adipose are widely used to monitor concentrations and the potential effects of legacy POPs (Dietz et al., 2019) and represent 75-90% of their total body burdens (Tanabe et al., 1981; Yordy et al., 2010). In general, methods to monitor Hg are relatively inexpensive and less time-consuming relative to POP analyses. In comparison, routine methods for POP determination tend to be costly, time and labor intensive, and require large volumes of toxic solvents, making these approaches inaccessible for some research groups. In addition, although legacy POPs, including the "dirty dozen", represent chemicals at some of the highest concentrations in marine mammals (Dietz et al., 2019), other contaminants, including chemicals of emerging Arctic concern (CEACs), are rarely, if at all, monitored in any marine mammals in the Arctic (Sonne et al., 2021). As such, although these marine predators may be exposed to many toxic, new/emerging contaminants, concentrations of these chemicals are entirely unknown (Sonne et al., 2021). In short, the implementation of more accessible and less costly methods to monitor both legacy and CEACs in such sentinel species is warranted.

To assess dietary accumulation of POPs, Hg, or even CEACs in marine predators, dietary tracers such as bulk stable isotopes (SI) of carbon ($\delta^{13}C$) and nitrogen ($\delta^{15}N$) are commonly employed (Hobson et al., 2002; Braune et al., 2005a; Remili et al., 2021). In general, the stable isotope ratios of $\delta^{13}C$ and $\delta^{15}N$ can be used to estimate feeding sources and trophic position of predators, respectively (Nielsen et al., 2018). However, interpretation of feeding patterns and contaminant uptake from bulk isotopes has several limitations, including spatial and temporal variation in baseline ("source") signals, the possibility of overlapping isotope values from different dietary resources, and limited representation of lipid and lipophilic contaminant flow through food webs. Due to these drawbacks, alternative or complementary approaches have

emerged, such as fatty acid signature (FAs) and their stable carbon isotopes (FA $\delta^{13}C$). However, FAs have rarely, if at all, been used to assess contaminant accumulation in Arctic marine mammals. Furthermore, FA $\delta^{13}C$ is a relatively new approach, yet may provide higher resolution assessments of diet than bulk SI (Twining et al., 2020), although values have not yet been monitored in most Arctic marine mammals and have never been used to assess contaminant accumulation. As such, due to the limitations of bulk SI approaches, the evaluation of newer, potentially higher resolution dietary tracers to assess contaminant accumulation in marine predators is warranted.

The objectives of this thesis were to develop and implement new approaches to: 1) improve monitoring of environmental contaminants in marine mammals and 2) gain new insights into contaminant accumulation in these species using novel dietary tracers. To address these objectives, we collected full-depth blubber samples from multiple marine mammal species in East Greenland (**Figure 1**) including killer whale (*Orcinus orca*), narwhal (*Monodon monoceros*), long-finned pilot whale (*Globicephala melas*), and polar bear. For the second objective, we also analyzed samples from a Cumberland Sound, Nunavut, Canada food web, from zooplankton to Greenland shark (*Somniosus microcephalus*). Chapters 3-6 address these objectives with the overarching goal to enhance our understanding of legacy and new/emerging contaminant dynamics in marine food webs, by gaining unique insights from new contaminant monitoring approaches and dietary tracers.

CHAPTER 2: COMPREHENSIVE REVIEW OF LITERATURE

2.1. CONTAMINANTS IN THE ARCTIC ENVIRONMENT

Persistent organic pollutants (POPs) are ubiquitous chemicals in the environment, showing long half-lives in water, sediment, air, and biota, up to several decades (Jones and Voogt, 1999). POPs are typically lipophilic (i.e., "fat-soluble" or "water-hating"), often partitioning into lipids in biota (Harrad, 2010). Due to their resistance to metabolism, POPs can also accumulate in fatty tissues overtime, increase in concentrations through food webs, and exert subsequent toxic effects in humans and wildlife (Scheringer et al., 2012; Solla, 2015). These concerns are reflected by the PBT concept (persistent, bioaccumulation, toxicity) that is often used by national chemical regulation programs (e.g., by the Registration, Evaluation, Authorisation, and Restriction of Chemicals [REACH] regulation in Europe) and used to assess and classify chemicals as POPs (Harrad, 2010).

In 2004, the Stockholm Convention on Persistent Organic Pollutants entered into force, globally restricting and/or banning the use and unintentional production of 12 POPs, referred to as the "Dirty Dozen," and was signed by 152 nations (Hagen and Walls, 2005). These POPs were initially identified due to their severe adverse effects on human and wildlife health, and included pesticides (e.g., dichlorodiphenyltrichloroetane [DDTs]), industrial chemicals (e.g., polychlorinated biphenyls [PCBs]), and some unintentionally produced byproducts from industrial practices (e.g., polychlorinated dibenzi-*p*-dioxins [PCDDs]) (The Stockholm Convention on Persistent Organic Pollutants, 2001; **Table 2.1**). However, recent evidence has suggested that the many signatory parties of the Stockholm Convention have failed to reduce environmental releases of many POPs, especially unintentional production of PCBs,

Hexachlorobenzene (HCB), and Hexabromocyclododecane (HBCDD; Wania and McLachlan, 2024).

Table 2.1: All Stockholm Convention-classified persistent organic pollutants (POPs) from its original ratification in 2004 banning the "dirty dozen" legacy POPs until present day.

Chemical Name	Chemical Use	Year Effective
"The Dirty Dozen" Legacy POPs		
Aldrin	Pesticide	2004
Chlordane (CHLs)	Pesticide	2004
Dichlorodiphenyltrichloroethane (DDTs)	Pesticide	2004
Dieldrin	Pesticide	2004
Endrin	Pesticide	2004
Heptachlor	Pesticide	2004
Hexachlorobenzene (HCB)	Pesticide	2004
Mirex	Pesticide	2004
Toxaphene	Pesticide	2004
Polychlorinated biphenyls (PCBs)	Industrial Chemical	2004
Polychlorinated dibenzo-p-dioxins (PCDD)	Byproduct	2004
Polychlorinated dibenzofurans (PCDF)	Byproduct	2004
New and Emerging POPs		
alpha-Hexachlorocyclohexane	Byproduct	2009
beta-Hexachlorocyclohexane	Byproduct	2009
Chlordecone	Pesticide	2009
Decabromodiphenyl ether	Industrial Chemical	2017
Dechlorane plus	Industrial Chemical	2019
Dicofol	Pesticide	2019
Endosulfan	Pesticide	2011
Hexabromobiphenyl	Industrial Chemical	2009
Hexabromocyclododecane (HBCDD)	Industrial Chemical	2013
Hexabromobiphenyl ether	Industrial Chemical	2009
Hexachlorobutadiene	Industrial Chemical	2015
Lindane	Pesticide	2009
Methoxychlor	Pesticide	2023
Pentachlorobenzene	Byproduct	2009
Pentachlorophenol	Pesticide	2015
Perfluorohexane sulfonic acid (PFHxS)	Industrial Chemical	2022
Perflurooctane sulfonic acid (PFOS)	Industrial Chemical	2019
Perfluorooctanoic sulfonic acid (PFOA)	Industrial Chemical	2009
Polychlorinated naphthalenes	Industrial Chemical	2015
Short chain chlorinated paraffins (SCCPs)	Industrial Chemical	2017
UV-328	Industrial Chemical	2023

DDT, in particular, was originally regarded as one of the most useful and successful insecticides globally, with over 1.8 million metric tonnes produced globally since the 1940s and was credited with helping over 1 billion people live free from malaria (Seagren, 2005). However, due its ubiquitous presence in the environment, its persistence and stability, and resistance to metabolism, high concentrations have been observed in humans and wildlife, often associated with carcinogenic and neurobehavioral effects (van Wendel et al., 2001). DDT half-lives are particularly long, with an estimated 10-20 years for a DDT exposure to be eliminated in humans; however, its stable metabolite DDE, can persist throughout an individual's entire life span (Turusov et al., 2002).

Similarly, PCBs were used widely in industrial and commercial practices due to their chemical stability, high boiling point, and electrical insulating properties (Safe, 1994), with an estimated 1.5 million metric tonnes produced globally since the 1930s (UNEP/POPS/COP.9/30). 209 congeners (i.e., individual chemicals) of PCBs exist that vary based on chemical structure and degree of chlorination, that largely impact their chemical properties. Although these properties made them attractive and inexpensive for industrial application, they also contributed to their environmental persistence. Given their high lipophilicity and resistance to degradation, they preferentially accumulate in fatty tissues and can biomagnify up terrestrial and aquatic food webs, causing potential endocrine disruption and carcinogenicity (Parkinson and Safe, 1987). Although production and use of PCBs and DDTs is highly restricted globally, they are still ubiquitous in the environment today, in the air (Schuster et al., 2021), water (Lohmann et al., 2021), soil and sediment (Wong et al., 2009), biota (Sonne et al., 2022), and even food for human consumption (Guo et al., 2019). However, the unintentional production of PCBs, most

notably from silicone and polyester production, continues to be a widespread source of PCB emissions globally (Wania and McLachlan, 2024).

Mercury (Hg) is similar to known POPs in its persistent, bioaccumulative, and toxic properties. Hg is a naturally occurring heavy metal in raw materials such as coal, crude oil, and other fossil fuels; however, anthropogenic inputs have increased Hg mobilization in the environment thorough coal combustion, mining, and waste incineration (Pirrone et al.,1996). In fact, coal-fired power plants were previously estimated to produce ~42% of global Hg emissions (Edgerton et al., 2006); although following regulation, this has been decreasing in more recent years (Maamoun et al., 2020). Still, anthropogenic releases of Hg in the atmosphere were more recently estimated to be 450% above natural levels in 2017 (UN Environment, 2019). Elemental mercury in aquatic environments can also undergo methylation and subsequent bioaccumulation up marine food webs as methyl Hg (MeHg; Brocza et al., 2024). Upper trophic levels organisms, consequently, tend to show elevated MeHg concentrations, and dietary consumption of marine fish is the primary route of Hg exposure in humans (Driscoll et al., 2013). Following incidents like the mass MeHg poisoning incident in Minamata, Japan, where >2,000 people consumed large amounts of contaminated fish, exposures to Hg were found to be associated with neurotoxicity in humans and wildlife (Lincoln et al., 2011), where pregnant women and some fish in Minamata showed MeHg concentrations >27 times higher than reference areas (Sakamoto et al., 2010). To address the issue of increasing global Hg contamination, the Minamata Convention of Mercury was signed by 128 nations in 2017, with the primary objective to regulate Hg supply and trade and reduce its use and emissions to the environment (The Minamata Convention on Mercury, 2017).

Despite long distances from primary sources, the Arctic acts as sink for POPs and Hg, showing elevated concentrations in water, sediment, air, and biota relative to lower latitude environments (AMAP, 2020). POPs and Hg can undergo long-range transport and subsequent deposition in the Arctic through atmospheric, oceanic, and riverine processes (Burkow and Kallenborn, 2000). The potential of POPs to be transported to the Arctic is determined by several characteristics including: 1) the chemical's persistence, 2) modes of emission (e.g., primary emissions in water, air, or soil), 3) the physical and chemical properties (e.g., water solubility, $\log K_{ow}$, vapor pressure), and 4) the spatio- and temporal conditions of the environmental media that hold the chemical (AMAP, 2002).

For most POPs and Hg, the atmosphere is the most significant and rapid pathway of transport to the Arctic, although ocean and riverine currents likely are a dominant pathway for some high molecular weight POPs (AMAP, 2002). Semi-volatile POPs and Hg show a cycle of deposition to the water column and then remobilization into the atmosphere, a phenomenon commonly referred to as the "grasshopper effect" (Wania and Mackay, 1993; Najam and Alam, 2023). The majority (~80%) of atmospheric contaminant deposition also occurs in snow, resulting in deposition in soil, transport into groundwater, or accumulation in ageing snow (Burkow and Kallenborn, 2000; AMAP, 2020; AMAP, 2021). However, although remobilization into the atmosphere is possible, year-round cold weather conditions limit these processes, where accumulation can instead occur over decades (AMAP, 2021). For example, for more volatile POPs, like hexachlorobenzene (HCB) and alpha-hexachlorocyclohexane (α-HCH), concentrations in Arctic biota are often higher compared to areas close to source emissions, postulated to be largely a consequence of atmospheric transport and preferential deposition in the Arctic (Haugen et al., 1998; Wang et al., 2020). Although, atmospheric transport of heavily

chlorinated PCBs is more limited (Burkow and Kallenborn, 2000; Wang et al., 2020), and may be instead occur by oceanic and riverine currents and sea ice. Regardless of mode of transport, deposition of POPs and Hg into the Arctic produces some of the highest observed concentrations in biota reported globally.

Although legacy POPs (i.e., "known" POPs like "the Dirty Dozen") and Hg constitute chemicals of high environmental concern and are still present in the Arctic in large quantities, new and replacement chemicals for POPs with pesticide and industrial application are currently produced in high volumes (Sonne et al., 2021; Prabhu and Lakshmipraba, 2022). Some of these chemicals show very similar properties to POPs and Hg including long-range transport potential to the Arctic, toxicity, and a bioaccumulative potential (Sonne et al., 2021). As such, some were added to the Stockholm Convention after its initial ratification, banning or restricting some new and replacement pesticides (**Table 2.1**). Still, many other new and replacement chemicals are largely unregulated today, and there is growing concern with potential accumulation and toxicity in biota. Although these chemicals likely show less persistence and toxicity relative to legacy POPs (Goldenman, 2017), their abundance in the Arctic and accumulation in biota is cause for concern, and as such, they are commonly classified as chemicals of emerging Arctic concern (CEACs) (AMAP, 2016; Reppas-Chrysovitsinos et al., 2017).

Multiple recent studies have detailed comprehensive assessments of CEACs that have the potential to cause toxicity and accumulate in marine food webs (**Table 2.2**; AMAP, 2016; AMAP 2020; Muir et al., 2019; Gibson et al., 2020). Muir et al. (2019) listed ~3,500 potentially PBT chemicals, some of which included high production volume (HPV) chemicals, with a potential for long-range transport to the Arctic. Furthermore, of >12,500 HPV chemicals recently evaluated, >24% of them were identified as having a greater long-range transport

potential than that of known Stockholm-regulated POPs (Breivik et al., 2023; Wania and McLachlan, 2024). International monitoring programs including AMAP have also compiled comprehensive assessments of CEACs detected in Arctic seawater and air including some per- and polyfluorinated substances (PFAS), brominated flame retardants (BFRs), organophosphate flame retardants (OPEs), personal and pharmaceutical care products (PPCPs), current-use pesticides (CUPs), marine plastics/microplastics, and plasticizers (AMAP, 2020). More recently, the Stockholm Convention has proposed further listings under the Convention including some CEACS, such as chlorinated paraffins, long-chain perfluorocarboxylic acids, and chlorpyrifos (The Stockholm Convention on Persistent Organic Pollutants). Of the AMAP-identified CEAC groups, and the ones proposed for inclusion in the Stockholm Convention, nearly all have been detected in some environmental media in the Arctic, in air (Wong et al., 2021), water (De Wit, 2022), and/or sediment (Spataro et al., 2023). However, the presence of most CEACs in Arctic marine biota, especially in upper trophic level consumers, is largely unknown.

Table 2.2: Chemicals of Emerging Arctic Concern (CEACs) classified by the Arctic Monitoring and Assessment Program (AMAP). This table was adapted from the 2020 AMAP report on POPs and CEACS: Influence of Climate Change

CEAC group	Abbreviation	Characteristic compounds
Brominated flame retardants	BFRs	decabromodiphenylether (PBDE-209)
Chlorinated flame retardants	CFRs	dechlorane plus
Current-use pesticides	CUPs	chlorpyrifos, chlorothalonil, dacthal
Halogenated natural products	HNPs	brominated phenols
Marine plastics and microplastics		polyethylene (PE), polypropylene (PP), polyvinyl chloride (PVC), and additives
Organophosphate-ester flame retardants	OPEs	chlorinated OPE such as tris(2-chloroethyl) phosphate (TCEP)
Organotins		triphenyl tin (TPT)
Pharmaceutical and personal care products	PPCPs	ibuprofen, caffein
Phthalates		diethyl phthalate
Polychlorinated naphthalenes	PCNs	halowax
Polycyclic aromatic hydrocarbons	PAHs	napthalene, anthracene
Siloxanes		decamethylcyclopentasiloxane (D5)
Unintentionally produced PCBs	uPCBs	PCB-11

2.2. CONTAMINANT EXPOSURE AND EFFECTS IN NORTHERN MARINE MAMMALS

Marine mammals are considered important sentinel species used by international (e.g., AMAP) and national programs (e.g., the Canadian Northern Contaminants Program [NCP]) for assessing exposures and effects of POPs, Hg, and CEACs. As sentinel species, marine mammals in the Arctic are often used to provide an early warning regarding potential negative impacts from emerging and neoplastic diseases, anthropogenic contamination, and even harmful algal blooms on ocean, wildlife, and human health (Bossart, 2011). In general, marine mammals are prime sentinel species as they are relatively long-lived, feed at high trophic positions, and possess unique fat stores (i.e., as blubber in cetaceans and subcutaneous adipose in polar bear) in which lipophilic chemicals, like POPs, are largely deposited (Bossart, 2011). As they often share coastal environments with humans and consume similar diets (e.g., fish or other marine mammal

species), they are also commonly used to monitor potential contaminant exposure in humans and other wildlife species (Bossart, 2011). Furthermore, human consumption of traditional foods, including marine mammals, is foundational to the cultural, spiritual, and physical health of Indigenous populations in the Arctic (AMAP, 2021). Marine mammals are also charismatic megafauna, eliciting considerable public response, attention, and outreach to support conservation efforts (Mazzoldi et al., 2019).

Among the eight nations collaborating on Arctic pollution under AMAP (Canada, Denmark, Finland, Iceland, Norway, Russia, Sweden, and the USA), a multitude of studies have detailed POP and Hg concentrations in marine mammals in the Arctic, where some populations are routinely investigated in some regions (Dietz et al., 2019). For example, a multitude of studies sampling among various regions and time periods across the Arctic have detailed long-term trends of POP concentrations in polar bear adipose from East Greenland (from 1983-2010; Dietz et al., 2013) and Hudson Bay, Canada (1968-2007; Braune et al., 2005b; McKinney et al., 2009). Similarly, the presence of killer whale has been well-documented in the Arctic during the ice-free months, and concentrations in blubber have been monitored in the Canadian Arctic (Nunavut from 2013-2019; Remili et al., 2023a; Desforges et al., 2024), East Greenland (2012-2014; Pedro et al., 2017), Iceland (2014-2016; Remili et al., 2021), the Faroe Islands (2008; Pedro et al., 2017), and Norway (2017-2019; Remili et al., 2023a). Across these studies on killer whale and polar bear, both species showed relatively high concentrations of POPs like PCBs and DDTs (ranging from 0.2-100 mg/kg lipid weight [lw] in killer whale and 0.1-10 mg/kg lw in polar bear) relative to other marine mammal consumers and lower trophic level prey (Dietz et al., 2019). In particular, killer whales likely feeding mostly on marine mammals in the Canadian Arctic and East Greenland (Pedro et al., 2017; Remili et al., 2023a) showed significantly higher

POP concentrations (up to 100 mg/kw lw) than reported for polar bear subpopulations (e.g., in East Greenland; Dietz et al., 2013). In comparison, Hg concentrations in protein-rich tissues (e.g., skin, muscle, liver) were similarly high in killer whale liver samples in the Faroe Islands and East Greenland (from 25-200 mg/kg wet weight [ww]; Dietz et al., 2022), while polar bear liver concentrations ranged widely among Beaufort Sea, Hudson Bay, and East Greenland subpopulations (1-400 mg/kg ww; Dietz et al., 2022).

Although a multitude of studies have investigated POP and/or Hg concentrations in some marine mammals, for other toothed whales, such as endemic narwhal and northward range-shifting long-finned pilot whale, POP concentrations are not well-documented. Only three studies, to date, have detailed PCB and DDT concentrations in narwhal, ranging up to ~0.2 mg/kg lw in West Greenland and Canadian Arctic blubber samples (Muir et al., 1992b; Dietz et al., 2004; Carlsson et al., 2014). Only three POP analyses exist for any pilot whale tissues, detailing PCB concentrations up to 4 mg/kg lw in blubber samples from the Faroe Islands and the North Atlantic (Borrell et al., 1995; Sonne et al., 2010; Hoydal et al., 2016). As such, a lack of studies for most legacy POPs in narwhal and pilot whale make it challenging to draw meaningful comparisons to other marine mammals and sampling locations. Year of collections can similarly impact POP levels in marine mammals, especially as legacy POP concentrations have generally decreased or leveled off following regional bans in the 1970s and 1980s (Dietz et al., 2013). However, the recent spatiotemporal cooccurrence of killer whale, narwhal, pilot whale, and polar bear in areas such as East Greenland (**Figure 2.1;** Higdon et al., 2014; Garde et al., 2015; Heide-Jørgensen et al., 2023) may now permit this region to serve as a suitable study location to directly compare contaminant concentrations among these species.

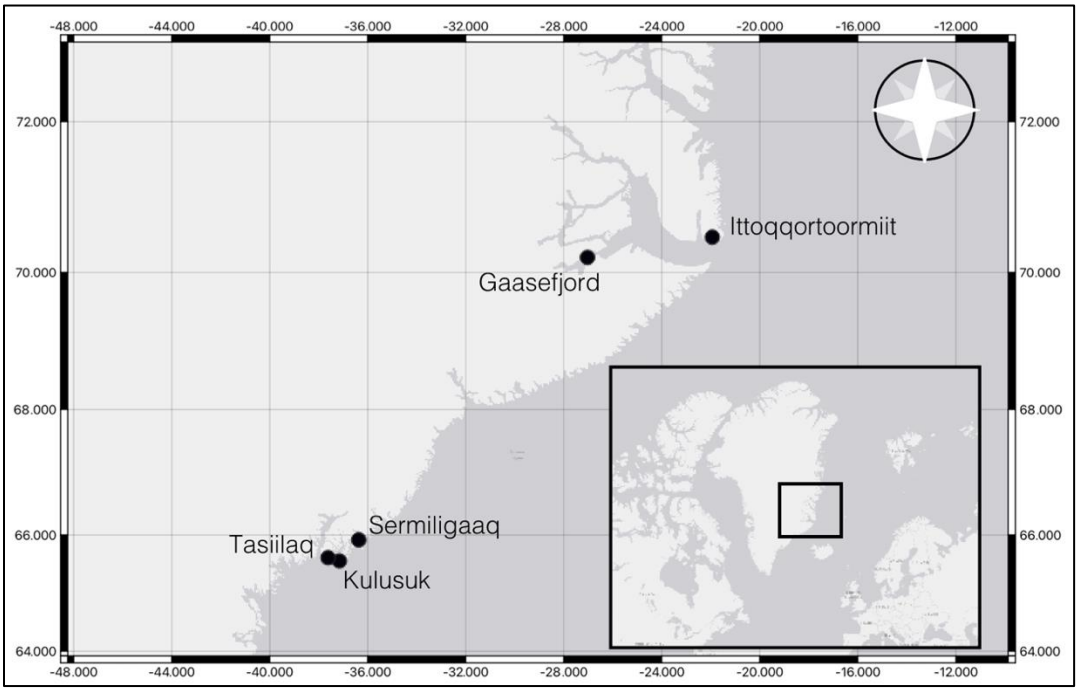

Figure 2.1: The broad region of East Greenland where a recent spatiotemporal cooccurrence of killer whale, narwhal, pilot whale, and polar bear has been observed recently.

The presence of new and emerging contaminants has also been documented in some marine mammals in the Arctic, although concentrations are generally far lower than legacy POPs and Hg. In fact, many Stockholm Convention-identified new and emerging POPs (**Table 2.1**) have been detected in many marine mammal species. For example, PFASs (including percussor compounds, replacement chemicals, and legacy PFASs) were measured in liver samples of polar bear (total PFAs at 2.3 mg/lg lw), killer whale (~0.3 mg/kg lw), and narwhal (<0.03 mg/kg lw) from Greenland, and pilot whale from the North Atlantic (<0.04 mg/kg lw) (Smithwick et al., 2005; Carlsson et al., 2014; Gebbink et al., 2016; Dassuncao et al., 2017). Similarly, HCBDD was detected in killer whale (~1.1 mg/kg lw) blubber and polar bear (~0.2 mg/kg lw) adipose tissue (McKinney et al., 2011a; Remili et al., 2023a), while SCCPs (0.88 mg/kg lw) and PCNs (<0.025 mg/kg lw) were also measured in polar bear adipose (Letcher et al., 2018).

Concentrations of most other contaminants that are not regulated by the Stockholm Convention, including most AMAP-classified CEACs, are not currently monitored in most marine mammal species in the Arctic (**Table 2.2**). For example, emerging flame retardants (e.g., organophosphate flame retardants [OPFRs]), siloxanes, PPCPs (e.g., antibiotics, antidepressants, fragrances, UV filters, etc.), and insecticides have been recently detected in Arctic environmental media including seawater, air, soil, sediments, and ice (Kallenborn et al., 2017; Lee et al., 2019); however, few of these chemicals, if any, have been investigated in any marine mammals. Many of these CEACs have also been recently identified in lower trophic species in the Arctic (e.g., zooplankton; Sørensen et al., 2023), and given a biomagnification potential for some, exposure to marine mammals is possible, but largely unexplored (Sonne et al., 2021). Furthermore, plastic additives like antioxidants and phthalates have been identified in Arctic seawater, with an estimated 30 and 190 tons per year atmospherically deposited to the Greenland Sea and Arctic Ocean, respectively (Xie et al., 2007). However, despite evidence of plastic additive accumulation in other lower trophic species (e.g., plankton, fish, seals, etc.), few studies to date have investigated the presence of plastic additives in marine mammals in the Arctic (Routti et al., 2021; Andvik et al., 2024). As such, CEAC presence (of emerging chemicals not regulated by the Stockholm Convention) in these predators is poorly understood

The accumulation of POPs and some CEACs in marine mammals is associated with toxic effects, including cancer, altered reproductive, endocrine, and immune function (Dietz et al., 2019; Sonne et al., 2020). DDT and its metabolites, organochlorine [OC] insecticides (e.g. mirex, CHLs, dieldrin, and mirex) and PCBs have been reported to have endocrine disruptive properties through disruptions in hormone levels (Colborn, 1993; Letcher et al., 2009). Recently, comprehensive assessments have detailed the cumulative effects of POPs on marine mammals in

the Arctic (e.g., Dietz et al., 2015; Desforges et al., 2018; Dietz et al., 2019). A toxic threshold in marine mammals from PCBs was suggested to be 9.0 mg/kg lw (Kannan et al., 2000), at which physiological effects were observed in experimental marine mammal studies. Several populations in the Arctic show concentrations above this threshold (Dietz et al., 2019). For example, polar bear adipose in East Greenland showed the highest risk of reproductive health effects and genotoxicity out of all studied polar bear subpopulations from Alaska to Norway, corresponding with higher concentrations of PCBs (Dietz et al., 2015). Similarly, all killer whale sampled in East Greenland (Pedro et al., 2017) and most pilot whale from the Faroe Islands (Hoydal et al., 2016) have previously show concentrations sufficiently high for major PCB-mediated effects on endocrine and/or immune function (Dietz et al., 2019).

MeHg, in comparison, is a known neurotoxin and health consequences are well-documented in many mammals (Mergler et al., 2007). A threshold associated for subtle neurological damage is suggested to be ~20 mg/kg dry weight in marine mammals, yet many populations have shown levels far exceeding these thresholds (Basu 2012; Basu, 2015; Dietz et al., 2019). In particular, up to 60% of pilot whale from the Faroe Islands are considered to be at high risk for Hg-mediated health risks, while ~33% of killer whale in the North Atlantic show substantial Hg contamination (Hoydal et al., 2016; Dietz et al., 2019). However, most narwhal populations show concentrations below expected toxic thresholds in East and West Greenland (Dietz et al., 2019). Although some polar bear populations have shown remarkably high concentrations (up to 414 mg/kg ww) in the Beaufort Sea, most polar bear (>90%) showed low to moderate risk for Hg-associated health risks, including in East Greenland (Dietz et al., 2019). Still, as concentrations of individual chemicals and cocktails can vary over time and are unknown in many populations, there is a need for further monitoring of legacy POPs and MeHg

in Arctic marine mammals, especially in regions such as East Greenland where tissue concentrations have previously shown to be some of the highest reported across the Arctic.

Furthermore, marine wildlife species are not exposed to single compounds individually, but instead to mixtures (sometimes referred to as "cocktails") of known chemicals (like POPs and MeHg) and yet to be identified compounds (like some potential CEACs). Although single contaminant exposure and effect studies, like those discussed herein, are useful to assess environmental risk of individual chemicals, they are not accurately reflective of real-world contaminant exposures (Jager et al., 2010). Furthermore, previous studies have suggested that the effects of mixtures may be greater than that of individual chemicals, and as such, even individuals showing concentrations below the suggested PCB toxic threshold at 9.0 mg/kg lw, for example, could still be above thresholds for immune, reproductive, and endocrine effects (Jager et al., 2010; Desforges et al., 2017; Sonne et al., 2021). Assessing mixture complexity and cumulative and/or synergistic effects in exposed wildlife is challenging, yet future studies should seek to establish toxicity thresholds for chemical mixtures, for example, using *in vitro* exposure experiments using marine mammal-derived chemical cocktails (e.g., Desforges et al., 2017). Physiologically based pharmacokinetic (PBPK) modeling should also be further employed to report risk quotients for individual contaminants and mixtures, which has been previously conducted in multiple marine mammal species, like polar bear, narwhal, long-finned pilot whale, and killer whale in East Greenland (AMAP, 2018; Dietz et al., 2019; Sonne et al., 2021).

2.3. DRIVERS OF CONTAMINANT ACCUMULATION IN MARINE MAMMALS

Contaminant accumulation in upper-level marine predators is primarily due to biomagnification from diet across food webs. Although definitions of biomagnification have

varied among studies, a widely accepted definition was coined by Gobas and Morrison (2000) as "the process in which chemical concentration in an organism achieves a level that exceeds that in the organism's diet, due to dietary accumulation." Biomagnification factors (BMFs) of contaminants have also been calculated for several decades using the following equation, where BMF > 1 indicates the occurrence of biomagnification (Hunt and Bischoff, 1960):

$$BMF_{lw} = \frac{Concentration\ in\ predator_{lw}}{Concentration\ in\ diet_{lw}}$$

Uptakes rates of many POPs are often similar among marine predator species, yet species-specific elimination and biotransformation rates determine if a chemical will biomagnify (i.e., if a chemical is quickly eliminated from a predator, it will not biomagnify; Drouillard and Norstrom, 2000). Contaminant accumulation in aquatic organisms may also directly occur from water. This process is referred to as bioconcentration, defined as the process in which the concentrations of a chemical in an organism are greater than that in water due to exposures of the waterborne chemical (Jensen, 1966). However, for most hydrophobic POPs, uptake from water is close to negligible compared to uptake from diet. Still, the term bioaccumulation is generally used instead, describing the uptake of chemicals from all environmental media, including sea water, sediments, suspended particles, and through dietary intake (Bryan and Darracott, 1979). Nonetheless, even when diet is the primary route of exposure to marine predators, bioaccumulation and biomagnification does not necessarily occur, as a wide variety of chemical and biological factors influence their accumulation or subsequent elimination from tissues (Borgå et al., 2004).

In particular, contaminant accumulation and biomagnification across food webs to top marine mammals are largely influenced by its chemical properties, mostly notably its hydrophobicity (Borgå et al., 2004). Hydrophobicity is often expressed using logK_{ow}, which

measures a chemical's solubility in water relative to octanol, a surrogate for lipids. Bioaccumulative compounds are typically defined as those with a logK_{ow} > 5, although certain compounds may still biomagnify with logK_{ow} < 5 but > 3.5 (Geyer et al., 2000). In general, bioaccumulation of most POPs increases with logK_{ow} while elimination decreases, although BMFs typically decrease for very hydrophobic POPs (e.g., logK_{ow} > 7.5; Fisk et al., 2001). In general, logK_{ow} values have also been shown to accurately predict a wide variety of other chemical and physical properties of contaminants, and even assess biomagnification potential (Meylan et al., 1999).

The position and number of chlorines (in PCBs and DDTs, for example) also impact bioaccumulation potential, where a greater number of chlorine atoms generally increase hydrophobicity and decrease elimination rates (Gobas, 1988). For example, tri-chlorinated PCBs (i.e., PCB isomers with three chlorine atoms) typically show logK_{ow} values 5-6 while hexa-chlorinated congers show values > 7 (Ballschmiter et al., 2005). Chlorine position also plays a role in the susceptibility of chlorinated-POPs to biotransformation. For example, PCB congeners lacking adjacent *para*- and *meta*-chlorines are more readily biotransformed and eliminated from predator bodies (Boon et al., 1989). As such, PCB congers like PCB-153, a hexa-chlorinated conger with chlorine atoms at *ortho*-, *meta*-, and *para*-positions, is highly recalcitrant, showing high BMFs in marine food webs and slow elimination rates, with half-lives between 10-15 years in fatty tissues (Crinnion, 2011).

Biological factors, including lipid content, body condition, age, sex, reproduction, biotransformation capacities, and feeding ecology, also play a large role in determining variation in POP concentrations within and between biota (Borgå et al., 2004). For example, lipid content plays a particularly important role in contaminant accumulation. The unique high fatty storage

tissues (i.e., blubber or adipose with > 70% lipid content) in marine mammals largely accounts for the accumulation of hydrophobic POPs. As lipid content often shows significant variation among species and populations (e.g., Fisk et al., 2001), comparative studies on lipophilic POPs in marine food webs and marine predators commonly lipid-normalize concentrations (i.e., concentrations/lipid content for units in lw; Thomann, 1989).

Variation in food availability and body condition also impact POP concentrations in biota, and lipophilic POP concentrations are typically higher in leaner relative to fatter animals (Tartu et al., 2017). For example, body condition and adipose reserves in fasting polar bear showed a significant negative correlation with concentrations of some lipophilic POPs (PCBs, chlordanes [CHLs], and chlorobenzenes [Clbzs]; Polischuk et al., 1995). As lipid stores decreased in these polar bears, POPs still remained in their fatty tissues, and thus become more concentrated (i.e., same amount of POPs in decreasing fat causes increases in POP concentrations; Tartu et al., 2017). Decreases in body condition and fatness in polar bear were also associated with declining sea ice extent and increases in POP concentrations in Norway and Hg concentrations in Alaska (McKinney et al 2017; Tartu et al., 2017). Here, biotransformation and subsequent elimination of PCBs was also more limited in leaner polar bears, as enzyme activities involved in contaminant biotransformation may also be regulated by nutritional status (i.e., leaner polar bear with poor body condition showed far lower biotransformation capacities and subsequent higher concentrations of PCBs; Letcher et al., 1996).

Other biological factors like age, sex, and reproduction also largely impact intraspecific variation of POPs. For example, as lipophilic POPs show long half-lives in biological tissues, continuous exposure over a lifetime may result in increases in concentrations with age until an equilibrium is reached between the exposure routes and the organism (Borgå et al., 2004). As

such, males, in particular, typically show increases in concentrations of lipophilic POPs with age. Instead, concentrations in females may decrease, remain relatively stable, or increase with age, albeit at slower rates than males. Lower concentrations in females are primarily a result of the transfer of hydrophobic chemicals to offspring during gestation and, particularly, lactation, where up to 60% of PCB burdens can be transferred to offspring (Jeong et al., 2018). Consequently, subadult marine mammals tend to show substantially higher concentrations than adult females (Pedro et al., 2017). Whether adult females undergo age-related changes in concentrations varies by species, locations, and the chemicals being examined; although, concentrations are likely influenced by their reproductive success, lipid investments in offspring during lactation and gestation, the frequency of offspring weaning, and levels of lipophilic contaminant exposure (Borgå et al., 2004). Numerous studies have demonstrated higher lipophilic POP concentrations in subadult marine mammals relative to adult females, including killer whale sampled in East Greenland (Pedro et al., 2017), polar bear in Hudson Bay, Canada (Letcher et al., 2018), pilot whale in the Faroe Islands (Hoydal et al., 2015), and narwhal from West Greenland (Carlsson et al., 2014). Comparing among taxa, toothed whales (e.g., killer whale, narwhal, and pilot whale) may also show higher accumulation over their lifetimes due to greater longevity (up to ~90 years in killer whale and ~ 50 years in narwhal and pilot whale) compared to polar bear (up to ~30 years) (Borgå et al., 2004; Hickie et al., 2007; Taylor et al., 2007; Garde et al., 2015).

Furthermore, variation in POP concentrations among species is likely tied to interspecific differences in biotransformation capacities and excretion routes. Biotransformation typically contributes to the elimination of a contaminant, and if the POP is biotransformed to a more polar (i.e., hydrophilic and water-soluble) compound, the metabolite will not bioaccumulate and can be

readily excreted (Borgå et al., 2004). For chlorinated POPs (e.g., PCBs and DDTs), biotransformation is enzyme-mediated by P450 monooxygenase (CYP) enzymes, although enzyme efficiencies often vary by sex and species (Honkakoski and Negishi, 2000). Multiple studies have detailed limited phase I cytochrome P450 xenobiotic biotransformation capability of toothed whales relative to Carnivora species, such as polar bear (Letcher et al., 2009; McKinney et al., 2011b; Sonne et al., 2010). Additionally, toothed whales cannot excrete contaminants through hair unlike polar bear (Dietz et al., 2006; Jaspers et al., 2010). Toothed whales also show limited biotransformation capacity due to functional loss of the Paraoxonase 1 gene (PON1) that plays a key role in the detoxification of some contaminants (Meyer et al., 2018). However, biotransformation of some lipophilic POPs is not necessarily a beneficial process, as the resulting metabolites may be more bioaccumulative and sometimes more toxic than parent compounds. For example, DDE is the primary metabolite of DDT, yet DDE has a higher biomagnification potential and a longer half-live than DDT (Fisk et al., 2001). In fact, DDE concentrations typically far exceed those of DDT in marine mammal blubber samples (e.g., Dietz et al., 2013; Pedro et al., 2017), resulting in ΣDDTs being used a common metric to monitor concentrations of DDT and its metabolites in marine biota. Similarly, PCBs can undergo hydroxylation and further transformations in biota to OH-PCBs and $MeSO_2$-PCBs (Letcher et al., 1998). These PCB metabolites are generally less hydrophobic than their respective parent compounds, but are still lipophilic, often showing high concentrations in blubber, blood, and liver (Tehrani and Van Aken, 2015; Letcher et al., 2009). OH-PCBs and $MeSO_2$-PCBs metabolite accumulation via PCB metabolism or from dietary intake is also associated with oxidative damage and endocrine disrupting effects (Tehrani and Van Aken, 2015).

Dietary intake and trophic position play a dominant role in determining recalcitrant POP concentrations in marine mammals. In fact, up to 99% of PCB exposure in predators was estimated to be derived from dietary exposure relative to intake from water (Thomann and Connolly, 1984; Borgå et al., 2004). As most hydrophobic POPs generally show high biomagnification potentials, concentrations in top marine predators are highly correlated with trophic position (see section 2.6; Cullon, 2010; Vergara et al., 2019; Madgett et al., 2022). For example, higher concentrations in killer whale feeding in East Greenland (up to 70 mg/kg lw; Pedro et al., 2017) was suggested to be from high consumption of harp (*Pagophilus groenlandicu*s) and hooded seal (*Cystophora cristata*) relative to fish-feeding populations in Iceland (Remili et al., 2021). Similarly, shifts in East Greenland polar bear diet from less contaminated ringed seal to more contaminated harp and hooded seal was correlated with increases in legacy POP concentrations over time (McKinney et al., 2013). Comparing among different sampling locations and time periods, other toothed whales like narwhal in West Greenland (Carlsson et al., 2014) and pilot whale in the Faroe Islands (Hoydal et al., 2015) likely show comparatively lower concentrations due to consumption on lower trophic position prey including fish and/or squid (Garde et al., 2015; Heide-Jørgensen et al., 2023).

MeHg behaves very similar to legacy POPs in its terms of its bioaccumulation and magnification across food webs, although, it preferentially accumulates in liver and other protein-rich tissue (skin, muscle, etc.) instead of fatty tissues (logK_{ow} ~ 2; Major et al., 1991). MeHg bioaccumulation in marine wildlife primarily occurs through diet, as lower concentrations in water result in minimal transfer via dermal exposure, similar to POPs (Rodgers, 1994; Hall et al., 1997). Yet, MeHg half-lives are far shorter than POPs in various tissues, between 10-15 days (Kershaw and Hall, 2019). Although diet is the primary route of exposure to Hg in marine

mammals, wide variation in tissue concentrations observed across the Arctic suggests geographic differences in release from sediment and local anthropogenic inputs (Braune et al., 2015; Kershaw and Hall, 2019). Marine organisms can also detoxify MeHg via demethylation in liver, where Hg binds with selenium (Se) to create biologically inert HgSe (Caurant et al., 1996; Wagemann et al., 1998). However, differences in species-specific detoxication rates are not entirely understood (Kershaw and Hall, 2019). Still, the primary drivers of intra- and interspecific differences in Hg concentrations in marine mammals are similar to known POPs, and include elimination rates, age, sex, trophic position, and dietary intake.

2.4. METHODS TO MONITOR LEGACY CONTAMIANTS IN MARINE MAMMALS

For developed methods in any laboratory setting, good quality measurement data and the production of reliable results is of utmost importance. Method validation is an internationally accepted means of ensuring analytical results are accurate and comparable, and multiple organizations such as the International Organization of Standardization have detailed method performance criteria for method validation that are used globally (International Organization for Standardization, 2017; Lees, 2022). In general, method validation determines that a procedure is "fit-for-purpose" and can be used for the determination of an analyte of interest and its range of concentrations in a particular matrix (Rambla-Alegre et al., 2012). To determine whether a method is "fit-for-purpose" (and validate the method), method performance criteria have been developed, where the determination of selectivity, accuracy, precision, repeatability, reproducibility, working range, and robustness is required (Rao, 2018). In brief, these method performance criteria for the validation of analytical methods are outlined in **Table 2.3**, with applications and examples for method validation to monitor contaminants in marine mammals.

Table 2.3: Method performance criteria for the validation of an analytical method, with examples applicable to contaminant analysis in marine mammal blubber and adipose samples. Organization guidelines taken from Rambla-Alegre et al., (2012). FDA = food and drug administration, ICH = International Conference on Harmonization, ISO = the International Organization for Standardization, IUPAC = the International Union of Pure and Applied Chemistry, and USP = the United States Pharmacopeia.

Method Performance Criteria	Description	Organization Guidelines	Approaches and Examples for Validation	References
Accuracy	The closeness of agreement between a test result and the accepted reference values of the property being measured	FDA, ICH, ISO 17025, USP.	Reported as percent recovery in SRMs or from matrix-spiked standards. Measures the difference between mean recoveries and the accepted true value	Thompson et al., 2006; Rambla-Alegre, 2012
Precision	The closeness of agreement between a series of measurements when a method is repeated under the same conditions	USP, ICH, FDA, IUPAC.	Calculated as the relative standard deviation of measurements from matrix-blank standard spikes or through SRM measurements	Rao, 2018
Repeatability	Precision under the same conditions over a short period of time with minor changes in laboratory conditions. Also referred to as intraday precision	ICH, ISO 17025	Calculated as precision across a minimum of nine determinations of analysis	Lees, 2022
Reproducibility	Precision between laboratories (i.e., with different operators and instruments)	ICH	Calculated a precision between laboratories and collaborative studies	Rambla-Alegre, 2012; Lees, 2022
Linearity	A method's ability to produce results that are proportional to the concentration of analytes within a given range in a sample	ICH, ISO 17025, IUPAC, USP	Determined using a minimum of five injections of different concentrations of analyte standards to generate a linear calibration curve	Rambla-Alegre, 2012; Rao, 2018

Limits of detection	The lowest amount of analyte that can be detected	FDA, ICH, ISO 17025, IUPAC, USP	3 × the signal-to-noise ratio × lowest concentration in samples or SRMs	Rambla-Alegre, 2012
Limits of quantification	The lowest amount of analyte that can be quantified	ICH, ISO 17025, IUPAC, USP	10 × the signal-to-noise ratio × lowest concentration in samples or SRMs	Rambla-Alegre, 2012
Robustness	The sensitivity of a method to small variation in the condition of analysis	FDA, ISP, USP	Generally not considered in most validation guidelines, but can be tested by deliberately external factors including reagents, period when analysis is normally conducted, and operator	Rambla-Alegre, 2012; Lees, 2022
Selectivity	The ability to measure an analyte in a matrix without interferences from other compounds of similar behavior	ICH, USP	Analyze samples with potential interferences around the retention time of analytes of interest and examining if their presence impacts analyte detection or quantitation	Rambla-Alegre, 2012

Robust and validated methods for the analysis of lipophilic POPs in marine mammal blubber and adipose have been routinely employed for several decades (Jensen et al., 1969) and have been adapted extensively overtime (e.g., Norstrom, 1988; Muir et al., 1988, Ford et al., 1993, Letcher et al., 1995, Verreault et al., 2005, McKinney et al., 2009). In general, current approaches to monitor legacy POPs are generally divided into four key steps: 1) sample homogenization, 2) analyte extraction 3) lipid removal, and 4) further clean-up (**Figure 2.2** for a method overview). In brief, recent methods typically homogenize samples using a mortar and pestle or tissue grinder with added anhydrous sodium sulfate or diatomaceous earth to remove moisture (Tsygankov and Boyarova, 2016; Pedro et al., 2017; Trukhin and Boyarova, 2020; Krasnova et al., 2021). Next, a mixture of standards, that are typically isotopically labelled with $\delta^{13}C$, are spiked into samples, typically at similar concentrations to those expected in samples and within the linear range of the instrument. Then, analyte extraction typically occurs using accelerated solvent extraction (ASE) or Soxhlet extraction, often using dichloromethane and/or hexane as extraction solvents. More recently, automated ASE is more commonly employed and is generally more efficient with higher analyte recovery, requiring less time and solvent use (Richter et al., 1996). Using ASE, elevated temperature and pressure are used to extract analytes from solid samples and increase their diffusion into the extraction solvent (Richter et al. 1996). Next, gel-permeation chromatography (GPC) is commonly used to remove any lipids remaining in the extracted samples. GPC uses size-exclusion to separate high-molecular weight compounds (like lipids) from analytes. Here, nonpolar analytes can be eluted from the column using an organic solvent such as hexane and/or dichloromethane. Then, further clean-up steps are often employed due to the complexity of the matrix and difficulties in providing lipid-free extracts. For example, solid-phase extraction (SPE) using silica gel can further remove any suspended polar

compounds (e.g., Pedro et al., 2017). Prepared extracts are then typically analyzed by gas chromatography – (single or triple quadrupole) mass spectrometry (GC-MS). These sample preparation techniques have shown acceptably clean extracts for GC-MS analysis, are generally consistent, and show sufficiently high recovery of selected PCB and other OC analytes, despite the challenges of working with lipid-rich matrices.

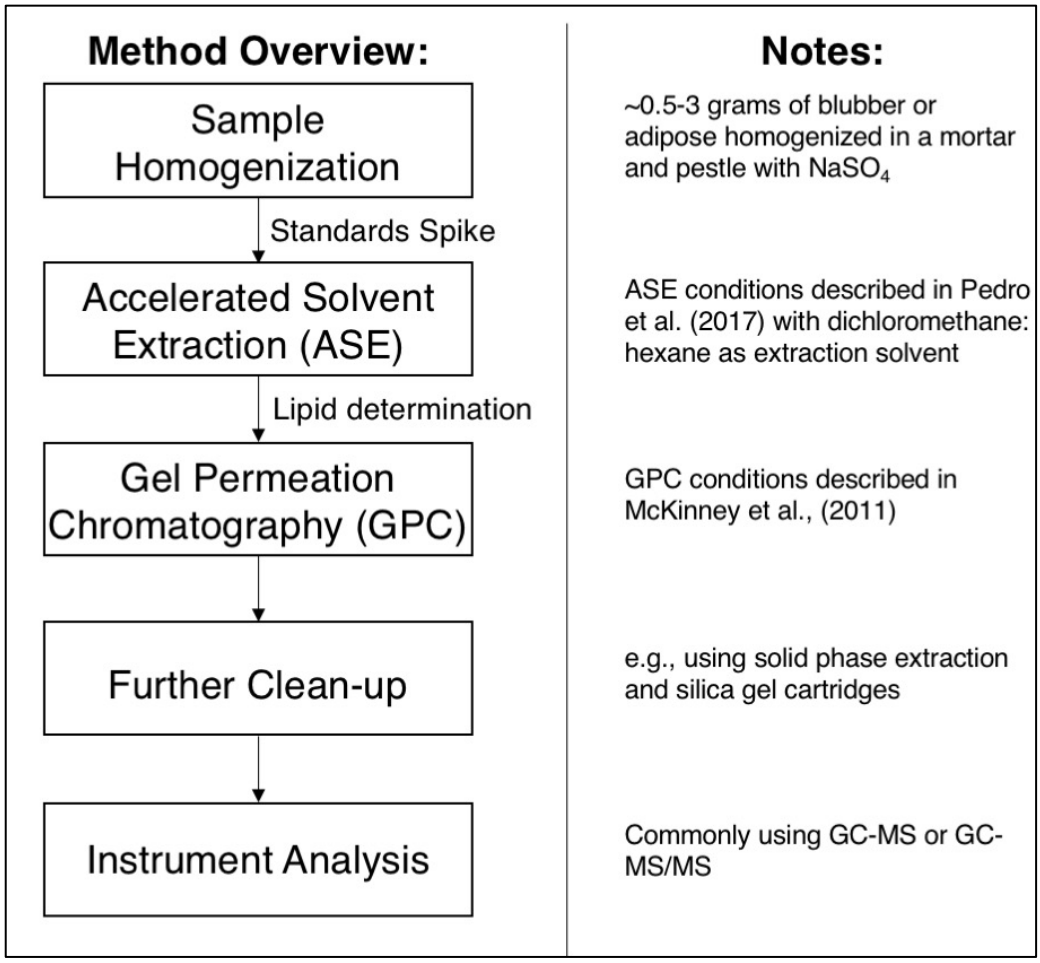

Figure 2.2: Method overview of current-use methods for the extraction of persistent organic pollutants (POPs) for marine mammal blubber and adipose tissues

Although these routine sample preparation methods for PCB and OC determination in blubber provide accurate and reproducible results, they possess some notable drawbacks in terms of cost, time and labor intensiveness, and a need for large volumes of toxic solvents. Both ASE

and automated GPC instruments are expensive to purchase and require ongoing costs to operate. An ASE run takes several hours for a typical batch of twelve samples, while a GPC will require more than 12 hours for a batch, and subsequently requires a few hours to reduce the sample extract volume back down prior to subsequent steps. Thus, in total, sample preparation for a batch of twelve samples takes around 16 hours (not including an overnight GPC run). The ASE and particularly the GPC steps also require relatively large quantities of toxic solvent to be used, which has associated expenses as well as potential for human exposure to these hazards (Joshi and Adhikari, 2019). For example, chronic exposures to hexane and dichloromethane, both heavily used in these current-use approaches, is associated with neurotoxicity and carcinogenicity in humans (Joshi and Adhikari, 2019). In short, although such approaches have been employed successfully for decades, they can be inaccessible for many research groups.

More recently, QuEChERS (quick, easy, cheap, effective, rugged, and safe) extraction methods have been highly successful in extracting numerous contaminants from a wide variety of fatty matrices. First described by Anastassiades et al. (2003), QuEChERS were originally detailed as single-phase liquid-liquid extraction methods, typically using acetonitrile as an extraction solvent, for pesticide analysis in fruits and vegetables (**Figure 2.3**). Further clean-up involves the simultaneous removal of residual matrix and water using dispersive solid-phase extraction (disperse-SPE) using magnesium sulfate and primary secondary amine sorbent (PSA). Coupled with GC-MS, this developed QuEChERS method presents a robust, cheaper, and effective method for providing acceptably clean extracts and accurate and precise results for pesticide analysis in some challenging matrices (including high percent recoveries of all lipophilic pesticides of interest like DDTs and endosulfans). Advantages of QuEChERS approaches include its simplicity, cost-effectiveness, and ability to recover a wider range of

analytes compared to current-use methods (i.e., **Figure 2.2**) and requiring less specialized equipment, expertise, and solvent usage (Kim et al., 2019).

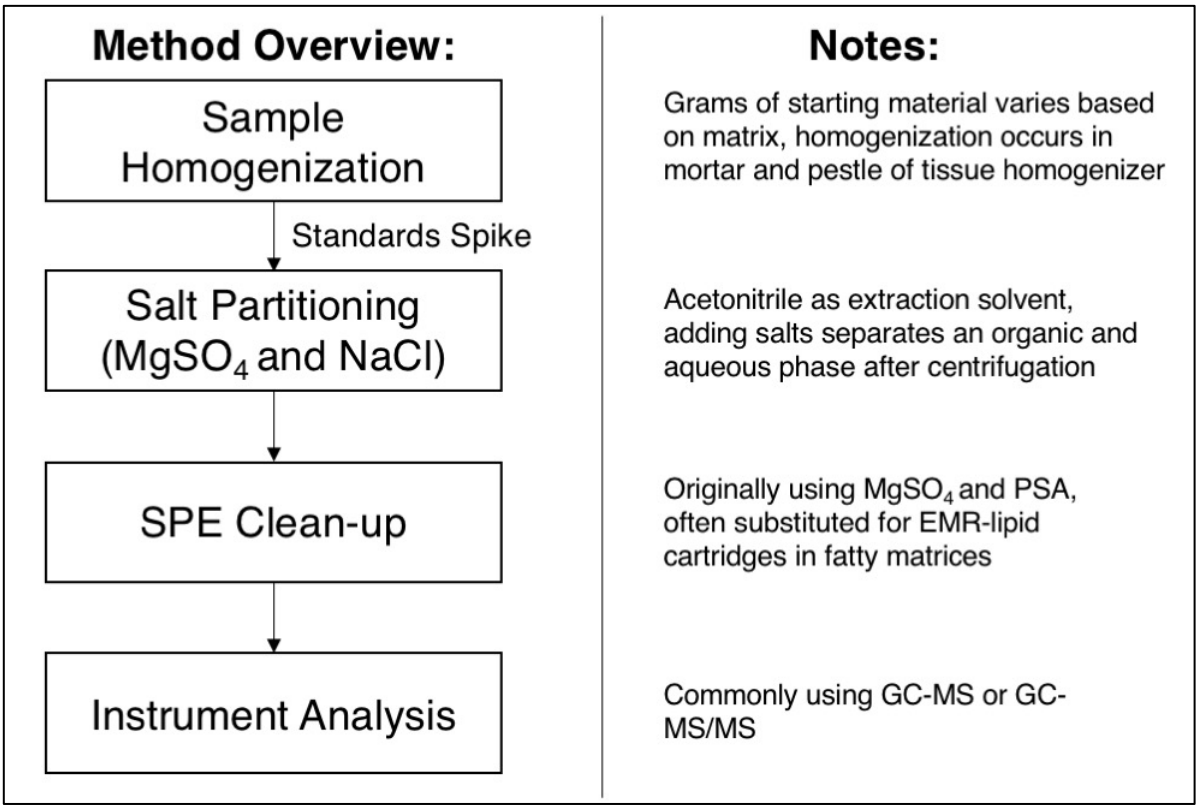

Figure 2.3: Method overview of the original QuEChERS (quick, easy, cheap, effective, rugged, and safe) method developed for the extraction of pesticides in fruits and vegetables

Despite challenges in the extraction of lipophilic contaminants from fatty tissues given their similar chemical properties, recent advancements in QuEChERS methodologies, such as SPE-based enhanced matrix removal-lipid (EMR-lipid) clean-up technology, have shown promise in effectively extracting lipophilic POPs including PCBs and OC pesticides from lipid-rich matrices. Fatty matrixes, like blubber and adipose generally show significant challenges due to the tendency of hydrophobic POPs to concentrate and remain in the lipids. Lipid-binding can also induce low analyte recoveries and trace fatty residues in final extracts can contribute to column contamination, ion suppression, and consequently, poor ion selectivity (Furey et al.,

2013). Therefore, additional clean-up steps are typically required to obtain high recoveries of lipophilic POPs in an ideally fat-free extract. For example, multiple recent studies have successfully employed QuEChERS-based methods coupled with EMR-lipid to extract lipophilic contaminants like OC pesticides, polycyclic aromatic hydrocarbons (PAHs), flame-retardants, and a few PCBs in fatty matrices such as animal fat and fatty foods (e.g., pork, fish, sausage, cheese, etc.; Slámová et al., 2020; Dai et al., 2023), edible oils (Sun and Wu, 2020), and chicken eggs (Guo et al., 2018). However, despite 1) the growing popularity of QuEChERS, 2) their effectiveness in extracting lipophilic contaminants, and 3) clear reductions in cost and time of extractions, they have not yet been tested in any marine mammal blubber or adipose tissues, to my knowledge. Additionally, even the studies on animal tissues and edible oils have not tested extractions on both an extensive suite of PCBs and OC pesticides, like DDT, which are vital for monitoring programs like AMAP.

2.5. METHODS TO MONITOR EMERGING CONTAMINANTS IN MARINE MAMMALS

Routine monitoring of legacy POPs (**Table 2.1**) in some northern marine mammal populations has typically relied on targeted screening approaches, where a select list of "known" chemicals (e.g., legacy POPs) are identified and quantified using authentic analytical standards. However, investigations into the presence of CEACS are other lesser-known chemicals is rarely, if at all, conducted. Although targeted screening approaches have produced accurate and reproducible results detailing POP concentrations in marine mammals for decades, they are often limited to (semi-)volatile compounds like PCBs and DDTs (Vinaixa et al., 2016). In addition, molecular ions are commonly absent or of low intensity from GC-MS with election ionization,

making molecular formula determination of unknown compounds, like most CEACs, challenging (Furey et al., 2013; Hollender et al., 2017). As such, unknown (or unexpected) compounds, including new/emerging contaminants, are inevitably missed by targeted screening approaches (Hollender et al., 2017). Yet, as multiple comprehensive assessments (e.g., AMAP, 2020) have already detailed the presence of many CEAC groups in Arctic seawater and air including OPFRs, paraffins, siloxanes, and plastics/plastic-related compounds (PRCs), such as phthalates, antioxidants, UV stabilizers, and micro/nanoplastics (**Table 2.2**; AMAP, 2020), CEAC presence in northern marine mammals is likely, but largely unknown (Sonne et al., 2021).

To identify unknown compounds, like CEACs and PRCs, in top marine mammals, a newer approach, nontarget screening, has been shown to be useful. Nontarget screening is a discovery-based approach, where organic chemicals can be detected without any prior information regarding their presence in samples (Manz et al., 2023). In a subcategory of nontarget screening, suspect screening, molecular features of a compounds of interest are compared against library databases with known molecular properties (Place et al., 2021). In comparison, in "true" nontarget analyses, compound presence is postulated without any suspect databases. Nontarget and suspect screening have allowed for the development of new analytical workflows for chemical analyses beyond the finite list commonly assessed via targeted analyses, which typically focus on relatively small number of compounds (e.g, < 500). In addition, nontarget and suspect screening could allow researchers to better characterize marine predator chemical exposome, defined as the totality of exposures individuals experience in their lifetime (Wild, 2012).

Although no routine nontarget/suspect approaches exist for the analysis of contaminants in marine mammal tissues, high-resolution mass spectrometry (HRMS) coupled with liquid or

gas chromatography (LC or GC) has allowed for the analysis of emerging contaminants in a wide variety of environmental matrixes, even some biological tissues (Schymanski et al., 2015; Hollender et al., 2017; Von Eyken and Bayen, 2019; Tian et al., 2020). In particular, using quadrupole time-of-flight (QTOF) LC-HRMS has been shown to provide high mass accuracy for formula generation and high confidence in structure prediction (Knolhoff et al., 2016a; Knolhoff et al., 2016b). Following instrument analysis and data processing, the Schymanski et al. (2014) scale also is commonly used to assess the identification confidence of a compound of interest, using its mass, isotope distributions, fragmentation data (from MS^2), and retention time (RT). For example, a confidence level 1 on the Schymanski et al. (2014) scale indicates a confirmed compound by a match to the RT, mass, and MS^2 between the sample and available standards. However, when a standard is not available for purchase, a level 2 score is given to indicate a probable structure via MS, mass, and MS^2 data matches to a library database. Similarly, level 3 indicates a tentative candidate from a library match, but insufficient evidence for one exact chemical structure (i.e., multiple similar chemical structures or isomers may show library matches). Finally, levels 4 and 5 indicate a lack of information for further identification, and only a molecular formula and exact mass, respectively, can be determined. An example nontarget and suspect workflow using LC-HRMS and the Schymanski et al. (2014) scale is available in **Figure 2.4.**

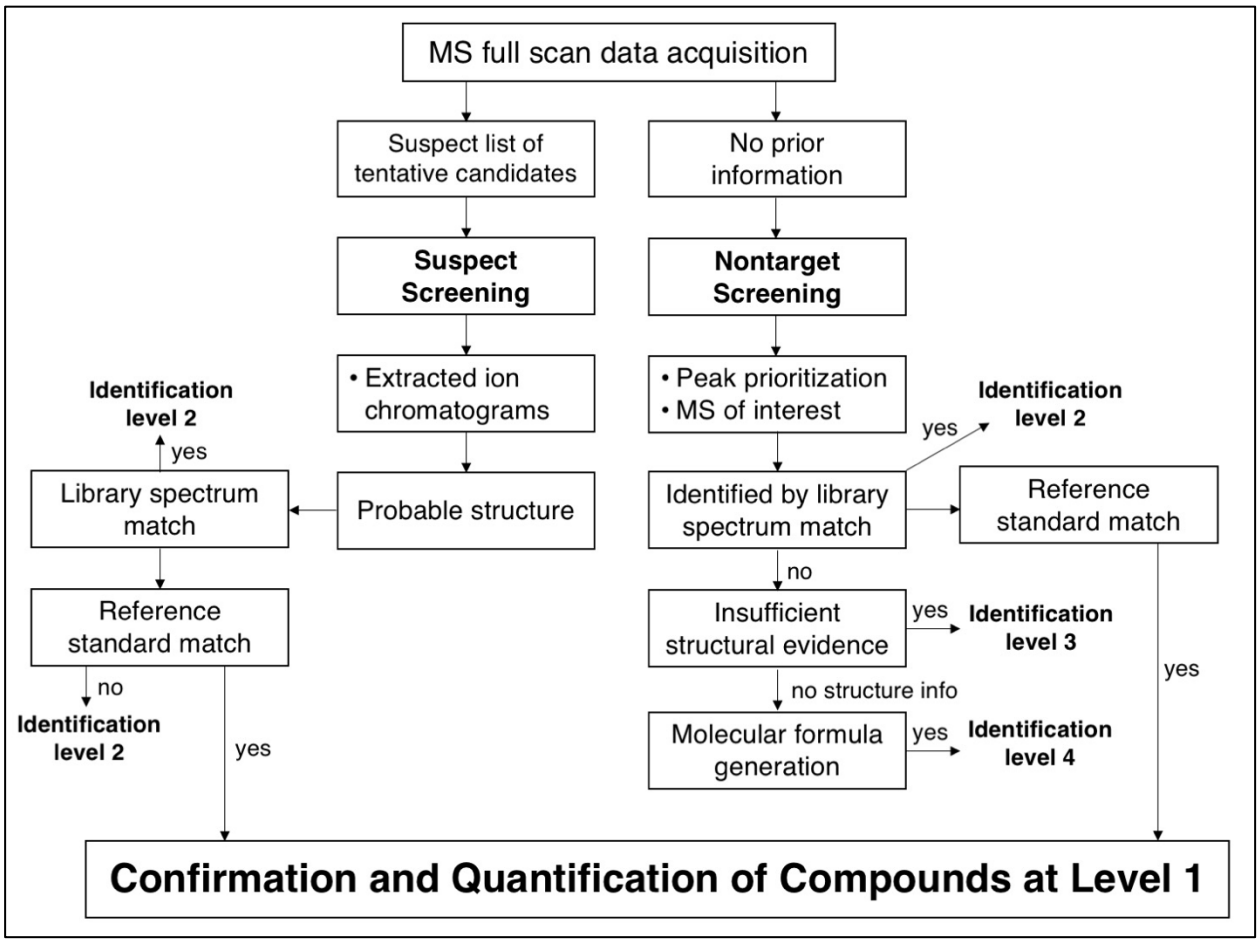

Figure 2.4: Example nontarget and suspect screening workflow for the identification of suspected or unknown compounds in a sample matrix, adapted from Rebryk and Haglund (2021) and El-Deen and Shimizu (2022). Identification confidence scale is based on Schymanski et al. (2014).

Nontarget/suspect approaches have rarely been used in any Arctic marine mammal species, although some studies exist in marine mammals studied elsewhere (**Table 2.4)**. For instance, multiple studies have monitored emerging contaminants in pinnipeds (e.g., mostly seals) using a nontarget or suspect approach in the Baltic Sea (Rebryk and Haglund, 2021), French Atlantic coast (Cariou et al., 2020) and Iceland, the eastern United States coast, and Sweden (Spaan et al., 2020). Two studies also used similar methods in bottlenose dolphin (*Tursiops truncates*) blubber samples from Brazil and the eastern United States, mostly showing high levels of halogenated natural products (HNPs; Shaul et al., 2015; Alonso et al., 2017).

However, the majority of other studies in marine mammals primarily used suspect approaches to monitor PFAS alone, including in the South China Sea (Wang et al., 2021), St. Lawrence Estuary, Canada (Barrett et al., 2021), and Iceland, Eastern United States, and Sweden (Spaan et al., 2020). Similarly, among the very limited studies in Arctic marine mammals, only PFAS was typically monitored, including in polar bear and killer whale from East Greenland (Spaan et al., 2020), long-finned pilot whale in East and West Greenland (Lauria et al., 2024), and polar bear in Hudson Bay, Canada (Chu and Letcher, 2024). However, one study in polar bear liver from Svalbard, Norway used a nontarget approach and detailed the presence of some phthalates, tonalide (a synthetic musk), and 4-nonylphenol, a PRC with known endocrine disrupting potential (Routti et al., 2016). As such, there is a severe lack of studies using nontarget/suspect screening approaches to detail any "unknown" contaminant presence in any Arctic marine mammals, other than for PFASs. As several other "unknown" and potentially toxic compounds may also be present, the implementation of a nontarget approach to identify never-before-screened chemicals, which may include CEACs, in these marine mammal sentinels is warranted.

Table 2.4: All available studies, to my knowledge, that used a nontarget or suspect screening approach to investigate some new/emerging contaminants in any marine mammal species globally. Refer to Table 1.1 for information on abbreviations.

Species	Scientific Name	Location	Tissue	Contaminants	Instrument	Reference
Humpback dolphin Finless porpoise	*Sousa chinensis* *Neophocaena phocaenoides*	South China Sea	Liver	PFASs	LC-QTOF-HRMS	Wang et al. (2021)
Harbor seal Harbor porpoise Gray seal	*Phoca vitulina* *Phocoena phocoena* *Halichoerus grypus*	Baltic Sea	Liver, Blubber, Muscle	HNPs Dechlorane 602 PRCs	GC-HRMS with ECNI	Rebryk and Haglund (2021)
Harbor porpoise Fin whale Bottlenose dolphin Harbor seal Sperm whale	*Phocoena phocoena* *Balaenoptera physalus* *Tursiops truncatus* *Phoca vitulina* *Physeter macrocephalus*	French Atlantic Coast	Blubber	Toxaphene Chlordanes OH-PCBs Dechlorane 603 HBCDD	LC/ESI-HRMS	Cariou et al. (2020)
Harbor seal Harbor porpoise Gray seal Killer whale Polar bear Minke whale	*Phoca vitulina* *Phocoena phocoena* *Halichoerus grypus* *Orcinus orca* *Ursus maritimus* *Balaenoptera acutorostrata*	East Greenland, Iceland, Eastern U.S, Sweden	Liver	PFASs	UPLC-Orbitrap-MS	Spaan et al. (2020)
Polar bear	*Ursus maritimus*	Norway	Liver, Adipose	Phthalates Tonalide Nonylphenols	HPLC-MS	Routti et al. (2016)
Beluga Whale	*Delphinapterus leucas*	St. Lawrence Estuary, Canada	Liver	PFASs	UHPLC-MS	Barrett et al. (2021)
White-beaked dolphin Long-fin pilot whale	*Lagenorhynchus albirosris* *Globicephala melas*	East and West Greenland	Liver	PFASs	UHPLC-ESI-MS/MS	Lauria et al. (2024)
Bottlenose dolphin	*Tursiops truncatus*	Brazil	Blubber	HNPs MeO-BDEs	GC×GC/TOF-MS	Alonso et al. (2017)
Bottlenose dolphin	*Tursiops truncatus*	Eastern U.S	Blubber	Legacy POPs HNPs	GC×GC/TOF-MS	Shaul et al. (2015)
Polar bear	*Ursus maritimus*	Hudson Bay, Canada	Liver	PFASs	UPLC-Orbitrap-HRMS	Chu and Letcher (2024)

2.6. METHODS TO ASSESS CONTAMINANT ACCUMULATION FROM DIET

Diet estimates are commonly used to assess the dietary accumulation of contaminants, like POPs and Hg (Iverson and Bowden, 2012). Although direct visual observations are, in principle, the best characterization of a predator's diet, dietary tracers like bulk stable isotope (SI) ratios in bulk (whole) tissues often provide insight into longer-term feeding patterns and contaminant accumulation in marine predators (Hobson et al., 2002; Braune et al., 2005a). Stable isotope of several elements (e.g., ^{2}H, ^{18}O, ^{13}C, ^{15}N, and ^{34}S) exist naturally in ecosystems, and calculating ratios of the heavy to light isotopes (e.g., $^{13}C/^{12}C$) can provide key information on habits, foraging and feeding (Hobson et al., 2002). To calculate isotope ratios, standards have been adopted for each tracer element, commonly using an isotope ratio mass spectrometer (IRMS; Garvey and Whiles, 2017). The common notation for calculating isotope ratios in a sample is:

$$\delta\,‰ = \left(\frac{R_{sample}}{R_{standard}} - 1\right) \times 1000$$

where:

$$R = \frac{{}^{H}E}{{}^{L}E}$$

with E representing the relative amount of the heavy (H) or light (L) isotope in the sample or standard.

SI of nitrogen ($^{15}N/\,^{14}N$ or $\delta^{15}N$) and carbon ($^{13}C/\,^{12}C$ or $\delta^{13}C$) in bulk tissues are commonly used to provide information on trophic position and feeding habitat of marine organisms, respectively (Gannes et al., 1997). SI methods are based on the assumption that a consumer's bulk stable isotope ratios reflect the composition of its diet items (Gannes et al., 1997). As the energy required to break interatomic bonds in heavy isotopes is significantly greater than for lighter isotopes (i.e., heavier isotopes react more slowly than lighter isotopes),

heavier isotopes can preferentially accumulate in predators from their diet (Garvey and Whiles, 2017). As $\delta^{15}N$ generally increases in consumer by ~3.4‰, trophic position (TP) can be calculated using the following equation:

$$TP = \lambda + (\delta^{15}N_{consumer} - \delta^{15}N_{primary\ consumer}) / 3.4‰$$

where λ equals the tropic position of the primary consumer (Post, 2002). However, more recently studies have indicated that this model is likely oversimplified and largely omits some known $\delta^{15}N$ variation (Hussey et al., 2014). $\delta^{13}C$ varies less predictably with trophic position and is instead often used to assess differences in predator feeding habitats, for example, between benthic and pelagic feeding, where $\delta^{13}C$ values tend to be lower in pelagic and higher in benthic marine environments (Le Loc'h et al., 2008).

As biomagnifying contaminants increase with trophic position and can vary based on feeding habit, bulk $\delta^{15}N$ and $\delta^{13}C$ are useful in assessing the bioaccumulation of Hg and lipophilic POPs. For example, using a simple linear regression between bulk $\delta^{15}N$ and contaminant concentrations, bulk SI have been used to assess variation in concentrations among diverse cetacean species, locations, years of collection, and feeding habitats (Nielsen et al., 2018). Furthermore, trophic magnification of Hg and/or POPs across diverse marine food webs has also been well documented using bulk $\delta^{15}N$ (Lavoie et al., 2013) or bulk $\delta^{15}N$-derived trophic position estimates (Fisk et al., 2002; McKinney et al., 2012).

Although bulk stable isotopes are routinely used to assess feeding habits and patterns, this approach has some notable drawbacks. In particular, bulk SI values vary widely based on geographic location, feeding habitat, and time (Goericke and Fry 1994), and as such, an isotope "baseline" (i.e. based on location) is commonly selected among primary consumers to correct for inherent differences in values characterized by a location. However, despite recommendations to

use longer-lived primary consumers with relatively consist SI values over time, there is currently widespread variation in selected baselines and statistical approaches used to estimate trophic positions relative to the baseline (or data is often not baseline corrected at all) among marine food web studies (Kjeldgaard et al., 2021). Furthermore, baseline values may not be entirely representative of omnivorous or highly mobile species (e.g., transient killer whale populations) feeding across different food webs and feeding habitats, making it difficult to characterize their feeding ecology from bulk SI alone (Jardine et al., 2006). Diet resolution is also often limited to predators with few prey items (~3-4) as $\delta^{13}C$ and/or $\delta^{15}N$ from district prey sources may overlap (Philips et al., 2014). Still, researchers often assess biomagnification of contaminants across food webs using bulk $\delta^{15}N$ (an estimated 88% of studies from Elliott et al., 2021).

Due to these drawbacks, alternative or complementary approaches have emerged, such as fatty acid (FA) signatures that are similarly transferred from predator to prey with little or predictable modification (Budge et al., 2006). FAs represent a group of biomolecules comprising the majority of lipids found in all species, varying based on carbon chain length (2 to 26 carbons) and number of double bonds (zero to six; Budge et al., 2006). FAs are commonly referred to using a shorthand notation of A:Bnx, where A represents the number of carbon, B is the number of double bonds, and x is the position of the first double bond relative to the methyl (CH_3) group. For example, 14:0 is a saturated FA (SFA) with no double bonds and 14 carbons, while 18:1n9 is a monounsaturated FA (MUFA) with 18 carbons and one double bond at the ninth carbon, and 22:6n3 is a polyunsaturated FA (PUFA) with 22 carbons, six double bonds with the first double bond on the third carbon from the methyl end (**Figure 2.5**). Long-chain PUFAs, in particular, with three or more double bonds are also essential for growth, reproduction, and neural development in humans and most animals (Menzel et al., 2018). However, biosynthesis of

PUFAs in humans and upper-trophic level consumers is limited, and thus they must be obtained through diet instead (Budge et al., 2006).

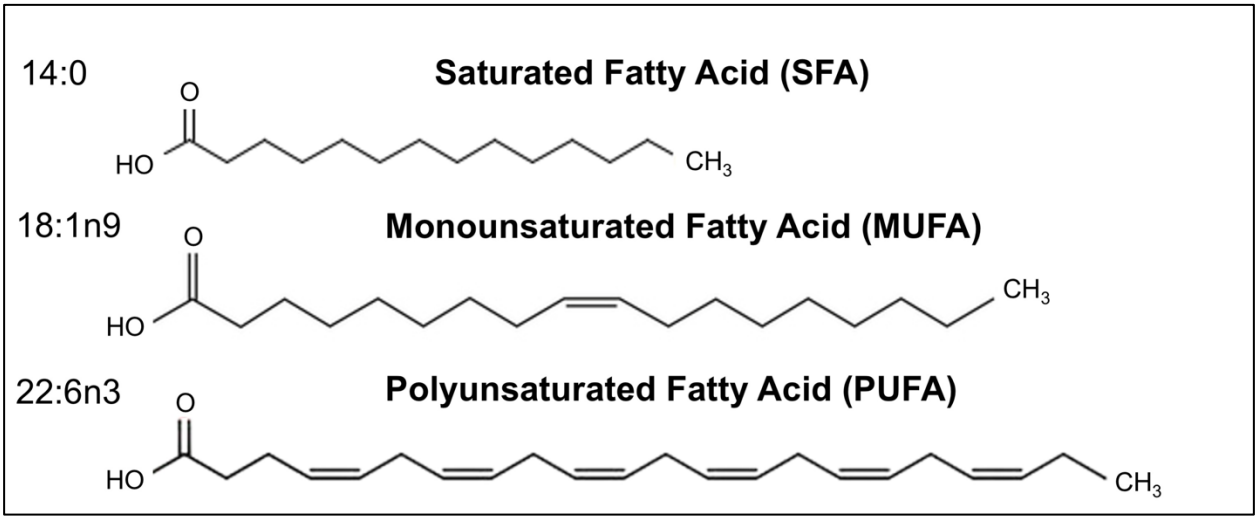

Figure 2.5: Examples of a saturated fatty acid with no double bonds (SFA), a monosaturated fatty acid with one double bond (MUFA), and a polyunsaturated fatty acid with multiple double bonds (PUFA).

FAs are typically attached to a glycerol backbone, called a triglyceride (Budge et al., 2006), which are the most common form of storage lipids found in marine mammal adipose and blubber. FA composition in these fatty tissues is, however, the result of three metabolic sources: 1) FAs from diet that are unmodified and directly deposited into adipose/blubber, 2) FAs from diet that are modified prior to deposition in fatty tissues, and 3) FA derived from *de novo* synthesis in a predator (i.e., the organism can biosynthesize the FA in its own body without acquiring it from diet; Budge et al., 2006). In general, *de novo* synthesis of FAs in birds and mammals is typically restricted to only SFAs and MUFAs, while biosynthesis of most PUFAs is not possible due to a lack of certain desaturase enzymes (Tocher, 2010). As such, PUFAs in predators are generally directly acquired from diet, and, therefore, they are the most commonly analyzed FAs for dietary analyses in top marine predators (Iverson et al., 2004). However, *de novo* synthesis of all FAs may still be inhibited during fasting and in the consumption of high-fat

diets (>30% of calories from fat), and thus, biosynthesis of MUFA and some SFAs may be limited in some marine mammals (Budge et al., 2006). Still, long-chain PUFAs and MUFAs (e.g., carbon length ≥ 18) in predators are of known dietary origin and, thus, are most likely used when reconstructing predator diet, while the predominant source of SFA and shorter-chain MUFAs in tissues is likely from relatively large contributions of both diet and *de novo* synthesis (Iverson et al., 2004).

FAs have successfully been used to trace diet in a wide variety of marine mammals in the Arctic. For example, a multitude of studies have used FAs to investigate sea ice-associated changes in diets in polar bear (McKinney et al., 2009), narwhal (Watt and Ferguson, 2014), and killer whale (Remili et al., 2023a). Furthermore, recent advancements in quantitative fatty acid signature analysis (QFASA) have provided estimates of predator diet, particularly in polar bear (Thiemann et al., 2008; McKinney et al., 2013) and killer whale (Remili et al., 2022; Remili et al., 2023b). However, despite FAs being routinely analyzed in many marine mammal populations in the Arctic, they have rarely, if ever, been used in assessments of contaminant accumulation and biomagnification. Without QFASA-based diet estimates, FAs may show also overlapping patterns among different prey items, similar to bulk SI.

Compound-specific isotope analysis (CSIA) of individual biomolecules, such as amino acids [AAs] and FAs (CSIA-FA) presents a newer approach that may offer greater sensitivity than bulk stable isotopes or FA signatures alone in describing feeding habits and assessing trophic transfer of contaminants (Twinning et al., 2020). Although bulk stable isotopes and FAs may overlap or occur at similar proportions among different diet resources, these FAs may still have distinct $\delta^{13}C$ values among prey. As such, CSIA-FA may offer higher-resolution insight into feeding patterns and food web contaminant dynamics (McKinney et al., 2013; Twining et

al., 2020). Multiple controlled-feeding experiments between lower trophic level organisms (e.g., phytoplankton and cyanobacteria) and primary consumers (e.g., snails, fish, and birds) have demonstrated the potential of $\delta^{13}C$ values of some dietary PUFAs, like 18:3n3 and 22:6n3, to be useful dietary tracers (Gladyshev et al., 2016; Fujibayashi et al., 2016; Burian et al., 2020). In these studies, $\delta^{13}C$ values of some PUFA between prey and their consumers showed little-to-no fractionation, defined as the difference in isotope values between consumers and their diets (Fujibayashi et al., 2016). As a low or predictable trophic fractionation is a very important characteristic of reliable dietary tracers, FA $\delta^{13}C$ values may show promise in assessing trophic relationships (Bec et al., 2011).

Although some studies have characterized trophic fractionation of FA $\delta^{13}C$ in controlled-feeding experiments (e.g., Budge et al., 2011; Fujibayashi et al., 2015; Burian et al., 2020), no studies to date, to my knowledge, have investigated FA $\delta^{13}C$ across complex natural food webs, ranging from primary consumers to top predators, nor has interspecific variation among mobile, higher-level consumers been explored. Furthermore, the utility of FA $\delta^{13}C$ to assess trophic transfer of contaminants is essentially unknown. For example, bulk isotopes and FA signatures were, instead, used to assess Hg biomagnification in a Cumberland Sound (CS; Nunavut, Canada) food web ranging from zooplankton, to primary consumers (e.g., shrimp), to piscivorous fish (e.g., Greenland halibut [*Reinhardtius hippoglossoides*], and Greenland shark (*Somniosus microcephalus*) (McKinney et al., 2012; McMeans et al., 2015). As food web structure and the trophic transfer of contaminants has been previously assessed with available bulk SI and FA data (McKinney et al., 2012; McMeans et al., 2015), this CS food web is likely suitable to monitor FA $\delta^{13}C$ fractionation and draw comparisons to other diet tracing approach (i.e., FA signatures and bulk SI).

$\delta^{13}C$ values of some FAs have been previously analyzed in two studies in some marine mammal species; however, few FAs were analyzed and no correlations to contaminants were discussed. For example, Budge et al. (2008) monitored FA $\delta^{13}C$ from primary producers to marine mammals in Barrow, Alaska to assess contribution of sea-ice algae to diets, yet only two FAs, 16:4n1 and 20:5n3, were monitored, and trophic fractionation and contaminant accumulation across the entire food web was not analyzed or discussed. McKinney et al., (2013) similarly analyzed dietary FA $\delta^{13}C$ in East Greenland polar bear; yet, only a select few FAs were monitored and fractionization across multiple trophic positions was not assessed. As such, further investigation is warranted into the trophic fractionation of dietary fatty acids (mostly PUFAs) and their utility to assess contaminant bioaccumulation 1) across complex, natural marine food webs (such as in CS) and 2) in mobile, top predator species (like among some marine mammal in East Greenland).

CHAPTER 3: DEVELOPMENT AND VALIDATION OF A MODIFIED QUECHERS METHOD FOR EXTRACTING POLYCHLORINATED BIPHENYLS AND ORGANOCHLORINE PESTICIDES FROM MARINE MAMMAL BLUBBER

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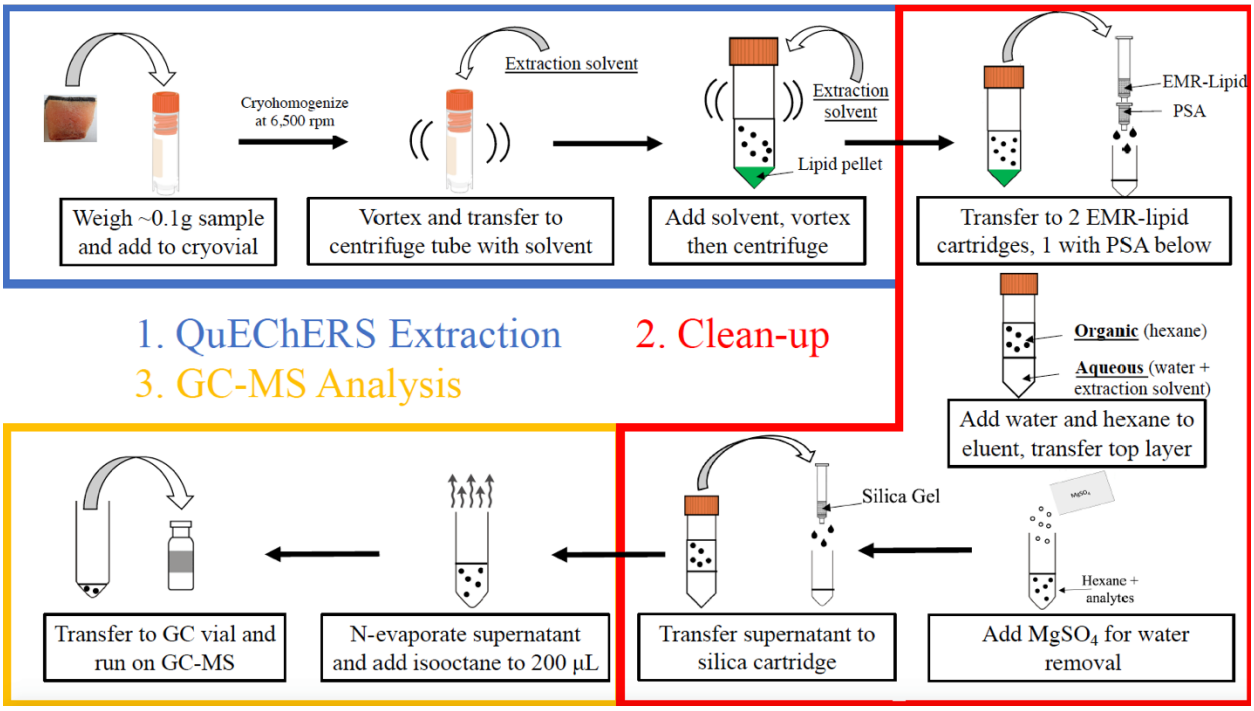
Highlights:

- QuEChERS method developed for extraction of persistent organic pollutants in blubber
- The method was validated using a NIST blubber standard reference material
- Method was applied to killer whales previously extracted by typical approaches
- Strong agreement between QuEChERS and current-use methods for most POPs
- The QuEChERS method reduces cost, time, and solvent-use

3.1. GRAPHICAL ABSTRACT



3.2. ABSTRACT

The monitoring of legacy persistent organic pollutants (POPs) in blubber of key sentinel marine mammal species has been conducted using established techniques for decades. Although these methods for polychlorinated biphenyl (PCB) and organochlorine (OC) pesticide determination provide accurate and reproducible results, they possess some drawbacks in terms of cost, time, and a need for large volumes of toxic solvents. QuEChERS (quick, easy, cheap, effective, rugged, and safe) extractions may help address these issues, but have not been applied to marine mammal blubber/adipose. As such, our aim was to develop, validate, and apply a QuEChERS method for the extraction of PCB and OC contaminants in marine mammal blubber. First, we tested multiple solid-phase extraction and clean-up steps to find the approach that provided the cleanest extracts along with consistent and acceptable analyte recovery, accuracy, and precision. QuEChERS extractions followed by two enhanced matrix removal-lipid (EMR-lipid), one primary-secondary amine (PSA), and one silica gel clean-up showed the highest matrix removal and acceptable recoveries of spiked internal (62-97%) and external standards (61-94%). Solvent usage was reduced by ~393% and extraction time was reduced by ~25% (from 16 to 12 hrs). Next, the method was validated using standard reference material (SRM) NIST 1945. Recovery experiments on SRM (n=5) showed acceptable recovery for 76% and 77% of PCBs and OC pesticides, respectively, and high precision for 73% and 69% of PCBs and OCs, respectively. Finally, the method was used on a set of southeast Greenland killer whales (n=13), with previously published PCB and OC data. Bland-Altman plots indicated good agreement between QuEChERS and current-use methods for ΣPCBs and some OCs with no significant constant or proportional bias. These results demonstrate that this QuEChERS extraction method represents

an effective, lower cost alternative to current-use extractions for PCBs and OCs in blubber, and likely other high-lipid samples.

3.3. INTRODUCTION

Marine mammals are important sentinels used in international monitoring programs including the Arctic Monitoring and Assessment Programme (AMAP) and national programs such as the Canadian Northern Contaminants Program (NCP) for assessing exposures and effects of persistent organic pollutants (POPs) (Muir et al., 2005; Dietz et al., 2019; Borgå et al., 2022). Most marine mammals often occupy high trophic positions as tertiary or even quaternary consumers within marine food webs and, consequently, relative to other marine organisms, tend to show high concentrations of biomagnifying POPs, including legacy polychlorinated biphenyls (PCBs) and organochlorine (OC) pesticides, such as chlordanes (CHLs), dichlorodiphenyltrichloroethanes (DDTs), and hexachlorocyclohexanes (HCHs) (McKinney et al., 2011a; Dietz et al. 2019; Remili et al., 2021). As PCBs and OCs are lipophilic, lipid-rich blubber is the primary site of accumulation of these POPs in marine mammals and represents around 75-90% of their total body burdens (Tanabe et al., 1981; Yordy et al., 2010). As such, blubber tissues are widely used to assess spatial and temporal variation in concentrations and the potential effects of legacy POPs and other lipophilic contaminants in pinniped and cetacean populations.

Sample preparation methods for PCBs and OCs in blubber (and other high lipid tissues like adipose) were first reported several decades ago (Jensen et al., 1969) and have been adapted extensively over the ensuing years (e.g., Norstrom, 1988; Muir et al., 1998, Ford et al., 1993, Letcher et al., 1995a, Verreault et al., 2005, McKinney et al., 2009). In brief, current approaches are generally divided into four key steps: 1) sample homogenization (and spiking with internal standards), 2) analyte extraction, e.g., using accelerated solvent extraction (ASE) or Soxhlet extraction, 3) lipid removal using gel permeation chromatography (GPC), 4) further clean-up,

e.g., by solid phase extraction. Prepared extracts are then typically analyzed by gas chromatography – (single or triple quadrupole) mass spectrometry (GC-MS) (Vaye et al., 2022). These sample preparation techniques have shown acceptably clean extracts for GC-MS analysis and generally consistent and sufficiently high recovery of selected PCB and OC analytes, despite the challenges of working with lipid-rich matrices.

Although these routine sample preparation methods for PCB and OC determination in blubber provide accurate and reproducible results, they possess some notable drawbacks in terms of cost, time and labor intensiveness, and a need for large volumes of toxic solvents. Both ASE and automated GPC instruments are expensive to purchase (~$50,000 each) and require ongoing costs to operate and repair. Assembling and disassembling the ASE cells is also time-consuming. An ASE run takes a few hours for a typical batch of twelve samples, while a GPC will require more than 12 hours for a batch, and subsequently requires a few hours to reduce the sample extract volume back down prior to subsequent steps. Thus, in total, sample preparation for a batch of twelve samples takes around 16 hr (not including an overnight GPC run) by this approach. The ASE and particularly the GPC steps also require relatively large quantities of toxic solvent to be used, which has associated expenses as well as potential for human exposure to these hazards (Joshi and Adhikari, 2018). In short, although such approaches have been employed successfully, they can be inaccessible for many research groups.

More recently, the QuEChERS (quick, easy, cheap, effective, rugged, and safe) extraction technique has been successfully used for extraction of a variety of different contaminants from multiple matrices. First described by Anastassiades et al. (2003), QuEChERS methods were originally described as single-phase liquid-liquid extraction techniques (commonly using acetonitrile) for the extraction of pesticides in fruits and vegetables. Currently,

to improve recoveries and reduce costs, QuEChERS methods have been employed to extract OC pesticides, PAHs (polycyclic aromatic hydrocarbons), flame-retardants, and a few PCBs in processed foods (dairy, meat products, eggs, cereals, fruits, oil, vegetables), fish, mussel, poultry muscle, cattle muscle tissues, and some environmental samples (Baduel et al., 2015; Haimovici et al., 2016; Han et al., 2016; Cloutier et al., 2017; Cunha et al., 2017; Babalola et al., 2018; Chiesa et al. 2018). Advantages of this method include its simplicity and cost-effectiveness, with the possibility of recovering even broader ranges of analytes than more targeted approaches, and requiring far less specialized equipment, knowledge, and solvent usage (Kim et al., 2019). In general, extraction of lipophilic contaminants from fatty tissues, given their similarity in chemical properties, can be particularly challenging as lipid-binding can induce low analyte recoveries and trace fatty residues can contribute to column contamination and ion suppression (Furey et al., 2013). Yet, recent studies have shown that solid phase extraction (SPE)-based enhanced matrix removal-lipid (EMR-lipid) clean-up technology may offer the possibility of effectively extracting OC pesticides from matrices containing lipids, including fatty foods, vegetable oils (nearly 100% lipid, mainly monounsaturated fatty acids in the form of triacylglycerols), and fish tissues (~10% lipid in the form of mixture of fatty acids including polyunsaturated fatty acids), with high sensitivity (Madej et al., 2018; Zhao et al., 2019; Cui et al., 2020; Drábová et al., 2022). However, despite the increasing popularity of QuEChERS methods, QuEChERS-based approaches, to our knowledge, have never been applied to marine mammal blubber tissues (>70% lipid in the form of a mixture of saturated, monounsaturated, and polyunsaturated fatty acids, plus some structural collagen) or other very lipid-rich animal tissues, and even the studies on fatty tissues and edible oils have not tested extractions on both an

extensive suite of PCBs and OC pesticides, which are key for on-going marine mammal monitoring programs.

This study developed a QuEChERS methodology for the extraction of an extensive suite of PCB and OC contaminants in marine mammal blubber. First, we tested multiple dispersive SPE and cartridge SPE extraction and clean-up steps to determine the approach providing the cleanest extracts along with consistent and acceptable analyte recovery, accuracy, and precision by GC-MS. We further checked a range of blubber sample starting masses and developed an optimized method that provided acceptable results, including sufficient lipid and fatty acid removal. Next, we evaluated method performance using U.S. National Institute of Standards and Technology (NIST) 1945 standard reference material (SRM) organics in whale blubber following SANTE guidelines (SANTE/11312/202). Finally, we applied the method to marine mammal blubber samples with previously published data, to demonstrate applicability of our QuEChERS method to lipid rich blubber/adipose tissues.

3.4. MATERIALS AND METHODS

3.4.1. Chemicals, Reagents, and Standards

All solvents (isooctane, acetonitrile, ethyl acetate, hexanes, dichloromethane, water, methanol) used for sample extractions were pesticide analysis grade and purchased from Fisher Scientific (Ottawa, ON, Canada). Native PCB (mixture of PCBs 17, 18, 28, 31, 33, 44, 49, 52, 70, 74, 82, 87, 95, 99, 101, 105, 110, 118, 128, 132, 138, 149, 151, 153, 156, 158, 169, 170, 171, 177, 180, 183, 187, 191, 194, 195, 199, 205, 206, 208, 209) and OC calibration standards (1,2,4,5-tetrachlorobenzene, 1,2,3,4-tetrachlorobenzene, pentachlorobenzene, hexachlorobenzene, α-HCH, β-HCH, γ-HCH, oxychlordane, *trans*-chlordane, *cis*-chlordane,

trans-nonachlor, *cis*-nonachlor, *p,p′*-DDE, *p,p′*-DDD, *p,p′*-DDT, mirex, heptachlor epoxide, dieldrin, methoxyclor, endosulfan II, and endosulfan sulfate) were purchased from Cambridge Isotope Labs (Andover, MA, USA). Isotopically-labeled internal standard PCBs ($^{13}C_{12}$-PCB-28, 52, 118, 138, 153, 180, 194) and OCs (chlorobenzene cocktail solution of $^{13}C_6$-1,2,4,5-tetrachlorobenzene, $^{13}C_6$-pentachlorobenzene, and $^{13}C_6$-hexachlorobenzene) were also purchased from Cambridge Isotope Labs (Andover, MA, USA). SPE cartridges (6 mL Captiva EMR-lipid SPE and Bond-Elut Jr PSA) and Bond-Elut EMR-lipid polish pouch (anhydrous $MgSO_4$) were purchased from Agilent Technologies (Folsom, CA, USA), and 6 mL HyperSep silica SPE cartridges were purchased from Thermo Fisher Scientific (Ottawa, ON, Canada).

3.4.2. Method Development

Here, we outline the optimized method, while providing details on method development in the Supporting Information. Multiple clean-up dSPE and SPE methods (Supporting Information S1) and multiple blubber starting weights (Supporting Information S2) were tested through the analytical procedure and matrix removal for each was assessed gravimetrically and by GC-MS in full scan mode (Figure S3.1, S3.2, S3.3, S3.4). The NIST 1945 SRM organics in whale blubber and calibration standard-spiked matrix blanks were used to test analyte recovery, accuracy, and precision during method development stages.

A graphical overview of the optimized analytical method workflow is shown in **Figure 3.1** and detailed step-by-step method description is available in Figure S3.5. Here, we provide an overview of the method. First, samples were prepared by sub-sampling 0.075-0.100 g of blubber and placing sub-samples into 2 mL pre-filled bead hard tissue homogenizing tubes (VWR, Mississauga, ON, Canada). A 1.25 mL aliquot of 20:80 (v:v) ethyl acetate:acetonitrile was then

added to each tube, and tubes were placed in a Precellys Evolution tissue homogenizer (Bertin Instruments, USA) at 6,500 rpm for 4 cycles of 30 sec (i.e. 30 sec homogenizer followed by 30 sec pause) at 0 °C.

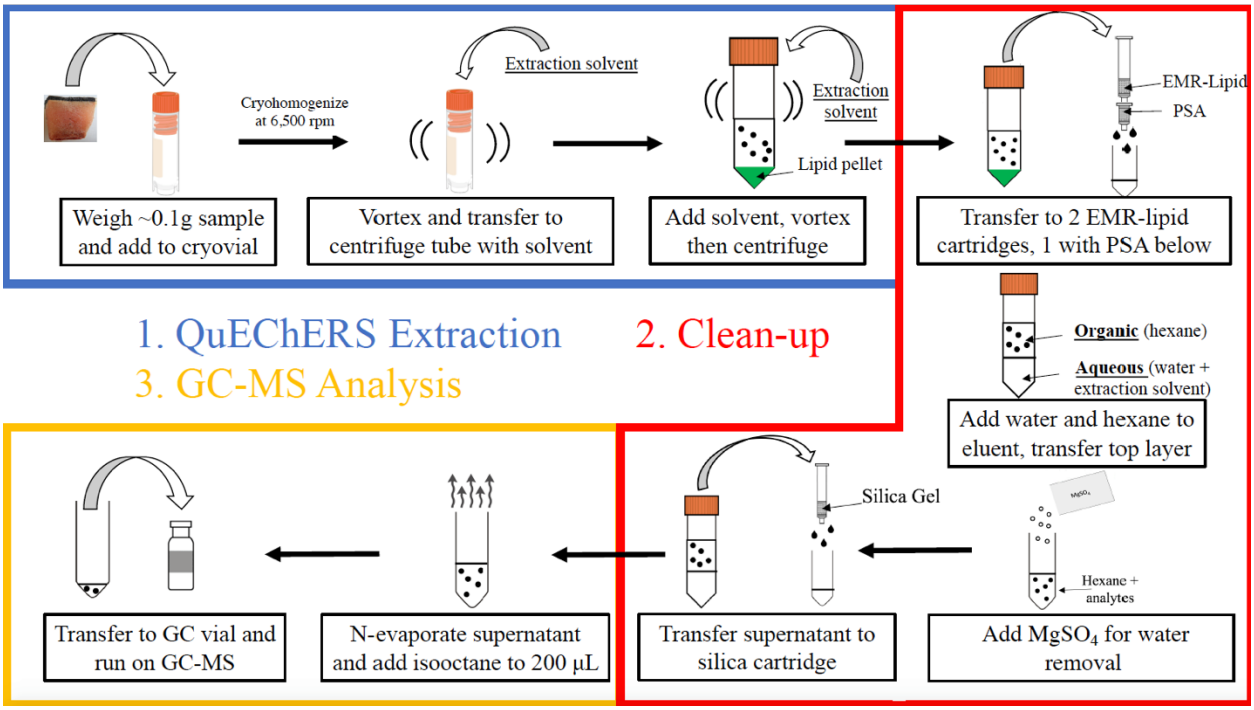


Figure 3.1: Graphical overview of the optimized modified QuEChERS method for extracting polychlorinated biphenyls (PCBs) and organochlorine (OC) pesticides from marine mammal blubber

vortexed, the solvent transferred to a polypropylene (PP) centrifuge tube (Tube 1), and then rinsed twice with 0.625 µL ethyl acetate:acetonitrile, used as the extraction solvent. We then spiked with 20 µL of mass labelled-PCB/OC internal standard (2000/2500 ng/ml) and vortexed. Tube 1 was centrifuged, and the supernatant (leaving behind a small lipid pellet) was transferred to a new PP centrifuge tube (tube 2). Tube 1 was rinsed twice with 1.25 mL extraction solvent (for a total of 5 ml) and then vortexed, centrifuged, and transferred to tube 2. A 0.95 mL (20% of the mixture) aliquot of pesticide grade water was then added. All of tube 2 was gravity eluted (followed by a vacuum elution once there was no visible liquid remaining) through a 6 mL

Captiva EMR-Lipid cartridge on a SPE vacuum manifold and collected in PP tube (tube 3), then tube 2 was rinsed with extraction solvent. This process was repeated with another EMR-lipid cartridge (i.e. the eluent was collected and then loaded onto a second EMR-Lipid cartridge), but also including a Bond-Elut Jr PSA cartridge fitted beneath, and the eluate was collected into a new PP tube (tube 4). Tube 4 was transferred to a 40 mL heavy-duty glass centrifuge tube (tube 5), and 11 mL of water and 5 mL of hexane were added to tube 5, then vortexed and centrifuged. The top layer was transferred to a new 10 mL glass tube (tube 6), and tube 5 was rinsed with 4.5 mL of hexane. To tube 6, ~1 g of anhydrous $MgSO_4$ was added and vortexed immediately, and then centrifuged at 2,000 rpm for 5 min. The supernatant was transferred to a glass tube (tube 7) and evaporated on a nitrogen evaporator to ~ 1 mL. All of tube 7 was gravity eluted through preconditioned (with dichloromethane [DCM], hexane, and methanol) silica cartridges and collected in a new 10 mL glass tube (tube 8). Tube 8 was evaporated under nitrogen to ~200 µL, and isooctane was added and then blown down to ~200 µL. Each extract was spiked with 20 µl of mass-labelled PCB-138 normalization standard (4000 ng/ml) to test for instrument variation. Tube 8 was vortexed and transferred to a 2 mL GC vial with glass insert. Vials were capped tightly and stored in a -20 ºC freezer or run immediately on the GC-MS.

3.4.3. Method Validation

The optimized method was validated using criteria outlined by SANTE guidelines (SANTE/11312/202) for analytical method validation, where acceptable accuracy ranges from 70-120% and acceptable precision (calculated as relative standard deviation; RSD) is less than 20%. The linearity and working range of the method were evaluated by building a calibration curve for each compound at five different concentrations using calibration standards (n = 3 at

each concentration). The method limit of detection (MLoD) was set to 3 × the signal-to-noise ratio, and method limit of quantification (MLoQ) was set to 10 × the signal-to-noise ratio for each compound. Matrix blanks spiked with internal and external standards (n = 5) were used to assess internal and external standard recoveries prior to further validation experiments. Accuracy was determined by measuring PCB and OC pesticide concentrations in NIST SRM 1945 organics in whale blubber (n = 5) using the optimized method (Certificate of Analysis, 1945; Kucklick et al., 2010). Recoveries for matrix blanks spiked with external and internal standards and for samples spiked with internal standards were calculated using the peaks areas in the spiked blanks/samples divided by the peak areas in standards prepared at the same concentration as in the spiked blanks/samples. A more detailed equation used to determine compound concentrations in blanks and samples is available in supporting information section S3.4. Intraday precision was determined by calculating the percent relative standard deviation (%RSD), based on a replicate analysis (n = 5) of the SRM.

3.4.4. Method Application

The newly optimized and validated method was then further tested by applying it to determine PCB and OC concentrations in southeast Greenland killer whale (*Orcinus orca*) blubber samples (n=13), for which previously reported PCB and OC pesticide concentration data were generated using current-use methods (Pedro et al., 2017). Based on sample availability and preservation, 13 samples (seven adult females, five subadults, and one fetus) were selected for this analysis and compared on a lipid weight (lw) basis. All samples were collected opportunistically by local communities in southeast Greenland, and all other sampling

information is available in Pedro et al. (2017). One NIST 1945 SRM was included in each batch of killer whales to calculate interday precision calculations.

3.4.5. Instrument Analysis

We monitored concentrated extracts for target PCBs and OC pesticides using a GC-MS system (Agilent Technologies, GC system 7820A, MSD 5977B) by selective ion monitoring (SIM) with one run for PCBs and a separate run for OCs, both on a fused silica DB-5 capillary column (30 m length x 0.25 mm I.D., 0.25 μm film thickness; Agilent Technologies (Folsom, CA, USA), with He as the carrier gas. Agilent MassHunter Workstation Plus 11.0 was used for data acquisition and processing. GC conditions are described elsewhere (Dietz et al., 2004; Pedro et al., 2017). Instrument blanks, internal standard spikes, and calibration standards were run in the beginning of a sequence and after every 12 samples. For the killer whale batches, a SRM NIST 1945 and a method blank were extracted with each batch of 10 samples. Trace amounts of CBs 52, 95, 101, 99, 149, 151, 118, 153, 180, 138, and *p,p'*-DDE and *trans*-nonachlor (<0.67 ng/mL) were found in some blanks. However, these levels were more than ten times lower than the concentrations found in samples and thus black subtraction was not performed. All contaminant concentrations are reported on a mg/kg lipid weight basis. Due to low recoveries of the chlorobenzenes, these, but no other OCs, were recovery-corrected from mass labelled chlorobenzene internal standards.

3.4.6. Data Analysis

Statistical analysis was conducted using Microsoft Excel 2017 and R (version 3.6.3). During method application, paired *t*-tests were used to test for differences between the

killer whale results using the current-use method relative to the optimized QuEChERS method for each PCB congener and individual OC pesticide. Bland-Altman plots were also generated to evaluate agreement between the two methods for ΣPCBs, ΣDDTs, ΣCHLs, and ΣHCHs. Bland-Altman plots are commonly used to assess agreement between two quantitative methods of measurements by estimating mean differences, limits of agreement (LoA), and biases between methods (both constant and proportional) (Giavarina, 2015). Bias is determined as the mean difference of measurements between methods. Constant bias is used to estimate any systemic differences between methods, while proportional bias is used to estimate differences at varying concentrations. LoA are calculated as the mean difference ± 1.96 standard deviation of the difference. All figures were generated in Microsoft Excel 2017 or R (version 3.6.3).

3.5. RESULTS AND DISCUSSION

3.5.1. Method Development and Utility

The optimized and validated method (**Figure 3.1)** showed very high matrix removal (~99.5%) relative to the other methods tests for NIST SRM 1945 whale blubber (Figure S3.1). Although other method tests should >98% matrix removal, our method showed the cleanest extracts by full scan GC-MS analyses (Figure S3.2). However, using only one EMR-lipid cartridge and without PSA, especially with less fatty tissues, may be sufficient when using more selective instrumentation (such as GC triple quadrupole MS) but requires further testing. Using the optimized method, 0.1 g of blubber samples showed high matrix removal, whereas clean-up was somewhat less effective for samples tested at 0.3 and 0.5 g (Figure S3.3). In addition, the 0.1 g sample showed much cleaner extracts than the larger sample sizes using GC-MS in full scan mode (Figure S3.4). As such, the combination of two EMR-lipid cartridges, one Bond-Elut Jr

PSA cartridge, one HyperSep silica cartridge, and 0.075-0.10 g of starting blubber was selected as the optimized method to be used for further validation and application phases.

Our QuEChERS method is a cheaper, faster alternative method to current-use methods and highlights many principles of green analytical chemistry (Gałuszka et al., 2013; Koel, 2016). Following the goal of eliminating or reducing the use of chemical substances, our method reduced solvent use by ~393%, saving hundreds of dollars in solvent cost per batch (Figure S3.6, **Table 3.1**) relative to current-use methods (e.g., Pedro et al., 2017). The largest reduction was in DCM, decreasing its use from ~200 mL per sample to ~8.5 mL. n-Hexane use was also reduced from ~63 mL per sample to ~27 mL. Through these reductions, we also increase safety for laboratory personnel, another goal of green analytical chemistry, as DCM and hexane are carcinogenic and neurotoxic, respectively (Lanska, 1999; Liu et al., 2013). Shorter extraction times (decreased from ~16 to ~12 hrs from our method, as well as avoiding overnight runs of GPC instrumentation) reduces exposures to these chemicals, lowers labor costs, and allows for more potentially sampling processing. As such, our optimized QuEChERs method enables PCB and OC contaminant analyses to be completed in shorter time frames with use of less chemical solvents, thus supporting the principles of green analytical chemistry.

Table 3.1: Summary of QuEChERS method verses current-use methods.

	QuEChERS	**Current-Use (Pedro et al. 2017)**
Extraction time per 12 samples	~12 hours	~16 hours
Solvent use (mL per sample)	53.6	264.3
Specialized Extraction Instrumentation	Cyrohomogenizer	Accelerated Solvent Extraction (ASE)
	SPE manifold	Gel Permeation Chromatography (GPC)
	N-evaporator	SPE manifold
		N-evaporator
Accuracy in SRM (% recovery, range)	ΣPCB: 86% (59-87)	ΣPCB: 80% (46-99)
	ΣOC: 84% (61-92)	ΣOC: 73% (50-98)

3.5.2. Method Validation

3.5.2.1. Linearity and Working Range

All calibration curves were linear with a coefficient of determination (r^2) ranging from 0.995-0.999 and 0.986-0.999 for PCBs and OCs, respectively (Table S3.1). Concentration ranges spanned by the calibration curves were similar to previous studies (McKinney et al., 2009; Pedro et al., 2017), and these ranges fully encompassed the analyte concentrations (in ng/g wet weight) found in SRM 1945 and the southeast Greenland killer whale samples that were investigated.

3.5.2.2. Limits of Detection and Quantification

The MLoDs ranged from 0.1-4.5 and 0.2-3.9 ng/g for PCBs and OCs, respectively, while MLoQs ranged from 0.4-12.3 and 0.5-12.9 ng/g for PCBs and OCs, respectively (Table S3.2). Method blanks were below the detection limit for most PCBs and OCs. All concentrations for PCBs and OCs in SRM NIST 1945 and in the killer whale batches used for method validation and application were above the MLoDs and MLoQs, with the exception of 1,2,3,5-tetrachlorobenzene concentrations in four killer whale samples, which were below the MLoQ for this compound and were excluded from further analyses.

3.5.2.3. External and Internal Standard Recoveries in Spiked Matrix Blanks

Recoveries of matrix blank external standard-spiked samples ranged from 61%-94% for PCBs and 70%-94% for most OC pesticides (n=5, Table S3.3, Figure S3.7 and S3.8). The mean recoveries of the chlorobenzenes were lower, ranging from 67 to 77%. Lower chlorobenzene recoveries are likely due to volatility-related losses during extraction, particularly concentration steps, and are consistent with previous studies (Pedro et al., 2017). For this reason, and as is

typically done (Vorkamp et al., 2004; McKinney et al., 2011), chlorobenzene concentrations were recovery-corrected using the mass-labelled chlorobenzene internal standards. Internal standard recoveries spiked to the SRM NIST 1945 ranged from 62%-97% for mass-labeled PCBs and 66%-76% for mass-labeled chlorobenzenes (Table S3.4).

From SANTE/11312/2021 guidelines (>70% recovery, <20% RSD), external standard recoveries for spiked matrix blanks were acceptable for 87% of PCBs and 90% of OCs. Similar to the chlorobenzenes, somewhat lower PCB-17, 18, and 33 recoveries are likely volatility-related; however, we did not have a surrogate standard to recovery correct. Somewhat lower recoveries of high molecular weight, high octanol-water partitioning coefficient PCBs, such as 194, 206, 209 ($\log K_{ow}$ from 7.56-8.18) and mirex ($\log K_{ow}$ ~6.89) were also apparent in the spiked matrix blanks. Other studies (He et al., 2017; Zhao et al., 2019) in edible oils found similar difficulty in recovering these compounds, most likely due to analyte partitioning to the lipid pellet during the initial QuEChERS extraction, retention in the EMR-lipid cartridge due to size exclusion, or solubility issues from the addition of 20% water. Increasing the solvent: sample ratio (i.e., using more 20:80 ethyl acetate acetonitrile and/or less starting blubber) or decreasing the water added to the extraction solvent (e.g. from 20% to 10%) has been shown to significantly increase the recovery of these hydrophobic analytes (Chamkasem and Harmon, 2015; He et al., 2017), and is an approach that could be employed if these are key analytes for a particular sample type. In addition, using matching mass-labelled internal standards can allow for recovery correction for research groups particularly interested in these compounds.

3.5.2.4 Accuracy and Precision using NIST 1945 Standard Reference Material

During method validation, we characterized analytical accuracy and precision using NIST 1945 extracted using the optimized modified QuEChERS method. Accuracy ranged from 65%-97% for individual PCB congeners (except for PCB 206 and 209, which were lower) and from 60%-92% for individual OCs, with overall mean accuracies of 86% for ΣPCBs, 82% for ΣDDTs, and 82% for ΣCHLs (**Table 3.2**). In total, we determined acceptable accuracies (>70%) for 76% and 77% of individual PCBs and OC pesticides, respectively. With the exception of PCB-206 and 209, all other PCBs still showed accuracies of > 65%. Although PCB 206 and 209 concentrations were also somewhat low in the external standard recovery experiments, high retention in the lipid pellet following QuEChERS extractions may explain even lower accuracies in the presence of the blubber matrix. Incorporating additional solvent rinses and increasing the solvent:sample ratios may increase recoveries of these compounds (Chamkasem and Harmon, 2015; He et al., 2017). Matrix effects around the retention times (Figure S3.2 and S3.3) of PCB 206 and 209 may also have led to some ion suppression of these analytes. Similarly, although hexachlorobenzene, dieldrin, and mirex showed accuracies outside acceptable ranges, they were still above 60%. For precision, values averaged 19% (ranging from 12%-36% RSD) for PCBs and 19% (ranging from 13%-34% RSD) for OCs. The mean precision was 15% for ΣPCBs, 15% for ΣDDTs, and 9% for ΣCHLs (**Table 3.2**). In total, we determined acceptable precision (<20% RSD) for 73% and 69% of individual PCBs and OC pesticides, respectively, with precisions generally not exceeding 30%. Based on both acceptable accuracy and precision, we can validate our QuEChERS method as sufficient in analyzing 16 PCBs and 9 OC pesticides based on SANTE/11312/2021 guidelines; however, many other PCBs and OC pesticides were close to

meeting threshold accuracy and precision cut offs. Using less strict guidelines at 60% recovery and <25% RSD, 23 PCBs and 11 OC pesticides (88% and 85%, respectively) are acceptable.

Table 3.2: Analytical accuracy (recovery %) and precision (RSD %) of the optimized modified QuEChERS method for analyzing polychlorinated biphenyls (PCBs) and organochlorine pesticides (OCs) in SRM NIST 1945 organics blubber (n=5) in ng/g lipid weight.

Chemical Class/Compound	Certified Value	Measured Concentration (means + SD)	Accuracy (% recovery, range in brackets)	Precision (mean % RSD)
PCBs[1]				
PCB-18	**6.1 ± 0.8**	**4.3 ± 1.0**	**71 (59-95)**	**20**
PCB-52	**57.2 ± 1.8**	**54.0 ± 19.0**	**95 (49-88)**	**13**
PCB-44	**17.0 ± 0.7**	**15.4 ± 4.4**	**91 (64-90)**	**16**
PCB-70	**15.5 ± 1.5**	**11.6 ± 2.7**	**76 (50-94)**	**19**
PCB-95	**47.7 ± 0.7**	**49.2 ± 12.2**	**97 (51-97)**	**19**
PCB-101	**109.7 ±16.7**	**98.0 ± 24.6**	**89 (60-96)**	**19**
PCB-99	82.3 ± 7.3	59.4 ± 19.1	72 (53-94)	23
PCB-87	**29.0 ± 3.6**	**31.5 ± 7.3**	**91 (46-99)**	**19**
PCB-110	**46.6 ± 3.2**	**41.6 ± 9.9**	**89 (60-94)**	**18**
PCB-151	**40.2 ± 1.8**	**30.8 ± 7.5**	**77 (49-90)**	**20**
PCB-149	**125.2 ± 9.6**	**98.8 ± 22.0**	**79 (53-90)**	**20**
PCB-118	**107.6 ± 4.0**	**110.9 ± 28.0**	**97 (52-94)**	**14**
PCB-153	**320.7 ± 13.9**	**228.4 ± 61.8**	**71 (52-98)**	**14**
PCB-105	**40.2 ± 1.7**	**44.2 ± 7.8**	**90 (64-95)**	**19**
PCB-138	**205.3 ± 18.1**	**192.6 ± 43.2**	**94 (64-98)**	**19**
PCB-158	12.8 ± 1.4	8.8 ± 2.2	69 (47-98)	19
PCB-187	**170.2 ± 15.3**	**118.3 ± 25.9**	**70 (48-96)**	**19**
PCB-183	53.4 ± 2.5	34.7 ± 8.6	65 (46-85)	25
PCB-128	32.3 ± 1.5	21.9 ± 4.7	68 (49-92)	17
PCB-156	16.0 ± 1.3	14.2 ± 2.8	89 (61-99)	21
PCB-180	194.1 ± 13.9	149.3 ± 25.8	77 (56-92)	22
PCB-170	59.9 ± 3.1	41.0 ± 8.8	69 (47-93)	19
PCB-195	20.1 ± 3.1	14.1 ± 6.0	70 (43-93)	36
PCB-194	**75.2 ± 7.2**	**89.5 ± 17.3**	**81 (69-97)**	**12**
PCB-206	63.2 ± 5.8	33.6 ± 11.8	53 (35-83)	29
PCB-209	24.2 ± 2.6	3.6 ± 1.2	15 (9-21.0)	28
ΣPCBs	**1947.6 ± 73.6**	**1682 ± 358.1**	**86 (59-87)**	**15**
OCs[1]				
Hexachlorobenzene	43.0 ± 2.1	26.5 ± 4.0	62 (45-96)	34
α-HCH	**23.8 ± 1.9**	**21.0 ± 2.0**	**88 (59-92)**	**17**
Heptachlor epoxide	**15.0 ± 0.01**	**13.6 ± 1.6**	**90 (62-93)**	**15**
cis-Chlordane	**67.7 ± 2.2**	**62.3 ± 6.0**	**92 (67-94)**	**13**
trans-Chlordane	**16.6 ± 0.7**	**13.3 ± 1.7**	**80 (54-83)**	**16**
Oxychlordane	**29.8 ± 1.5**	**24.7 ± 2.7**	**83 (42-86)**	**15**
cis-Nonachlor	64.4 ± 4.6	54.2 ± 8.7	84 (51-86)	25
trans-Nonachlor	**278.5 ± 22.2**	**222.5 ± 20.8**	**80 (70-91)**	**11**
***p,p′*-DDT**	**327.7 ± 11.1**	**253.7 ± 33.5**	**77 (51-86)**	**17**
***p,p′*-DDD**	**168.8 ± 1.7**	**144.4 ± 18.7**	**86 (57-87)**	**15**
***p,p′*-DDE**	**699.0 ± 26.4**	**587.6 ± 73.2**	**84 (57-86)**	**15**
Dieldrin	70.5 ± 5.7	100.6 ± 9.2	60 (36-68)	23
Mirex	43.6 ± 4.7	28.0 ± 3.4	64 (44-92)	27
ΣDDTs	**1195.5 ± 39.2**	**985.8 ± 125.3**	**83 (55-83)**	**14**
ΣCHLs	**457.0 ± 31.3**	**377.0 ± 38.0**	**83 (66-86)**	**9**

[1]Bolded values indicate values meeting acceptance criteria for accuracy and precision from SANTE/11312/2021.

3.5.3. Method Application

Mean ΣPCB concentrations across all killer whale samples using the modified QuEChERS method were 45.3 (± 8.6) mg/kg lw and were not significantly different from concentrations reported from the current-use method (**Figure 3.2A**, Table S3.5; Pedro et al., 2017). Comparisons across age class and sex showed similar results and are available in Figure S3.9. A more detailed comparison of PCBs according to degree of chlorination also showed no differences between the two methods for concentrations of tetra- through deca-chlorinated PCBs (Table S3.6), with the exception of ΣtriPCB concentrations, which were significantly higher using the QuEChERS method (*p=0.02*, **Figure 3.2B**). Of the two tri-chlorinated PCBs compared, only PCB-28/32 was significantly different (*p=0.001*, Table S3.5) and was likely volatility-related. That is, current-use methods require evaporation to concentrate extracts after ASE or (Soxhlet extraction) of ~50 mL of solvent per sample and after GPC of ~100 mL per sample; these large evaporation steps are absent from the QuEChERS method, and as a result, less loss of the more volatile PCBs, such as PCB-28/32, may occur through evaporation during the QuEChERS extraction. Lower volatility-related losses have also been reported in previous QuEChERS studies relative to standard approaches (Pinto et al., 2010; Rouvière et al., 2012).

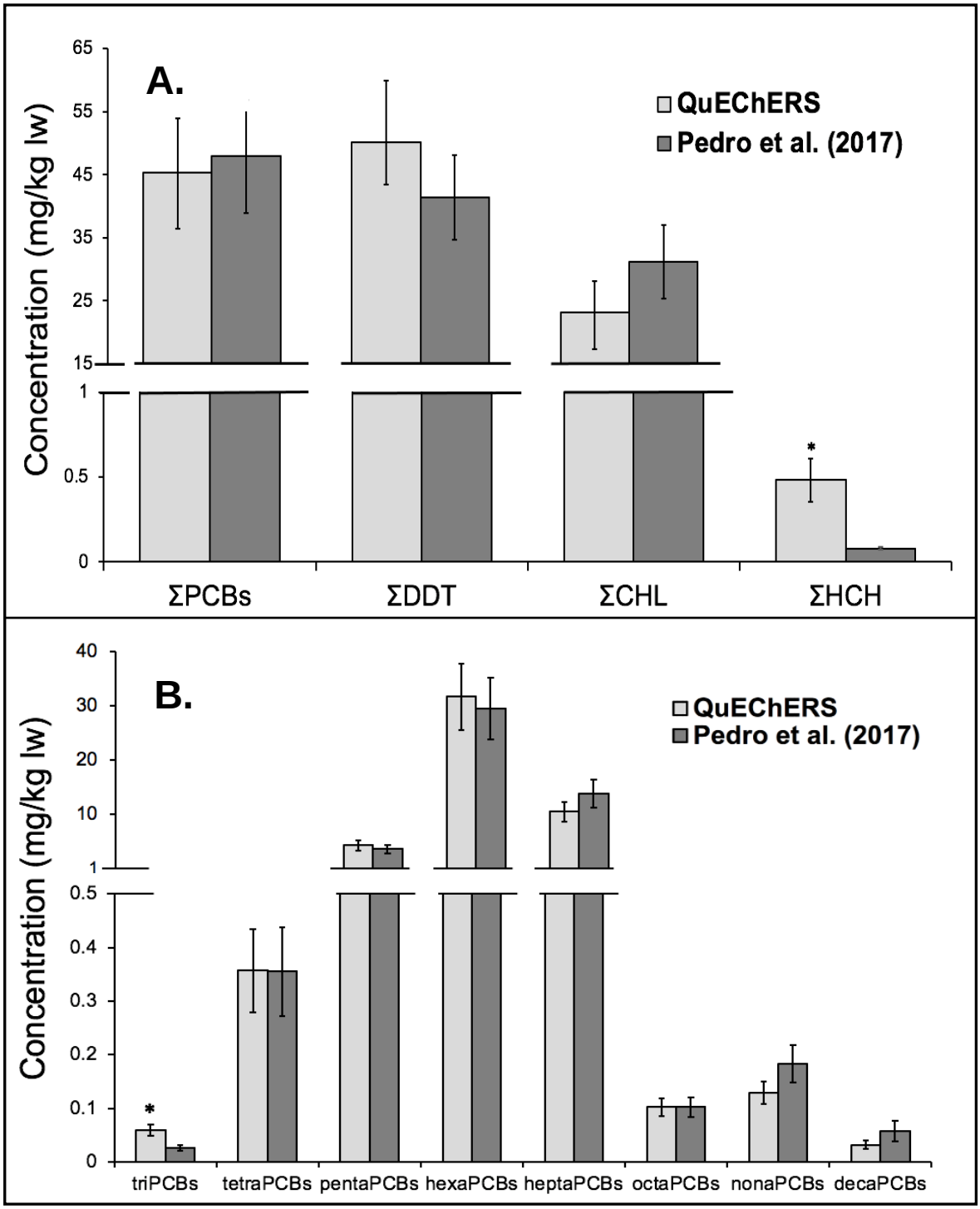


Figure 3.2: Mean concentrations (±standard error) in mg/kg lipid weight across all killer whale (Orcinus orca) samples extracted using QuEChERS (light gray) and current-use (dark gray; Pedro et al. 2017) methods for polychlorinated biphenyls (PCBs) based on (A) mean concentrations for ΣPCBs, Σhexachlorocyclohexanes (ΣHCHs), Σchlordanes (ΣCHLs), and Σdichlorodiphenyltrichloroethanes (ΣDDTs), and (B) degree of chlorination of PCBs. Asterisks (*) represent statistical differences ($p<0.05$) from paired t-tests between methods.

For OCs, mean ΣDDT, ΣCHL, and ΣHCH concentrations across all killer whale samples were 50.2 (± 9.8), 23.2 (± 4.9), and 0.47 (± 0.13) mg/kg lw, respectively (**Figure 3.2A**, Table S3.5). Relative to current-use methods (Pedro et al., 2017), ΣDDTs and ΣCHLs were not significantly different; however, ΣHCH concentrations from the QuEChERS extraction were significantly higher (*p=0.002*, **Figure 3.2A**). Of the two HCHs compared, only β-HCH was significantly different (*p=0.002*, Table S3.5), and similarly to PCB-28/32, may be volatility-related. β-HCH has been tested through similar QuEChERS extractions with EMR-lipid clean-up with acceptable recoveries (Sanchez Costa et al., 2018) and our external standard mean recovery was acceptable (79.7%; Table S3.3). Remili et al. (2021) also reported β-HCH in Icelandic marine mammal-feeding killer whales that likely fed on marine mammals and showed mean concentrations of 0.12 mg/kg, about three times higher than mean values found in Pedro et al. (2017), but still less than our reported 0.44 mg/kg value. Unfortunately, certified β-HCH concentrations are not available in SRM NIST 1945 so testing for accuracy of this compound remains difficult; therefore, further examination of β-HCH across extraction methods and among laboratories is warranted, and perhaps with the addition of a mass-labelled β-HCH standard.

To test in detail for any systemic differences in results between the two methods, Bland-Altman analyses were used (**Figure 3.3**). For ΣPCB concentrations, there was no significant constant bias (intercept of -0.70 mg/kg lw; 95% CI: -8.5 to 7.1) or proportional bias (slope was -0.02; 95% CI: -1.7 to 1.5), and only one sample was outside of the LoA. Similarly, ΣDDTs showed no significant constant bias (intercept of 8.8 mg/kg lw; 95% CI: -0.49 to 18.0) or proportional bias (slope was -0.004; 95% CI: -0.14 to 0.62), with just one sample outside the LoA. There was significant constant bias for ΣCHLs (intercept of -8.2 mg/kg lw; 95% CI: -1.5 to -15.8), but no significant proportional bias (slope was -0.17; 95% CI: -43 to 0.101), and all

samples were inside the LoA. For ΣHCHs, no significant constant bias (intercept of 0.4 mg/kg lw; 95% CI: 0.13 to 0.68) was present, but there was significant proportional bias (slope was 1.9; 95% CI: -0.06 to -0.33), although only one sample was outside the LoA.

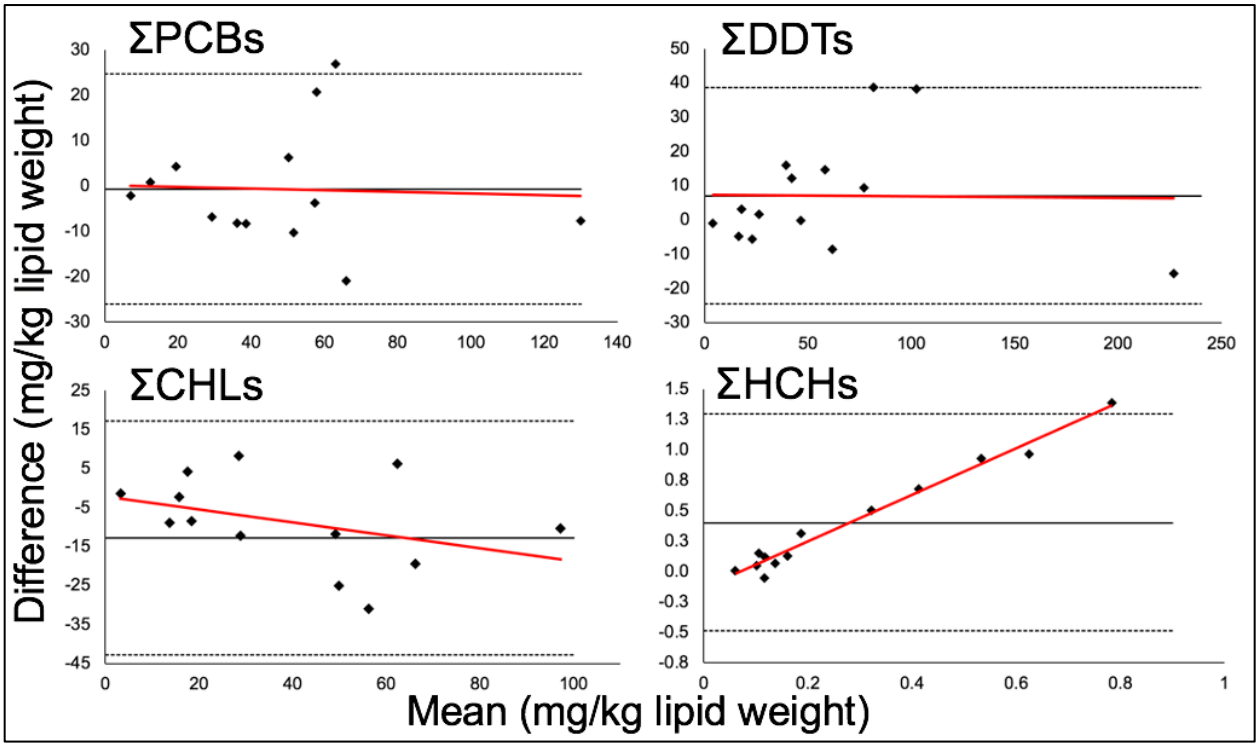


Figure 3.3: Bland-Altman plots of differences (y-axis) between QuEChERS and current-use extraction methods for polychlorinated biphenyl (ΣPCBs), Σhexachlorocyclohexanes (ΣHCHs), Σchlordanes (ΣCHLs), and Σdichlorodiphenyltrichloroethanes (ΣDDTs) concentrations in mg/kg lipid weight using killer whale (Orcinus orca) samples analyzed using both approaches. The solid black line (in the middle of each pane) indicates the bias, while the dashed line (from the top to the bottom of each pane) represents the upper limits of agreement and lower limits of agreement. The solid red line represents the proportional bias trend line.

The results from Bland-Atlman plots demonstrate good agreement between methods for most PCBs and OC pesticides. Given no significant differences in concentrations between methods and no significant constant or proportional biases for ΣPCBs and ΣDDTs, our modified QuEChERS method is suitable to monitor these groups of contaminants. For ΣCHLs, constant bias in this group is most likely due to significantly lower concentrations of heptachlor epoxide

relative to data from the current use method (*p=0.02*, Table S3.5; Pedro et al., 2017); nonetheless, there was no significant differences based on *t*-tests for ΣCHLs or for most individual CHL compounds. In addition, external standard recoveries and concentrations in NIST 1945 of heptachlor epoxide were acceptable (**Table 3.2**, Table S3.3), and this compound has also been tested in similar QuEChERS methods with EMR-lipid clean-up (Cui et al., 2020). Therefore, our heptachlor epoxide results are likely acceptable. For HCHs, significant proportional bias is likely due to significantly higher concentrations of β-HCHs, especially at high concentrations. Similar to heptachlor epoxide, all other quality control data (e.g., recovery of spiked matrix blanks) were acceptable, suggesting that β-HCH concentrations as measured by this modified QuEChERs method may also be acceptable. However, unlike heptachlor epoxide, β-HCH concentrations are not available for NIST 1945, therefore further checks of the accuracy of β-HCH concentrations in blubber using this modified QuEChERS method may be required.

3.6. CONCLUSION

This study presents a simple, robust, and cost-effective alternative for the analysis an extensive suite of PCB and OC pesticides in complex, lipid-rich matrices. This modified QuEChERS method produced sufficiently clean extracts yielding accurate and precise results for marine mammal blubber using NIST 1945 as a reference material. Our study also shows relatively good agreement between current-use methods and our QuEChERS method using killer whale samples with known PCB and OC pesticide concentrations. Our method helps to overcome the high costs of current-use methods, while enabling contaminant analyses to be done in short time frames and using less toxic solvent, thus supporting the principles of green analytical chemistry. Moving forward, this method can be applied to more blubber and adipose

tissues to better understand the benefits and limitations from adopting this method for more routine legacy contaminant analyses by marine mammal monitoring programs.

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3.9. SUPPORTING INFORMATION

S3.1. Supplemental details on the development of the method – clean-up testing and matrix removal

We compared the matrix removal of 0.1 grams of SRM NIST 1945 organics in whale blubber between seven different combinations of both dSPE and SPE clean-up methods following QuEChERS liquid-liquid extractions: 1) one EMR-lipid cartridge, 2) two EMR-lipid cartridges, 3) two EMR-lipid cartridges and one Bond-Elut Jr PSA cartridge, 4) two EMR-lipid cartridges and one HyperSep silica cartridge, 5) one EMR-lipid cartridge, one Bond-Elut Jr PSA cartridge, and one HyperSep silica cartridge, 6) two EMR-lipid cartridges, one Bond-Elut Jr PSA cartridge, and one HyperSep silica cartridge, and 7) one dSPE Bond-Elut EMR-lipid and one HyperSep silica cartridge. The combination of two EMR-lipid cartridges, one Bond-Elut Jr PSA cartridge, and one HyperSep silica cartridge provided the highest average matrix removal (99.5%) from a duplicate analysis (**Figure S3.1)** and cleanest extracts by GC-MS (**Figure S3.2**). Matrix removal was assessed gravimetrically, i.e., by blowing concentrated extracts in GC vials to dryness, weighing on an analytical balance, and then using the follow equation:

$$\%\ matrix\ removed = 100 - \frac{grams\ remaining\ in\ GC\ vial}{grams\ of\ starting\ material} \times\ 100$$

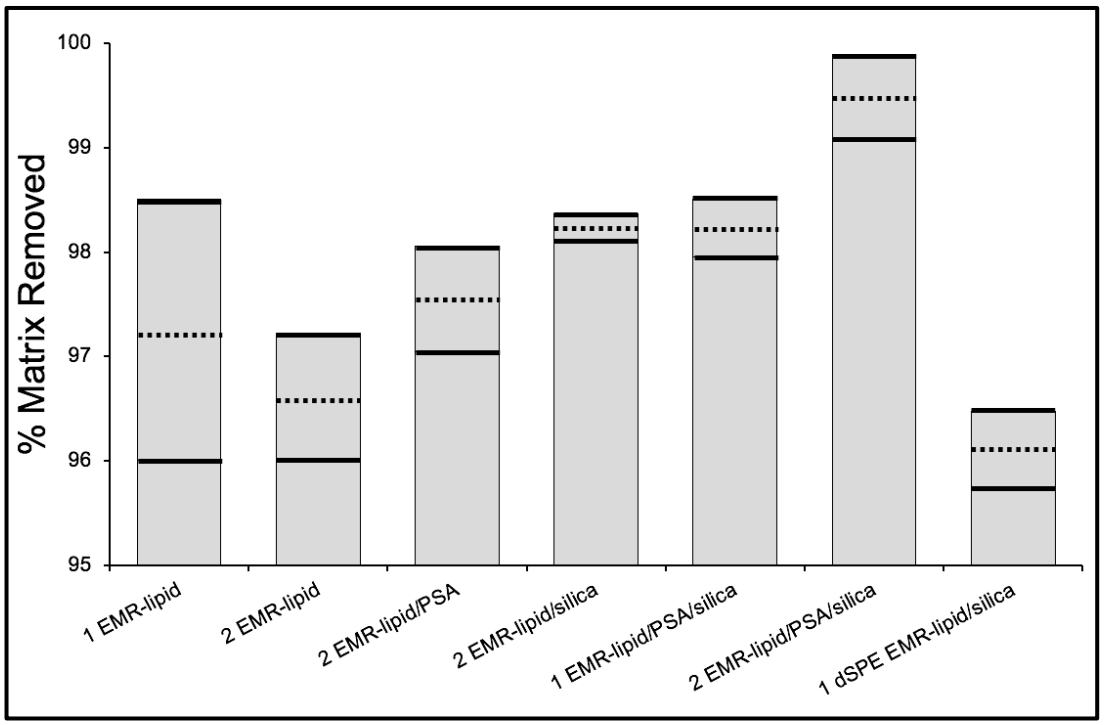

Figure S3.1: Percent matrix removal determined gravimetrically for different combinations of dispersive solid phase extraction (dSPE) and SPE clean-up methods following QuEChERS liquid-liquid extractions from duplicates of SRM NIST 1945 organics in whale blubber. Bolded lines in bars represent the upper and lower ranges of matrix removal, while dashed lines represent their means

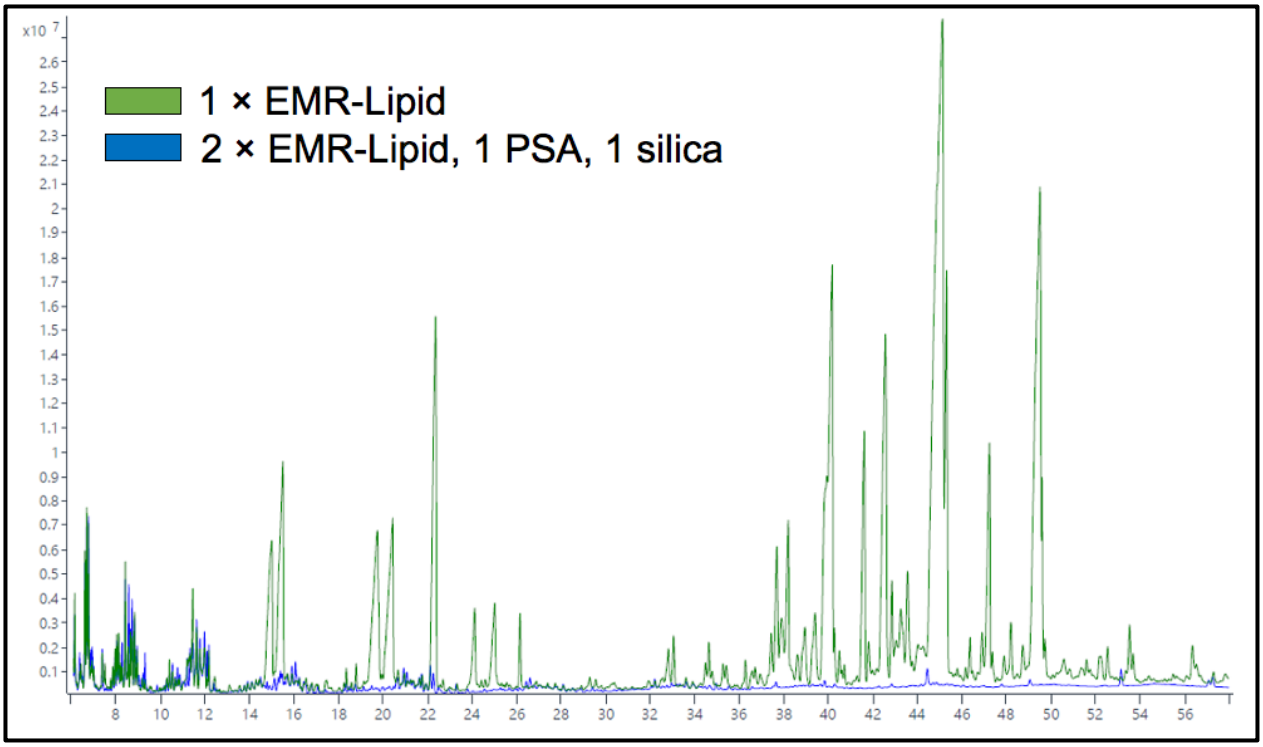

Figure S3.2: Chromatogram in full scan mode (polychlorinated biphenyl method) from GC-MS analysis of extracts using two combinations of clean-up steps: one EMR-lipid cartridge (green) and two EMR-lipid cartridges, one Bond-Elut Jr PSA cartridge, and one HyperSep silica cartridge (blue).

S3.2. Supplemental details on the development of the method – starting material mass testing

We compared the matrix removal gravimetrically (see S2) of SRM NIST 1945 organics in whale blubber using 3 different starting masses: 0.1, 0.3, and 0.5 g. The optimized method from S1 was used (two EMR-lipid cartridges, one Bond-Elut Jr PSA cartridge, and one HyperSep silica cartridge) following QuEChERS liquid-liquid extraction. A mass of 0.1 g of starting material provided the highest average matrix removal (99.5%) from a duplicate analysis (**Figure S3.3)** and cleanest extracts from GC-MS (**Figure S3.4**).

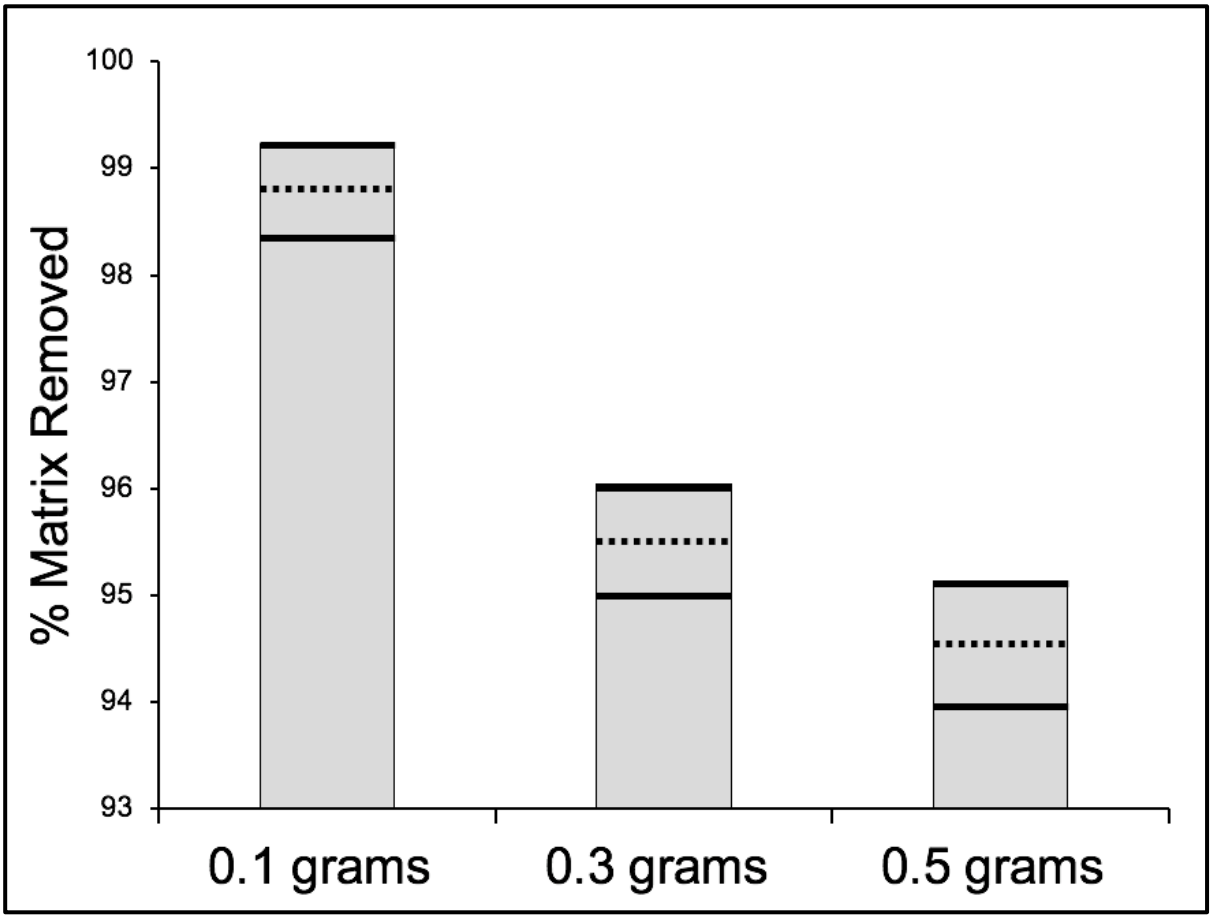

Figure S3.3: Percent matrix removal assessed gravimetrically using 3 different starting weights of 0.1, 0.3, and 0.5 g following QuEChERS liquid-liquid extractions from a duplicate analysis of SRM NIST 1945. Bolded lines in bars represent the upper and lower ranges of matrix removal, while dashed lines represent their means.

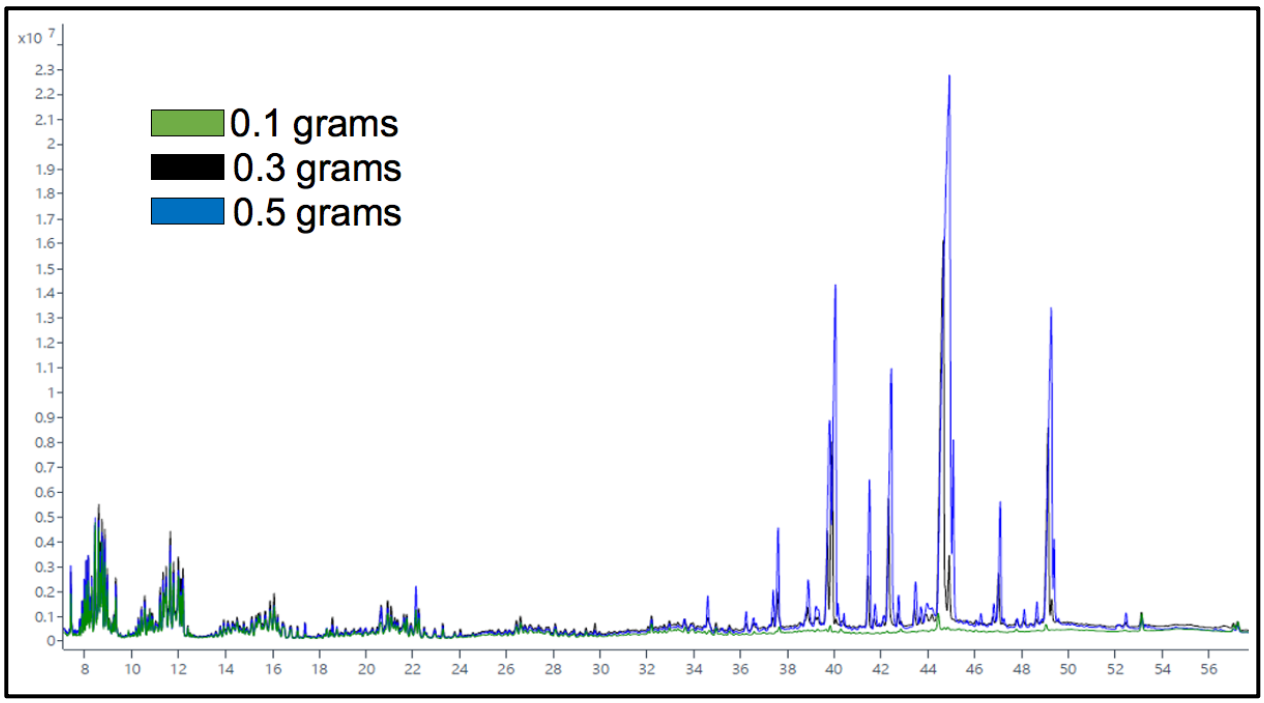

Figure S3.4: Chromatograms in full scan mode (polychlorinated biphenyl method) from GC-MS analysis using 3 starting material masses: 0.1 grams (green), 0.3 grams (black), and 0.5 grams (blue).

S3.3. Supplemental details on the in-depth optimized method

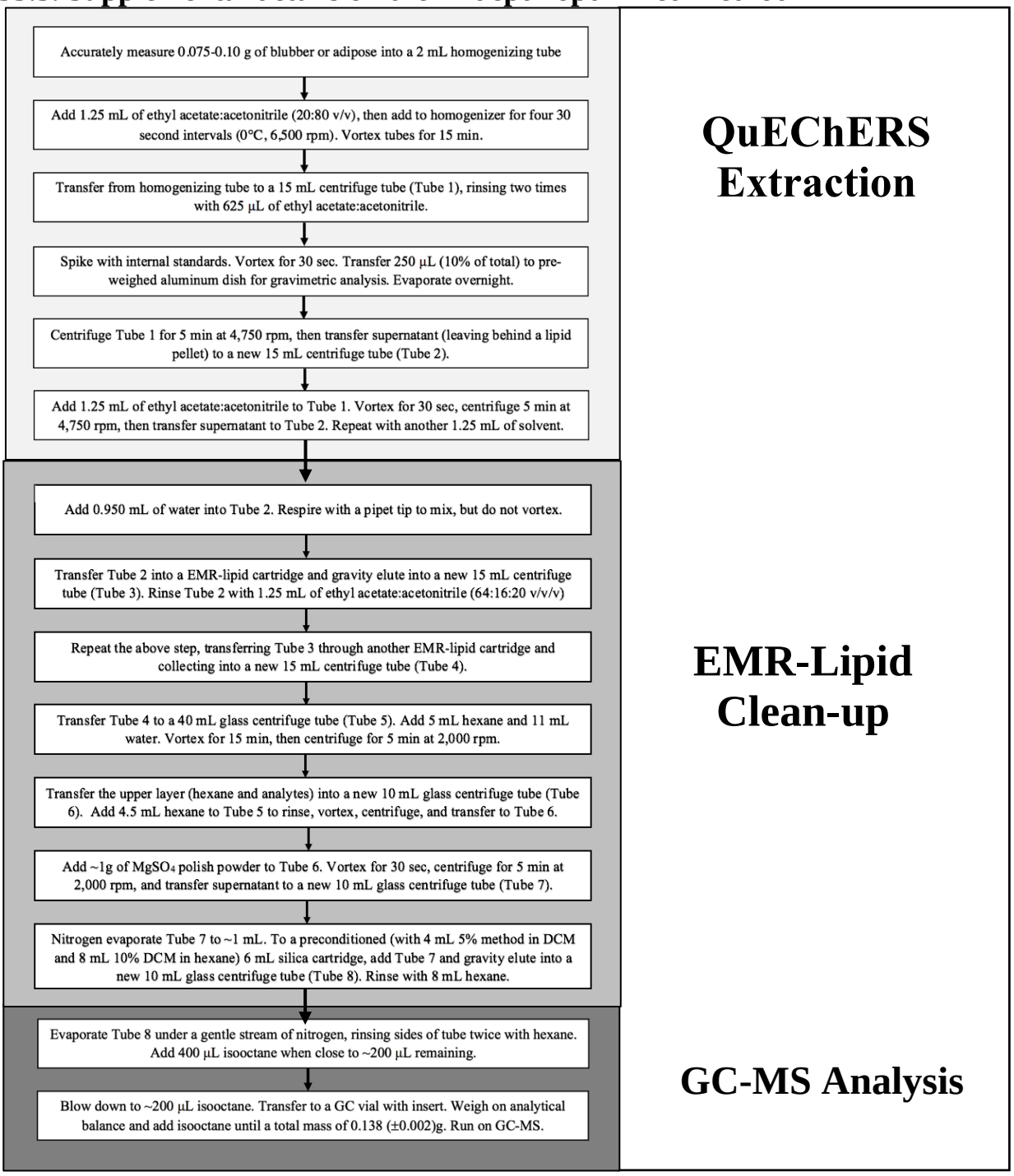

Figure S3.5: Detailed breakdown of the optimized QuEChERS method for extracting polychlorinated biphenyls (PCBs) and organochlorine (OC) pesticides from marine mammal blubber

S3.4. Supplemental details on the calculation of PCB and OC pesticide analyte concentration

A Microsoft Excel spreadsheet is used to calculate analyte concentrations as follows:

$$C_s = [(A_s/A_{std}) \times C_{std}] \times [(V_{Sf}/W_s)] \times 10^{-3} \ (or\ 10^{-6})$$

where C_s = analyte concentration in the sample in μg/g (wet weight): A_s = area counts of analyte (PCB or OC) in the sample; A_{std} = area counts of analyte in the injected standard; C_{std} = analyte concentration in the standard solution in pg/μL: V_{Sf} = final volume of the sample, in μL; W_S = sample weight in g (wet weight); 10^{-3} to convert to ng/g or 10^{-6} to convert to mg/kg

S3.5. Supplemental details on cost analysis

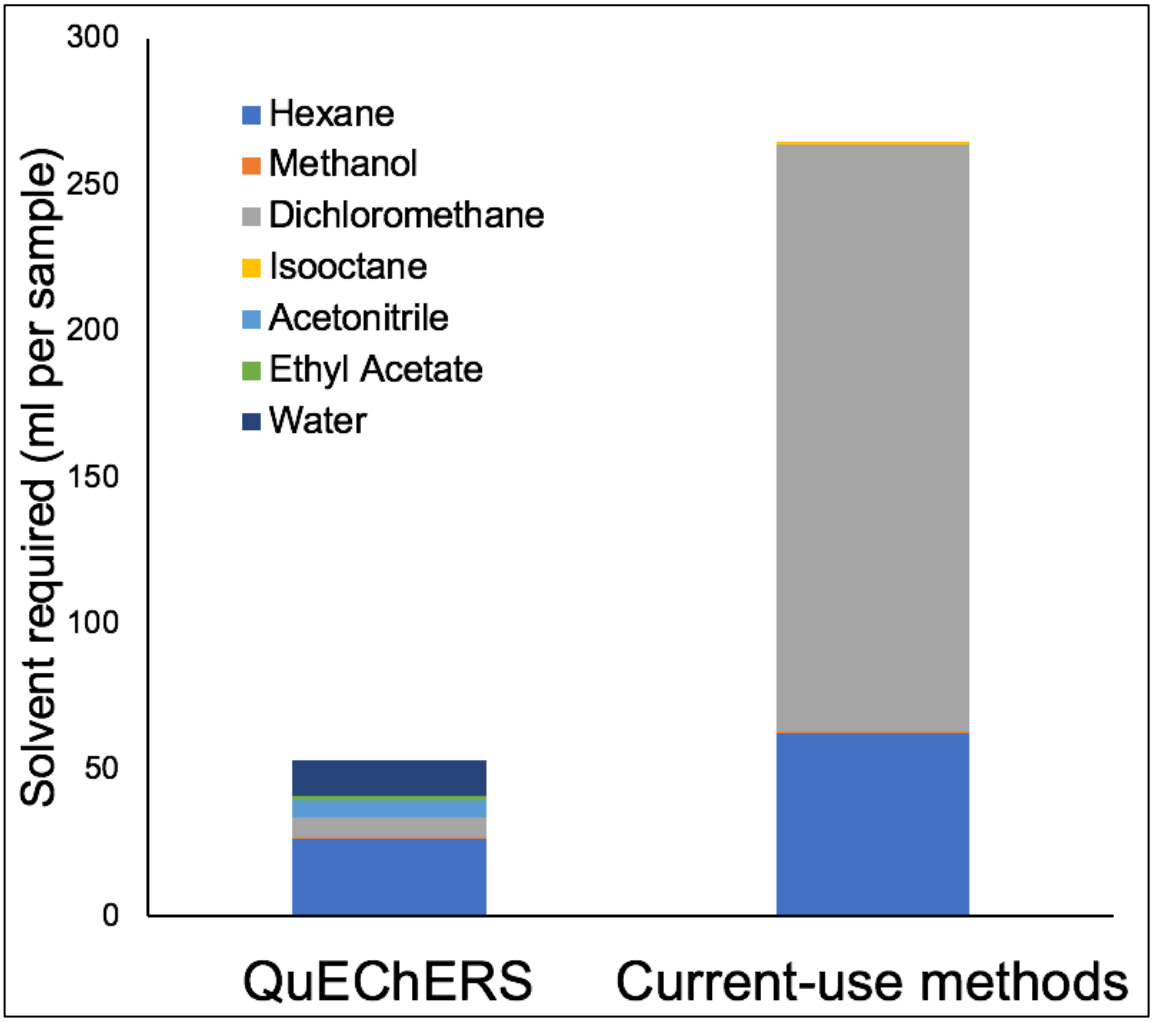

Figure S3.6: Volume (in mL) of solvent used per one sample based on the optimized QuEChERS methods as compared to current-use methods detailed in Pedro et al. (2017)

S3.6. Supplemental details on the development of the method – linearity

Table S3.1: Nominal calibration standard (CS) concentration in ng/mL used to create calibration curves for each polychlorinated biphenyl (PCB) and organochlorine (OC) pesticide. r^2 values were determined by a linear regression.

Chemical Class/Compound	CS1	CS2	CS3	CS4	CS5	r^2	Equation of line
Organochlorines							
1,2,4,5-Tetrachlorobenzene	1000	500	300	100	30	0.997	y = 612.629x – 2801.282
1,2,3,4-Tetrachlorobenzene	1000	500	300	100	30	0.997	y = 449.212x – 3826.694
Pentachlorobenzene	1000	500	300	100	30	0.996	y = 406.278x – 2384.675
Hexachlorobenzene	1000	500	300	100	30	0.996	y = 348.693x – 2073.934
α-Hexachlorocyclohexane	1000	500	300	100	30	0.996	y = 159.136x – 2808.363
β-Hexachlorocyclohexane	1000	500	300	100	30	0.994	y = 104.436x – 2351.924
Oxychlordane	3000	1500	900	450	90	0.991	y = 116.045x – 12884.522
trans-Chlordane	2000	1000	600	300	60	0.993	y = 158.847x – 10909.271
cis-Chlordane	2000	1000	600	300	60	0.991	y = 142.453x – 28523.455
trans-Nonachlor	2000	1000	600	300	60	0.994	y = 168.618x – 11143.718
cis-Nonachlor	1000	500	300	100	30	0.993	y = 75.733x – 6492.273
p,p'-DDE	3000	1500	900	450	90	0.992	y = 368.449x – 32634.909
p,p'-DDD	3000	1500	900	450	90	0.990	y = 561.162x – 98012.458
p,p'-DDT	3000	1500	900	450	90	0.994	y = 364.530x – 88624.322
Mirex	1000	500	300	100	30	0.995	y = 269.504x – 7949.189
Heptachlor Epoxide	1000	500	300	100	30	0.989	y = 122.585x – 4222.372
Dieldrin	2000	1000	600	300	60	0.991	y = 124.631x – 5621.562
Methoxychlor	1000	500	300	100	30	0.983	y = 3621.121x – 3204.136
Endosulfan II	1000	500	300	100	30	0.986	y = 1080.421x – 83275.52
Polychlorinated Biphenyls							
PCB-17	375	150	60	15	1.5	0.997	y = 269.239x – 156.716
PCB-18	1500	600	240	60	6	0.998	y = 268.959x – 230.339
PCB-28	1500	600	240	60	6	0.999	y = 388.417x – 545.421
PCB-31	1125	450	180	45	4.5	0.998	y = 419.431x – 2325.579
PCB-33	1500	600	240	60	6	0.999	y = 269.239x – 156.716
PCB-44	1500	600	240	60	6	0.999	y = 400.125x – 3534.132
PCB-49	1500	600	240	60	6	0.999	y = 241.025x – 3191.188
PCB-52	1500	600	240	60	6	0.999	y = 285.542x – 3385.275
PCB-70	1500	600	240	60	6	0.999	y = 388.754x – 5909.007
PCB-74	1500	600	240	60	6	0.999	y = 389.239x – 6489.975
PCB-82	375	150	60	15	1.5	0.998	y = 184.814x – 1019.980
PCB-87	1500	600	240	60	6	0.999	y = 227.622x – 4482.170
PCB-95	725	290	116	29	2.9	0.999	y = 237.648x – 1595.394
PCB-99	1500	600	240	60	6	0.999	y = 274.825x – 4870.950
PCB-101	1500	600	240	60	6	0.999	y = 253.293x – 4501.950
PCB-105	375	150	60	15	1.5	0.997	y = 357.759x – 2382.759
PCB-110	1500	600	240	60	6	0.999	y = 320.666x – 6216.693
PCB-118	1500	600	240	60	6	0.998	y = 351.617x – 8045.382
PCB-128	1500	600	240	60	6	0.998	y = 267.368x – 7734.242
PCB-138	1500	600	240	60	6	0.995	y = 170.749x – 4731.113
PCB-149	1500	600	240	60	6	0.998	y = 189.198x – 3917.044
PCB-151	1500	600	240	60	6	0.999	y = 188.694x – 3316.913
PCB-153	1500	600	240	60	6	0.998	y = 226.779x – 5245.251

PCB-156	1500	600	240	60	6	0.995	y = 241.592x – 10159.823
PCB-158	375	150	60	15	1.5	0.998	y = 265.383x – 1874.749
PCB-169	1500	600	240	60	6	0.997	y = 201.491x – 5703.982
PCB-171	1500	600	240	60	6	0.997	y = 190.207x – 6212.427
PCB-177	1500	600	240	60	6	0.998	y = 151.527x – 4465.817
PCB-180	1500	600	240	60	6	0.996	y = 138.250x – 4932.105
PCB-183	1500	600	240	60	6	0.997	y = 132.776x – 3720.619
PCB-187	1500	600	240	60	6	0.998	y = 159.548x – 4020.346
PCB-191	1500	600	240	60	6	0.997	y = 148.553x – 3975.569
PCB-194	1500	600	240	60	6	0.998	y = 142.658x – 4435.666
PCB-195	1500	600	240	60	6	0.995	y = 112.175x – 4570.508
PCB-199	1125	450	180	45	4.5	0.995	y = 118.886x – 3654.968
PCB-205	1500	600	240	60	6	0.998	y = 83.456x – 2430.701
PCB-208	1500	600	240	60	6	0.996	y = 121.781x – 3988.373
PCB-209	1500	600	240	60	6	0.997	y = 88.170x – 2934.470

S3.7. Supplemental details on the development of the method – limits of detection and quantification

Table S3.2: Method limit of detection (MLoD; 3 × the signal-to-noise ratio) and method limit of quantification (MLoQ;10 × the signal-to-noise ratio) for each polychlorinated biphenyl (PCB) congener and organochlorine (OC) pesticide in the optimized method

Chemical Class/Compound	LOD_{method} (ng/g)	LOQ_{method} (ng/g)
Organochlorines		
1,2,4,5-Tetrachlorobenzene	0.3	1.0
1,2,3,4-Tetrachlorobenzene	0.2	0.5
Pentachlorobenzene	0.3	1.0
Hexachlorobenzene	0.4	1.5
α-Hexachlorocyclohexane	0.3	1.1
β-Hexachlorocyclohexane	0.3	1.0
Oxychlordane	1.9	6.2
trans-Chlordane	0.5	1.6
cis-Chlordane	0.2	0.8
trans-Nonachlor	0.2	0.6
cis-Nonachlor	0.5	1.7
p′p-DDE	2.5	8.3
p′p-DDD	2.4	9.6
p′p-DDT	3.2	12.2
Mirex	3.9	12.9
Heptachlor Epoxide	2.2	7.3
Dieldrin	2.1	8.7
Polychlorinated Biphenyls		
PCB-17	0.2	0.8
PCB-18	0.3	0.8
PCB-31/28	0.5	1.7
PCB-33	1.8	5.8
PCB-44	0.7	2.2
PCB-49	0.5	1.6
PCB-52	0.6	1.9
PCB-70	0.8	2.7
PCB-74	0.8	2.8
PCB-82	4.5	12.3
PCB-87	0.4	1.3
PCB-95	3.4	11.3
PCB-99	0.1	0.4
PCB-101	0.3	1.0
PCB-105	0.4	1.3
PCB-110	0.3	0.8
PCB-118	3.0	10.1
PCB-128	0.8	2.5
PCB-138	0.3	1.0
PCB-149	1.1	3.7
PCB-151	1.7	5.6
PCB-153	0.1	0.4
PCB-156	0.4	1.4
PCB-158	0.3	1.0

PCB-169	1.4	4.6
PCB-170	0.5	1.8
PCB-177	0.2	0.6
PCB-180	0.2	0.5
PCB-183	0.2	0.7
PCB-187	0.3	1.0
PCB-191	3.6	12.1
PCB-194	0.7	2.4
PCB-195	0.6	2.0
PCB-199	0.6	1.9
PCB-205	0.5	1.8
PCB-206	0.6	2.0
PCB-208	0.9	3.1
PCB-209	0.5	1.7

S3.8. Supplemental details on external standard recovery

Table S3.3: Average recovery of external standards for each polychlorinated biphenyl (PCB) congener and organochlorine (OC) pesticide spiked to matrix blanks (n=5) and ran through the optimized QuEChERS method. Chlorobenzenes, but no other OCs, were internal standard recovery-corrected.

Chemical Compound	Accuracy (% recovery, min/max in brackets)	Chemical Compound	Accuracy (% recovery, min/max in brackets)
Polychlorinated Biphenyls		***Organochlorines***	
PCB-18	60.5 (40.9-80.2)	1,2,4,5-Tetrachlorobenzene	73.5 (47.5-81.3)
PCB-17	66.2(54.5-85.6)	1,2,3,4-Tetrachlorobenzene	67.1 (57.5-85.3)
PCB-31/28	70.3 (56.7-91.8)	Pentachlorobenzene	76.9 (61.1-78.3)
PCB-33	68.8 (56.4-89.6)	α-Hexachlorocyclohexane	83.8 (75.5-98.4)
PCB-52	71.02 (56.5-92.0)	Hexachlorobenzene	76.3 (66.1-83.0)
PCB-49	78.8 (67.3-89.7)	β-Hexachlorocyclohexane	79.7 (71.3-86.3)
PCB-44	76.3 (61.5-90.4)	Heptachlor epoxide	74.2 (68.6-116.3)
PCB-74	84.2 (66.6-90.4)	Oxychlordane	92.7 (80.4-108.9)
PCB-70	83.4 (55.4-90.7)	trans-Chlordane	88.4 (81.6-95.6)
PCB-95	82.7 (67.5-89.5)	cis-Chlordane	92.0 (79.9-110.1)
PCB-101	85.6 (82.0-94.5)	trans-Nonachlor	90.0 (80.0-99.3)
PCB-99	84.7 (66.5-98.1)	p′p-DDE	86.3 (75.5-97.1)
PCB-87	85.4 (68.9-94.6)	Dieldrin	89.1 (79.0-102.7)
PCB-110	84.1 (68.9-95.3)	Endosulfan II	91.0 (80.9-109.5)
PCB-82	87.3 (73.3-102.7)	p′p-DDD	87.4 (74.2-112.1)
PCB-151	85.4 (68.6-94.4)	cis-Nonachlor	91.8 (72.2-115.3)
PCB-149	82.6 (77.1-92.6)	Endosulfan sulfate	93.9 (82.3-106.8)
PCB-118	79.1 (59.3-93.8)	p′p-DDT	87.3 (71.0-104.0)
PCB-153	76.0 (60.3-84.2)	Methoxychlor	88.0 (73.4-105.4)
PCB-105	78.4 (63.4-93.3)	Mirex	69.7 (57.2-89.9)
PCB-138	81.8 (63.9-91.2)		
PCB-158	92.6 (70.7-109.7)		
PCB-187	88.1 (67.4-107.6)		
PCB-183	86.0 (65.7-96.1)		
PCB-128	80.9 (64.9-91.7)		
PCB-177	91.8 (69.6-108.4)		
PCB-156	89.4 (68.0-103.4)		
PCB-180	88.1 (60.4-94.7)		
PCB-191	78.5 (68.3-109.2)		
PCB-169	89.6 (73.2-108.5)		
PCB-170	93.8 (68.8-109.1)		
PCB-199	91.4 (51.5-86.7)		
PCB-208	70.7 (44.9-85.8)		
PCB-194	67.7 (60.2-91.2)		
PCB-205	71.6 (65.2-83.9)		
PCB-206	63.6 (48.7-79.1)		
PCB-209	67.1 (58.5-79.7)		

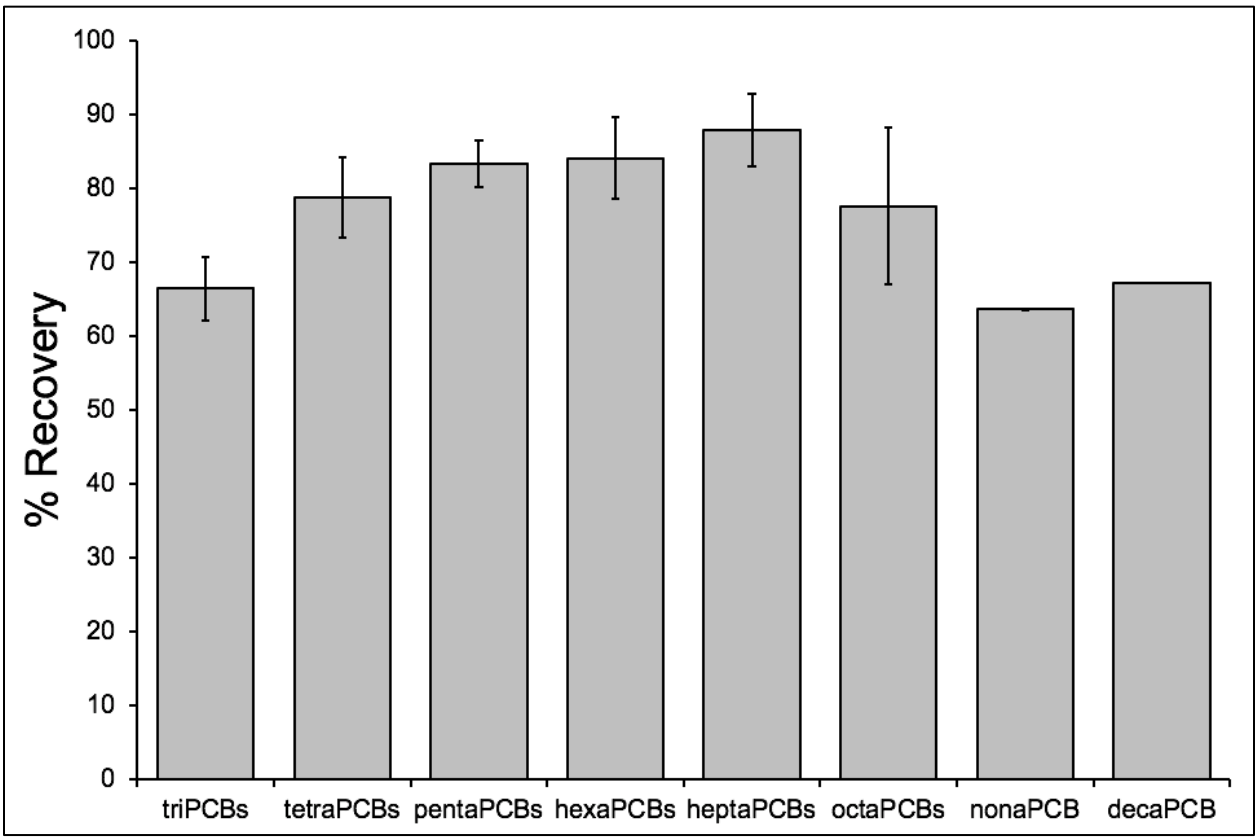

Figure S3.7: Average recoveries of external standards per PCB congener class spiked to matrix blanks (n=5) and run through the optimized modified QuEChERS method. Error bars represent one standard deviation from the mean.

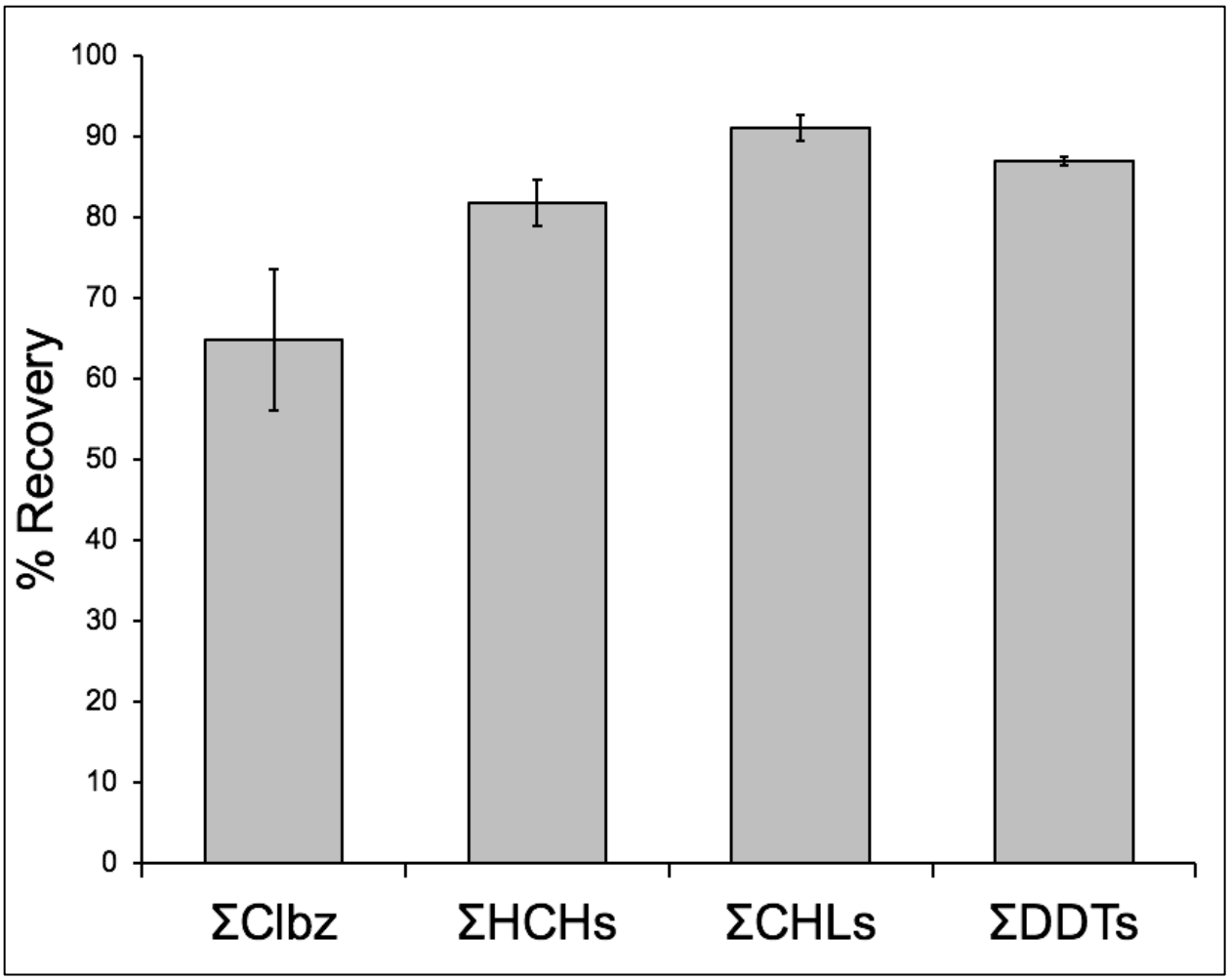

Figure S3.8: Average recoveries of external standards for Σchlorobenzenes (ΣClbzs), Σhexachlorocyclohexanes (ΣHCHs), Σchlordanes (ΣCHLs), and Σdichlorodiphenyl-trichloroethanes (ΣDDTs) from matrix blanks (n=5) ran through the optimized modified QuEChERS method. Error bars represent one standard deviation from the mean.

S3.9. Supplemental details on internal standard recovery

Table S3.4: Average recovery of internal standards from spiked SRM NIST 1945 (n=5) ran through the optimized method.

Chemical Class/Compound	Averaged % Recovery
Organochlorines	
$^{13}C_6$-1,2,4,5-tetrachlorobenzene	70.1 (59.6-85.9)
$^{13}C_6$-1,2,4,5-pentachlorobenzene	65.8 (62.4-70.0)
$^{13}C_6$-1,2,4,5-hexachlorobenzene	75.7 (68.9-82.0)
Polychlorinated Biphenyls	
$^{13}C_{12}$-PCB-28	79.1 (75.3-80.0)
$^{13}C_{12}$-PCB-52	97.0 (86.3-100.6)
$^{13}C_{12}$-PCB-118	73.0 (69.5-78.2)
$^{13}C_{12}$-PCB-153	72.0 (67.8-76.6)
$^{13}C_{12}$-PCB-180	80.0 (66.1-93.0)
$^{13}C_{12}$-PCB-194	61.7 (50.1-68.8)

S3.10. Supplemental details on the application of the method- southeast Greenland killer whale method comparison

Table S3.5: Comparison of polychlorinated biphenyl (PCB) congener and organochlorine (OC) pesticide mean concentrations in killer whale (Orcinus orca) samples between QuEChERS extractions and current-use extractions (n=13). Bolded values indicate p-values less than 0.05 as determined by a paired t-test. Due to low recoveries of the chlorobenzenes, they were internal standard recovery-corrected.

Chemical Class/Compound	QuEChERS (mg/kg lw)	Pedro et al. (2017) (mg/kg lw)	Percent Difference	p-value
Organochlorines				
1,2,4,5-Tetrachlorobenzene	0.02 (0.01-0.04)	0.04 (0.005-0.1)	63.6	**0.01**
1,2,3,4-Tetrachlorobenzene	0.001 (0.01-0.01)	0.002 (0.0001-0.005)	42.7	0.23
Pentachlorobenzene	0.02 (0.006-0.03)	0.04 (0.002-0.08)	60.3	**0.002**
α-Hexachlorocyclohexane	0.03 (0.005-0.06)	0.03 (0.04-0.05)	8.2	0.72
Hexachlorobenzene	0.5 (0.05-2.1)	1.3 (0.15-4.6)	59.2	0.05
β-Hexachlorocyclohexane	0.4 (0.04-1.4)	0.04 (0.01-0.09)	941.7	**0.002**
Heptachlor epoxide	1.8 (0.1-5.5)	5.1 (1.6-9.5)	64.8	**0.02**
Oxychlordane	6.4 (0.4-17.5)	7.4 (2.5-12.9)	14.4	0.63
trans-Chlordane	0.3 (0.04-0.9)	0.2 (0.1-0.7)	11.7	0.74
cis-Chlordane	0.5 (0.05-1.8)	0.8 (0.9-1.4)	40.2	0.17
trans-Nonachlor	12.9 (1.0-33.0)	16.1 (14.2-21.4)	20.2	0.42
p′p-DDE	46.2 (3.0-110.2)	37.8 (30.1-41.4)	22.1	0.45
Dieldrin	2.6 (0.2-9.8)	2.8 (1.7-5.6)	7.7	0.83
cis-Nonachlor	1.5 (0.1-4.5)	1.5 (0.2-3.9)	3.6	0.90
p′p-DDD	1.5 (0.1-4.4)	2.2 (0.2-6.3)	30.8	0.30
p′p-DDT	2.5 (0.2-7.0)	1.4 (0.6-4.0)	76.3	0.07
Mirex	0.9 (0.3-2.2)	0.8 (0.5-1.6)	8.2	0.72
ΣDDTs	50.2 (3.3-121.6)	41.4 (4.4-72.2)	21.2	0.47
ΣHCHs	0.5 (0.06-1.5)	0.1 (0.02-0.14)	515.4	**0.003**
ΣCHLs	23.2 (1.7-63.2)	31.2 (2.9-77.7)	26.2	0.31
Polychlorinated Biphenyls				
PCB-18	0.02 (0.007-0.06)	0.01 (0.001-0.06)	51.5	0.45
PCB-28/31	0.04 (0.007- 0.03)	0.01 (0.004-0.02)	256.8	**0.001**
PCB-44	0.05 (0.004-0.03)	0.06 (0.007-0.16)	9.0	0.24
PCB-74	0.3 (0.02-0.7)	0.3 (0.04-0.9)	12.8	0.44
PCB-87	0.3 (0.02-0.4)	0.2 (0.02-0.4)	110.7	0.19
PCB-95	0.6 (0.03-2.0)	0.3 (0.01-1.2)	94.5	0.39
PCB-99	3.3 (0.2-9.1)	3.1 (0.3-9.5)	5.2	0.93
PCB-110	0.1 (0.01-1.2)	0.04 (0.003-0.1)	228.7	0.60
PCB-118	1.1 (0.09-3.1)	1.1 (0.1-3.5)	0.8	0.77
PCB-128	0.7 (0.05-1.9)	0.8 (0.07-2.2)	23.0	0.60
PCB-138	12.2 (1.1-32.2)	13.8 (1.7-37.5)	11.9	0.60
PCB-149	1.3 (0.08-3.5)	1.1 (0.07-3.6)	15.0	0.64
PCB-151	0.4 (0.03-1.3)	0.3 (0.01-1.2)	25.7	0.53
PCB-153	16.0 (1.6-43.4)	12.2 (1.7-34.8)	30.7	0.66
PCB-156	0.2 (0.03-0.4)	0.2 (0.02-0.5)	22.8	0.23
PCB-180	5.1 (1.1-12.7)	8.5 (1.4-20.5)	40.3	0.11
PCB-183	1.3 (0.3-3.3)	2.0 (0.4-5.6)	32.4	0.20
PCB-187	4.1 (0.9-6.0)	3.4 (0.9-11.5)	19.9	0.97
PCB-195	0.1 (0.05-0.2)	0.1 (0.009-0.2)	6.4	0.58
PCB-206	0.1 (0.1-0.2)	0.2 (0.1-0.5)	34.2	0.11
PCB-209	0.03 (0.006-0.1)	0.06 (0.002-0.3)	47.7	0.20
ΣPCBs	45.3 (6.0-126.0)	47.9 (12.0-133.7)	1.3	0.98

Table S3.6: Comparison of averaged polychlorinated biphenyl (PCB) congeners sorted by degree of chlorination between QuEChERS extractions and current use killer whale (Orcinus orca) extractions (n=13). Bolded values indicate p-values less than 0.05 as determined by a paired student's t-test.

PCB Class	QuEChERS (mg/kg lw)	Pedro et al. (2017) (mg/kg lw)	% Difference	p-value
triPCBs	0.06 (0.01-0.2)	0.02 (0.006-0.08)	144.2	**0.007**
tetraPCBs	0.4 (0.03-1.0)	0.4 (0.04-1.1)	2.2	0.95
pentaPCBs	4.3 (0.3-12.7)	3.6 (0.4-11.2)	19.6	0.56
hexaPCBs	31.6 (3.0-85.4)	29.4 (3.6-82.8)	7.4	0.79
heptaPCBs	10.5 (2.3-26.0)	13.9 (2.7-37.6)	24.3	0.30
octaPCBs	0.1 (0.02-0.2)	0.1 (0.008-0.2)	6.4	0.77
nonaPCB	0.1 (0.01-0.5)	0.2 (0.01-0.5)	34.2	0.10
decaPCB	0.03 (0.002-0.3)	0.06 (0.002-0.3)	47.7	0.16

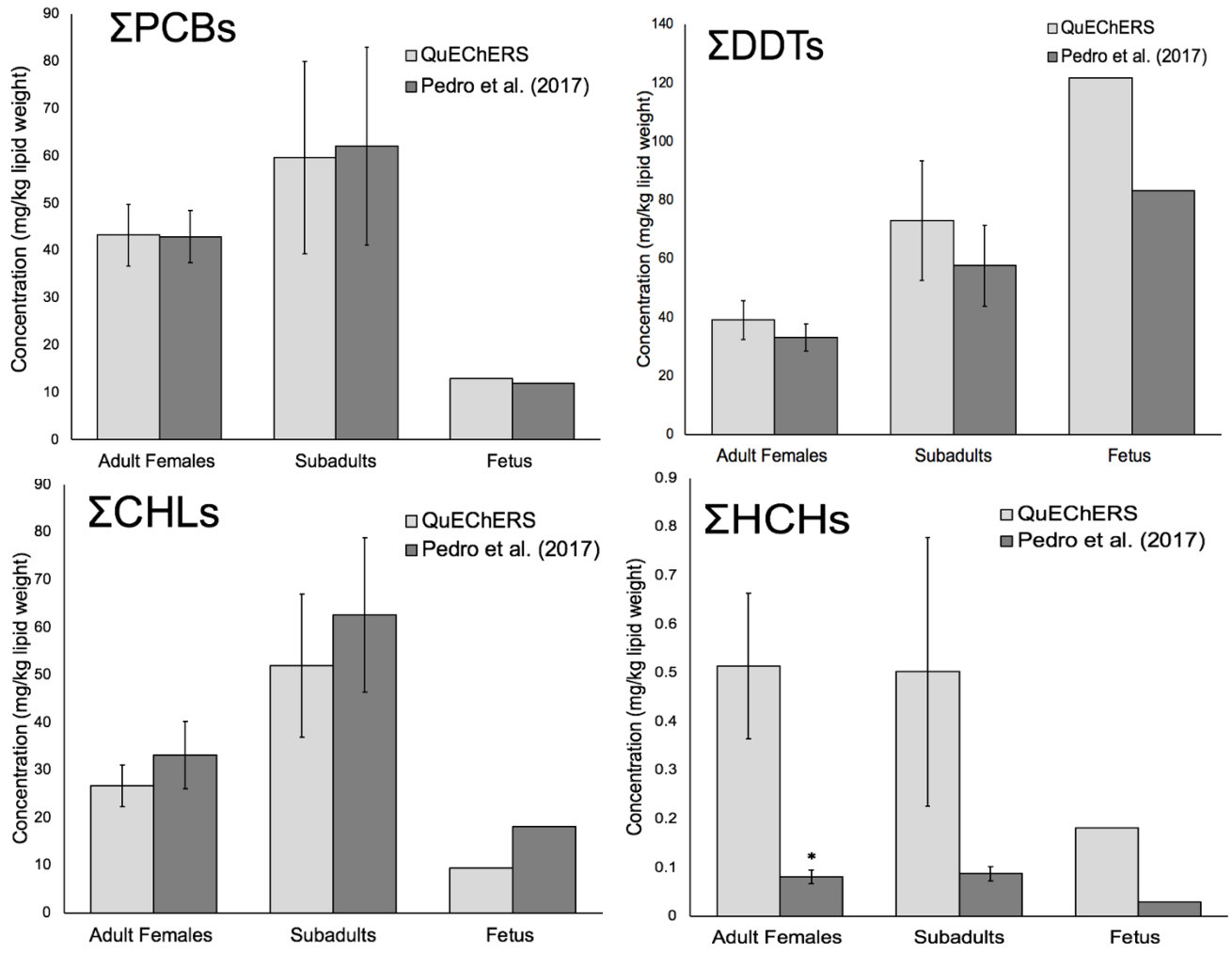

Figure S3.9: Comparison of mean Σpolychlorinated biphenyl (ΣPCB), Σhexachlorocyclohexanes (ΣHCHs), Σchlordanes (ΣCHLs), and Σdichlorodiphenyltrichloroethanes (ΣDDTs) concentrations between QuEChERS extractions and current-use extraction methods for killer whale (Orcinus orca) grouped by sex/age class. Only 1 fetus was used the analysis, so statistical analyses was not performed for that class. Error bars represent one standard deviation from the mean. Asterisks (*) represent significant differences ($p<0.05$) from paired t-tests.

CONNECTING TEXT

In Chapter 3, from the development of this modified QuEChERS approach, we successfully demonstrated its use to extract an extensive suite of lipophilic POPs from marine mammal blubber. However, this method was not tested for its ability to effectively extract any other chemicals, including CEACs. As the approach was specifically developed for the recovery of hydrophobic analytes (i.e., PCBs, DDTs, CHLs, HCH, ClBzs) with particularly high octanol-water partition coefficients ($LogK_{ow}$ > ~5), other chemicals in the blubber matrix with similar chemical properties should, in theory, also be present in the final extracts. Yet, given a lack of studies on other contaminants in marine mammal blubber and adipose tissues (see chapter 2.5), especially on AMAP-identified emerging chemicals, the identity of potential co-extracted lipophilic chemicals is not known.

Chapter 4 discuss the implementation of a newer approach, nontarget screening, that was used to simultaneously screen for hundreds to thousands of unknown lipophilic chemicals in marine mammal blubber and adipose. Using a subset of nontarget screening, suspect screening, we were also able to create a personalized library database to screen for several hundreds of AMAP-identified CEACs. The remaining killer whale extracts from Chapter 3 were included in this analysis, but we also ran several polar bear, long-finned pilot whale, and narwhal blubber/adipose tissues (n=15 per species) through the same QuEChERS approach. Results indicate the presence of several never-before-screened and potentially toxic chemicals (e.g., PRCs) in >50% of all individuals. Chapter 4 also indicates the successful use of the developed QuEChERS extraction for other, non-legacy contaminants including CEACS.

CHAPTER 4: NONTARGET AND SUSPECT SCREENING REVEALS THE PRESENCE OF MULTIPLE PLASTIC RELATED COMPOUNDS IN POLAR BEAR, KILLER WHALE, NARWHAL AND LONG-FINNED PILOT WHALE BLUBBER FROM EAST GREENLAND

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4.1. ABSTRACT

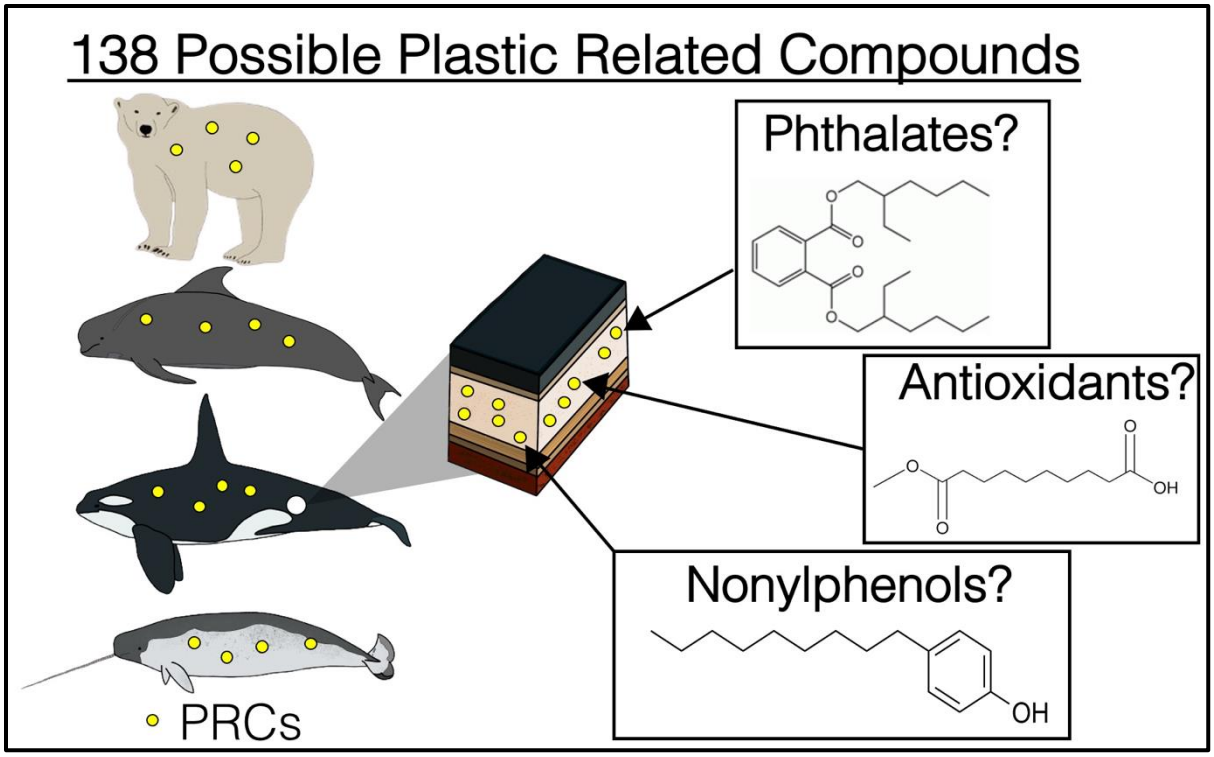
The monitoring of legacy contaminants in sentinel northern marine mammals has revealed some of the highest concentrations globally. However, investigations into the presence of chemicals of emerging Arctic concern (CEACs) and other lesser-known chemicals are rarely conducted, if at all. Here, we used a nontarget/suspect approach to screen for thousands of different chemicals, including many CEACs and plastic-related compounds (PRCs) in blubber/adipose from killer whales (*Orcinus orca*), narwhals (*Monodon monoceros*), long-finned pilot whales (*Globicephala melas*), and polar bears (*Ursus maritimus*) in East Greenland. 138 compounds were tentatively identified mostly as PRCs, and four were confirmed using authentic standards: di(2-ethylhexyl) phthalate (DEHP), diethyl phthalate (DEP), di(2-propylheptyl) phthalate (DPHP), and one antioxidant (Irganox 1010). Three other PRCs, a nonylphenol isomer, 2,6-di-*tert*-butylphenol, and dioctyl sebacate, exhibited fragmentation patterns matching those in library databases. While phthalates were only above detection limits in some polar bear and narwhal, Irganox 1010, nonylphenol, and 2,6-di-*tert*-butylphenol were detected in >50% of all samples. This study represents the first application of a nontarget/suspect screening approach in Arctic cetaceans, leading to the identification of multiple PRCs in their blubber. Further nontarget analyses are warranted to comprehensively characterize the extent of CEAC and PRC contamination within Arctic marine food webs.

Keywords: *phthalates, suspect screening, Irganox 1010, cetacean, HPLC-QTOF-MS, chemicals of emerging Arctic concern (CEACs)*

Highlights

- Marine mammal blubber was nontarget/suspect screened for environmental contaminants
- Suspect screening revealed 138 compounds, mostly plastic related compounds (PRCs)
- Phthalates were only detected in a few individuals, but concentrations ranged up to ~7 mg/kg
- Irganox 1010, an antioxidant, and alkyl phenols were detected in >50% of all samples
- Biomagnification of these PRCs is likely limited relative to legacy persistent organic pollutants

4.2. GRAPHICAL ABSTRACT



4.3. INTRODUCTION

Marine mammals in the Arctic, including polar bear (*Ursus maritimus*) and toothed whales (*Odontocetes*), are considered sentinels for assessing exposures and effects of contaminants in the Arctic (Dietz et al., 2019; Borgå et al., 2022). As some populations of these species show among the highest concentrations globally of many "known" legacy contaminants (McKinney et al., 2011a; Desforges et al., 2018; Letcher et al., 2018; Dietz et al., 2019), they are routinely monitored for persistent organic pollutant (POPs) using targeted screening approaches (Dietz et al., 2013; Desforges et al., 2018; Dietz et al., 2019). Routine monitoring employs established methods to identify and quantify a suite of targeted compounds using authentic analytical standards (de Boer et al., 2022). Although this approach has produced accurate and reproduceable results for decades, it has historically been limited to (semi-)volatile compounds including legacy contaminants (e.g., polychlorinated biphenyls [PCBs] and dichlorodiphenyltrichloroethanes [DDTs]; Vinaixa et al., 2016). In addition, molecular ions are commonly absent or of low intensity in targeted gas chromatography mass spectrometry with election ionization (GC-EI-MS), making molecular formula determination of unknown compounds challenging (Furey et al., 2013; Hollender et al., 2017). As such, unknown (or unexpected) compounds, including new/emerging contaminants, are inevitably missed by targeted screening approaches (Hollender et al., 2017).

With many target-screened contaminants already banned/regulated nationally and globally by the Stockholm Convention, new replacement chemicals are being produced, and many of these in high production (Goldenman et al., 2017), defined as high production volume (HPV) chemicals (OECD, 2023). Some of these current-use chemicals have been detected in the Arctic; however, for many, their bioaccumulation, biomagnification, and toxicity in marine

mammals is largely unknown (Sonne et al., 2021). Multiple recent studies have detailed comprehensive assessments of new/emerging chemicals that have a high potential reach the Arctic and accumulate in marine food webs (AMAP, 2016; Muir et al., 2019; Gibson et al., 2020). Muir et al. (2019) listed ~3,500 potentially persistent, bioaccumulative, and toxic chemicals, some of which included HPV chemicals, with a potential for long-range transport to the Arctic. A subset of compounds from this list, those with the highest toxic, bioaccumulative, and long-range transport potential (i.e., "POP-like" potential) were designated as chemicals of emerging Arctic concern (CEACs; Muir et al., 2019; AMAP, 2020). International monitoring programs including the Arctic Monitoring and Assessment Program (AMAP) and national programs such as like Canada's Northern Contaminants Program (NCP) have also compiled comprehensive assessments of CEACs detected in Arctic seawater and air including organophosphate flame retardants, paraffins, siloxanes, and plastics/plastic-related compounds (PRCs), such as phthalates, antioxidants, UV stabilizers, and micro/nanoplastics (AMAP, 2020; NCP, 2024). As marine mammals in the Arctic often occupy high trophic positions, are long-lived, and possess large quantities of fatty storage tissues (Borgå et al., 2004), bioaccumulation of CEACs and/or mixtures of them is possible, but largely unknown (Sonne et al., 2021).

To identify new CEACs in marine mammal tissues, a newer approach, nontarget screening, may be useful. In the absence of authentic standards, nontarget approaches can identify and semi-quantify a wide range of "unknown" chemical compounds (Díaz et al., 2012; Pieke et al., 2018; Manz et al., 2023). A subcategory of nontarget screening, suspect screening, involves the automated detection of compounds in comparison to the mass spectra of compound libraries (Krauss et al., 2010; Díaz et al., 2012). As true nontarget analysis involves the detection of compounds without any suspect compound information or database, suspect screening is

typically used to tentatively identify compounds of potential interest (Hollender et al., 2017; Manz et al., 2023). Although no routine nontarget/suspect approach exists for the analysis of contaminants in marine mammal blubber, chromatography coupled to high resolution MS (HRMS) has been increasingly popular in the nontarget/suspect analyses of emerging contaminants in a wide variety of challenging environmental matrixes, including some biological tissues (Schymanski et al., 2015; Hollender et al., 2017, Von Eyken et al., 2019; Tian et al., 2020b). In particular, using quadrupole time-of-flight (QTOF) HRMS in nontarget analysis has been shown to provide high mass accuracy for the formula generation and high confidence in structure prediction (Knolhoff et al., 2016a; Knolhoff et al., 2016b).

Nontarget/suspect approaches have rarely been used in any Arctic marine mammal species, despite calls by international monitoring programs such as AMAP for the development of nontarget approaches to aid in identification of potential chemicals of concern (AMAP, 2016). In fact, for most sub-Arctic or Arctic toothed whales, including killer whale (*Orcinus orca*), narwhal (*Monodon monoceros*), and long-finned pilot whale (*Globicephala melas*), a nontarget/suspect screening approach to identify any "unknown" or predicted contaminants of concern, including most AMAP-identified CEACs, has not been reported. Similarly, only two studies to date has used a nontarget/suspect approach in polar bear, identifying some emerging halogenated organics and PRCs in adipose and liver samples (Routti et al., 2016) and per- and polyfluorinated compounds (PFAS) in liver (Chu and Letcher, 2024). As several other "unknown" and potentially toxic compounds may also be present, the implementation of a nontarget approach to identify never-before-screened chemicals, which may include CEACs, in marine mammal sentinels is warranted.

Here, we apply nontarget and suspect screening approaches to 1) screen for "unknown" environmental contaminants, 2) confirm contaminant presence using authentic standards, 3) use semi-quantitative approaches to estimate concentrations of a subset of these confirmed compounds, and 4) compare levels of confirmed compounds to legacy contaminants in the same samples of blubber/adipose in multiple marine mammal species sampled in East Greenland, including polar bear and narwhal and northward-range expanding killer whale and pilot whale. To date, this study is the first to implement a nontarget/suspect workflow to investigate unknown contaminant presence in any cetacean in the Arctic, to our knowledge.

4.4. MATERIALS AND METHODS

4.4.1. Sample Collection

A subset of the samples used in Pedersen et al. (2024), which analyzed these same four species for PCBs and DDTs, were included in the current study. In short, 15 killer whale in 2012-2014 (n = 13) and 2021 (n = 2), 15 narwhal in 2015, 15 long-finned pilot whale in 2021, and 15 polar bear in 2021 (Table S4.1) were opportunistically collected during subsistence harvests by local hunters from East Greenland communities in Ittoqqortoormiit, Tasiilaq and Kulusuk (**Table 4.1**; Figure S4.1). Full-blubber depth samples collected from each whale and subcutaneous adipose from polar bear were stored at -20 °C until they arrived at McGill University, where they were then stored at -80°C until time of analysis. Further information on age class and sex determination is available in Pedersen et al. (2024).

Table 4.1: Sampling location and GPS coordinates, years of collection, and sample size for each location and year for each of blubber/adipose samples (n=15 per species) from East Greenland

Species	Year Collected	Sampling Location	GPS Coordinates	Sample Size
Killer whale	2012	Tasiilaq, Greenland	65°37 N 37°57 W	3
	2013	Tasiilaq, Greenland	65°37 N 37°57 W	3
	2013	Kulusuk, Greenland	65°20 N 37°10 W	2
	2014	Tasiilaq, Greenland	65°37 N 37°57 W	5
	2021	Kulusuk, Greenland	65°20 N 37°10 W	1
	2021	Ittoqqortoomiit, Greenland	70°29 N 21°58 W	1
Narwhal	2015	Gaasefjord, Greenland	70°10 N 27°15 W	15
Long-finned pilot whale	2021	Tasiilaq, Greenland	65°37 N 37°57 W	10
	2021	Kulusuk, Greenland	65°20 N 37°10 W	5
Polar bear	2021	Ittoqqortoomiit, Greenland	70°29 N 21°58 W	15

4.4.2. Sample Extraction

All samples were extracted using a modified QuEChERS (quick, easy, cheap, effective, rugged and safe) method that we previously developed (Pedersen et al., 2023) and all contaminant extraction information was described previously (Pedersen et al., 2024). All authentic analytical standards (Table S4.2; 45 standards) were purchased from Toronto Research Chemicals (Toronto, Canada) or Sigma-Aldrich (St. Louis, MO). After analysis for legacy PCBs and OC pesticides, GC-MS extracts were reconstituted in methanol by blowing down the original isooctane solvent on a nitrogen evaporator to ~50 µL, adding 200 µL of methanol, and evaporating again to ~50 µL. Extracts were transferred to a new HPLC vial along with 1 mL of 50:50 (v:v) methanol: acetonitrile. The solution was passed through a 3 mL syringe attached to a 0.2 µm filter (Fisher Scientific, Pittsburg, PA, USA) prior to instrument analysis.

4.4.3. Background contaminant control

To avoid plastic-related contamination during the sample collection and extraction, the use of plastic labware was limited as much as possible. Following collection, large pieces of blubber/adipose (ranging from 25-100 g) from all narwhal, polar bear, and killer whale were subset and wrapped in a sheet of acetone-rinsed aluminum foil, while large pilot whale samples (ranging from 115-200 g samples) were placed directly in plastic bags, then all samples were shipped to McGill University. Prior to chemical extraction at McGill University, only the innermost portion (0.1 g) was sampled from the innermost portion of each large piece of blubber (i.e., was not touching the foil or plastic) using an acetone-rinsed metal scalpel blade. During the chemical extraction, plastic equipment was limited to the clean-up cartridges (see Pedersen et al., 2023) and filter syringes. All glassware was cleaned with deionized water and solvent rinsed three times, dried, and then solvent rinsed again three times prior to experimentation. As the usage of plastic was unavoidable, one procedural blank was also extracted with each batch of samples (for a total of five) and was processed and analyzed on the instrument the same way as blubber/adipose samples. Although field blanks were not taken, contamination from field sampling was previously shown to not be a source of PRCs (i.e., all field blanks showed no PRC contamination; Routti et al., 2021). Although pilot whale samples were placed directly in plastic bags, they did not show a greater number of nontarget or suspect screened compounds (see results sections 3.1 and 3.2). As such, sampling from the innermost layer of blubber is likely sufficient to avoid background PRC contamination from packaging.

4.4.4. Instrument analysis

Samples were analyzed using a 1290 Infinity II LC from Agilent Technologies (Santa, Clara, USA) coupled to an Agilent 6545 Q-TOF MS, in both positive (ESI^+) and negative (ESI^-) electrospray ionization modes. The LC system was equipped with a Poreshell120 EC-C18 analytical column (Agilent Technologies; 2.7 μm × 3 mm × 100 mm) fitted with a Poroshell 120 (EC-C18; 2.7μm × 3.0 mm × 5 mm) guard column (Agilent Technologies). The mobile phase consisted of water (solvent A) and methanol/acetonitrile (1:1 vol/vol, solvent B), both containing 5mM ammonium acetate, at a flow rate of 0.3 mL/min. The percentage of organic mobile phase B increased linearly as follows: initially at 5% for 0.5 min, then increased to 100% from 1 to 8 min, and then maintained at 100% from 8-13 min; reduced to 5% from 13-13.5 min, held at 5% from 13.5-15 min, followed by 1.5 min post run. The injection volume was 10 μL and the column temperature was set to 30 °C. MS conditions were: drying gas temperature = 175°C, drying gas flow rate = 10 L/min, sheath gas temperature = 375°C, sheath gas flow rate = 12 L/min, nebulizer pressure = 30 psi, capillary voltage = 4000 V, fragmentor voltage = 125 V, skimmer voltage = 50 V, and nozzle voltage = 1000 V (ESI^+) or at 2000 V (ESI^-). Full scan MS data were recorded at a mass-to-charge ratio (*m/z*) range from 100 to 1700 with a scan rate of 2 spectra/sec and were collected using both centroid and profile modes. Targeted MS/MS data for features of interest and analytical standards was collected with three different collision energies in succession (10, 20, and 40 V). Two reference ions (*m/z* at 121.0508 and 922.0098 for ESI^+, 112.9856 and 1033.9881 for ESI^-) were used in each ion mode for automatic mass recalibration during data acquisition. For the targeted compounds, target m/z and retention times are available (Table S4.3).

4.4.5. Quality assurance/quality control

As pooled quality assurance/quality control (QA/QC) samples are essential when conducting nontarget analysis (Gika et al., 2014), one pooled QC samples were prepared by mixing 10 µL of each sample. The pooled QC sample was analyzed every 20 marine mammal samples (5 times total) to control for instrument background noise, mass measurement reproducibility, and retention time drifts.

4.4.6. Nontarget screening, suspect screening, and data filtering

Nontarget analysis of MS-full scan data was performed using the software MassHunter Profinder B.10.00 from Agilent Technologies. Molecular features in all data including blanks and pooled QC samples were first extracted by the "*Batch Recursive Feature Extraction*" algorithm (RT tolerance ± 0.15 min, mass tolerance ± 20 ppm, absolute height threshold ≥ 5,000 counts, score ≥ 70). The total molecular features extracted in each ion mode were filtered based on following criteria: detection frequency of features in the five pooled QC data ≥ 40%, and relative standard deviation (RSD%) of features' abundance in the five pooled QC data <40%. Hierarchical clustering analysis with Euclidean distances were performed on the filtered molecular features to explore groupings within the dataset using Mass Profiler Professional 15.1 (MPP, Agilent Technologies).

Suspect screening was also conducted on the same dataset in "*Batch Targeted Feature Extraction"* mode (RT tolerance ± 0.05 min, mass tolerance ± 20 ppm, absolute height threshold ≥ 5000 counts), and the resulting MS information was screened against the *Extractables & Leachables PCDL* (Personal Compound Database and Library; Agilent Technologies). This database was selected as it contains and many CEAC groups including PFAS, polycyclic

aromatic hydrocarbons (PAHs), antioxidants, UV stabilizers, phthalates, plasticizers, and many others; however, we also personalized this database with the addition of another >100 compounds that are likely CEACs from AMAP 2016 and 2020 assessments (Table S4.4). The minimum total score for the identification of a compound was set to 80%. The total score indicates the probability that the feature is the actual compound in the matching library (i.e., a score of 100% is a perfect match) and is based on: an isotope abundance score, an isotope spacing score and a mass match score (Knolhoff et al., 2016a). A list of possible compound candidates was generated and further sequentially filtered using the same QC data filters as the nontarget screening, but the following filters were added: maximum peak area of each feature > mean plus 3 times of standard deviation of signals in procedural blanks; maximum peak area of each feature > 100,000. Targeted MS/MS spectra of features of interest were compared either with PCDL MS/MS spectra library or subjected to SIRIUS for structure prediction (Schymanski et al., 2015; Dührkop et al., 2019; Schmid et al., 2023). 45 authentic standards (Table S4.2), were used to confirm the tentatively identified molecular features based on the retention time and targeted MS/MS fragment patterns.

Compound identification confidence was also based on Schymanski et al. (2014), where Level 3 indicates a tentative candidate (but insufficient evidence for one exact structure), Level 2 indicates a probable structure (from literature or library spectrum match from MS and MS/MS), and Level 1 indicates a confirmed structure via an appropriate reference standard (with matching less than 0.1 min difference in retention time and matching targeted MS/MS fragmentation patterns).

4.4.7. Semi-quantification of select compounds

A subset of identified and confirmed compounds were semi-quantified; however, this was only done for compounds with an available mass-labelled authentic standard (Table S4.2), which were unavailable for many of the tentatively identified compounds. To determine percent recovery (calculated as [peak area in sample/peak area in standard] *100), we spiked three blubber samples with the mass-labelled standard mix (mix 5) prior to the QuEChERS extraction, then injected them on the LC-QTOF post-extraction. Limits of detection (LODs) and quantification (LOQs) were calculated as the average concentration of the compound in the procedural blanks plus three and ten times of the standard deviation, respectively.

4.4.8. Comparisons to legacy contaminants

For a subset of confirmed compounds, we compared peak areas (divided by starting material weight, i.e., ~0.1 g) to concentrations (in wet weight) of the recalcitrant legacy contaminant, PCB-153 (Pedersen et al., 2024), using linear correlations as a preliminary indication of biomagnification. As PCB-153 is highly biomagnifying and increases with trophic position in food webs (and previously shown to be higher in likely marine mammal-feeding polar bear and killer whale relative to fish/squid feeding narwhal and pilot whale; Pedersen et al., 2024), significant and positive correlations likely suggest similar characteristics for the nontarget screened compound to PCB-153. Furthermore, information regarding toxicity and "POP-like" potential for all confirmed and tentatively identified PRCs was available and compiled from the PlastChem Database on the State of the Science on Plastic Chemicals (Wagner et al., 2024). All mg/kg concentrations and peak areas were log(x+1) transformed, and all data achieved normality.

4.5. RESULTS AND DISCUSSION

4.5.1. QA/QC and clustering analysis

Mean recovery for the 11 mass-labelled standard mix was 63.9 ± 18.1% (Table S4.5) from matrix-spiked samples, demonstrating sufficient analyte recovery. The mean mass accuracies for all mass labelled standards were acceptable, with mean accuracies of 0.86 ± 0.24 ppm (Table S4.5). Peak areas of mass-labelled standard post-spiked in sample matrix were similar to the corresponding value of standard in pure solvent at the same concentration level, indicating no significant matrix effects. Thus, the concentration of confirmed PRCs were semi-quantified via one-point calibration (see Equation 1 in Supporting Information). Contamination of a few PRCs was also evident in procedural blanks, and as such, concentrations in the samples were also corrected for the presence of each respective compound found in the procedural blanks.

To ensure the repeatability/reproducibility of the analysis, we verified the position of the pooled QA/QC injections in the hierarchical clustering analysis from the filtered features from nontarget screening (**Figure 4.1**), suspect screening (Figure S4.2 and S4.3), and from the PCA (Figure S4.4). From the nontarget and suspect screenings, QA/QC injections in each analysis were grouped together, indicating the analysis was repeatable and could be included in the next steps for data treatment (Sangster et al., 2006).

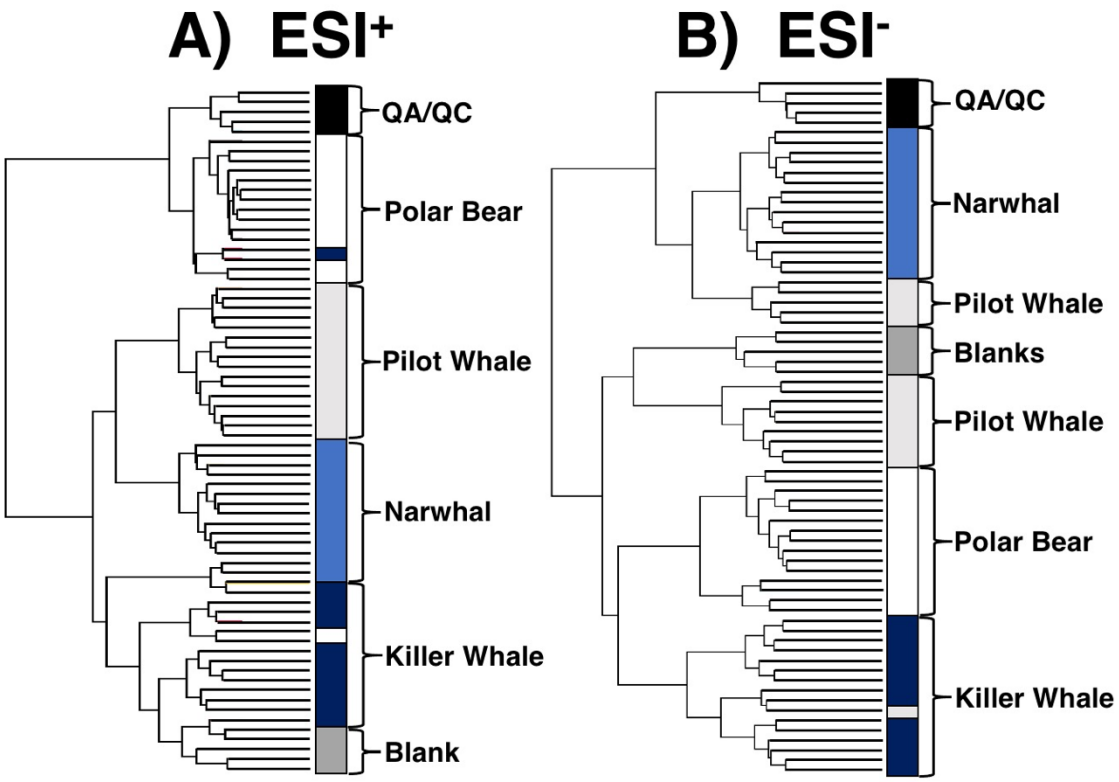


Figure 4.1: Hierarchical clustering analysis (A) in ESI^+ and (B) ESI^- mode by LC-QTOF-MS based on the peak areas from all nontarget screening features in individual marine mammal blubber samples.

Both the nontarget and suspect screening clustering analyses also indicates distinct groupings based on species in both ESI^+ and ESI^-, suggesting interspecific differences in nontarget screened chemical profiles. However, as some individuals in each species cluster outside of their respective groupings, other factors, such as differences in sex/age class (i.e. adult male, adult female, and subadult), may also impact individual chemical profiles. In particular, adult males tended to cluster outside of their species groupings. For example, two male polar bears (in ESI^+) and two adult male killer whale (in ESI^+) clustered separately from adult females and subadults (Figure S4.3). Although trends vary based on legacy contaminant, the more recalcitrant PCBs (e.g., CB-153, 180) tended to show higher concentrations in adult males and subadults relative to adult females (Pedersen et al., 2024). In general, adult male marine mammals tend to show increasing concentrations of POPs with age due to a lack of capacity to

offload burdens to young that females have through gestation and particularly lactation (Pedero et al., 2017; Dietz et al., 2019). As such, the particular feature groupings, with some adult males showing distinct patterns from adult females, could suggest some features behave similar to known POPs in terms of bioaccumulation in males and offloading of burdens in females to offspring. However, as patterns are not entirely discernable among all individuals when comparing across age class/sex groupings, other factors still likely influence differences in individual chemical profiles, such as diet, body condition, migration, seasonality, year of collection, and lipid content.

4.5.2. Data Filtering

From the nontarget screening approach, 10,927 unique molecular features were obtained from both ESI^+ (6,115 features) and ESI^- (4,825 features) for all 60 blubber samples (**Figure 4.2**). From the suspect screening, 1,830 features (972 in ESI^+ and 856 in ESI^-) were tentatively identified with a matching score of >80% in the library database. Of these features, most (~83%) were simultaneously detected in ~20% of individuals above the mean + 3σ of the blanks (Figure S4.5). The mean number of features above the mean + 3σ of the blanks also varied significantly by species with: narwhal (83 features) = pilot whale (79) > killer whale (74) = polar bear (70) (Figure S4.5).

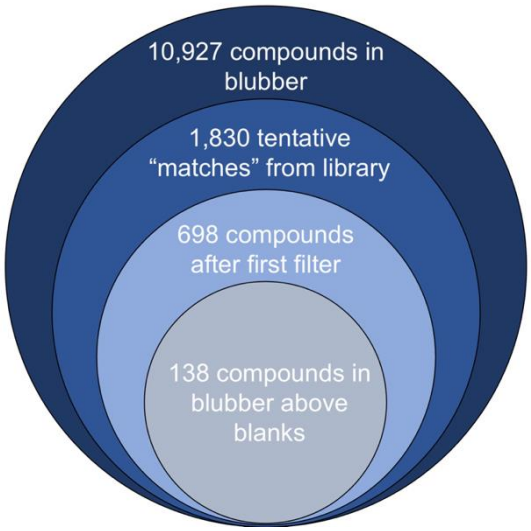


Figure 4.2: Graphical representation of the feature filtering steps (from both ESI^+ and ESI^-) from 1) the total initial features (outermost circle) from nontarget screening, 2) tentative matching features to personalized library database with matching score of >80% from suspect screening, 3) filtering from pooled quality assurance/quality controls injections and 4) filtering by compounds above the mean + 3σ of the blanks (innermost circle).

From the suspect screening approach, filtering from the tentative matching features from the pooled QA/QC injections yielded 698 features (240 in ESI^+ and 458 in ESI^-). Out of these compounds, 138 (86 in ESI^+ and 52 in ESI^-) were above the mean + 3σ of the blanks (see Table S4.6 for full list of compounds). This number of suspect-screened features is similar to those reported elsewhere, including in water samples from an urban estuary (205 features; Tian et al., 2020a), Arctic marine zooplankton (127 features; Sorensen et al., 2023), and bottlenose dolphin (*Tursiops truncates*) blubber from Brazil (158 features; Alonso et al., 2017).

Although this subset of 138 compounds details a comprehensive list of CEACs in Arctic marine mammal blubber/adipose, including some phthalates and their metabolites (e.g., di-(2-ethylhexyl) phthalate [DEHP] and mono-(2-ethylhexyl) phthalate [MEHP]), pesticides (e.g., Triclosan), fluorinated compounds (e.g., perfluorohexanesulfonic acid), UV stabilizers (e.g., UV-320, and Irgacure 369), antioxidants (e.g., Ethanox 702, Irganox 1010), synthetic dyes (e.g.,

Sudan III, Malachite Green), and surfactants (Surfynol 104), these compounds are only a tentative confirmation of the respective compounds, equated to a confidence Level 4 on the Schymanski et al. (2014) scale. As the confirmation of 138 compounds across 60 blubber samples would be prohibitively costly and time-consuming, a subset of this list was instead identified based on available standards (i.e., for Level 1 confidence), as detailed in Sections 3.3 to 3.6.

4.5.3. Phthalates

Features at m/z 223.0971 ($[M+H]^+$, 8.21 min), 391.2848 ($[M+H]^+$, 11.79 min), and 447.3482 ($[M+H]^+$, 14.08 min) were identified in the library as diethyl phthalate (DEP), di(2-ethylhexyl) phthalate (DEHP), and di(2-propylheptyl phthalate) (DPHP). The identification for all three compounds was confirmed (i.e. identification confidence Level 1; Schymanski et al., 2014) with a retention time match of less than 0.1 min difference and MS/MS fragmentation patterns match relative to the available authentic standards (**Table 4.2**, Figure S4.6).

Table 4.2: Nontarget identification of select plastic related compounds with high identification confidence in marine mammal blubber/adipose.

Feature m/z	RT (min) in standard	Molecular formula	Suspected ID from library	RT match from standard	MS/MS match from standard	MS/MS match from library	Identification confidence*
ESI$^+$							
223.0971	8.210	$C_{12}H_{14}O_4$	Diethyl phthalate (DEP)	Yes	Yes	NA	1
391.2848	11.792	$C_{24}H_{38}O_4$	Di(2-ethylhexyl) phthalate (DEHP)	Yes	Yes	NA	1
447.3482	14.079	$C_{28}H_{46}O_4$	Di(2-propylheptyl) phthalate (DPHP)	Yes	Yes	NA	1
1194.8160	13.253	$C_{73}H_{108}O_{12}$	Irganox 1010	Yes	Yes	NA	1
ESI$^-$							
205.1603	9.78**	$C_{14}H_{22}O$	2,6-Di-*tert*-Butylphenol	NA	NA	Yes***	2
219.1758	10.16**	$C_{15}H_{24}O$	Nonylphenol (or isomers)	NA	NA	Yes***	3
427.3777	14.25**	$C_{26}H_{50}O_4$	Dioctyl sebacate (or isomers)	NA	NA	Yes***	3
498.9299	8.668	$C_8HF_{17}O_3S$	Perfluorooctanesulfonic acid (PFOS)	Yes	Yes	NA	1

*From Schymanski et al. (2014)

**Average retention time in samples, since no standard was available

***SIRIUS score >85

Several other features were tentatively identified as phthalates, including dibutyl phthalate, benzyl butyl phthalate, and dibenzyl phthalate, respectively. These compounds showed a retention time match with available standards, but MS/MS spectra in samples was of low quality (i.e., very small peaks), likely from relatively small signals from parent ions, preventing further confirmation (see Table S4.7).

For phthalates with level 1 identification confirmation (i.e., DEP, DEHP, DPHP), detection frequencies (calculated as the number of samples above the blank mean + 3σ/15 *100) of these compounds varied widely by species (**Table 4.3**). DEP was detected in 20% of polar bear (3/15 individuals), DEHP was detected in 20% (3/15 individuals) of polar bear and 13% (2/15 individuals) of narwhal, while DPHP was only detected in the same two narwhal. DEP, DEHP, and DPHP were not detected in any killer whale or pilot whale. Correlations of phthalate peak areas/starting material weight with concentrations of legacy contaminants (PCB-153 in wet weight) in the same individuals showed no significant correlation for DEP and DEHP ($R^2 = 0.01$ and $R^2 = 0.02$, respectively), but a significant and negative correlation for DPHP ($R^2 = 0.21$ and $p < 0.01$; Figure S4.7). These models likely suggest limited or no biomagnification potential of these phthalates (as supported elsewhere; Gobas et al., 2003; Mackintosh et al., 2004; Lynch et al., 2022), and even potential trophic dilution (as seen in DPHP; Figure S4.7), also supported elsewhere in both aquatic (Gobas et al., 2003) and terrestrial (McLachlan, 1996; Franco et al., 2007) food webs.

Table 4.3: Detection frequencies in % (ND = nondetected) of all plastic related compounds with high identification confidence (level 1, 2, or 3) in blubber/adipose samples.

Compound name	Detection Frequency (%)*			
	Killer whale	Narwhal	Pilot whale	Polar bear
Phthalates				
Diethyl phthalate (DEP)	ND	ND	ND	20
Di(2-ethylhexyl) phthalate (DEHP)	ND	13	ND	20
Di(2-propylheptyl) phthalate (DPHP)	ND	13	ND	ND
Antioxidant				
Irganox 1010	67	80	ND	13
Alkyl Phenols				
2,6-di-*tert*-butylphenol	40	27	53	67
Nonylphenol isomer	80	80	7	33
Misc. Compounds				
Dioctyl sebacate (or isomers)	27	33	13	7
Perfluorooctanesulfonic acid (PFOS)	ND	13	ND	20

*darker colors indicate higher detection frequencies

For semi-quantified phthalate concentrations (i.e. DEP and DEHP, based on available mass-labelled standards), DEP concentrations ranged from <0.14-0.25 mg/kg wet weight (ww), but DEHP ranged slightly higher from <0.54-7.29 mg/kg ww in all blubber/adipose samples. Phthalate concentrations were relatively high in blanks, likely from contamination during chemical extraction, as DEP and DEHP can migrate from plastic (e.g., plastic tubing, cartridges, syringes, etc.) to surrounding materials (García Ibarra et al., 2018; Rastkari et al., 2018); due to blank subtraction, this led to high limits of detection, which are similar to those reported previously (Fankhauser-Noti et al., 2007; Routti et al., 2021).

Table 4.4: Semi-quantified concentrations (mg/kg wet weight) of phthalates (based on available mass-labelled standard) in blubber/adipose sample.

Feature m/z	Killer whale	Narwhal	Pilot whale	Polar bear
Diethyl phthalate (DEP)	<0.14	<0.14	<0.14	<0.14-0.25*
Di(2-ethylhexyl) phthalate (DEHP)	<0.54	<0.54-1.83	<0.54	<0.54-7.29

*Ranges from samples below detection limits to samples above detection limits.

Phthalates are AMAP-classified CEACs and many are considered HPV PRCs (AMAP, 2016; AMAP, 2020). DEHP, in particular, has received intensive scientific interest as a likely endocrine disrupting chemical by the World Health Organization and United Nations Environmental Program (WHO/UNEP, 2013). As such, many phthalates, including DEHP have been globally identified as substances of high concern with regional bans/restrictions, mostly in cosmetics, children's toys, and childcare products (CEPA 1999; ECHA, 2015; Wang and Qian, 2021). More recently, DEP has been also been classified as a highly hazardous compound due to its reproductive and specific target organ toxicity, although no current regional or global regulation exist (Wagner et al., 2024). Information on DPHP toxicity is more limited, although a potential for endocrine disruption has been reported (Wagner et al., 2024).

Targeted screening studies have previously identified both DEHP and DEP across the Arctic in air, water, sediment, and some biota (Vorkamp et al., 2004; Schlabach et al., 2009; Remberger et al., 2013; Routti et al., 2021. Similar to our findings, DEHP was the most abundant phthalate detected in Norwegian polar bear adipose and cetacean blubber (ranging from <0.012-0.39 mg/kg ww; Routti et al., 2021) and polar bear liver from Greenland (0.13-0.15 mg/kg ww; Vorkamp et al., 2004). Our detection frequencies and limits of detection in polar bear adipose are comparable to those reported elsewhere (8.3% and 0.1 mg/kg ww, respectively; Routti et al., 2021). DEP was similarly detected at lower concentrations (0.016-0.024 mg/kg ww) relative to DEHP in Greenlandic polar bear liver (Vorkamp et al., 2004), although our reported concentrations in adipose were substantially higher. In Norwegian cetaceans, all DEP concentrations in cetacean blubber were similarly below detection limits, although our detection in polar bears was higher (i.e., not detected in Routti et al., 2021 compared to 20% in the present

study). However, the present study is the first to confirm the presence of phthalates (DEP and DPHP) in any narwhal, to our knowledge, albeit at low detection frequencies.

The sources and pathways of phthalates to marine mammal blubber/adipose are not fully known. However, high concentrations of phthalates, most notably DEHP, have been identified in high Arctic seawater, with an estimated 30 and 190 tons per year atmospherically deposited to the Greenland Sea and Arctic Ocean, respectively (Xie et al., 2007). Following deposition to surface waters, phthalate ingestion has been shown to occur in plankton, yet studies suggest limited biomagnification potential of phthalates to top predators (Mackintosh et al., 2004; Kim et al., 2016). Instead, trophic dilution of phthalate diesters and their monoester metabolites has been reported, suggesting further metabolic breakdown/and or rapid excretion in high trophic level marine organisms (Hu et al., 2016). No phthalate metabolites were identified in the current study, further suggesting high xenobiotic biotransformation potential across all studied species, although extraction-based losses of these more hydrophilic metabolites may also be likely. As such, given low detection frequency across all species, and a likely limited biomagnification potential, phthalate bioaccumulation, at least for DEP, DEHP, and DPHP, to top predator marine mammals in the Arctic is likely relatively low, especially compared to known concentrations of legacy contaminants.

4.5.4. Antioxidants

The feature at *m/z* 1194.8160 ($[M+Na]^+$, 13.25 min) was identified in the library as Irganox 1010. The identification was confirmed at confidence Level 1 (**Table 4.2**, Figure S4.8). Another antioxidant was detected at m/z 357.1894 ($[M+H]^+$, 10.69 min) and was tentatively identified as Irganox 1081. However, although the retention time in samples matched the

available standard, peak areas were too low (mean ~1,000) in pooled QA/QC injections and thus did not met QA/QC criterion (see section 2.6).

Detection frequencies for Irganox 1010 were highest in killer whale (67%) and narwhal (80%), lower in polar bear (13%), and not detected in pilot whale (**Table 4.3**). As mass labelled standards were not available and were not extracted with samples in the method procedure, concentrations were not quantified. Linear correlations comparing Irganox 1010 to PCB-153 in the same individuals were not significant ($R^2 = 0.03$; Figure S4.7).

Irganox 1010, a high molecular weight HPV chemical, is a plastic additive used in most polyolefins such as polyethylene, polypropylene, and polybutene (OECD, 2005). Despite its widespread global usage, information on its environmental presence is currently severely lacking (Wagner et al., 2024). High concentrations of Irganox 1010 (up to 1,600 µg/g) have been reported in plastic debris and new plastic products (Rani et al., 2017). Although Irganox 1010 has not yet been classified has a CEAC, plastics (i.e. micro- and nanoplastics) and plastic additives (e.g., phthalates) are classified as CEACs (AMAP, 2016; AMAP, 2020), especially as widespread observations of plastic pollution have been observed across the Arctic (Bergmann et al., 2022) and in East Greenland (Morgana et al., 2018). Nonetheless, the present study is the first to identify Irganox 1010 in any marine wildlife tissue, to our knowledge, although similar antioxidant compounds have been detected in seawater (Suhrhoff et al., 2016).

Ingestion of plastic debris has been suggested as a source of exposure to plastic additives in marine mammals (Fossi et al., 2016; Baini et al., 2017; Routti et al., 2021. In Northeast Greenland, plastic ingestion by Arctic fishes, harp seals (*Pagophilus groenlandicus*), and hooded seals (*Cystophora cristata*) has been recently observed (Morgana et al., 2018; Pinzone et al., 2021), with evidence of polyethylene, polypropylene, and polyvinyl chloride (PVC)

accumulation in gastrointestinal (GI) tracts and livers. As Irganox 1010 is one of the most common additives in polyethylene- and polypropylene-based plastics (Hahladakis et al., 2018), subsequent assimilation into marine mammal tissue post-ingestion may be possible, yet the extent to which sorbed additives can transfer from plastics to animal tissues is currently uncertain. However, Irganox 1010 has been shown to significantly migrate from plastic into fatty/oily substrates in a laboratory setting (Marcato et al., 2003). Direct consumption of Irganox 1010 from seawater (i.e., after leeching from plastic) is also unlikely due to its hydrophobicity and high octanol-water partitioning coefficient (19.06; Lynch et al., 2022), although some sorbed additives may accumulate in lower trophic organisms such as plankton (Xin et al., 2023). Direct plastic ingestion has also been shown to be a negligible source of some PRCs (e.g., phthalates) compared to dietary intake (Bakir et al., 2016), suggesting potential accumulation from trophic transfer. However, biomagnification potential is not likely (Figure S4.7; given nonsignificant correlations with PCB-153) as biomagnification of large size plastic additives is generally limited (Miller et al., 2020), although it has not yet been investigated for any Irganox antioxidants in any other studies, to our knowledge.

Given the high detection frequencies of Irganox 1010 in the present study, further investigation into the sources, transfer, and toxicity of antioxidants to marine mammal predators is warranted. Differences in feeding habitat and individual diet may impact plastic ingestion as indicated elsewhere (Hahladakis et al., 2018; Pinzone et al., 2021), which may explain our reported interspecific differences in detection frequencies. Toxicity is expected to be low, with high LD_{50} observed in *Daphnia magna* (86 mg/L) and other animals (USFDA, 2019); although, a recent study indicated decreased growth and survival in Irganox 1010-exposed sea urchins (*Echinus sp.*; Shore et al., 2022). However, targeted analyses are required to confirm the presence

of Irganox 1010 and better assess whether the concentrations exceed expected nontoxic thresholds.

4.5.5. Alkylphenols

Features at m/z 219.1758 ($[M-H]^-$, 10.16 min) and 205.1603 ($[M-H]^-$, 9.78 min) were initially identified by the library as 4-nonylphenol and 2,6-di-*tert*-butylphenol, respectively (**Table 4.2**). However, the MS/MS fragmentation and retention time of an available 4-nonylphenol standard did not match with samples (Table S4.7). A branched nonylphenol standard, 4(1-ethyl-1methylhexyl) phenol, was also tested and matched retention time, but with a different fragmentation abundance pattern. Instead, SIRIUS predicted six nonylphenol isomer structures with a high degree of confidence (>84% match), and as such, a confidence level of 3 was assigned, as the confirmation of one nonylphenol structure was not possible. For the other feature 205.1603 ($[M-H]^-$, 9.78 min), targeted MS/MS showed a matched fragmentation pattern as 2,6-di-*tert*-butylphenol with a 96% matching score from SIRIUS prediction (Figure S4.10). Thus, a confidence level of 2 was assigned.

For 2,6-di-*tert*-butylphenol, detection frequencies were as follows: polar bear (67%) > pilot whale (53%) > killer whale (40%) > narwhal (27%). Patterns differed for the nonylphenol isomer compound, with killer whale (80%) = narwhal (80%) > polar bear (33%) > pilot whale (7%). Linear regressions comparing nonylphenol and 2,6-di-*tert*-butylphenol peak areas to PCB-153 in the same individuals[28] were also nonsignificant ($R^2 = 0.10$ and $R^2 = 0.01$, respectively; Figure S4.7).

2,6-di-*tert*-butylphenol and some nonylphenols are degradation products of alkylphenol ethoxylates, commonly used as additives in plastics (commonly PVC and polystyrene),

detergents, paints, lubricants, and some pesticides (Sharma et al., 2009). In accordance with our findings, multiple C_8- (like 2,6-di-*tert*-butylphenol) and C_9-alkylphenols (i.e. nonylphenols) were also detected in polar bear plasma from Svalbard (Simon et al., 2013). More recently, 4-nonylphenol, a known persistent and moderately bioaccumulative endocrine disrupting chemical (Soares et al., 2008), was also identified in polar bear liver samples from Svalbard (Routti et al., 2016) and in killer whale liver from the northeast Pacific (Lee et al., 2023) using targeted approaches. 2,6-di-*tert*-butylphenol has not yet been identified in any marine mammal species, to our knowledge, yet recent assessments have detailed a high potential for specific target organ toxicity, although limited environmental persistence (Wagner et al., 2024). Confirming alkylphenol presence via a nontarget approach is challenging due to the vast number of octyl- and nonyl-alkylphenol constitutional isomers (e.g., >200 nonylphenol isomers; Guenther et al., 2006), making standard purchases and analyses costly and time intensive. However, future studies should aim to screen for the alkylphenols of the highest concern (i.e. 4-nonylphenol; Guenther et al., 2006), detail concentrations, and to confirm 2,6-di-*tert*-butylphenol presence in marine mammal blubber/adipose.

4.5.6. Other Compounds of Potential Concern

The feature at m/z 427.3777 ($[M-H]^-$, 14.25 min) in samples was identified in the library as dioctyl sebacate. Detection frequencies were as follows: narwhal (33%) > killer whale (27%) > pilot whale (13%) > polar bear (7%). Standards were not available to confirm this compound. However, based on targeted MS/MS fragmentation patterns, SIRIUS predicted six different confirmations of dioctyl sebacate with matching scores > 87%, and as such, a confidence level of 3 was assigned. Dioctyl sebacate and its configurational isomers are PRCs used as plasticizers

(Mahrous et al., 1999), with a potential for toxicity in wildlife (Wagner et al., 2024). However, information of their presence in any environmental compartment is severely lacking (Wagner et al., 2024), and to our knowledge, they have not been reported in any marine wildlife tissues. As such, further investigation using authentic standards is required to confirm its, or its isomers, presence.

The feature at m/z 498.9299 ($[M-H]^-$, 8.67 min) was identified in the library as perflurooctanesulfonic acid (PFOS) and was confirmed with a retention time match less than 0.1 min difference and MS/MS fragmentation patterns match to the standard (**Table 4.2**, see Figure S4.11). PFOS was only detected in polar bear (20%) and narwhal (13%). PFOS and other fluorinated compounds have been previously analyzed and detected in killer whale (Gebbink et al., 2016), narwhal (Carlsson et al., 2014), pilot whale (Dassuncao et al., 2017), and polar bear (Boisvert et al., 2019) liver samples given their proteinophilic nature and accumulate to a far lower degree in fatty tissues (Kelly et al., 2009), likely explaining our lower detection frequencies in blubber/adipose across all individuals. Although our detection frequencies were far lower than those reported elsewhere in polar bear adipose (Boisvert et al., 2019), this is likely a result of extraction-based losses.

Several other compounds of interest are also likely present in these blubber samples but may be missing from the selected library database, concentrated in other tissues (e.g. in muscle or liver), or were not detected due to extraction-based losses. For example, biomagnifying halogenated natural products and metabolites such as hydroxylated and methoxylated polybrominated diphenyl ethers (OH- and MeO-PBDEs) may still be present (Kelly et al., 2008), but were absent in the selected library database. For other chemicals that were included in the library database like bisphenol A (BPA) and tetrabromobisphenol A (TBBPA), mass-labelled

BPA spikes carried out through our QuEChERS approach were not detected post-extraction (likely maintained in the aqueous fraction, while the organic fraction was collected). As such, they were likely not detected due to extraction-based loses but may still be present, especially as BPA and TBBPA presence has been documented across the subarctic and Arctic, including in subarctic marine mammal liver (e.g., fin whale, sperm whale, minke whale in South China Sea; Guo et al., 2023), in other Arctic biota (fishes and mussel; Evenset et al., 2009), and in Greenland shark (*Somniosus microcephalus*) liver from the Greenland Sea (Ademollo et al., 2018). Furthermore, chemicals with a lower octanol-water partition coefficient, like BPA and some phthalate metabolites like MEHP, may concentrate in marine mammal liver and may be nondetectable in blubber. In addition, different data treatment approaches, such as those provided by machine learning-based retention time predictions, could be employed in future work to provide higher confidence in the identification of individual compounds, including more hydrophilic chemicals (Song et al., 2024). As such, although a large number of unexpected chemicals were both tentatively identified and confirmed in the present study, further investigation using similar nontarget/suspect approaches with different library databases, in other marine mammal tissues (e.g., skin, muscle, liver), and using different analytical extraction methodologies is warranted, especially as some non-detected, yet toxic and persistent chemicals (or chemicals that were not screened) or their primary metabolites are still likely present.

4.6. CONCLUSIONS

Here, we present the results of the first nontarget/suspect screening workflow specifically developed for the identification of novel and “unknown” contaminants in Arctic marine mammal

toothed whales. Tentatively identifying 138 features, predominantly comprising of CEACs and PRCs, our comprehensive analysis compared retention time and MS/MS fragmentation patterns for ~50 compounds with available authentic standards. We successfully confirmed the presence of multiple PRCs, including three phthalates (DEP, DEHP, DPHP) and one antioxidant, Irganox 1010. Three additional PRCs, a nonylphenol, 2,6-di-*tert*-butylphenol, and dioctyl sebacate, exhibited MS/MS fragmentation patterns matching those in library databases. While the low detection frequencies of the identified phthalates suggest limited bioaccumulation and even trophic dilution in Arctic marine mammals, the high detection frequencies of Irganox 1010 and limited information on its usage, toxicity, and environmental persistence indicate the need for further investigation into its environmental fate and uptake in marine wildlife. In addition, the presence of some alkylphenols, especially those with known endocrine disrupting potential (i.e., sone nonylphenols) warrants prioritization in future research. As indicated by the large number of unknown or unexpected chemicals, both tentatively identified and confirmed in this study, our current understanding of contaminant exposure in marine mammal predators is likely incomplete. Therefore, further nontarget analyses are essential to better characterize the magnitude of CEAC contamination in the Arctic marine food webs.

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4.9. SUPPORTING INFORMATION

Table S4.1: Biological data (Age/age class and sex) for each toothed whale/ursid individual from East Greenland and collected from 2012 to 2021 that were used in the nontarget screening analysis. For pilot whale and polar bear, age-specific data is available, but this was converted to age class during future modeling analyses.

Species	ID	Sex	Age/Age Class	Year Collected	Location
Killer Whale	48338	female	adult	2012	Tasiilaq
	48337	ND	subadult	2012	Tasiilaq
	48336	female	adult	2012	Tasiilaq
	48335	female	adult	2012	Tasiilaq
	48736	female	adult	2013	Tasiilaq
	48733	female	adult	2013	Kulusuk
	48732	male	adult	2013	Tasiilaq
	35143	female	adult	2013	Kulusuk
	51607	ND	subadult	2014	Tasiilaq
	51613	male	subadult	2014	Tasiilaq
	51610	male	subadult	2014	Tasiilaq
	51606	ND	subadult	2014	Tasiilaq
	51601	male	subadult	2014	Tasiilaq
	GL-01	male	adult	2021	Ittoqqortoormitt
	64752	female	adult	2021	Kulusuk
Narwhal	53802	female	adult	2015	Gaasefjord
	53812	male	adult	2015	Gaasefjord
	53823	male	subadult	2015	Gaasefjord
	58324	male	subadult	2015	Gaasefjord
	53825	female	subadult	2015	Gaasefjord
	53835	female	adult	2015	Gaasefjord
	53839	female	subadult	2015	Gaasefjord
	53840	male	subadult	2015	Gaasefjord
	53834	male	subadult	2015	Gaasefjord
	53801	female	adult	2015	Gaasefjord
	53845	female	subadult	2015	Gaasefjord
	53811	female	adult	2015	Gaasefjord
	53842	female	adult	2015	Gaasefjord
	53844	female	adult	2015	Gaasefjord
	53846	female	subadult	2015	Gaasefjord
Pilot Whale	64702	female	adult	2021	Tasiilaq
	64703	female	adult	2021	Tasiilaq

	64705	female	adult	2021	Tasiilaq
	64709	male	subadult	2021	Tasiilaq
	64710	female	subadult	2021	Tasiilaq
	64711	female	adult	2021	Kulusuk
	64712	male	adult	2021	Tasiilaq
	64714	female	adult	2021	Tasiilaq
	64720	male	adult	2021	Kulusuk
	64721	female	adult	2021	Kulusuk
	64722	male	subadult	2021	Kulusuk
	64723	female	subadult	2021	Tasiilaq
	64724	male	subadult	2021	Tasiilaq
	64727	male	subadult	2021	Tasiilaq
	64728	female	subadult	2021	Tasiilaq
Polar Bear	61866	male	subadult	2021	Ittoqqortoormitt
	61867	female	adult	2021	Ittoqqortoormitt
	61868	female	subadult	2021	Ittoqqortoormitt
	61869	female	adult	2021	Ittoqqortoormitt
	61870	female	adult	2021	Ittoqqortoormitt
	61871	male	adult	2021	Ittoqqortoormitt
	61872	female	subadult	2021	Ittoqqortoormitt
	61873	male	adult	2021	Ittoqqortoormitt
	61874	male	adult	2021	Ittoqqortoormitt
	61875	female	adult	2021	Ittoqqortoormitt
	61876	female	subadult	2021	Ittoqqortoormitt
	61877	male	subadult	2021	Ittoqqortoormitt
	61878	female	subadult	2021	Ittoqqortoormitt
	61879	male	adult	2021	Ittoqqortoormitt
	61880	male	adult	2021	Ittoqqortoormitt

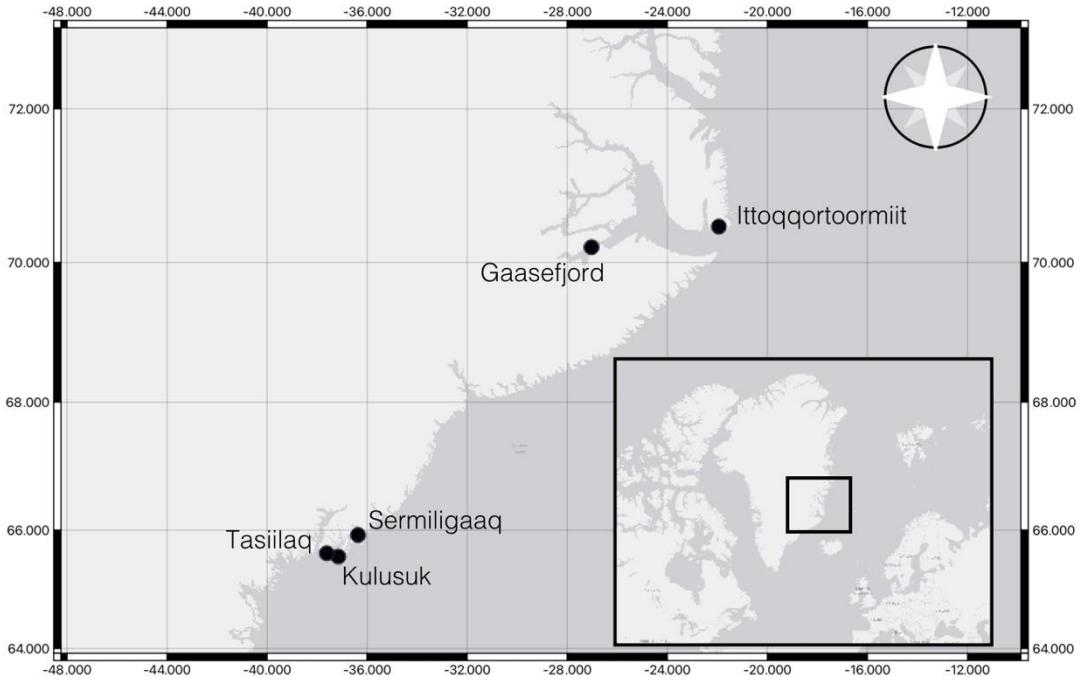

Figure S4.1: Sampling location for all killer whale (Orcinus orca), long-finned pilot whale (Globicephala melas), narwhal (Monodon monoceros), and polar bear (Ursus maritimus), sampled in Greenland from 2012-2021. Map adapted from Pedersen et al. 2023.

Table S4.2: Standard mixes with individual standards in each mix and associated concentrations used for compound confirmation.

Compound	Polarity	Chemical formula	m/z*	Retention time (min)
Mix 1 (100 ppb)				
Mercaptobenzothiazole	ESI^+	$C_7H_5NS_2$	167.9941	6.97
Benzothiazole	ESI^+	C_7H_5NS	136.0221	7.00
Hexa(methoxymethyl)melamine	ESI^+	$C_{15}H_{30}N_6O_6$	391.2305	7.65
6-PPD quinone	ESI^+	$C_{18}H_{22}N_2O_2$	299.1760	9.31
Dibutyl phthalate	ESI^+	$C_{16}H_{22}O_4$	279.1596	9.68
Dipentyl phthalate	ESI^+	$C_{18}H_{26}O_4$	307.1909	10.12
Dihexyl phthalate	ESI^+	$C_{20}H_{30}O_4$	335.2222	10.24
Diheptyl phthalate	ESI^+	$C_{22}H_{34}O_4$	363.2535	11.24
Di(2-ethylhexyl) phthalate	ESI^+	$C_{24}H_{38}O_4$	391.2848	11.76
Decyl-octyl-phthalate	ESI^+	$C_{26}H_{42}O_4$	419.3161	13.39
Irganox1010	ESI^+	$C_{73}H_{108}O_{12}$	1194.8160	13.25
Diphenol A	ESI^-	$C_{15}H_{16}O_2$	227.1072	7.83
Irganox 1081	ESI^-	$C_{22}H_{30}O_2S$	357.1894	10.69
Mix 2 (100 ppb)				
5-hydroxyquinoline	ESI^+	C_9H_7NO	146.0604	5.74
8-hydroxyquinoline	ESI^+	C_9H_7NO	146.0604	5.74
Triethylene glycol monobutyl ether	ESI^+	$C_{10}H_{22}O_4$	224.1865	6.74
Trioctyl trimellitate	ESI^+	$C_{33}H_{54}O_6$	547.4015	10.25
Diisononyl phthalate (DINP)	ESI^+	$C_{26}H_{42}O_4$	419.3175	12.94
Di(2-propylheptyl) phthalate	ESI^+	$C_{28}H_{46}O_4$	447.3482	14.07
Sebacic acid	ESI^-	$C_{10}H_{18}O_4$	201.1132	3.82
Butyl butyrate	ESI^-	$C_8H_{16}O_2$	143.108	6.93
Perfluorobutanesulfonic acid (PFBS)	ESI^-	$C_4HF_9O_3S$	298.9424	6.98
Perfluorooctanesulfonic acid (PFOS)	ESI^-	$C_8HF_{17}O_3S$	498.9299	8.66
Diphenol TMC	ESI^-	$C_{21}H_{26}O_2$	309.187	9.49
4-dodecylbenzenesulfonic acid	ESI^-	$C_{18}H_{30}O_3S$	325.1848	9.71
2,4,7,9-Tetramethyl-5-decyne-4,7-Diol (Surfynol 104)	ESI^-	$C_{14}H_{26}O_2$	225.1863	9.78
Mix 3 (50 ppb)				
Dimethyl phthalate	ESI^+	$C_{10}H_{10}O_4$	195.0657	7.22
Diethyl phthalate	ESI^+	$C_{12}H_{14}O_4$	223.0971	8.22
Benzyl butyl phthalate	ESI^+	$C_{19}H_{20}O_4$	313.144	9.54
Dioctyl phthalate	ESI^+	$C_{24}H_{38}O_4$	391.2848	12.13
Diisobutyl phthalate	ESI^+	$C_{16}H_{22}O_4$	279.1596	9.62
Di(2-ethylhexyl) adipate	ESI^+	$C_{22}H_{42}O_4$	371.3162	11.89
Mix 4 (50 ppb)				
Diphenol S	ESI^-	$C_{12}H_{10}O_4S$	249.0224	6.16
Diphenol F	ESI^-	$C_{13}H_{12}O_2$	199.0753	7.16
Diphenol E	ESI^-	$C_{14}H_{14}O_2$	213.0914	7.52

Diphenol A	ESI^-	$C_{15}H_{16}O_2$	227.1068	7.82
Diphenol B	ESI^-	$C_{16}H_{18}O_2$	241.1227	8.24
Diphenol AF	ESI^-	$C_{15}H_{10}F_6O_2$	335.0501	8.37
Diphenol AP	ESI^-	$C_{20}H_{18}O_2$	289.1231	8.44
Diphenol C	ESI^-	$C_{14}H_{10}Cl_2O_2$	255.1382	8.53
Diphenol Z	ESI^-	$C_{18}H_{20}O_2$	267.1384	8.74
Diphenol BP	ESI^-	$C_{25}H_{20}O_2$	351.1394	8.96
Diphenol P	ESI^-	$C_{24}H_{26}O_2$	345.1864	9.35
Mix 5 (100 ppb)				
Dimethyl phthalate-d4	ESI^+	$C_{10}H_6D_4O_4$	199.0903	7.16
Mono-n-butyl phthalate-d4	ESI^+	$C_{12}H_{10}D_4O_4$	227.1222	9.62
Diethyl phthalate-d14	ESI^+	$C_{12}D_{14}O_4$	237.1844	8.15
Diallyl phthalate-d4	ESI^+	$C_{14}H_{10}D_4O_4$	251.1216	8.58
Di-iso-butyl Phthalate--d4	ESI^+	$C_{16}H_{18}D_4O_4$	283.1848	9.62
Mono(ethylhexyl) phthalate -d4	ESI^+	$C_{16}H_{18}D_4O_4$	283.1848	9.62
Benzyl n-Butyl Phthalate-d4	ESI^+	$C_{19}H_{16}D_4O_4$	317.1685	9.53
Dicyclohexyl phthalate-d4	ESI^+	$C_{20}H_{22}D_4O_4$	335.2155	10.26
Di-n-octyl Phthalate--d4	ESI^-	$C_{24}H_{34}D_4O_4$	395.3094	12.13
Di(ethylhexyl) phthalate -d38	ESI^+	$C_{24}D_{38}O_4$	429.5228	11.63
Di-iso-decyl Phthalate-d4	ESI^+	$C_{28}H_{42}D_4O_4$	451.3720	10.03
Di-n-decyl phthalate-d4	ESI^+	$C_{28}H_{42}D_4O_4$	451.3720	14.64

*$[M + H]^+$ for ESI+ compounds and $[M - H]^-$ for ESI- compounds

Table S4.3: The 16 compounds (six with an available analytical standard) that were analyzed using Target MS/MS mode) to confirm their structure in marine mammal blubber/adipose samples after suspect identification.

Compound	Polarity	Chemical formula	m/z	Retention time (min)
Di(2-ethylhexyl) phthalate (DEHP)	ESI^-	$C_{24}H_{38}O_4$	391.2848	11.79
Diethyl phthalate (DEP)	ESI^-	$C_{12}H_{14}O_4$	223.0971	7.00
Di(2-propylheptyl) phthalate (DPHP)	ESI^-	$C_{28}H_{46}O_4$	447.3482	7.65
Irganox1010	ESI^-	$C_{73}H_{108}O_{12}$	1194.8160	13.25
2,4,7,9-Tetramethyl-5-decyne-4,7-diol (Surfynol 104)	ESI^-	$C_{14}H_{26}O_2$	225.1863	9.79
Perfluorooctanesulfonic acid (PFOS)	ESI^-	$C_8HF_{17}O_3S$	498.9299	8.69
Dibenzyl phthalate (DBZP)	ESI^+	$C_{22}H_{18}O_4$	347.1251	NA*
Irganox 1425	ESI^+	$C_{15}H_{25}O_4P$	301.1568	NA*
Topanol CA (TPNC)	ESI^+	$C_{37}H_{52}O_3$	545.4036	NA*
Di-3,4-dimethyl-dibenzylidene sorbitol (DMDBA)	ESI^+	$C_{24}H_{30}O_6$	415.2117	NA*
Dioctyl sebacate	ESI^+	$C_{26}H_{50}O_4$	427.3777	NA*
Trioctyl trimellitate	ESI^+	$C_{33}H_{54}O_6$	547.3962	NA*
2,6-Ditert-Butylphenol	ESI^-	$C_{14}H_{22}O$	205.1603	NA*
p-Nonylphenol (4-Nonylphenol or 4-Nonylphenol-branched)	ESI^-	$C_{15}H_{24}O$	219.1758	NA*
Cyanox 1790	ESI^-	$C_{42}H_{57}N_3O_6$	698.4167	NA*
Di 2,4-di-tert-butylphenyl phosphite	ESI^-	$C_{28}H_{43}O_3P$	457.2956	NA*

*No available standards with which to compare MS/MS patterns, therefore patterns were analyzed instead using SIRIUS 5 (https://bio.informatik.uni-jena.de/software/sirius/).

Table S4.4: Additional compounds (including some Arctic Monitoring and Assessment Programme-identified chemicals of emerging Arctic concern (CEACs)) added to the Agilent Extractable & Leachable LC/QTOF PCDL library for the identification of contaminants in East Greenland polar bear adipose and toothed whale blubber collected from 2012 to 2021.

Chemical Name	CAS	Chemical Formula
Phthalates*		
dioctyl phthalate (DnOP)	117-84-0	$C_{24}H_{38}O_4$
di-(2-ethylhexyl) terephthalate	6422-86-2	$C_{24}H_{38}O_4$
di-(2-ethylhexyl) phthalate	117-81-7	$C_{24}H_{38}O_4$
dibutyl phthalate (DnBP)	84-74-2	$C_{24}H_{38}O_4$
diisobutyl phthalate (DiBP)	84-69-5	$C_{16}H_{22}O_4$
diisodecyl phthalate	26761-40-0	$C_{28}H_{46}O_4$
dinonyl phthalate (DnNP)	84-76-4	$C_{26}H_{42}O_4$
diisononyl phthalate (DiNP)	28553-12-0	$C_{26}H_{42}O_4$
butyl benzyl phthalate (BBP)	85-68-7	$C_{19}H_{20}O_4$
diethyl phthalate (DEP)	84-66-2	$C_{12}H_{14}O_4$
dicyclohexyl phthalate (DCHP)	84-61-7	$C_{20}H_{26}O_4$
di(4-methyl-2-pentyl) phthalate	84-63-9	$C_{20}H_{30}O_4$
dihexyl phthalate (DnHxP)	84-75-3	$C_{20}H_{30}O_4$
di(2-ethylhexyl) phthalate (DEHP)	117-81-7	$C_{24}H_{38}O_4$
diisodecyl phthalate (DiDP)	26761-40-0	$C_{28}H_{46}O_4$
octyldecyl phthalate	119-07-3	$C_{26}H_{42}O_4$
benzyl isooctyl phthlate	27215-22-1	$C_{23}H_{28}O_4$
diisooctyl phthalate (DIOP)	3198-29-6	$C_{24}H_{38}O_4$
dioctyl phthalate (DNOP)	27554-26-3	$C_{24}H_{38}O_4$
diheptyl phthalate (DHP)	3648-21-3	$C_{22}H_{34}O_4$
hexyl octyl phthalate	61827-62-1	$C_{22}H_{34}O_4$
2-ethylhexyl hexyl phthalate (HEHP)	75673-16-4	$C_{22}H_{34}O_4$
dimethyl phthalate (DMP)	131-11-3	$C_{10}H_{10}O_4$
dipentyl phthalate (DnPEP)	131-18-0	$C_{18}H_{26}O_4$
diisopentyl phthalate (DIPeP)	605-50-5	$C_{18}H_{26}O_4$
didecyl phthalate (DnDP)	84-77-5	$C_{28}H_{46}O_4$
Phthalate metabolites		
monomethyl phthalate (MMP)	4376-18-5	$C_9H_8O_4$
monoethyl phthalate (MEP)	2306-33-4	$C_{10}H_{10}O_4$
mono(2-ethyl-5-oxohexyl) phthalate (MEOHP)	40321-98-0	$C_{16}H_{20}O_4$
monoisobutyl phthalate (MiBP)	30833-53-5	$C_{12}H_{14}O_4$
monobutyl phthalate (MnBP)	131-70-4	$C_{12}H_{14}O_4$
mono(2-ethyl-5-hydroxyhexyl) phthalate (MEHHP)	40321-99-1	$C_{16}H_{22}O_5$

mono(2-ethyl-1-hexyl) phthalate (MEHP)	4376-20-9	$C_{16}H_{22}O_4$
monoisononyl phthalate	106-61-0	$C_{17}H_{24}O_4$
monooctyl phthalate (MOP)	5393-19-1	$C_{16}H_{22}O_4$
monobutyl phthalate (MBP)	130-70-4	$C_{12}H_{14}O_4$
monopentyl phthalate (MPEP)	24539-56-8	$C_{13}H_{16}O_4$
monohexyl phthalate (MHXP)	24539-57-9	$C_{14}H_{18}O_4$
monocyclohexyl phthalate (MCHP)	7517-36-4	$C_{14}H_{16}O_4$
monoheptyl phthalate (MHPP)	24539-58-0	$C_{15}H_{20}O_4$
monobenzyl phthalate (MBZP)	2528-16-7	$C_{15}H_{12}O_4$
monodecyl phthalate (MDP)	24539-60-4	$C_{18}H_{26}O_4$
monononyl phthalate (MNP)	24539-59-1	$C_{17}H_{24}O_4$
Antioxidants		
Irgafos 168 Phosphate	31570-04-4	$C_{42}H_{63}O_4P$
Irgafos 126 (Antioxidant 24)	26-74-1	$C_{33}H_{50}O_6P$
Ethanox 702	118-82-1	$C_{29}H_{44}O_2$
Ethanox 703	88-27-7	$C_{17}H_{29}NO$
di-(2-ethylhexyl) sebacate (BEHS)	122-6-23	$C_{26}H_{50}O_4$
dioctyl Decanedioate	2432-87-3	$C_{26}H_{50}O_4$
dibutylmaleate (DBM)	105-76-0	$C_{12}H_{20}O_4$
dibutyl itaconate	2155-60-4	$C_{13}H_{22}O_4$
1,4-Dioxacyclotetradecane-5,14-dione	5578-82-5	$C_{12}H_{20}O_4$
Irganox 1010	6683-19-8	$C_{73}H_{108}O$
Irganox 1310	90804-34-5	$C_{17}H_{26}O_3$
Acrylic acid, n-octyl ester	79-10-7	$C_{11}H_{20}O_2$
di(2-ethylhexyl) adipate (DEHA)	103-23-1	$C_{22}H_{42}O_4$
dioctyl Adipate	123-79-5	$C_{22}H_{42}O_4$
Organophosphate Flame Retardants*		
Tri (2-chloroethyl) phosphate (TCEP)	115-96-8	$C_6H_{12}Cl_3O_4P$
Tri (chloropropyl) phosphate (TCPP)	13674-84-5	$C_9H_{18}Cl_3O_4P$
Tri (dichloropropyl) phosphate (TDCP)	13674-87-8	$C_9H_{15}Cl_6O_4P$
Triphenyl phosphate (TPhP)	115-86-6	$C_{18}H_{15}O_4P$
Tricresyl phosphate (TCrP)	78-30-8	$C_{21}H_{21}O_4P$
Tripropyl phosphate (TPrP)	513-08-6	$C_9H_{21}O_4P$
Tri-n-butyl phosphate (TnBP)	126-73-8	$C_{12}H_{27}O_4P$
Triisobutyl phosphate (TiBP)	126-71-6	$C_{12}H_{27}O_4P$
Tributoxyethyl phosphate (TBEP)	78-51-3	$C_{18}H_{39}O_7P$
Tripentyl phosphate (TPeP)	2528-38-3	$C_{18}H_{15}O_4P$
Tri(2-ethylhexyl) phosphate (TEHP)	78-42-2	$C_{24}H_{51}O_4P$
Dibutylphenylphosphate (DBPhP)	2528-36-1	$C_{14}H_{23}O_4P$

Diphenylbutylphosphate (DPhBP)	981-40-8	$C_{12}H_{11}O_4P$
Trischresylphosphate (TCrP)	78-32-0	$C_9H_{15}O_6P$
4-isopropylphenyl diphenyl phosphate (4IPPDPP)	55864-04-5	$C_{21}H_{21}O_4P$
Di(4-isopropylphenyl) phenyl phosphate (B4IPPPP)	69500-29-4	$C_{24}H_{27}O_4P$
Isopropyl phenyl phosphate (IPPP)	68937-41-7	$C_{21}H_{21}O_4P$
Triphenylphosphine oxide (TPPO)	791-28-6	$C_{18}H_{15}OP$
Tris(1,3-dichloro-2-propyl) phosphate (TDCPP)	136-87-8	$C_9H_{15}Cl_6O_4P$
Siloxanes*		
Hexamethylcyclotrisiloxane (D3)	541-05-9	$C_6H_{18}O_3Si_3$
Octamethylcyclotetrasiloxane (D4)	556-67-2	$C_8H_{24}O_4Si_4$
Decamethylcyclopentasiloxane (D5)	541-02-6	$C_{10}H_{30}O_5Si_5$
Dodecamethylcyclohexasiloxane (D6)	540-97-6	$C_{12}H_{36}O_6Si_6$
Hexamethyldisiloxane (MM)	107-46-0	$C_6H_{18}OSi_2$
Octamethyltrisiloxane (MDM)	107-51-7	$C_6H_{24}O_2Si_3$
Decamethyltetrasiloxane (MD2M)	141-62-8	$C_{10}H_{30}O_3Si$
Dodecamethylpentasiloxane (MD3M)	141-63-9	$C_{12}H_{36}O_4Si_5$
Phenols		
Tetrabromodiphenol A (*TBBPA*)	79-94-7	$C_{15}H_{12}Br_4O_2$
Diphenol A	80-05-7	$C_{15}H_{16}O_2$
Diphenol E	2081-08-5	$C_{12}H_{10}O$
Diphenol F	620-92-8	$C_{13}H_{12}O_2$
Diphenol S	80-09-1	$C_{12}H_{10}O_4S$
Diphenol Z	843-55-0	$C_{18}H_{20}O_2$
4,4’-Biphenol	92-88-6	$C_{12}H_{10}O_2$
2,4-dichlorophenol	120-83-2	$C_6H_4Cl_2O$
2,5-dichlorophenol	583-78-8	$C_6H_4Cl_2O$
Triclosan	3380-34-5	$C_{12}H_7Cl_3O_2$
4-nonylphenol	104-40-5	$C_{15}H_{24}O$
4-octylphenol	1806-26-4	$C_{14}H_{22}O$
2,6-di-tert-butylphenol	128-39-2	$C_{14}H_{22}O$

*AMAP classified CEAC group

Table S4.5: Recovery ([peak area in sample/peak area in standard]*100) for n=3 marine mammal blubber-spiked standards. Based on standard availability, only standard mix 5 (Table S4.1) were spiked into blubber samples (n=3).

Compound Name	Mean ± Standard Deviation % Recovery	Mass Accuracy (ppm)
Dimethyl phthalate-d4	25.4 ± 10.2	1.00
Diethyl phthalate-d14	49.5 ± 11.2	3.08
Diallyl phthalate-d4	63.7 ± 5.6	0.84
Di-iso-butyl phthalate-d4	79.0 ± 15.0	0.40
Mono(2-ethylhexyl) pthalate-d4	82.2 ± 10.3	0.64
Benzyl n-Butyl Phthalate-d4	65.2 ± 12.5	1.77
Dicyclohexyl phthalate-d4	81.3 ± 10.2	0.63
Di-n-octyl phthalate -d4	65.4 ± 5.2	0.30
Di(2-ethylhexyl) phthalate -d38	58.8 ± 13.4	0.51
Di-iso-decyl phthalate-d4	84.4 ± 8.4	0.23
Di-n-decyl phthalate-d4	47.8 ± 15.6	0.66

Equation 1: Supplemental details on the calculation of analyte concentrations

A Microsoft Excel spreadsheet was used to calculate analyte concentrations as follows:

$$C_s = [(A_s/A_{std}) \times C_{std}] \times [(V_{Sf}/W_s)] \times 10^{-3} \ (or\ 10^{-6})$$

where C_s = analyte concentration in the sample in μg/g (wet weight): A_s = area counts of analyte (PCB or OC) in the sample; A_{std} = area counts of analyte in the injected standard; C_{std} = analyte concentration in the standard solution in pg/μL: V_{Sf} = final volume of the sample, in μL; W_S = sample weight in g (wet weight); 10^{-3} to convert to ng/g or 10^{-6} to convert to mg/kg

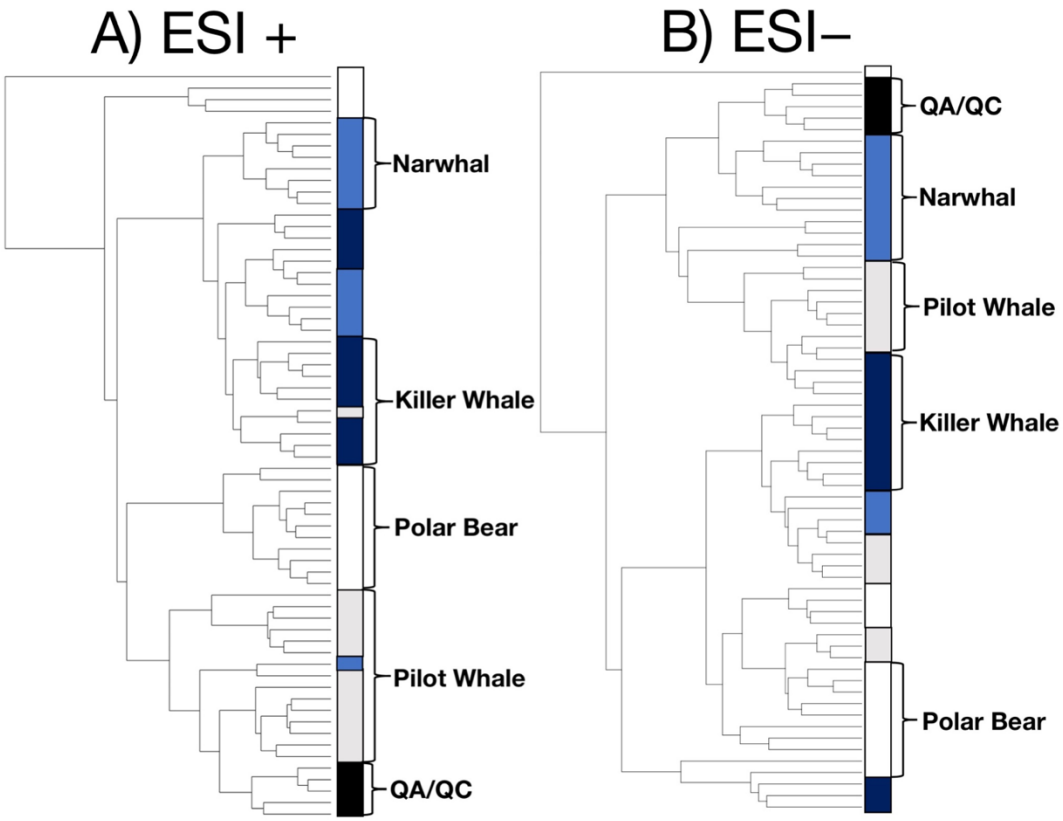

Figure S4.2: Hierarchical clustering analysis based on the peak areas from all features in individual marine mammals (killer whale [*Orcinus orca*], narwhal [*Monodon monoceros*], long-finned pilot whale [*Globicephala melas*], and polar bear [*Ursus maritimus*]) grouped by age class/sex following filtering from the pooled quality assurance/quality control injections (n=5; 2,496 total features), from the nontarget screening approach. The figures were generated using Mass Profiler Professional 15.1 (MPP, Agilent Technologies).

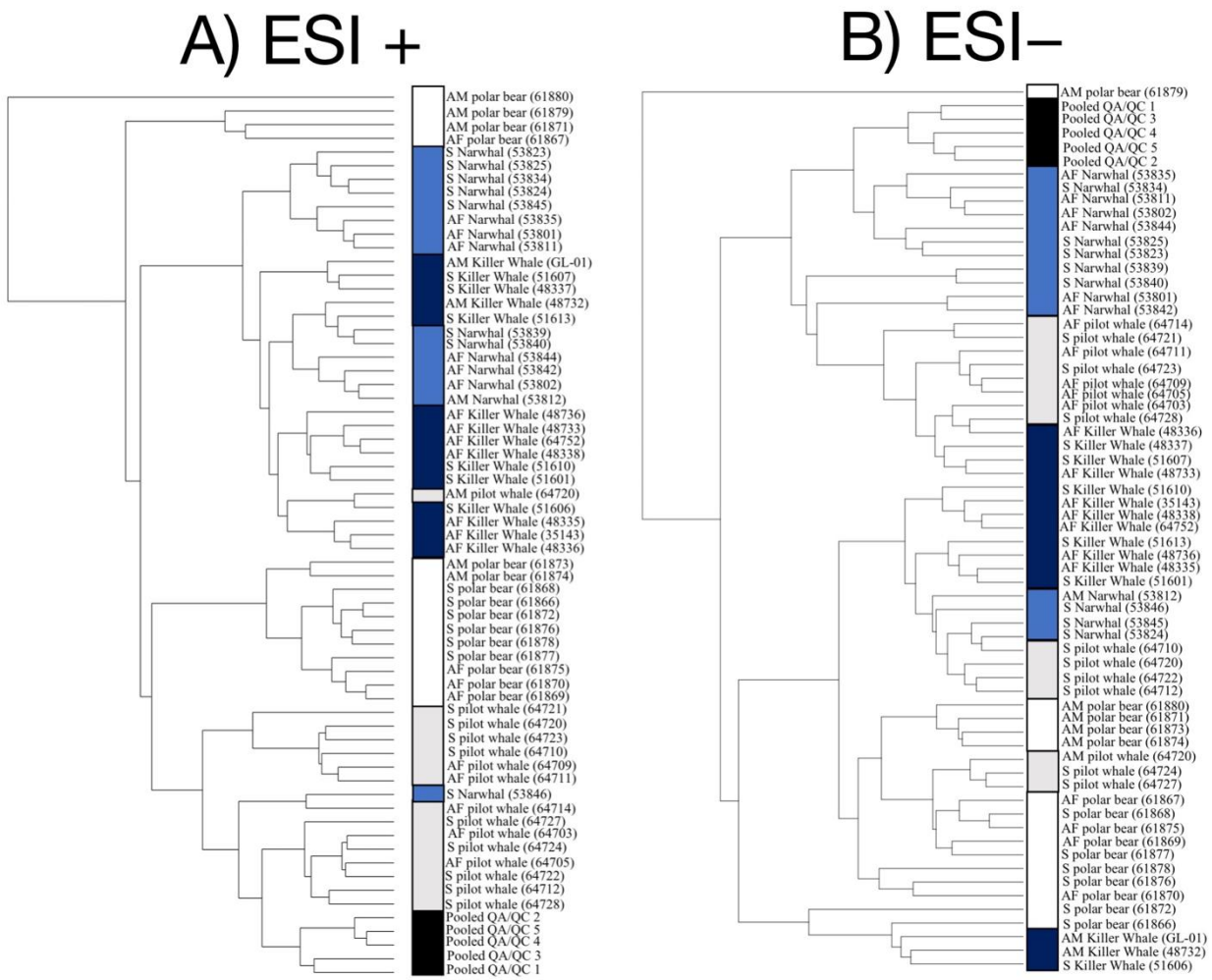

Figure S4.2: Hierarchical clustering analysis based on the peak areas from all features in individual marine mammals (killer whale [Orcinus orca], narwhal [Monodon monoceros], long-finned pilot whale [Globicephala melas], and polar bear [Ursus maritimus]) grouped by age class/sex following filtering from the pooled quality assurance/quality control injections (n=5), method detection limits, and from features in blanks from the suspect screening approach. AM= adult male, AF = adult females, S = subadult.

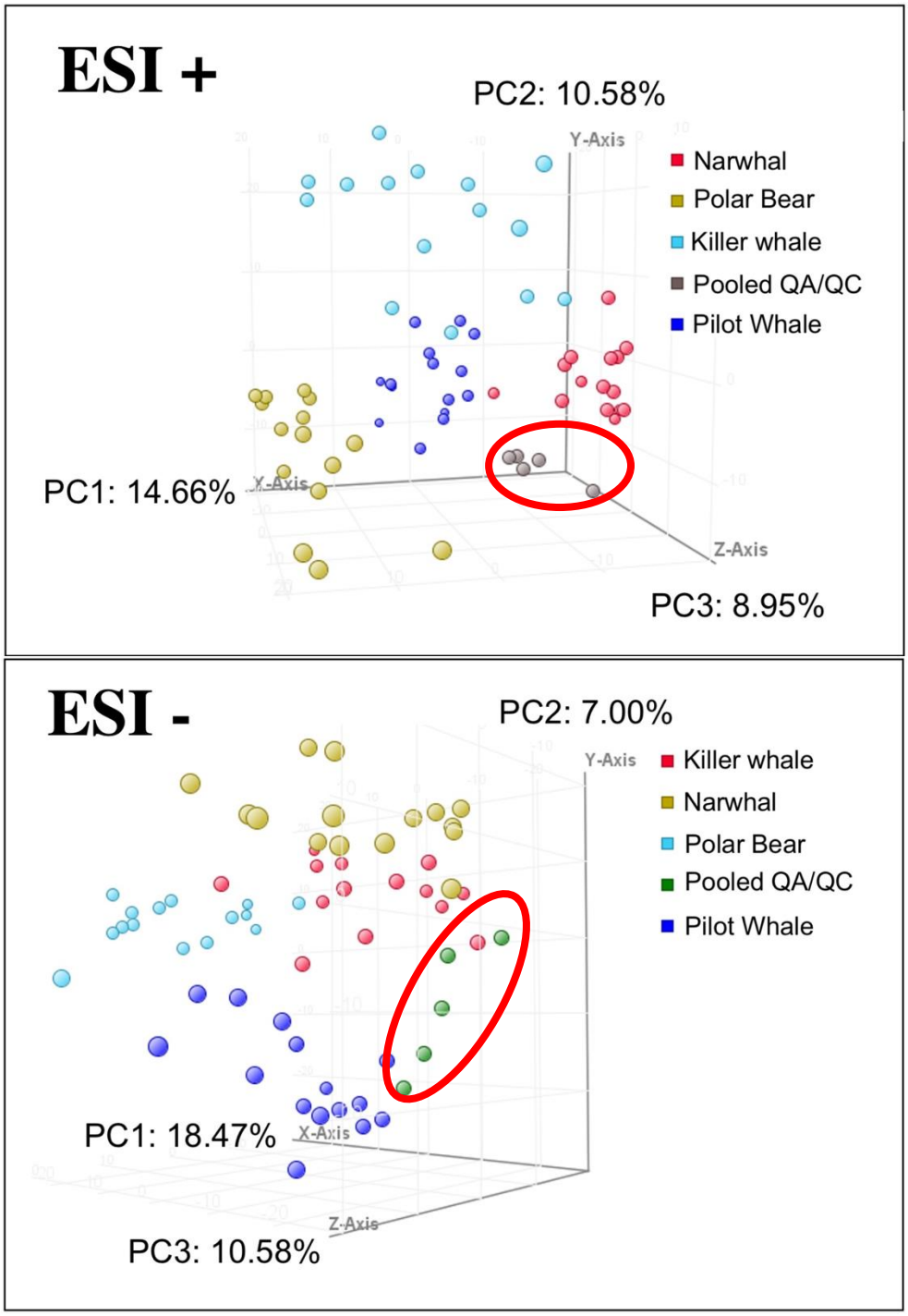

Figure S4.3: Principal components analysis based on the peak areas from all features in individual marine mammals (killer whale [Orcinus orca], narwhal [Monodon monoceros], long-finned pilot whale [Globicephala melas], and polar bear [Ursus maritimus]) following filtering from the pooled quality assurance/quality control injections (n=5). ESI+ monitored 1,645 features, while ESI- monitored 1,031 features. The pooled QA/QC samples are circled in each PCA.

Table S4.6: All 138 features present in in East Greenland polar bear adipose and toothed whale blubber collected from 2012 to 2021 with detection > 3 and a relative standard deviation (RSD) < 40% in pooled QA/QC and above the mean + 3σ of the blanks in both ESI+ and ESI- from suspect screening. The following is provided: chemical formula, the mean mass (and its relative standard deviation (RSD)) across all samples, the mean retention time across all samples, the mean peak area across all samples, and the mean library match score across all samples.

Chemical Name	Chemical Formula	Mass (mean)	Mass (RSD)	Retention Time (Mean)	Peak Area (Mean)	Matching Score (mean)
ESI+						
Diethylene glycol dibenzoate	$C_{18}H_{18}O_5$	314.1157	1.19	8.91	6018	99.7
Myristamine oxide	$C_{16}H_{35}NO$	257.2716	0.27	9.81	48853	99.7
N-Methylpyrrolidone	C_5H_9 NO	99.0682	0.73	8.11	110912	99.8
Sorbic acid	$C_6H_8O_2$	112.0523	1.54	8.53	13420	99.6
1,4-Cyclohexanedione	$C_6H_8O_2$	112.0523	1.54	8.53	13420	99.6
Caprolactone	$C_6H_{10}O_2$	114.0682	1.79	8.49	10010	87.7
2-Hydroxycyclohexanone (Adipoin)	$C_6H_{10}O_2$	114.0682	1.79	8.49	10010	87.7
Dibutylamine	C_8 H_{19} N	129.1517	0.22	5.00	89812	100
Aminocaproic acid	$C_6H_{13}NO_2$	131.0945	0.77	8.13	10819	99.8
3,4-Dimethylbenzaldehyde	$C_9H_{10}O$	134.0728	1.06	8.84	9281	96
4-Ethylbenzaldehyde	$C_9H_{10}O$	134.0728	1.06	8.84	9281	96
Phthalic anhydride	$C_8H_4O_3$	148.0159	0.58	11.8	109128	100
Cinnamic acid	$C_9H_8O_2$	148.0522	0.84	8.91	5711	99.7
Mesitaldehyde	$C_{10}H_{12}O$	148.0888	0.55	8.84	15719	87.8
Cumene hydroperoxide	$C_9H_{12}O_2$	152.0829	0.93	1.57	9264	82.7
1,4-Diacetylbenzene	$C_{10}H_{10}O_2$	162.0678	0.37	9.5	82264	99.7
1,3-Benzenedicarboxylic acid	$C_8H_6O_4$	166.0266	0.47	11.8	19637	99.9
Terephthalic acid	$C_8H_6O_4$	166.0266	0.47	11.8	19637	99.9
Phthalic acid	$C_8H_6O_4$	166.0266	0.47	11.8	19637	99.9
Butyl 4-hydroxybenzoate	$C_{11}H_{14}O_3$	194.0932	9.24	8.92	19121	99.9
Ethyl 4-ethoxybenzoate	$C_{11}H_{14}O_3$	194.0932	9.24	8.92	19121	99.9
Tetraethyleneglycol	$C_8H_{18}O_5$	194.1153	0.29	3.77	79443	100
2,2,6,6-Tetramethypiperidinol	$C_{11}H_{23}NO_2$	201.1727	0.42	1.63	305904	99.8
2,2,6,6-Tetramethypiperidinol	$C_{11}H_{23}NO_2$	201.1727	0.34	3.2	170889	99.8
tert-Dodecylmercaptan	$C_{12}H_{26}S$	202.1758	0.37	3.19	21322	86.1

Triethylene glycol monobutyl ether	$C_{10}H_{22}O_4$	206.1511	0.69	6.06	9301	98.8
Diethyl phthalate (DEP)	$C_{12}H_{14}O_4$	222.0892	0.46	8.21	39172	98.9
Diethyl terephthalate	$C_{12}H_{14}O_4$	222.0892	0.46	8.21	39172	98.9
Diethyl isophthalate	$C_{12}H_{14}O_4$	222.0892	0.46	8.21	39172	98.9
Monoisobutyl phthalic acid (MIBP)	$C_{12}H_{14}O_4$	222.0892	0.46	8.21	39172	98.9
Monobutyl phthalate	$C_{12}H_{14}O_4$	222.0892	0.46	8.21	39172	98.9
Dibutylmaleate (DBM)	$C_{12}H_{20}O_4$	228.1358	0.8	12.87	27040	99.7
1,4-Dioxacyclotetradecane-5,14-dione	$C_{12}H_{20}O_4$	228.1358	0.8	12.87	27040	99.7
Dibutyl itaconate	$C_{13}H_{22}O_4$	242.1516	0.43	13.31	45731	99.7
2,4-Diethylthioxanthone	$C_{17}H_{16}OS$	268.0919	2.23	10.7	2811	99.2
Stearylamine (ODA)	$C_{18}H_{39}N$	269.3078	0.27	9.09	36346	99.5
N,N-Dimethylcetylamine	$C_{18}H_{39}N$	269.3078	0.27	9.09	36346	99.5
Lauroylsarcosine	$C_{15}H_{29}NO_3$	271.2144	1.35	9.41	9067	97.3
Octyldimethyl PABA (Padimate O)	$C_{17}H_{27}NO_2$	277.2042	1.54	10.53	21591	86.1
DBP / Dibutyl phthalate	$C_{16}H_{22}O_4$	278.1516	0.3	11.8	70351	99.9
Mono-n-octyl phthalate	$C_{16}H_{22}O_4$	278.1516	0.3	11.8	70351	99.9
Mono-(2-ethylhexyl) phthalate (MEHP)	$C_{16}H_{22}O_4$	278.1516	0.3	11.8	70351	99.9
Diisobutyl phthalate (DIBP)	$C_{16}H_{22}O_4$	278.1516	0.3	11.8	70351	99.9
Stearamide (Octadecanamide)	$C_{18}H_{37}NO$	283.2872	0.28	11.7	64598	99.6
2,2-(Tridecylazanediyl)diethanol	$C_{17}H_{37}NO_2$	287.2823	0.24	10.3	163189	99.5
Dimantine (Dymanthine)	$C_{20}H_{43}N$	297.3393	0.21	9.57	87810	99.8
Irganox 1425 degradation product	$C_{15}H_{25}O_4P$	300.1501	4.92	9.6	7697	93.6
Tri(propylene glycol) diacrylate	$C_{15}H_{24}O_6$	300.1577	2.23	8.53	12324	99.8
Diethoxyneopentyl glycol diacrylate	$C_{15}H_{24}O_6$	300.1577	2.23	8.53	12324	99.8
Dehydroabietic acid	$C_{20}H_{28}O_2$	300.2055	4.04	11.04	28492	95.4
Tinuvin 329	$C_{20}H_{25}N_3O$	323.1972	2	6.38	8228	81.8
Tinuvin 320	$C_{20}H_{25}N_3O$	323.1972	2	6.38	8228	81.8
Leuco Malachite Green	$C_{23}H_{26}N_2$	330.2099	1.69	9.78	29665	99.3
Erucamide (Erucic amide)	$C_{22}H_{43}NO$	337.3345	0.42	13.25	1230655	99.8
1,4-Bis{2-[(2-methyl-2-propanyl) peroxy]-2-propanyl}benzene	$C_{20}H_{34}O_4$	338.2454	0.96	11.29	3450	84.6
Octadecyl methacrylate	$C_{22}H_{42}O_2$	338.3194	5.56	11.36	2777	87.2
Erucic acid	$C_{22}H_{42}O_2$	338.3194	5.56	11.36	2777	87.2
2-Ethylhexyl fumarate (DOF)	$C_{20}H_{36}O_4$	340.2607	1.07	12	18683	99.7
Dibenzyl phthalate (DBZP)	$C_{22}H_{18}O_4$	346.1178	0.29	9.35	9150	84.8

Sudan III	$C_{22}H_{16}N_4O$	352.131	0.76	9.69	20813	87.4
Gylceryl linoleate (1-Monolinolein)	$C_{21}H_{38}O_4$	354.2761	1.29	12.82	14296	99.6
Irgacure 369	$C_{23}H_{30}N_2O_2$	366.2298	3.31	10.28	9863	96.9
Di(2-ethylhexyl) terephthalate (DEHT)	$C_{24}H_{38}O_4$	390.2771	0.27	11.8	1329267	99.8
Dioctyl phthalate (DNOP)	$C_{24}H_{38}O_4$	390.2771	0.27	11.8	1329267	99.8
Diisooctyl phthalate (DIOP)	$C_{24}H_{38}O_4$	390.2771	0.27	11.8	1329267	99.8
Di(2-ethylhexyl) phthalate (DEHP)	$C_{24}H_{38}O_4$	390.2771	0.27	11.8	1329267	99.8
Triethylene glycol bis(2-ethylhexanoate)	$C_{22}H_{42}O_6$	402.2977	2.14	10.46	11078	98.7
Triethylene glycol dicaprylate	$C_{22}H_{42}O_6$	402.2977	2.14	10.46	11078	98.7
Bis (3,4-dimethyl-dibenzylidene sorbitol)	$C_{24}H_{30}O_6$	414.2044	0.15	8.84	623512	99.8
Bis (3,4-dimethyl-dibenzylidene sorbitol)	$C_{24}H_{30}O_6$	414.204	0.19	9	105746	99.9
Dinonyl phthalate (DNP)	$C_{26}H_{42}O_4$	418.3081	0.45	12.49	103212	99
Diisononylphthalate (DINP)	$C_{26}H_{42}O_4$	418.3081	0.45	12.49	103212	99
Octyl decyl phthalate	$C_{26}H_{42}O_4$	418.3081	0.45	12.49	103212	99
Ethanox 702	$C_{29}H_{44}O_2$	424.3337	0.6	12.04	58030	96
Dioctyl Decanedioate	$C_{26}H_{50}O_4$	426.3647	11.27	14.25	15684	83.1
Bis-(2-ethylhexyl) sebacate (BEHS)	$C_{26}H_{50}O_4$	426.3647	11.27	14.25	15684	83.1
2,5-bis(5-tert-Butyl-2-benzoxazolyl)thiophene (BBOT)	$C_{26}H_{26}N_2O_2S$	430.1745	1.88	10.49	29363	90.3
Tocopherol (Vitamin E)	$C_{29}H_{50}O_2$	430.3812	5.73	10.72	6466	87.4
Topanol CA (TPNC)	$C_{37}H_{52}O_3$	544.3943	1.23	11.12	16961	80.8
Trioctyl trimellitate	$C_{33}H_{54}O_6$	546.3898	0.63	9.79	738676	90.6
Trioctyl trimellitate	$C_{33}H_{54}O_6$	546.3889	0.46	14.66	27975	80.5
TOTM / Tri-2-ethylhexyl trimellitate	$C_{33}H_{54}O_6$	546.3898	0.63	9.79	738676	90.6
TOTM / Tri-2-ethylhexyl trimellitate	$C_{33}H_{54}O_6$	546.3889	0.46	14.66	27975	80.5
Mark PEP 36	$C_{35}H_{54}O_6P_2$	632.3382	0.46	13.4	15313	93.8
Diisooctyl phthalate (DIOP)	$C_{24}H_{38}O_4$	390.2771	0.27	11.8	1329267	99.8
Bis-(2-ethylhexyl) sebacate (BEHS)	$C_{26}H_{50}O_4$	426.3647	11.27	14.25	15684	83.1
ESI-						
Malic acid	$C_4H_6O_5$	134.0215	0.4	1.57	5278	99.6
Decanoic acid (Capric acid)	$C_{10}H_{20}O_2$	172.1465	0.33	8.47	33385	99.8
6-Methylheptyl methacrylate	$C_{12}H_{22}O_2$	198.1619	0.43	8.96	5654	87.4
4-Octylphenol	$C_{14}H_{22}O$	206.1675	0.34	9.78	5795001	98.5
2,6-Di-tert-butylphenol	$C_{14}H_{22}O$	206.1675	0.34	9.78	5795001	98.5
2,4-Di-tert-butylphenol	$C_{14}H_{22}O$	206.1675	0.34	9.78	5795001	98.5

4-tert-Octylphenol	$C_{14}H_{22}O$	206.1675	0.34	9.78	5795001	98.5
2,6-di-tert-butyl-p-Cresol (BHT)	$C_{15}H_{24}O$	220.1828	0.37	10.16	38688	99.9
p-Nonylphenol (4-Nonylphenol)	$C_{15}H_{24}O$	220.1828	0.37	10.16	38688	99.9
NP / Nonylphenol (4-Nonylphenol-branched)	$C_{15}H_{24}O$	220.1828	0.37	10.16	38688	99.9
2,5-Di-tert-butylhydroquinone	$C_{14}H_{22}O_2$	222.1621	0.41	9.51	131079	99.4
Isobornyl methacrylate	$C_{14}H_{22}O_2$	222.1621	0.41	9.51	131079	99.4
Surfynol 104	$C_{14}H_{22}O_2$	226.1932	0.32	9.75	29799	87.2
Dibutyl itaconate	$C_{13}H_{22}O_4$	242.152	0.46	7.3	10968	99.5
Pentadecanoic acid	$C_{15}H_{30}O_2$	242.2246	0.2	10.6	103287	100
Methyl tetradecanoate	$C_{15}H_{30}O_2$	242.2246	0.2	10.6	103287	100
Palmitoleic acid	$C_{16}H_{30}O_2$	254.2248	0.36	10.36	128379	86.7
Tridecyl acrylate	$C_{16}H_{30}O_2$	254.2248	0.36	10.36	128379	86.7
Benzenemethanol, 4-[1-[(1,1-dimethylethyl) dioxy]-1-methylethyl]- Î±,Î±-dimethyl-	$C_{16}H_{26}O_3$	266.1887	0.28	9.77	346035	99.4
7,9-Di-tert-butyl-1-oxaspiro(4,5)deca-6,9-diene-2,8-dione	$C_{17}H_{24}O_3$	276.1723	1.85	8.74	6879	85.5
Linolenic acid	$C_{18}H_{30}O_2$	278.2247	0.4	10.09	17353	99.7
Linoleic acid	$C_{18}H_{32}O_2$	280.2406	0.58	10.5	71412	95.4
Methyl oleate	$C_{19}H_{36}O_2$	296.2714	0.66	11.49	9241	85.9
Hexadecyl acrylate (Cetyl acrylate)	$C_{19}H_{36}O_2$	296.2714	0.66	11.49	9241	85.9
Dehydroabietic acid	$C_{20}H_{28}O_2$	300.2092	0.34	10.03	68996	92.5
Hexadecyl methacrylate	$C_{20}H_{38}O_2$	310.2873	0.6	12	332841	98.5
Ethyl oleate	$C_{20}H_{38}O_2$	310.2873	0.6	12	332841	98.5
Arachidic acid (Eicosanoic acid)	$C_{20}H_{40}O_2$	312.3029	0.21	13.41	74659	100
Ethyl stearate	$C_{20}H_{40}O_2$	312.3029	0.21	13.41	74659	100
Malachite Green (Basic Green)	$C_{23}H_{25}N_2$	329.199	0.96	10.33	16114	83.9
Erucamide (Erucic amide)	$C_{22}H_{43}NO$	337.3345	0.63	13.19	21130	96.4
Octadecyl methacrylate (Stearyl methacrylate)	$C_{22}H_{42}O_2$	338.3189	0.37	13.32	203894	99.2
Erucic acid	$C_{22}H_{42}O_2$	338.3189	0.37	13.32	203894	99.2
Behenic acid	$C_{22}H_{44}O2$	340.334	0.32	14.56	6257	99.9
2-Ethylhexyl hexyl phthalate (HEHP)	$C_{22}H_{34}O_4$	362.2456	0.8	10.14	21743	99.8
Hexyl octyl phthalate	$C_{22}H_{34}O_4$	362.2456	0.8	10.14	21743	99.8
Diheptyl phthalate (DHP)	$C_{22}H_{34}O_4$	362.2456	0.8	10.14	21743	99.8

Diisoheptyl phthalate (DIHP)	$C_{22}H_{34}O_4$	362.2456	0.8	10.14	21743	99.8
Lignoceric acid	$C_{24}H_{48}O_2$	368.3654	0.33	13.23	9675	99.9
Monoester analog of Irganox 1010	$C_{22}H_{36}O_6$	396.2515	0.76	11.42	10381	99.7
Perfluorohexanesulfonic acid	$C_6HF_{13}O_3S$	399.9445	1.28	7.95	3915	99.6
Sudan 410	$C_{26}H_{24}N_4O$	408.1948	0.79	9.72	20161	95.2
2,2',6,6'-Tetra-tert-butyldiphenylquinone	$C_{28}H_{40}O_2$	408.3031	1.63	12.71	3404952	98.6
Docusate hydrogen	$C_{20}H_{38}O_7S$	422.234	0.21	9.62	171926	99.4
Bis 2,4-di-tert-butylphenyl phosphite	$C_{28}H_{43}O_3P$	458.2975	12.89	10.69	13397	94
Perfluorooctanesulfonic acid (PFOS)	$C_8HF_{17}O_3S$	499.9375	0.3	8.67	131353	100
Cinnamate derivative of Irganox 1076	$C_{35}H_{60}O_3$	528.4542	0.84	12.54	70001	96.2
Quinonemethide derivative of Irganox 1076	$C_{35}H_{60}O_3$	528.4542	0.84	12.54	70001	96.2
Cyanox 1790	$C_{42}H_{57}N_3O_6$	699.4241	1.34	13.3	4810	98.4
Triclosan	$C_{12}H_7Cl_3O_2$	287.9513	0.39	9.54	53422	99.7
Triester analog of Irganox 1010	$C_{56}H_{84}O_{10}$	916.6053	0.29	12.45	100540	99.4
Irganox 1010	$C_{73}H_{108}O_{12}$	1176.7818	1.04	13.24	1754104	98.8

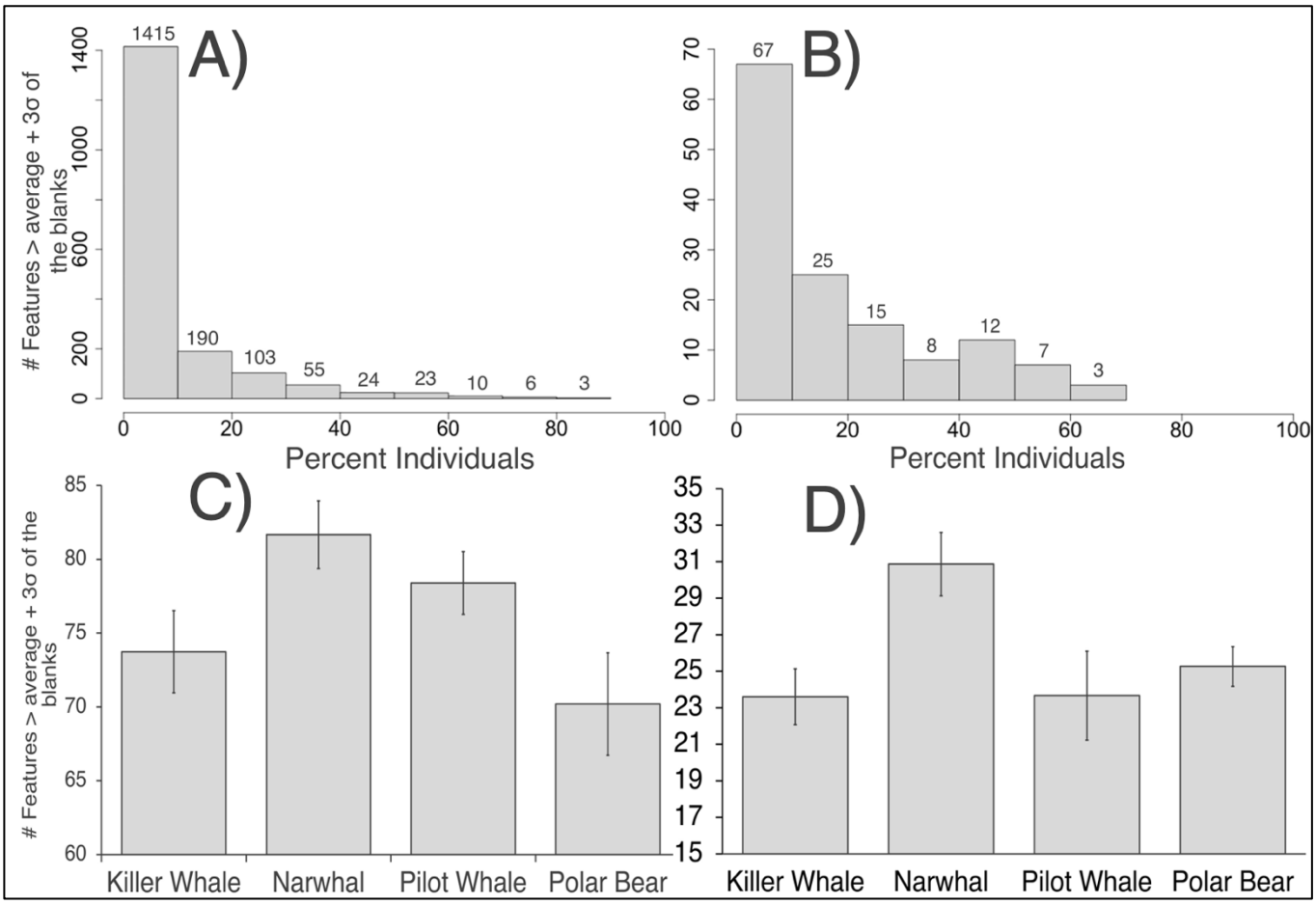

Figure S4.4: All features pre- (A and C) and post-(B and D) pooled QA/QC filtering above the mean + 3σ of the blanks in both ESI+ and ESI- for all sample from East Greenland polar bear adipose and toothed whale blubber collected from 2012 to 2021. Figures A and B: frequency plot of all features across all samples and Figures C and D: Mean number of features per species and standard error bars.

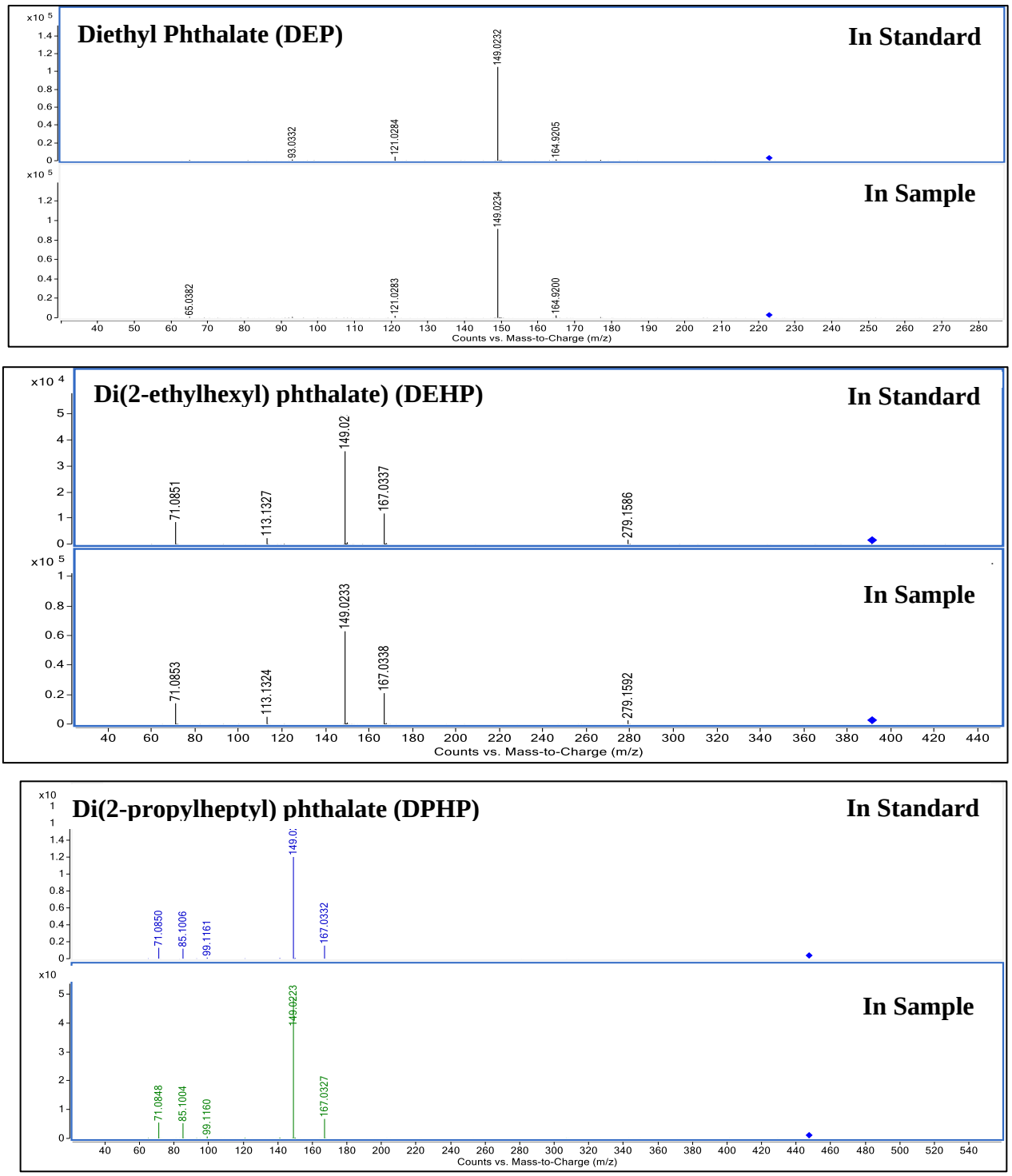

Figure S4.5: MS/MS fragmentation patterns for diethyl phthalate (DEP; top), di(2-ethylhexyl) phthalate) (DEHP; middle) and di(2-propylheptyl) phthalate (DPHP; bottom). Patterns in authentic analytical standards are provided in the top of each pane and matching patterns in a marine mammal blubber sample indicate compound confirmation and presence in samples.

Table S4.7: A confirmation information (retention time and MS/MS fragmentation pattern) from available standards to matches in at least one East Greenland polar bear adipose and/or toothed whale blubber collected from 2012 to 2021. Dark shading indicates confirmed compounds (Level 1 confirmation identification; Schymanski et al., 2014), while lighter shade compounds indicate tentatively identified compounds

Feature m/z	RT in standard	Molecular formula	Standard Name	Abbreviation	RT match from standard	MS/MS match from standard
ESI+						
195.0657	7.22	$C_{10}H_{10}O_4$	Dimethyl phthalate	DMP	No	NA
223.0971	8.22	$C_{12}H_{14}O_4$	Diethyl phthalate	DEP	**Yes**	**Yes**
279.1596	9.67	$C_{16}H_{22}O_4$	Dibutyl phthalate	DBP	**Yes**	NA*
313.144	9.54	$C_{19}H_{20}O_4$	Benzyl butyl phthalate	BBP	**Yes**	NA*
391.2848	12.13	$C_{24}H_{38}O_4$	Dioctyl phthalate	DOP	No	NA
419.3175	12.94	$C_{26}H_{42}O_4$	Diisononyl phthalate	DINP	No	NA
447.3482	14.08	$C_{28}H_{46}O_4$	Di(2-propylheptyl) phthalate	DPHP	**Yes**	**Yes**
391.2848	11.75	$C_{24}H_{38}O_4$	Di(2-ethylhexyl) phthalate	DEHP	**Yes**	**Yes**
279.1596	9.62	$C_{16}H_{22}O_4$	Diisobutyl phthalate	DIBP	No	NA
307.1909	10.11	$C_{18}H_{26}O_4$	Dipentyl phthalate	DPP	No	NA
363.2535	11.24	$C_{22}H_{34}O_4$	Diheptyl phthalate	DHP	No	NA
419.3161	13.38	$C_{26}H_{42}O_4$	Decyl octyl phthalate		No	NA
335.2222	10.24	$C_{20}H_{30}O_4$	Dihexyl phthalate	DnHP	**Yes**	NA*
1194.8160	13.25	$C_{73}H_{108}O_{12}$	Irganox 1010		**Yes**	**Yes**
357.1894	10.69	$C_{22}H_{30}O_2S$	Irganox 1081		**Yes**	NA
146.0604	5.74	C_9H_7NO	5-hydroxyquinoline		No	NA
146.0604	5.74	C_9H_7NO	8-hydroxyquinoline		No	NA
224.1865	6.74	$C_{10}H_{22}O_4$	Triethylene glycol monobutyl ether		No	NA
547.4015	10.25	$C_{33}H_{54}O_6$	Trioctyl trimellitate		No	NA
ESI-						
298.9424	6.98	$C_4HF_9O_3S$	Perfluorobutanesulfonic acid		No	NA
498.9299	8.66	$C_8HF_{17}O_3S$	Perfluorooctanesulfonic acid	PFOS	**Yes**	**Yes**
201.1132	3.82	$C_{10}H_{18}O_4$	Sebacic acid		No	NA
143.1080	6.93	$C_8H_{16}O_2$	Butyl butyrate		**Yes**	No
309.1870	9.49	$C_{21}H_{26}O_2$	Diphenol TMC		No	NA
325.1848	9.71	$C_{18}H_{30}O_3S$	4-dodecylbenzenesulfonic acid		No	NA

225.1863	9.78	$C_{14}H_{26}O_2$	2,4,7,9-Tetramethyl-5-decyne-4,7-Diol	Surfynol 104	**Yes**	NA*
220.1828	10.16	$C_{15}H_{24}O$	4-Nonylphenol		No	NA
220.1828	10.16	$C_{15}H_{24}O$	4-Nonylphenol-branched)		**Yes**	No

*MS/MS spectra quality too low for compound confirmation

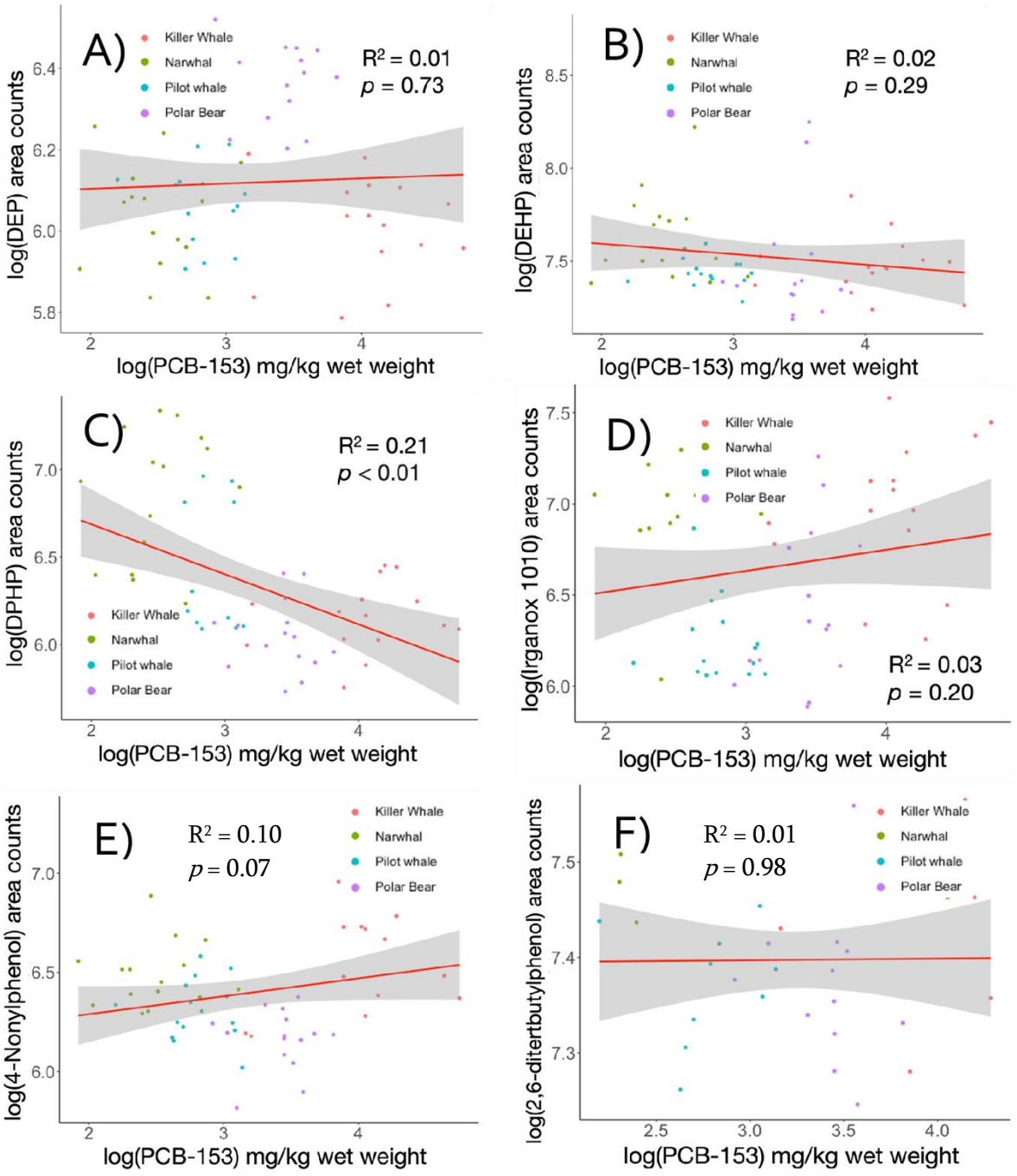

Figure S4.6: Linear regressions comparing nontargeted contaminants to PCB-153 concentrations (mg/kg wet weight) in the same killer whale, narwhal, pilot whale, and polar bear blubber/adipose tissues for area counts (divided by wet weight) of diethyl phthalate (DEP), Di(2-ethylhexyl) phthalate (DEHP), Di(2-propylheptyl) phthalate (DPHP), Irganox 1010, 4-nonylphenol (or isomers), and 2,6-ditertbutylphenol (or isomers)

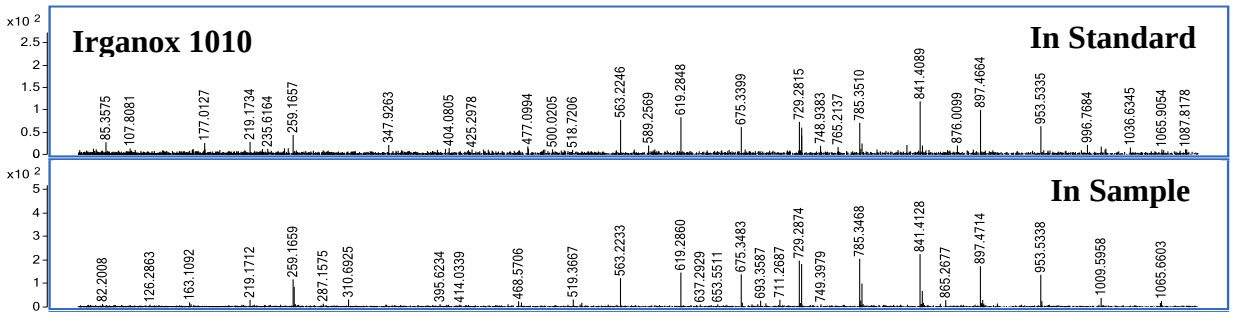

Figure S4.7: MS/MS fragmentation patterns for Irganox 1010. Patterns in authentic analytical standards are provided in the top of each pane and matching patterns in a marine mammal blubber sample indicate compound confirmation and presence in samples.

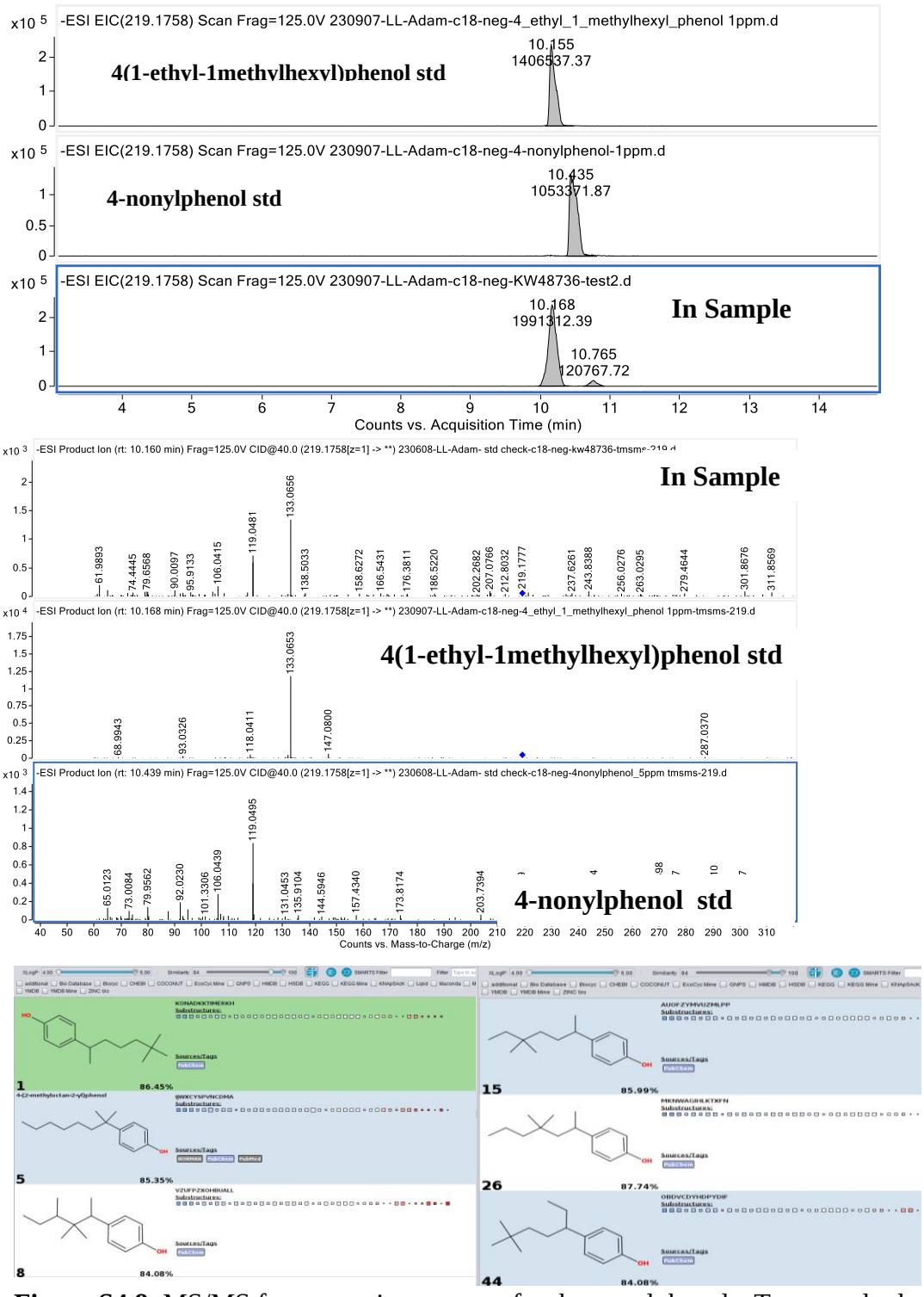

Figure S4.8: MS/MS fragmentation patterns for the nonylphenols. Two standards, 4-nonylphenol and 4(1-ethyl-1methylhexyl)phenol were compared to the retention time and fragmentation patterns in samples, but did not match (top and middle figures). We then compared targeted MS/MS patterns to those existed in a SIRIUS library. The corresponding compounds with a fragmentation pattern match >84% are shown in the bottom image.

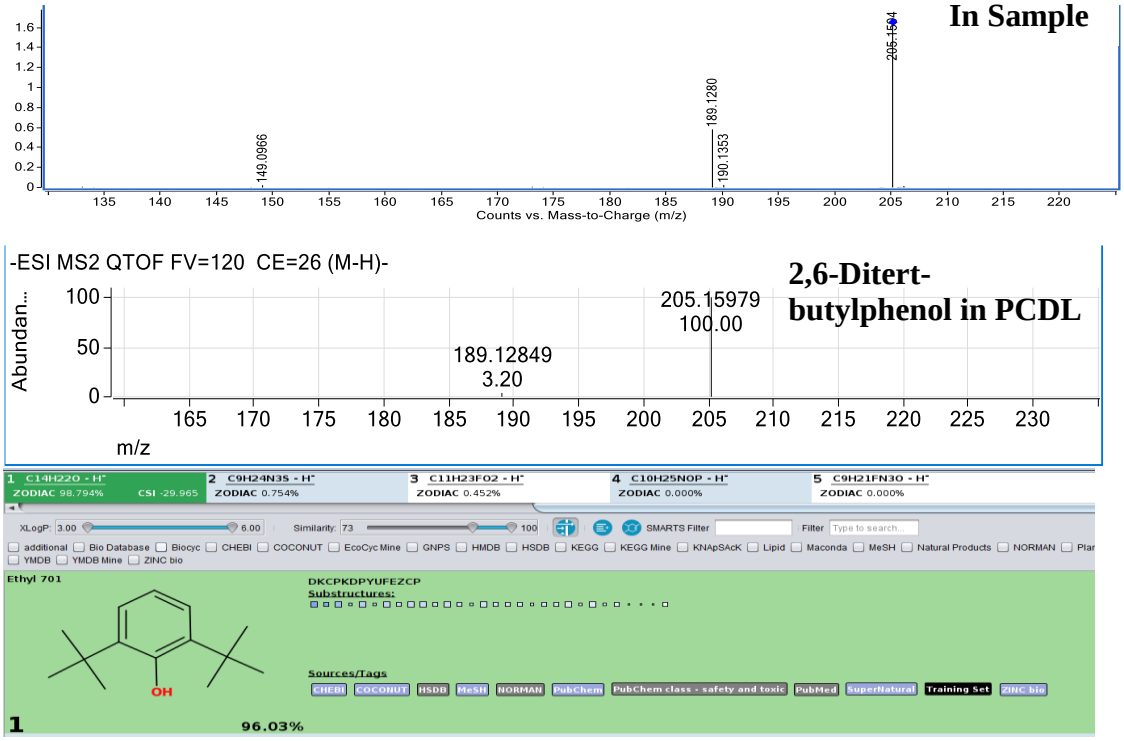

Figure S4.9: MS/MS fragmentation patterns for the 2,6-ditert-butylphenol. As standards were not available, we compared targeted MS/MS patterns to those existed in a SIRIUS library. The corresponding compound with a fragmentation pattern match at ~96% is shown in the bottom image.

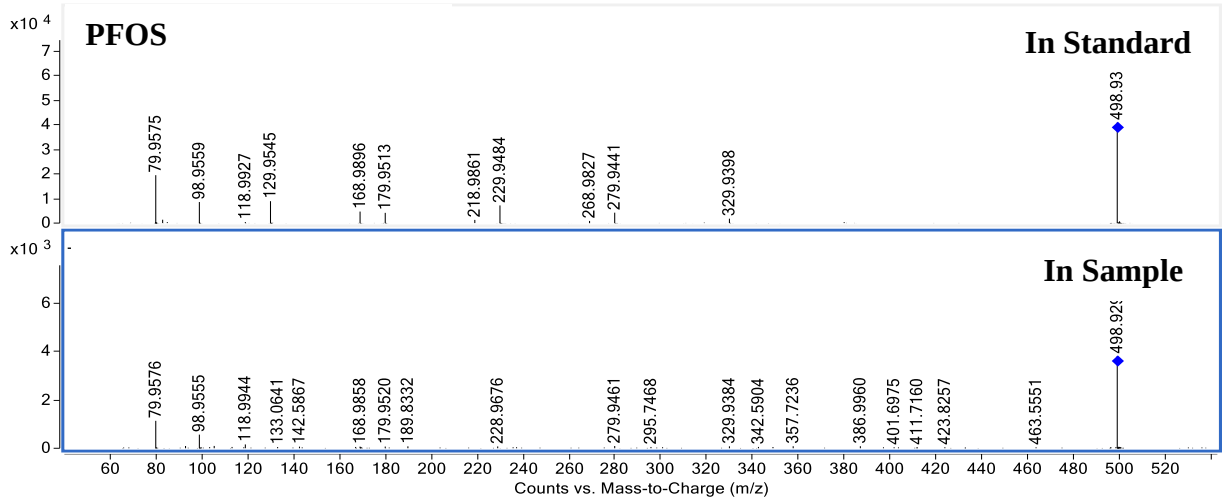

Figure S4.10: MS/MS fragmentation patterns for perflurooctanesulfonic acid (PFOS). Patterns in authentic analytical standards are provided in the top of each pane and matching patterns in a marine mammal blubber sample indicate compound confirmation and presence in samples.

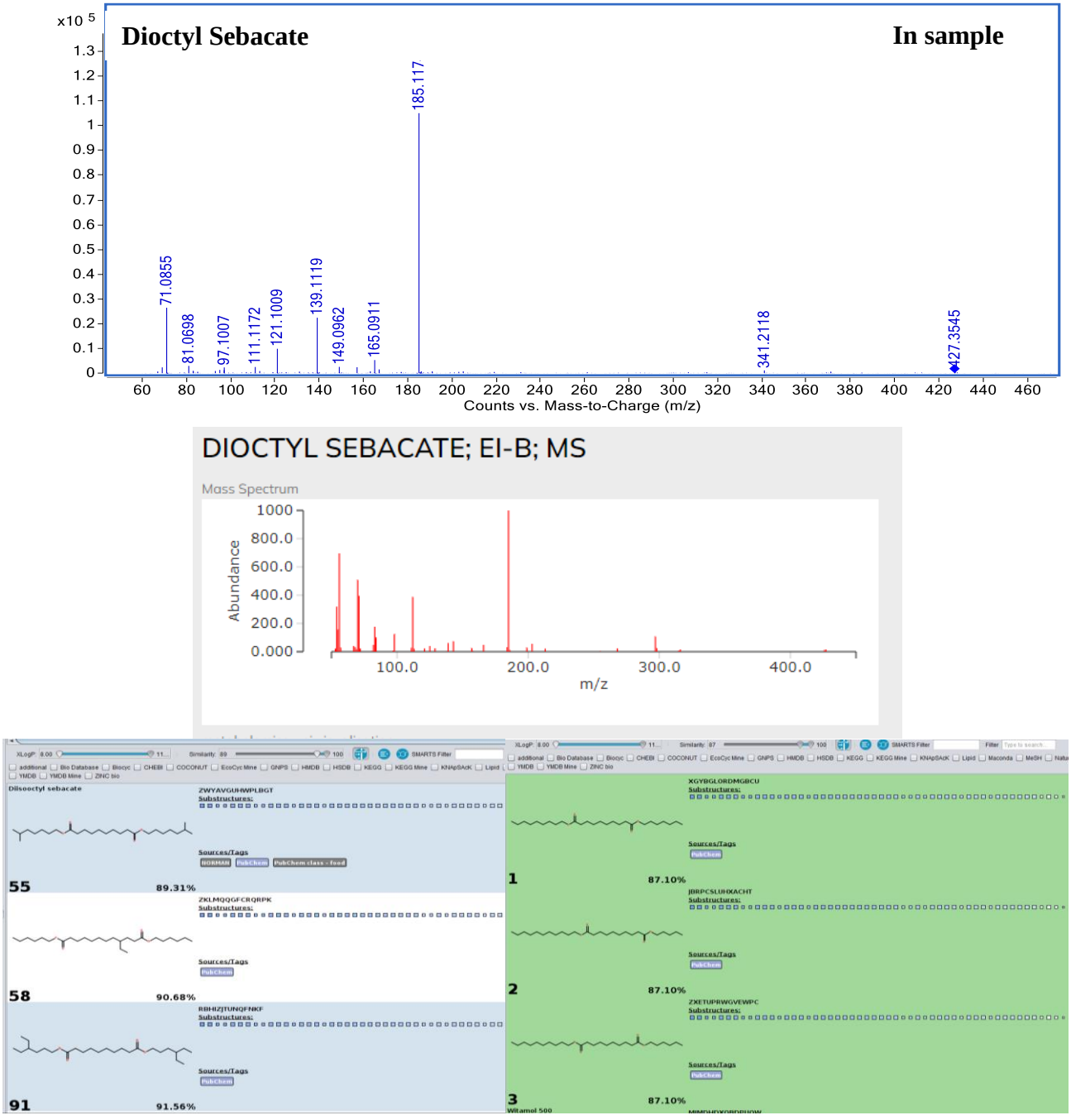

Figure S4.11: MS/MS fragmentation patterns for the dioctyl sebacate. As standards were not available, we compared targeted MS/MS patterns to those existed in a SIRIUS library. The corresponding compounds with a fragmentation pattern match >87% are shown in the bottom images.

CONNECTING TEXT

Chapters 3 and 4 successfully developed new approaches to monitor concentrations of legacy and emerging contaminants using a QuEChERS-based approach coupled with nontarget and suspect screening. However, tracing the accumulation of these contaminants into marine mammal blubber and adipose tissues was not yet discussed. As described in Chapter 2.3, the bioaccumulation of both new and emerging contaminants in marine mammal fatty tissues is anticipated to be mostly from diet. Although some commonly used tracing approaches currently are used to assess the accumulation of these contaminants from diet and biomagnification, including bulk SI, they can have drawbacks and lack sufficient resolution to detail some dietary patterns in mobile marine predators (see Chapter 2.6).

As such, instead, Chapter 5 discusses the use of FA signatures as a newer, higher resolution dietary tracer to assess the accumulation of contaminants in marine mammals. The QuEChERS method developed in Chapter 3 was used here to extract legacy POPs in polar bear, killer whale, and long-finned pilot whale, and all killer whale legacy contaminant data was already available from Chapter 3. Generalized linear models using FAs were then used to assess the role of diet in determining interspecific differences in these concentrations. Unfortunately, as concentration data was not available for most of the confirmed nontarget/suspect screened chemicals (see Chapter 4.4.7), they were not included in Chapter 5 analysis. Using FA signatures may provide new, potentially higher resolution insights into the role of diet in determining differences in legacy POP concentrations among these marine mammal species.

CHAPTER 5: FEEDING AND BIOLOGICAL DIFFERENCES INDUCE WIDE VARIATION IN LEGACY PERSISTENT ORGANIC POLLUTANT CONCENTRATIONS AMONG TOOTHED WHALES AND POLAR BEAR IN THE ARCTIC

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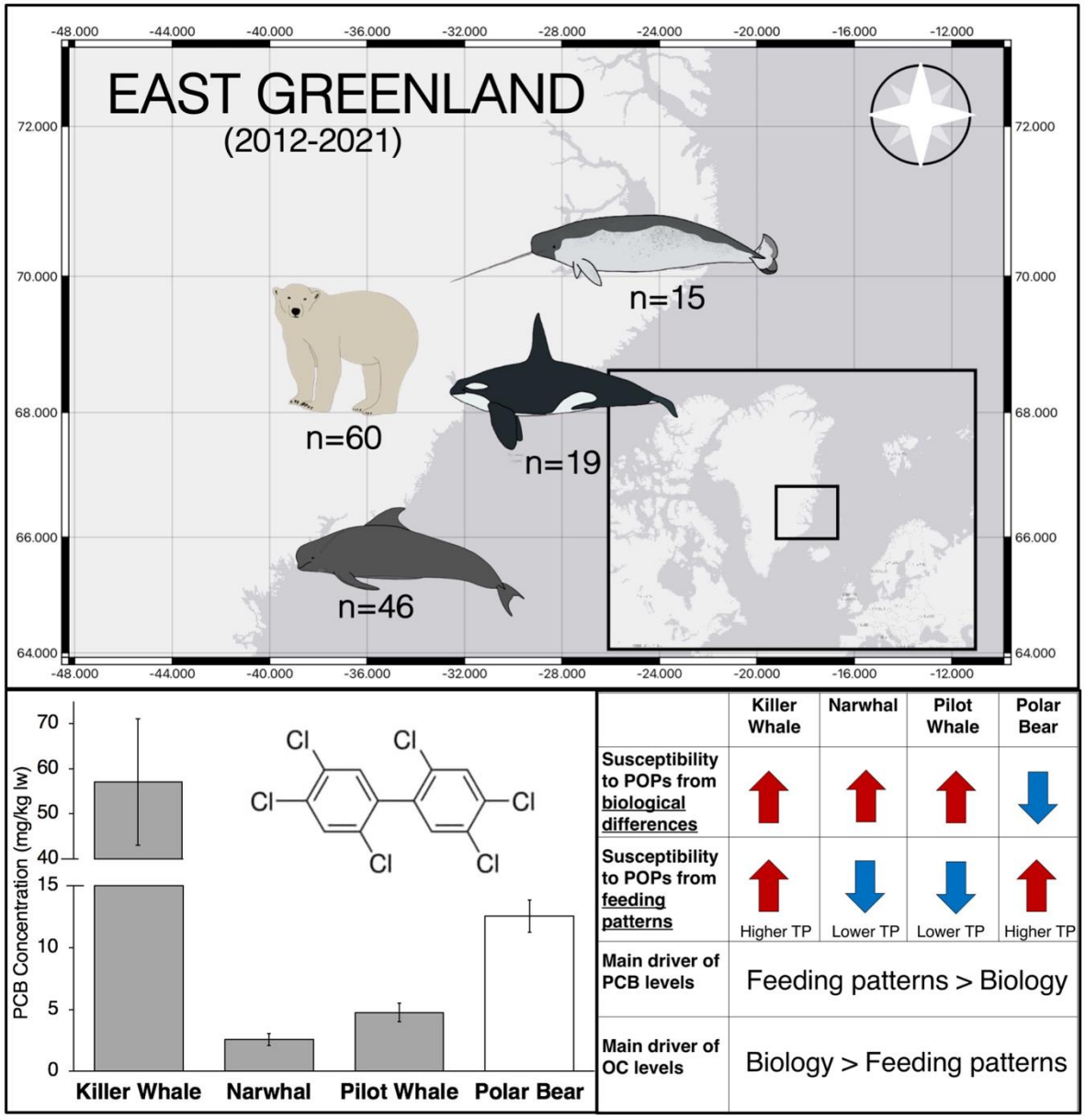
5.1. ABSTRACT

Polar bear and toothed whales in the Arctic exhibit orders of magnitude differences in concentrations of legacy persistent organic pollutants (POPs), which may be attributed to comparisons made across regions and different time frames. These interspecific differences could be influenced by variations in biological susceptibility, including differences in xenobiotic biotransformation between polar bear, from the order Carnivora, and toothed whales, from the order Artiodactyla, as well as ecological factors, such as variation in feeding patterns. Here, we analyzed samples from subsistence-harvested toothed whales and polar bear in East Greenland collected between 2012-2021 and quantitatively compared interspecific differences in blubber/adipose polychlorinated biphenyl (PCB) and organochlorine (OC) pesticide concentrations. We further determined fatty acid (FA) signatures as dietary tracers to evaluate how feeding patterns influence POP concentrations relative to the influence of biological differences between taxa. Killer whale exhibited the highest mean concentrations of ΣPCBs (57.0 ± 14.0 mg/kg lw), Σdichlorodiphentlytrichloroethanes (ΣDDTs; 55.7 ± 13.1), and Σchlordanes (ΣCHLs; 23.1 ± 5.6 mg/kg lw), while polar bear showed the second highest concentrations for ΣPCBs (12.5 ± 1.3 mg/kg lw), but comparable or even lower levels of all OCs relative to narwhal and pilot whale. Linear models using FA patterns as explanatory variables for POP concentrations demonstrated that, for ΣPCBs, diet differences explained most of the variation. Conversely, biological differences explained more of the variation for most OCs, especially for DDT, for which polar bear showed the lowest concentrations despite feeding on similarly high trophic position prey as killer whale. This novel quantitative comparison confirms that significant differences in legacy POP concentrations occur among Arctic marine mammal predators. Furthermore, the drivers of these differences are contaminant-specific, with feeding

patterns primarily influencing PCB concentrations, taxa-specific biological characteristics (e.g., in xenobiotic biotransformation capacity) affecting DDT concentrations, and both factors contributing to variations in other OCs.

Keywords: POPs, polar bear, killer whale, narwhal, long-finned pilot whale, fatty acids

5.2. GRAPHICAL ABSTRACT



5.3. INTRODUCTION

Some marine mammals in the Arctic, particularly polar bear (*Ursus maritimus*) and toothed whales (*Odontocetes*), show among the highest concentrations worldwide of persistent organic pollutants (POPs), including polychlorinated biphenyls (PCBs) and organochlorine (OC) pesticides, such as dichlorodiphenyltrichloroethanes (DDTs), chlordanes (CHLs), chlorobenzenes (ClBzs), and hexachlorocyclohexanes (HCHs) (e.g. McKinney et al., 2011a; Desforges et al., 2018; Letcher et al., 2018; Dietz et al. 2019). These legacy POPs have long been banned or restricted internationally under the Stockholm Convention (United Nations Environmental Programme, 2009). However, due to their environmental persistence, long-range transport potential, and tendency to bioaccumulate and biomagnify in marine food webs (Borgå et al., 2004), they are still among the most predominant synthetic organic contaminants in the environment, including in the Arctic (Borgå et al., 2022). Given the persistence and bioaccumulation potential of these POPs, their toxicity in predator marine mammals is of concern, and thus concentrations in blubber/adipose are routinely monitored in certain locations throughout the Arctic (Dietz et al., 2019). Elevated concentrations of lipophilic PCBs and OC pesticides in these marine mammals may be explained, at least in part, by their high trophic positions within Arctic marine food webs as tertiary or even quaternary consumers, as well as their often lipid-rich diets (Borgå et al., 2004; Chen et al., 2022).

Despite these overall elevated POP concentrations reported in polar bear and toothed whales, blubber/adipose POP concentrations among these species, when qualitatively compared among studies, have been suggested to vary by one or even two orders of magnitude (McKinney et al., 2011a; Carlsson et al., 2014; Pedro et al., 2017). Nonetheless, comparisons among studies with vast geographic differences in sampling locations and disparate time frames makes it

challenging to draw meaningful conclusions. In East Greenland, for example, annual monitoring of adipose concentrations of PCBs and OC pesticides in polar bear has occurred for decades since 1983, and data from 2011 showed mean DDT concentrations at 0.39 ± 0.11 mg/kg lipid weight lipid weight (lw) (Dietz et al., 2013; McKinney et al., 2013; Dietz et al., 2018). In comparison, killer whale (*Orcinus orca*) are range shifting northward into multiple Arctic regions including East Greenland (Higdon et al., 2014; Bourque et al., 2018) and some harvested in 2012-2014 in East Greenland showed substantially higher mean DDT concentrations at 52 +/- 11 mg/kg lw (Pedro et al., 2017). For other toothed whales, such as the endemic narwhal (*Monodon monoceros*) and range-shifting long-finned pilot whale (*Globicephala melas*), PCB and OC pesticide concentrations are much less well known with existing data only from different locations and much earlier timepoints (Muir et al., 1992; Borrell et al., 1995; Dietz et al., 2004; Sonne et al., 2010; Carlsson et al., 2014; Dietz et al., 2021). However, the recent spatiotemporal cooccurrence of killer whale, narwhal, pilot whale and polar bear in areas such as East Greenland (Higdon et al., 2014; Garde et al., 2015; Hansen et al., 2019; Heide-Jørgensen et al., 2023) may now permit this region to serve as a suitable study location to directly compare contaminant concentrations among these species.

If such direct comparisons were made, differences in POP concentrations among these marine predators could be related to a variety of factors, including interspecific biological differences (Borgå et al., 2004), such as xenobiotic biotransformation capacity, excretion routes, and longevity. Multiple studies have detailed limited phase I cytochrome P450 xenobiotic biotransformation capability of toothed whales relative to Carnivora species, such as polar bear (Letcher et al., 2009; McKinney et al., 2011b; Sonne et al., 2018). Toothed whales also show limited biotransformation capacity due to function loss of the Paraoxonase 1 gene (PON1; Meyer

et al., 2018). Additionally, toothed whales cannot excrete contaminants through hair unlike polar bear (Dietz et al., 2006; Jaspers et al., 2010). Toothed whales may also show higher accumulation over their lifetimes due to greater longevity (up to ~90 years in killer whale and ~50 years in narwhal and pilot whale) compared to polar bear (up to ~30 years) (Borgå et al., 2004; Hickie et al., 2007; Taylor et al., 2007; Garde et al., 2015). As a result of these particular biological characteristics, relative to polar bear, toothed whales may be more susceptible to contamination (**Table 5.1**).

Table 5.1: Possible biological and ecological drivers of potential differences in susceptibility to accumulation of legacy persistent organic pollutants among toothed whales (killer whale, narwhal, and pilot whale) and polar bear.

	Killer Whale	Narwhal	Pilot Whale	Polar Bear	References
Increased susceptibility to contamination from biological characteristics	Yes	Yes	Yes	No	Houde et al., 2005 Borga et al., 2004 Norstorm et al., 1992
Limited biotransformation potential	Yes	Yes	Yes	No*	Meyer et al., 2018 Letcher et al. 2009 Letcher et al., 1998 Boon et al., 1997
Limited excretion capacity	Yes	Yes	Yes	No**	Jaspers et al., 2010 Dietz et al., 2006
Longevity	Yes	Yes	Yes	No	Garde et al., 2015 Taylor et al., 2007 Hickie et al., 2007 Abend and Smith, 1999
Increased susceptibility to contamination from feeding patterns	Yes	No	No	Yes	Heide-Jørgensen et al., 2023 Garde et al., 2022 Remili et al., 2022 McKinney et al., 2013
Primary diet items	Tertiary and secondary consumers (seal and fish)	Secondary and primary consumers (fish and invertebrates)	Tertiary/ secondary consumers (cephalopods)	Tertiary consumers (Seal)	Heide-Jørgensen et al., 2023 Garde et al., 2022 Remili et al., 2022 McKinney et al., 2013

*At least for the biotransformation of DDT and some PCBs (that are meta-para unsubstituted)
**Potentially for PCB and OC pesticide excretion through hair

In addition to these biological factors, feeding patterns may play a role in interspecific variation in legacy contaminant concentrations among these species. In East Greenland, killer whale and polar bear have been recently estimated to consume mostly seal, while narwhal and pilot whale likely feed at lower trophic positions on fish and/or invertebrates (**Table 5.1**). The killer whale and polar bear diet estimates are based on fatty acid (FA) signature analysis, which provides information on the long-term species composition of their diets, while similar and thus more comparable diet analyses have not been performed for narwhal and pilot whale in this region. Many FAs consumed by predators, like toothed whales and polar bear, are deposited into blubber/adipose tissues with little or predictable modification (Budge et al., 2006). As such, FA signatures in these predators reflect those assimilated from their prey, allowing for insights into feeding patterns and direct comparison among them. As the legacy POPs are generally highly lipophilic, FA signatures may be regarded as useful tools to assess the role of dietary patterns in explaining variation in contaminant concentrations among multiple predator marine mammals.

The first objective of the present study is to assess interspecific variation in concentrations of PCBs and OC pesticides among the three toothed whales species killer whale, narwhal, pilot whale and polar bear collected in East Greenland from 2012-2021. Secondly, we compare dietary patterns among these species using FA signatures. Lastly, we test how variation in dietary patterns influences interspecific differences in these legacy POP concentrations, relative to influences of biological differences between toothed whales and polar bear. If differences in contaminant concentrations among these species are driven by both variation in diet and biological susceptibility (**Table 5.1**), then we hypothesize that killer whale will show the highest concentrations due to feeding on high trophic position prey and high biological susceptibility. Instead, narwhal and pilot whale will show lower concentrations due to lower

trophic feeding but high biological susceptibility, and polar bear will also show lower levels due to feeding at high trophic position but low biological susceptibility.

5.4. METHODS

5.4.1 Sample Location and Collection

Samples from 19 killer whale collected in 2012-2014 and 2021, 15 narwhal in 2015, 46 pilot whale in 2016, 2018, and 2021, and 60 polar bear in 2012-2016 and 2021 (see Table S5.1 for details on regions, years and biological information) were opportunistically collected from the local subsistence harvest with help from local hunters of East Greenland communities (**Table 5.2;** map available in Figure S5.1). For each whale, a full-blubber depth sample was taken, while for polar bear, a sample of subcutaneous adipose was collected, and then stored at -20°C until they arrived at McGill University, where they were then stored at -80°C until time of analysis. For all samples, sex was determined visually. Age classes (i.e., adult or subadult, based on sexual maturity) of killer whale and narwhal were determined based on animal size and sexual maturity (e.g., by confirming size of dorsal fin; Perrin, 1982; Perrin and Reilly, 1984; Garde et al., 2015). For pilot whale samples collected in 2021 and all polar bear, individual ages were determined by counting annual growth layer groups of the I_3 tooth after decalcification using methods described elsewhere (Dietz et al., 1991). To create a comparable dataset across all species, we grouped individual ages in each species to age class. For polar bear, age classifications were: adult males ≥ 6 years of age, adult females ≥ 5 years, and subadults consisted of all others (Rosing-Asvid et al., 2002). For pilot whale, age classifications were adult males ≥ 13 years, adult females ≥ 6 years, and subadults consisted of all other individuals (Betty et al., 2022). For pilot whale collected in 2016 and 2018, neither age nor age class data were determined.

Table 5.2: Sampling location and GPS coordinates, years of collection, and sample size for all killer whale (Orcinus orca), narwhal (Monodon monoceros), long-finned pilot whale (Globicephala melas), and polar bear (Ursus maritimus) blubber/adipose included in this study.

Species	Year Collected	Sampling Location	GPS Coordinates	Sample Size
Killer whale	2012	Tasiilaq, Greenland	65°37 N 37°57 W	6
	2013	Tasiilaq, Greenland	65°37 N 37°57 W	3
	2013	Kulusuk, Greenland	65°20 N 37°10 W	2
	2014	Tasiilaq, Greenland	65°37 N 37°57 W	5
	2021	Kulusuk, Greenland	65°20 N 37°10 W	1
	2021	Ittoqqortoomiit, Greenland	70°29 N 21°58 W	2
Narwhal	2015	Gaasefjord, Greenland	70°10 N 27°15 W	15
Pilot Whale	2016*	Tasiilaq, Greenland	65°37 N 37°57 W	9
	2018*	Sermiligaaq, Greenland	65°54 N 36°22 W	7
	2021	Tasiilaq, Greenland	65°37 N 37°57 W	20
	2021	Kulusuk, Greenland	65°20 N 37°10 W	10
Polar bear	2012	Ittoqqortoomiit, Greenland	70°29 N 21°58 W	9
	2013	Ittoqqortoomiit, Greenland	70°29 N 21°58 W	7
	2014	Ittoqqortoomiit, Greenland	70°29 N 21°58 W	10
	2015	Ittoqqortoomiit, Greenland	70°29 N 21°58 W	10
	2016	Ittoqqortoomiit, Greenland	70°29 N 21°58 W	9
	2021	Ittoqqortoomiit, Greenland	70°29 N 21°58 W	15

*Age class and sex data not available for these samples.

5.4.2. Contaminant Analysis

The killer whale, narwhal, pilot whale, and 2021 polar bear tissues were extracted and analyzed for PCBs and OC pesticides at McGill University (Sainte-Anne-de-Bellevue, Quebec, Canada) using established methods (Pedersen et al. 2023). From a 0.075-0.100 g piece of tissue, the target analytes were extracted using a modified QuEChERS (quick, easy, cheap, effective, rugged, and safe) approach (see SI Section S3.3) and spiked with 20 µL of mass labelled-PCBs ($^{13}C_{12}$-PCB-28, 52, 118, 138, 153, 180, 194) and OC pesticides ($^{13}C_6$-1,2,4,5-tetrachlorobenzene, $^{13}C_6$-pentachlorobenzene, and $^{13}C_6$-hexachlorobenzene). Final extracts were analyzed for 41 PCB congeners and 19 OC pesticides including DDTs, CHLs, ClBzs, and HCHs (Table S5.2) on an

Agilent 7820A gas chromatograph with mass spectrometer (GC-MS) (Agilent Technologies, Santa Clara, CA, USA; GC system 7820A, MSD 5977B) using selective ion monitoring (SIM). For each batch of 10 samples, a National Institute of Standards and Technology (NIST) standard reference material (SRM) sample (1945 pilot whale for killer whale and 1946 Lake Superior fish tissue for narwhal, pilot whale, and 2021 polar bear) and a method blank were also extracted. The method limit of detection (MLoD) was set to 3 × the signal-to-noise ratio, and method limit of quantification (MLoQ) was set to 10 × the signal-to-noise ratio for each compound, and MLoD ranged from 0.1-3.6 ng/g and MLoQ ranged from 0.4-12.9 ng/g. For SRM 1945, mean accuracies (calculated as [accepted value in NIST SRM - our measured value]/ [accepted value in NIST SRM] *100) across all batches were 16.6 ± 9.8% and 19.0 ± 12.9%, for ΣPCBs and ΣOCs, respectively (Table S5.3), and for SRM 1946, mean ΣPCBs and ΣOCs accuracies were 20.5 ± 13.4% and 14.6 ± 6.5%, respectively, across all batches (Table S5.3). Internal standard spikes showed recoveries for mass-labelled PCBs and ClBzs at 81.4 ± 16.4% and 62.3 ± 15.6%, respectively, across all batches (Table S5.4). Due to low recoveries of the ClBzs, these, but no other OCs, were recovery-corrected. Trace amounts of some PCBs and *p,p'*-DDE and *trans*-nonachlor (<0.88 ng/mL) were found in some blanks. However, these levels were more than ten times lower than the concentrations found in samples and thus black subtraction was not performed.

The 2012-2016 polar bear samples were extracted and analyzed at Environment and Climate Change Canada (Organic Contaminants Research Laboratory, National Wildlife Research Centre Carleton University, Ottawa, Canada). More detailed contaminant analysis information is available in Supporting Information Section S5.3. Briefly, 0.1 to 0.2 g of adipose tissue were extracted using established methods reported elsewhere (Letcher et al., 2009;

McKinney et al., 2010, 2011a). 74 PCB congeners and 20 OC pesticides including DDTs, CHLs, ClBz, and HCHs were monitored (see Table S5.2). Extracts were analyzed on an Agilent 6890 GC coupled with a 5973 MSD in the positive EI mode and using SIM. For each batch of 10 samples, a NIST SRM sample (1945 pilot whale) and a method blank sample were also extracted. The PCB and OC mean accuracies across all batches were 8.6 ± 5.0% and 12.1 ± 3.5%, respectively (Table S5.3). These accuracies (as well as those reported from samples extracted at McGill University) met analytical performance guidelines detailed by SANTE/11312/202.

To ensure comparability between labs, only a subset of congeners and compounds that were extracted in both labs were included in the data analyses. Between these two extraction techniques, we have previously (Pedersen et al. 2023) shown no significant differences (by paired *t*-tests) for ΣPCBs, ΣDDTs, and ΣCHLs (and nearly all individual compounds). As such, these contaminant classes, as well as some individual compounds, were included in our statistical analyses, as there should be minimal difference in the datasets between the two labs. Contaminant concentrations are reported on a mg/kg lw basis.

5.4.3. FA Signature Analysis

The same blubber/adipose samples for each animal were also extracted and analyzed for FA signatures using established procedures (Budge et al., 2006; McKinney et al., 2013). The FA data for the killer whale was previously analyzed and reported elsewhere (Bourque et al., 2018), as were the FA data for the 2016 and 2018 pilot whale and for all narwhal (Land-Miller et al. 2023). All polar bear and 2021 pilot whale samples were analyzed for FAs at McGill University. Briefly, each tissue piece was shaved to reveal fresh blubber/adipose. From a 0.4-0.5 g piece

(ensuring full-depth blubber for the whales to avoid issues of FA stratification with blubber depth; Koopman, 2007; Bourque et al., 2018), lipids were quantitatively extracted using the Folch method (Remili et al., 2021; Saini et al., 2021; Land-Miller et al., 2023), and lipid content was determined gravimetrically. Using the Hilditch reagent, FAs were *trans*-esterified to produce fatty acids methyl esters (FAMEs). The FAMEs were quantified as mass percent of total FAME on an Agilent 8860 gas chromatograph with flame ionization detection (GC-FID) using a DB-23 column (Agilent Technologies, Santa Clara, CA, USA). Either ~0.1 g of NIST SRM 1945 (for 2016 and 2018 pilot whale, all narwhal, 2012-2016 polar bear, and all killer whale) or ~0.1 g of NIST RM 8037 krill oil (for 2021 polar bear and 2021 pilot whale) were analyzed in a batch of 10 samples, along with and a duplicate of a random sample. SRM 1945 runs averaged 14.0 ± 5.1% compared to published values (Kucklick et al., 2010) and RM 8037 values averaged 18.0 ± 1.1% of the certified values for the 20 reported FAMEs (NIST Report of Investigation, 2020). All duplicates averaged 6.0 ± 1.4% of the values reported in corresponding samples, and thus, samples and their respective duplicate were averaged for each batch (see section S5.6 for more detailed QA/QC information).

5.4.4. Data Analysis

We tested for interspecific differences in concentrations of ΣPCBs (and each homolog group, e.g., tri-chlorinated PCBs), ΣDDTs (and *p,p'*-DDT, *p,p'*-DDE, *p,p'*-individually), ΣCHLs (parent compounds: *trans*-chlordane, *cis*-chlordane, *trans*-nonachlor, *cis*-nonachlor and metabolites: oxychlordane and heptachlor epoxide), ΣClBzs, ΣHCHs, and dieldrin and mirex (Table S5.2). All individuals were included in this analysis. We also calculated ratios of some metabolites relative to the known parent compound(s) (i.e. oxychlordane/[*trans*-chlordane+*cis*-

chlordane+*trans*-nonachlor+*cis*-nonachlor] and DDE/DDT). All mg/kg concentrations were first lipid normalized (Thomann, 1989), then log(x+1) transformed, and all data were tested for normality prior to further statistical analysis, and log-transformed data achieved normality. One-way analysis of variance (ANOVAs) with *post-hoc* Tukey pairwise comparisons were used to test for differences in mean concentrations among species. Additionally, as contaminant trends may be influenced by year of collection (Dietz et al. 2013), we tested for variation in concentrations among years for each species using the same statistical analyses (Table S5.5), with no significant differences found between any years for all species.

We next investigated interspecific variation in dietary patterns based on the FA signatures (Table S5.6). To ensure a sufficient sample to variable ratio for multivariate analysis, only a subset of FAs was selected. First, only FAs that were above >0.1% of total FAME on average (Pedro et al., 2020) were used to avoid influence of minor FAs. From these, only those FAs considered to be present largely through dietary intake and not from biosynthesis (Iverson et al., 2004) were chosen. This reduced the set of FAs for analysis to 16 (Table S5.7). The proportions of these FAs were then arcsin-transformed (Budge et al., 2006), and then a principal component analysis (PCA) was performed to visualize variation in FA signatures among species. We then used multivariate analysis of variance (MANOVA) with Euclidian distances to test for differences in FA proportions among species, followed by *post-hoc* one-way ANOVA and Tukey pairwise comparisons. Because FA signatures in young marine mammals are influenced by nursing (Birkeland et al., 2005; Figure S5.2), we excluded all individuals from this analysis that were of an age when they were likely nursing, including nine pilot whale subadults of four years of age and younger (Betty et al., 2022). No killer whale or narwhal were excluded since age-specific data was not available, and all subadult individuals showed similar patterns as

adults. As polar bear of nursing age are legally protected from being hunted (Sandell and Sandell, 1996), all polar bear, which were either subadults and adults, were included in this analysis.

To test the influence of dietary patterns from FA signatures on POP variations, relative to the biological differences between toothed whales and polar bear, we used linear regression models (LM) with the following variables: FA PC scores 1, 2, and 3 (the significant PCs in the PCA of the FAs), age class/sex (adult male, adult female, subadult), and taxa (with two categories: toothed whales and polar bear). Linear regression diagnostic plots were run for each model to ensure assumptions were met. We used variation inflation factors (VIF) to assess multicollinearity among these variables with a cutoff of 5. We then tested every possible combination of variables for each contaminant class. The models were ranked using Akaike's information criterion (AIC) and then top ($AIC < 2$) models were averaged to produce the top average model for each contaminant class. We also determined the semi-partial correlation coefficient squared of each variable for top averaged models, to evaluate the unique contribution of each individual variable (i.e., without the influence of any other variables; Eckardt and Mateu, 2021). The same subset of individuals that were included in dietary pattern analysis were analyzed here, except for the 2016 and 2018 pilot whale, as they did not have age class and/or sex data available. As > 15 individuals per species were included in this analysis (and only five variables were included in the models), the sample size is suitable for this analysis (Dang et al., 2008.) As there were no differences in FA signatures or POP concentrations for pilot whale (or any other species) among years, this reduced set of pilot whale should not influence the results. All statistical analyses were performed using R (version 3.6.3) and with α set to 0.05.

5.5. RESULTS AND DISCUSSION

5.5.1. Interspecific variation in PCB and OC pesticide concentrations

Mean ΣPCB concentrations varied widely among species (ANOVA $F_{3,24} = 48.7$, $p < 0.001$), with concentrations five times higher in killer whale at 57.0 ± 14.0 mg/kg lw than in polar bear at 12.6 ± 1.3 mg/kg lw, and lowest at 4.8 ± 0.7 in pilot whale and 2.6 ± 0.5 mg/kg lw in narwhal, with significance of killer whale > polar bear > narwhal = pilot whale (*post-hoc* $p \leq 0.001$, except $p = 0.75$ between narwhal and pilot whale) (**Figure 5.1,** Table S5.8). Similar trends among species were present for each age class/sex grouping (Figure S5.3), even with the subset of subadults from the dietary pattern analysis. For PCB homologue groups (Table S5.8), tri- and tetra-chlorinated PCBs were still highest in killer whale, but with significance of killer whale > narwhal = pilot whale > polar bear ($p \leq 0.001$), while penta-PCBs concentrations were killer whale > narwhal = pilot whale = polar bear ($p \leq 0.001$). However, for hexa- and hepta-PCBs, patterns were the same as for ΣPCBs, with killer whale > polar bear > narwhal = pilot whale ($p < 0.001$). Finally, for octa- and deca-chlorinated PCBs, polar bear showed the highest concentrations, with trends polar bear > killer whale > narwhal = pilot whale for octa-PCBs, and polar bear = killer whale > narwhal = pilot whale for deca-PCB.

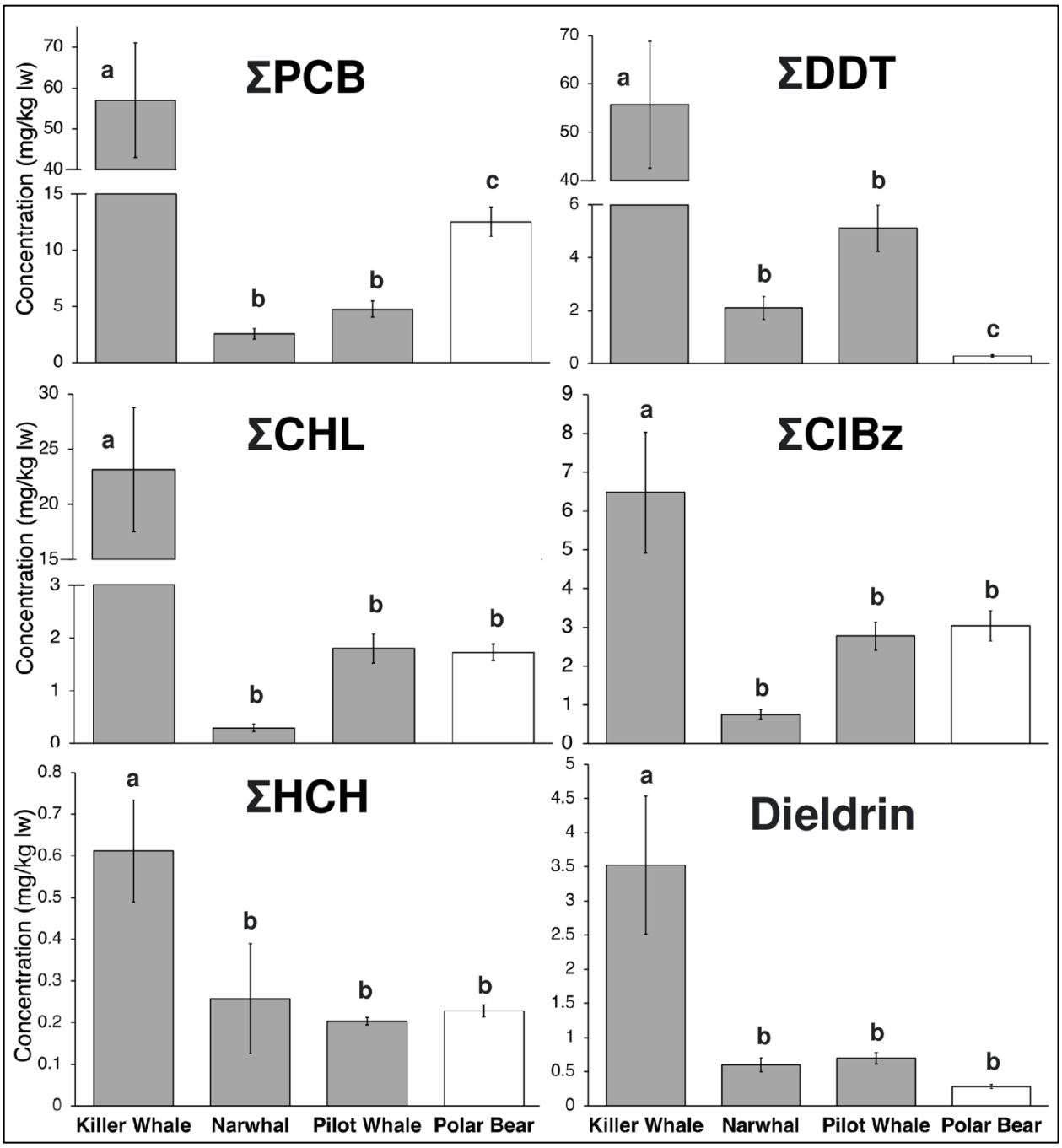


Figure 5.1: Comparison of legacy contaminant levels for mean ± standard error for Σpolychlorinated biphenyls (ΣPCBs) and organochlorine (OC) pesticides, such as Σdichlorodiphenyltrichloroethanes (ΣDDTs), Σchlordanes (ΣCHLs), Σchlorobenzenes (ΣClBzs), Σhexachlorocyclohexanes (ΣHCHs), and dieldrin in there toothed whales (in gray): killer whale (Orcinus orca; n =19), narwhal (Monodon monoceros; n = 15), and 46 long-finned pilot whale (Globicephala melas; n = 46) and one ursid species (in white): polar bear (Ursus maritimus; n = 60). Significant differences are represented by different letters (a,b,c) above the measurement.

Similar to ΣPCBs, concentrations were substantially higher for ΣDDTs, ΣCHLs, ΣClBz, ΣHCHs, and dieldrin in killer whale than in any other species; however, concentrations were generally not significantly different among polar bear, narwhal and pilot whale, except for DDTs (**Figure 5.1,** Table S5.8). For all OC pesticides, similar trends among species were also present when analyzed separately for each age class/sex grouping (Figure S5.4 and S5.5). For ΣDDTs (ANOVA $F_{3,24} = 22.5$, $p < 0.001$), mean concentrations were ~200 times higher in killer whale (55.7 ± 13.1 mg/kg lw) relative to polar bear (0.28 ± 0.05 mg/kg lw), and ~10-25 times higher in killer whale than in pilot whale (5.11 ± 0.8 mg/kg lw) and narwhal (2.1 ± 0.4 mg/kg lw), with significance of killer whale > pilot whale = narwhal > polar bear ($p \leq 0.001$, except $p = 0.61$ between narwhal and pilot whale). The same trends were present for the DDT metabolites, DDE and DDD. The DDE/DDT ratio also differed among species (ANOVA $F_{3,24} = 11.9$, $p < 0.001$), with ratios not significantly differing for killer whale and polar bear (18.6 ± 2.2 and 19.6 ± 2.9, respectively), but significantly higher than narwhal and pilot whale ($p \leq 0.01$; 3.4 ± 0.3 and 7.2 ± 0.4, respectively; Figure S5.6). For ΣCHLs, ΣClBz, ΣHCHs, and dieldrin (ANOVA $F_{3,24} > 6.1$, $p < 0.001$), killer whale showed the highest mean concentrations, but mean concentrations were not significantly different between narwhal, pilot whale, and polar bear, i.e., killer whale > polar bear = pilot whale = narwhal (all *post-hoc* $p \leq 0.01$ between killer whale and each species). The ratios of oxychlordane/ΣCHL parent compounds (Figure S5.6) were not significantly different between all toothed whales, but over eight times higher (and significantly different, $p<0.001$) in polar bear.

Although interspecific differences in contaminants have been compared among other top predators in the Arctic (e.g., Hoekstra et al., 2003), the present study is the first to compare

trends among any killer whale, narwhal, pilot whale, and polar bear sampled under a similar spatio-temporal scale, and to confirm that orders of magnitude differences exist among species. When qualitatively compared among studies and across regions, killer whale sampled elsewhere (e.g. in Alaska, the Northeast Pacific, Iceland, and Northwest Pacific) have similarly shown at least five times higher (and at most >100) mean PCB concentrations than narwhal, at least those sampled in the Canadian Arctic, in Norway, and in West Greenland, and pilot whale in the North Atlantic and the Faroe islands (Muir et al., 1992; Borrell et al., 1995; Hayteas et al., 2000; Herman et al., 2005; Kajiwara et al., 2006; Wolkers et al., 2006; Sonne et al., 2010; Carlsson et al., 2014; Remili et al., 2021).

Higher PCB concentrations in killer whale relative to polar bear in this present study are largely consistent with previous reports. Nonetheless, this depends somewhat on the particular killer whale populations studied as, e.g., Alaskan resident killer whale and polar bear in Barents Sea and Hudson Bay showed similar levels (Dietz et al., 2019), while other killer whale transients show several times higher concentrations (Desforges et al., 2018). However, DDT concentrations have also shown orders of magnitude differences across many different regions between killer whale (e.g., >200 mg/kg lw in Barents Sea transients; Krahn et al., 2007) and polar bear (e.g. 0.1 mg/kg in the Hudson Bay; McKinney et al., 2010). As such, the magnitude of our reported interspecific differences is generally consistent with those compared among studies, confirming substantial, orders of magnitude interspecific differences in POP concentrations, especially between many killer whale populations and the other toothed whales for PCBs, and between killer whale and polar bear for DDTs.

5.5.2. FA signature variation among species

The FA signatures significantly differed among species (MANOVA $F_{3,54} = 44.6$, $p < 0.001$) (Table S5.7). Similarly, FA signatures largely clustered by species in the PCA, with most separation observed along the first principal component (PC1) axis between polar bear, which loaded positively, and the three toothed whales, for which nearly all individuals loaded negatively (**Figure 5.2A**). PC1 explained 43.4% of the variation, with FAs 20:1n9, 20:1n7, 22:6n3, 20:2n6, 22:1n9, and 21:5n3 contributing most to this variation and loading positively towards polar bear clustering (**Figure 5.2B)**. A PCA including age class/sex groupings for each species showed similar results for this PC axis and with distinct groupings among species (Figure S5.7).

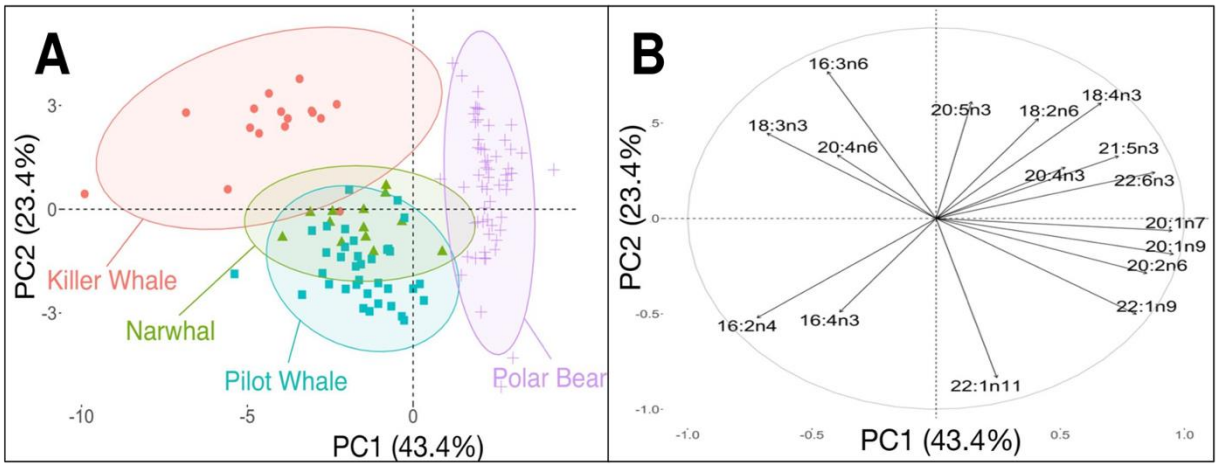


Figure 5.2: A: Principal component analysis of the 16 highest proportion dietary fatty acids in killer whale (Orcinus orca), narwhal (Monodon monoceros), long-finned pilot whale (Globicephala melas), and polar bear (Ursus maritimus). The first dimension of the PCA accounted for 43.4% of the total variation, and the second dimension accounted for 23.4%. Ellipses represent 90% confidence intervals. B: Variable correlation plot of the 16 fatty acids used in the PCA with average contribution greater than 5%.

The second principal component (PC2) axis in the PCA may show significant differences between the higher trophic position species, killer whale and polar bear, and the lower trophic position species, narwhal and pilot whale, where all killer whale and most (~75%) polar bear

loaded positively, while all but a few narwhal and pilot whale loaded negatively (**Figure 5.2A**). PC2 explained 23.4% of the variation in the PCA, with 22:1n11, 16:3n6, 20:5n3, 18:4n3, 18:2n6, 16:2n4 contributing the most to this variation. Of these FAs, all loaded positively towards polar bear and killer whale except 22:1n11 and 16:2n4 (**Figure 5.2B**). For these two FAs, pilot whale showed significantly higher proportions relative to all other species (p<0.001), while narwhal showed intermediate levels (Table S5.7**)**.

In general, these distinct differences among species along FA-PC2 may reflect differences in trophic position, as East Greenland polar bear have previously been estimated to consume almost exclusively seal (McKinney et al., 2013) and East Greenland killer whale diet was estimated to average ~80% marine mammal, also mostly seal (Remili et al., 2022; Remili et al., 2023). Lower proportions of certain FAs, such as 22:1n11, in killer whale and polar bear are consistent with marine mammal feeding, as this FA has been reported as significantly lower in killer whale feeding on marine mammals versus those feeding on fish (Bourque et al., 2018). Similarly, the three FAs significantly and positively associated with killer whale and polar bear on PC2, 18:4n3 and 18:2n6 (but not 16:3n6) were higher in proportion (>5 times higher for 18:4n3 but only slightly higher for 18:2n6) in the primary diet items of killer whale and polar bear i.e. ringed, harp, and hooded seal than in narwhal (Thiemann et al., 2008). However, variation of other individual FAs is more difficult to interpret along this axis, but may, at least in part, be tied to differences in feeding habitats (e.g., benthic verses pelagic verses ice-associated). For example, 20:5n3 (that was more associated in killer whale and polar bear) was previously reported as higher in fish-feeding versus marine mammal feeding killer whale (Bourque et al., 2018); however, 20:5n3 may instead reflect more association with sea ice food webs in polar bear and killer whale relative to pilot whale (Dalsgaard et al., 2003; McKinney et al., 2013). As

the diets of narwhal and pilot whale are not well known in East Greenland, further dietary analyses, including quantitative fatty acid signature analysis (QFASA; Iverson et al., 2004; Remili et al., 2022) would help confirm our interpretations along this axis, especially to account for potential interspecific differences in predator metabolism of FAs (Galloway and Budge, 2020).

Although explaining only 15.1% of the variation, the third principal component axis (PC3) detailed some differences between pilot whale and the other three species (Figure S5.8). Here, pilot whale loaded almost exclusively positively, while most killer whale (85%), narwhal (57%), and polar bear (65%) loaded negatively. The FAs, 20:4n6, 20:5n3, 22:1n11, 20:4n3, 16:4n3, and 16:2n4 contributed most to the variation along PC3, with all loading positively. Of these, all were highest in pilot whale (Table S5.7).

While FA-PC2 may distinguish feeding at different trophic positions, variation along FA-PC3 may be explained by high invertebrate consumption in pilot whale, and to a lesser extent in narwhal. Although pilot whale diets in East Greenland have not been quantified, conspecifics in the North Atlantic have shown specialization on cephalopods, i.e., squid and octopus (Monteiro et al., 2015), and the armhook squid (*Gonatus fabricii*) has shown very high abundance in East/West Greenland (Zumholz et al., 2006). FA analysis of this squid also showed high proportions of in 22:1n11 (Hooker et al., 2001), and 22:1n11 was significantly higher in our pilot whale than all other species. Our FA analysis of this squid (n =2; Table S5.9, unpublished) also revealed similar proportions of 20:4n6, 20:4n3, and 22:1n11 as in the pilot whale, which showed higher proportions of all three of these FAs relative to the other predator species. High consumption of pelagic cephalopods may also explain significantly higher proportions of the C_{16} polyunsaturated FAs, 16:2n4 and 16:4n3, in pilot whale, as these FAs are associated with pelagic

feeding (Kelly and Scheibling, 2012). Recent East Greenland stomach content data of narwhal have also indicated regular consumption of *Gonatus fabricii* (Garde et al., 2022), likely explaining partial overlap of narwhal and pilot whale along all PC axes.

However, as killer whale and pilot whale are only present in East Greenland seasonally, these FA signatures may also reflect feeding further south in the North Atlantic at other times during the year. Especially as dietary patterns and associated FAs are changing rapidly the Arctic (Laidre et al., 2008; Borgå et al., 2022), QFASA diet estimates for narwhal and pilot whale, similar to what was done in these same killer whale (Remili et al., 2022) and polar bear (McKinney et al., 2013), along with stable isotope, $\delta^{15}N$ and $\delta^{13}C$ (for information on trophic position and carbon source, respectively; Herman et al., 2000), would be useful to further confirm our interpretations of dietary patterns based on FA patterns alone.

5.5.3. Influence of dietary patterns on interspecific variation on PCB concentrations

Five variables, FA-PC1, FA-PC2, FA-PC3, age class/sex, and taxa (toothed whales or ursid [i.e., polar bear]) were initially examined for their influence on variation in contaminant classes and individual contaminants using LMs. However, a high correlation between FA-PC1 and taxa was demonstrated in the VIF analysis (VIF>8), and as such, we removed FA-PC1 from our models, as regardless of whether FA-PC1 or taxa was included, they showed very similar results (see Table S5.10 for taxa, see Table S5.11 for FA-PC1). For ΣPCBs, the top averaged model (using AIC <2) explained 38% of variation among species and included all four variables, and all were also significant predictors (confidence intervals not overlapping zero; **Figure 5.3**). From squared semi-partial correlation coefficients for each variable, FA-PC2 and FA-PC3 explained the most variation in the model at 10% and 18% respectively, while taxa explained

~7%. For PCB homolog groups (Table S5.8, Figure S5.9), taxa, FA-PC2, and FA-PC3 were significant variables in most top models. In general, taxa explained most of the variation in each model for tri-, tetra-, penta-, and octa-PCBs (50%, 51%, 22%, 20%, respectively), while the dietary variables contributed less than 6%. However, for hexa- and hepta-PCBs, which showed the highest concentrations in all species, FA-PC3 explained most of the variation (14% for each), while FA-PC2 explained ~5%, and taxa was less than 2%. When significant, estimates for FA-PC2 were always positive and FA-PC3 always negative, while taxa varied based on homolog group.

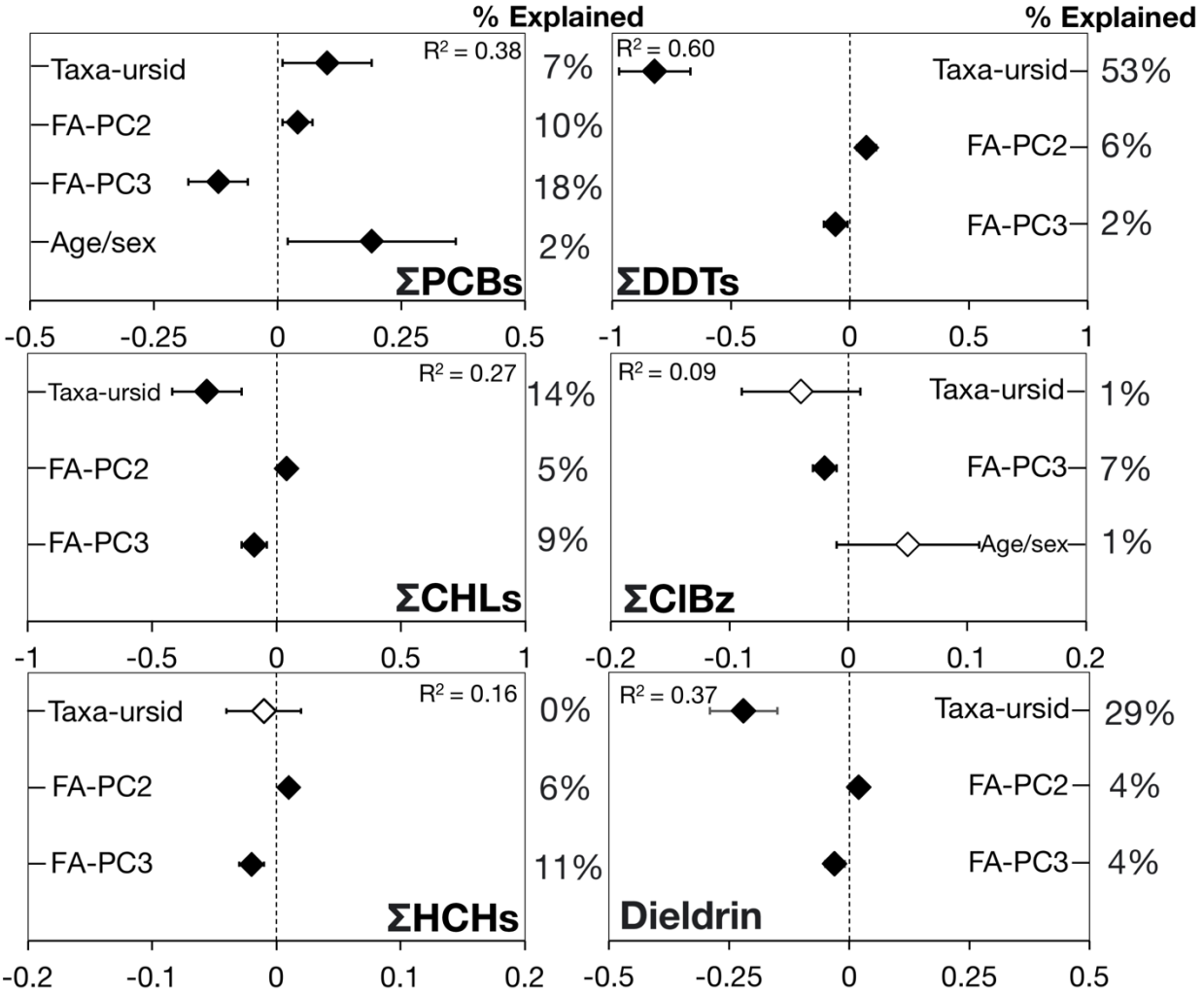


Figure 5.3: Confidence interval figures for top averaged models (AIC<2) for Σpolychlorinated biphenyls (ΣPCBs) and organochlorine (OC) pesticides, such as Σdichlorodiphenyltrichloroethanes (ΣDDTs), Σchlordanes (ΣCHLs), Σchlorobenzenes (ΣClBzs), Σhexachlorocyclohexanes (ΣHCHs), and dieldrin in killer whale (Orcinus orca), narwhal (Monodon monoceros), long-finned pilot whale (Globicephala melas), and polar bear (Ursus maritimus) collected between 2012-2021 in East Greenland. Significant (when confidence intervals do not cross zero) variables in top models are indicated by a black symbol (◆), while nonsignificant variables are white (◇). Percent explained by each variable, from squared semi-partial correlation coefficients, is next to each variable.

As ΣPCB concentrations in polar bear were significantly higher than lower trophic position narwhal and pilot whale, and FA-PC2 (10%) and FA-PC3 (18%) explained most of the total explained variation (i.e. 38%) in this model, feeding patterns likely drive most of the

variation among the toothed whales and polar bear for ΣPCBs (**Table 5.3**). Significant and positive estimates for FA-PC2 likely suggest increased PCB contamination from consumption at higher trophic positions, which has been also reported elsewhere (Dietz et al., 2019; Remili et al., 2021). Negative FA-PC3 estimates suggest that higher invertebrate consumption is associated with lower ΣPCB concentrations relative to fish and seal-feeding individuals, as shown elsewhere (Corsolini et al., 2016). Relative to feeding patterns, taxa-related differences were not as influential in explaining variation in ΣPCB concentrations, although other factors that were not included in the model, such as body condition and reproductive status, may also impact PCB variation (Borgå et al., 2004).

Table 5.3: Summary of the results from modeling analyses assessing the relative influence of biological characteristics (i.e. taxa) compared to feeding patterns (i.e. from FA-PC2 and FA-PC3) between three toothed whales and one ursid species for Σpolychlorinated biphenyls (ΣPCBs), Σdichlorodiphenyltrichloroethanes (ΣDDTs), Σchlordanes (ΣCHLs), Σchlorobenzenes (ΣClBzs), Σhexachlorocyclohexanes (ΣHCHs), and dieldrin

Contaminant Class	Relative Influence on Contaminant Variation
ΣPCBs	Feeding patterns > Biological characteristics
Lower-chlorinated congers	Biological characteristics >> Feeding patterns
Higher-chlorinated congers	Feeding patterns >> Biological characteristics
ΣDDTs	Biological characteristics >> Feeding patterns
ΣCHLs	Biological characteristics = Feeding patterns
Parent compounds	Biological characteristics > Feeding patterns
Metabolites	Feeding patterns >> Biological characteristics
ΣClBz	Feeding patterns > Biological characteristics*
ΣHCH	Feeding patterns > Biological characteristics*
Dieldrin	Biological characteristics >> Feeding patterns

*low model correlation (low R^2), other factors may better explain contaminant variation.

However, investigating PCBs by homolog group may provide more insight than ΣPCB concentrations alone, as significant variables (and % explained by each) in each model varied widely by PCB homolog group, and degree of chlorination has been previously shown to impact PCB metabolism (Bucheli and Fent, 1995; Goksøyr, 1995; Boon et al., 1997). For tri-, tetra-, and

penta-chlorinated PCBs, as taxa explained nearly all total explained variation in these models, polar bear likely possess sufficiently higher biotransformation capabilities for these compounds, leading to the lowest concentrations in polar bear of all species. However, for hexa- and hepta-PCBs, that include some of the most persistent congeners (Goksøyr, 1995; Houde et al., 2005; Grimm et al., 2015), differences in feeding patterns likely, and nearly exclusively, dictate species-specific bioaccumulation, consistent with killer whale and polar bear having higher concentrations than pilot whale and narwhal. These results align with previously published biomagnification factors (BMFs) of many PCB congeners compared between multiple toothed whales and Carnivora ringed seal (Fisk et al., 2001; Hoekstra et al., 2003). For example, Fisk et al. (2001) detailed similar CB-153 and CB-180 BMFs between Arctic cod-feeding beluga whale and ringed seal, yet significantly higher BMFs in beluga for most tri- through penta-PCBs (e.g. CB-118 was over ten times higher in beluga than ringed seal). As such, our findings are consistent with previous studies where interspecific differences in PCBs are likely congener-specific, with dietary patterns explaining most of the variation in the concentrations of highly chlorinated, persistent congeners, while biological differences among taxa, such as xenobiotic biotransformation capacities, largely dictate differences for lower-chlorinated congeners.

5.5.4. Influence of dietary patterns on interspecific variation on OC pesticide concentrations

For all OC pesticides, taxa and the two dietary variables were included in nearly all top averaged models (Table S5.10). For ΣDDTs, the top model explained 60% of variation among species, with taxa, FA-PC2, and FA-PC3 as significant variables. Taxa explained nearly all variation in this model at 53%, while the dietary variables explained less than 7% combined. The same trends were observed for each individual DDT compound/metabolite (Table S5.10). For

ΣCHLs, 27% of the variation was explained by top averaged models with taxa, FA-PC2, and FA-PC3 as significant variables. Variation explained exclusively by taxa was ~14%, while the dietary variables explained 5% and 9%, respectively. For each parent chlordane and nonachlor compound, the same variables were significant in most top models, and taxa alone contributed most to this variation (ranging from 14-36%). For the chlordane metabolite, oxychlordane, both dietary variables, but not taxa, were significant. However, for the ratio of oxychlordane/parent compounds, taxa and FA-PC3 were significant, but taxa explained nearly all (>61%) of the total explained variation (64%). For ΣClBz and ΣHCHs, R^2 values were low at 9% and 16%, respectively.

As polar bear showed similar or lower concentrations of OC pesticides compared to lower trophic position-feeding toothed whales, and as taxa explained most of the variation in each OC model, biological differences likely drive most of the variation between the toothed whales and polar bear for most OCs. This was particularly evident for ΣDDTs and each individual compound/metabolite, where concentrations in polar bear were significantly lower than all toothed whales despite feeding on a similar diet as killer whale. Polar bear metabolism of DDT into DDE is well-documented with high efficiencies (Letcher et al., 1998; Letcher et al., 2009), and comparative studies assessing concentrations between other toothed whales and Carnivora species have detailed similarly large differences (Fisk et al., 2001; Hoekstra et al., 2003). Although DDE/DDT ratios were not significantly different between killer whale and polar bear, this is more likely a result of high metabolic breakdown of DDT in seal prey, which has been detailed elsewhere (Letcher et al., 2009). Dietary patterns likely still have some partial influence for DDTs, however, as FA-PC2 and FA-PC3 were significant in top models. This may explain why, despite similar biological susceptibility to DDT and CHL contamination, killer

whale still had higher concentrations than pilot whale and narwhal. For ΣCHLs, feeding patterns and taxa explained the same amount of variation and thus, likely have a relatively similar impact; however, trends for parent compounds were very similar to ΣDDTs (especially in CHLs at the highest concentration, i.e., *cis*- and *trans*-nonachlor), likely indicating that chlordanes and nonachlors are better metabolized to oxychlordane in polar bear. A capacity for CHL biotransformation has also been reported in other Carnivora marine mammals (Wiberg et al., 2000). Similar to DDE, oxychlordane has been shown to be primarily formed in seal and accumulate in top predators through diet (Wiberg et al., 2000). However, large and significant differences in oxychlordane/parent compound ratios between all toothed whales and polar bear likely indicate higher metabolism of parent compounds in polar bear, yet similarly limited biotransformation of oxychlordane in both groups, where feeding patterns play a larger role in variation.

For ΣClBzs and ΣHCHs, neither dietary variables nor taxa explained much variation. Relative to ΣDDTs and ΣCHLs, the magnitude of differences in concentrations among species is far lower (only 2-3 times higher in killer whale). As such, more similar concentrations across all species (and high variability within them), may explain the low variation explained in our models, and other factor such as body condition or reproductive status may better explain interspecific differences of these compounds (Tartu et al., 2017), although some influences of diet are still likely (Hoekstra et al., 2003).

These results provide further confirmation of striking differences in legacy POP concentrations among marine mammal predators in the Arctic, and that whether these differences are driven largely by diet or largely by biological characteristics is contaminant-specific. For DDTs and parent CHLs, killer whale and polar bear are likely exposed to similarly high

concentrations; however, polar bear likely possess more efficient detoxification mechanisms resulting in correspondingly lower concentrations. Other biological differences, such as longevity between taxa, may contribute to POP variation, particularly in males where concentrations tend to increase with age (Borgå et al., 2004). However, even with a lower number of adult male toothed whales in our dataset (and only two male killer whale), killer whale still showed the highest concentrations. Additionally, polar bear may exhibit lower concentrations due to an additional excretion route through hair, although hair concentrations were found to be less than 3% of those in adipose (Jaspers et al., 2010). Thus, the influence of both longevity and excretion routes may be overshadowed by differences in biotransformation capacity. Instead, polar bear likely showed lower levels of OCs due to lower biological susceptibility despite occupying high trophic positions **(Table 5.3)**. In contrast, significantly higher contamination in killer whale, who feed at a similar high trophic position as polar bear, is likely a result of high biological susceptibility (i.e. low xenobiotic transformation capacity). While narwhal and pilot whale likely possess similar biological susceptibility as killer whale, they likely exhibit considerably lower concentrations due to feeding at lower trophic positions, where the bioaccumulation of lipophilic POPs is less substantial. As some toothed whales in the Arctic are among the most contaminated individuals globally by legacy POPs (Desforges et al., 2018), further investigation into their dietary uptake and xenobiotic transformation potential towards lesser-known chemicals of emerging Arctic of concern is warranted.

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5.8. SUPPORTING INFORMATION

Section S5.1: Supplemental information on the sampling location

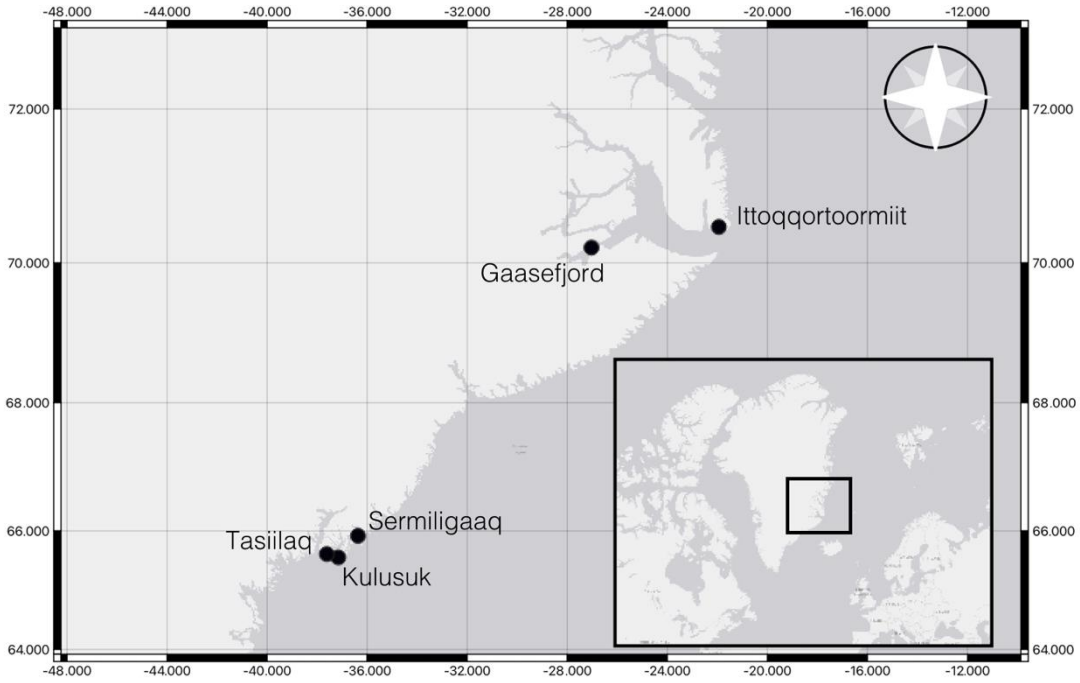

Figure S5.1: Sampling location for all killer whale (*Orcinus orca*), polar bear (*Ursus maritimus*), long-finned pilot whale (*Globicephala melas)*, and narwhal (*Monodon monoceros*) sampled in this study from 2012-2021.

Section S5.2: Supplemental information of biological data for each individual

Table S5.1: Biological data (Age/age class and sex) for each toothed whale/ursid individual, when available (ND is not determined), for all samples. 19 killer whale (9 adult female, 2 adult males, 8 subadults), 15 narwhal (6 adult female, 2 adult males, 12 subadults), 46 pilot whale (15 adult female, 3 adult males, 10 subadults, 18 ND), and 60 polar bear (10 adult female, 23 adult males, 27 subadults) were sample.

Species	ID	Sex	Age/Age Class	Year Collected	Location
Killer Whale	38340	male	subadult	2012	Tasiilaq
	48339	male	subadult	2012	Tasiilaq
	48338	female	adult	2012	Tasiilaq
	48337	ND	subadult	2012	Tasiilaq
	48336	female	adult	2012	Tasiilaq
	48335	female	adult	2012	Tasiilaq
	48736	female	adult	2013	Tasiilaq
	48735	female	adult	2013	Tasiilaq
	48733	female	adult	2013	Kulusuk
	48732	male	adult	2013	Tasiilaq
	35143	female	adult	2013	Kulusuk
	51607	ND	subadult	2014	Tasiilaq
	51613	male	subadult	2014	Tasiilaq
	51610	male	subadult	2014	Tasiilaq
	51606	ND	subadult	2014	Tasiilaq
	51601	male	subadult	2014	Tasiilaq
	GL-01	male	adult	2021	Ittoqqortoormitt
	GL-03	female	adult	2021	Ittoqqortoormitt
	64752	female	adult	2021	Kulusuk
Narwhal	53802	female	adult	2015	Gaasefjord
	53812	male	adult	2015	Gaasefjord
	53823	male	subadult	2015	Gaasefjord
	58324	male	subadult	2015	Gaasefjord
	53825	female	subadult	2015	Gaasefjord
	53835	female	adult	2015	Gaasefjord
	53839	female	subadult	2015	Gaasefjord
	53840	male	subadult	2015	Gaasefjord
	53841	female	adult	2015	Gaasefjord
	53843	female	subadult	2015	Gaasefjord
	53845	female	subadult	2015	Gaasefjord
	53811	female	adult	2015	Gaasefjord
	53842	female	adult	2015	Gaasefjord

	53844	female	adult	2015	Gaasefjord
	53846	female	subadult	2015	Gaasefjord
Pilot Whale	GR1	ND	ND	2016	Sermiligaaq
	GR2	ND	ND	2016	Sermiligaaq
	GR13	ND	ND	2016	Sermiligaaq
	GR14	ND	ND	2016	Sermiligaaq
	GR15	ND	ND	2016	Sermiligaaq
	GR16	ND	ND	2016	Sermiligaaq
	GR17	ND	ND	2016	Sermiligaaq
	GR18	ND	ND	2016	Sermiligaaq
	GR19	ND	ND	2016	Sermiligaaq
	GM03	ND	ND	2018	Tasiilaq
	GM05	ND	ND	2018	Tasiilaq
	GM06	ND	ND	2018	Tasiilaq
	GM07	ND	ND	2018	Tasiilaq
	GM12	ND	ND	2018	Tasiilaq
	GM13	ND	ND	2018	Tasiilaq
	GM14	ND	ND	2018	Tasiilaq
	64701	female	0.0	2021	Kulusuk
	64702	female	19.0	2021	Tasiilaq
	64703	female	16.0	2021	Tasiilaq
	64704	female	28.0	2021	Tasiilaq
	64705	female	23.0	2021	Tasiilaq
	64706	male	0.0	2021	Tasiilaq
	64707	female	1.0	2021	Kulusuk
	64708	female	6.0	2021	Tasiilaq
	64709	male	1.5	2021	Tasiilaq
	64710	female	4.0	2021	Tasiilaq
	64711	female	8.0	2021	Kulusuk
	64712	male	10.0	2021	Tasiilaq
	64713	female	16.0	2021	Kulusuk
	64714	female	7.5	2021	Tasiilaq
	64715	ND	8.0	2021	Tasiilaq
	64716	female	12.0	2021	Tasiilaq
	64717	ND	2.0	2021	Tasiilaq
	64718	female	11.0	2021	Tasiilaq
	64719	female	15.0	2021	Kulusuk
	64720	male	18.5	2021	Kulusuk
	64721	female	13.0	2021	Kulusuk

	64722	male	11.5	2021	Kulusuk
	64723	female	1.0	2021	Tasiilaq
	64724	male	1.0	2021	Tasiilaq
	64725	female	0.0	2021	Tasiilaq
	64726	female	19.0	2021	Kulusuk
	64727	male	8.5	2021	Tasiilaq
	64728	female	2.5	2021	Tasiilaq
	64729	female	0.0	2021	Kulusuk
	64730	female	14.0	2021	Tasiilaq
Polar Bear	35163	male	13	2014	Ittoqqortoormitt
	35164	female	2	2014	Ittoqqortoormitt
	35165	male	13	2014	Ittoqqortoormitt
	35166	male	6	2014	Ittoqqortoormitt
	35167	male	4	2014	Ittoqqortoormitt
	35168	male	11	2014	Ittoqqortoormitt
	35169	male	8	2014	Ittoqqortoormitt
	35170	male	4	2014	Ittoqqortoormitt
	35171	female	3	2014	Ittoqqortoormitt
	35172	male	5	2014	Ittoqqortoormitt
	46751	male	2	2012	Ittoqqortoormitt
	46752	male	10	2012	Ittoqqortoormitt
	46753	male	6	2012	Ittoqqortoormitt
	46754	female	7	2012	Ittoqqortoormitt
	46755	female	5	2012	Ittoqqortoormitt
	46756	female	2	2012	Ittoqqortoormitt
	46757	male	7	2012	Ittoqqortoormitt
	46758	male	5	2012	Ittoqqortoormitt
	46760	male	2	2012	Ittoqqortoormitt
	48703	female	13	2013	Ittoqqortoormitt
	48704	male	2	2013	Ittoqqortoormitt
	48705	male	8	2013	Ittoqqortoormitt
	48706	male	14	2013	Ittoqqortoormitt
	48707	male	9	2013	Ittoqqortoormitt
	48708	male	8	2013	Ittoqqortoormitt
	48710	male	3	2013	Ittoqqortoormitt
	50413	female	19	2015	Ittoqqortoormitt
	50414	male	4	2015	Ittoqqortoormitt
	50415	male	5	2015	Ittoqqortoormitt
	50416	male	21	2015	Ittoqqortoormitt

50417	female	4	2015	Ittoqqortoormitt
50418	male	1	2015	Ittoqqortoormitt
50419	male	13	2015	Ittoqqortoormitt
50420	female	12	2015	Ittoqqortoormitt
50421	male	7	2015	Ittoqqortoormitt
50422	male	6	2015	Ittoqqortoormitt
53412	male	12	2016	Ittoqqortoormitt
53421	male	16	2016	Ittoqqortoormitt
53423	ND	11	2016	Ittoqqortoormitt
53424	male	4	2016	Ittoqqortoormitt
53425	male	4	2016	Ittoqqortoormitt
53426	male	2	2016	Ittoqqortoormitt
53427	male	2	2016	Ittoqqortoormitt
53428	male	2	2016	Ittoqqortoormitt
53429	female	8	2016	Ittoqqortoormitt
61866	male	4	2021	Ittoqqortoormitt
61867	female	7	2021	Ittoqqortoormitt
61868	female	4	2021	Ittoqqortoormitt
61869	female	5	2021	Ittoqqortoormitt
61870	female	6	2021	Ittoqqortoormitt
61871	male	9	2021	Ittoqqortoormitt
61872	female	4	2021	Ittoqqortoormitt
61873	male	8	2021	Ittoqqortoormitt
61874	male	9	2021	Ittoqqortoormitt
61875	female	5	2021	Ittoqqortoormitt
61876	female	4	2021	Ittoqqortoormitt
61877	male	4	2021	Ittoqqortoormitt
61878	female	4	2021	Ittoqqortoormitt
61879	male	10	2021	Ittoqqortoormitt
61880	male	9	2021	Ittoqqortoormitt

Section S5.3: Supplemental information on the contaminant analysis methods

Quechers extractions: All information is available in Pedersen et al. (2023). Briefly, samples were homogenized in a tissue homogenizer and then spiked with 20 µL of mass labelled-PCB ($^{13}C_{12}$-PCB-28, 52, 118, 138, 153, 180, 194) and OC pesticide ($^{13}C_6$-1,2,4,5-tetrachlorobenzene, $^{13}C_6$-pentachlorobenzene, and $^{13}C_6$-hexachlorobenzene) internal standards at 2000 and 2500 ng/ml, respectively. Extractions proceeded using liquid-liquid extractions using 20:80 (v:v) ethyl acetate:acetonitrile as the extraction solvent. 10% of the extract was removed to determine lipid content gravimetrically. Extracts were subject to subsequent clean-up steps using enhanced matrix removal (EMR)-lipid, primary-secondary amine (PSA), and silica gel cartridges and water removal using anhydrous $MgSO_4$. Extracts for target PCBs and OC pesticides were analyzed using a gas chromatography mass spectrometry (GC-MS) system (Agilent Technologies, GC system 7820A, MSD 5977B) by selective ion monitoring (SIM) with one run for PCBs and a separate run for OCs, both on a fused silica DB-5 capillary column (30 m length x 0.25 mm I.D., 0.25 µm film thickness; Agilent Technologies [Folsom, CA, USA]), with He as the carrier gas. Agilent MassHunter Workstation Plus 11.0 was used for data acquisition and processing.

Polar bear extraction (2012-2016): Briefly, a portion of fat tissue was sub-sampled while still frozen. Tissue masses of approximately 0.15 g were sub-sampled from polar bear samples. As samples were not stored in solvent-cleaned aluminum foil, the outer tissue was shaved off and discarded prior to taking a sub-section for contaminant analysis, such that no contamination from the storage vessel (clear plastic bag) occurred. This sub-sample was accurately weighed into a mortar, cut into small pieces using a scalpel, and homogenized (using a pestle) with 5 g of pre-cleaned diatomaceous earth (DE). The mixture was quantitatively transferred to a stainless steel cell for accelerated solvent extraction (ASE; the cell was initially rinsed with acetone and then hexanes), and was spiked with a mass-labeled OC/PCB/BFR mixed internal standard (25 µL spike). The ASE was performed using a 50:50 mix of DCM:hexanes, after which the sample extracts were evaporated to around 2 mL and filtered through sodium sulfate to remove residual moisture. The sodium sulfate was washed with a 50:50 mix of DCM:hexanes, and the volume was brought to 10 mL using nitrogen evaporation. After taking 1 mL (10% of the original) extract volume for lipid determination, the remaining portion of the extract was cleaned up further by gel permeation chromatography (GPC). The GPC was set to a flow rate of 5 mL/min of DCM/hexane (1:1). The "dump" time was 28 min, and thus the first 140 mL of eluant was discarded. The second "collect" time was set to 40 min, and thus the PCB/OC/PBDE fraction of 200 mL was collected. In between sample runs there was a 3 min wash time. The collected fraction was roto-evaporated to approximately 2 mL, quantitatively transferred to a graduated test tube and reduced to 0.5 mL under nitrogen. The reduced GPC extract was cleaned up on a silica LC-Si SPE cartridge (500 mg X 6 mL; 6 gram; J.T. Baker, USA) (Saito et al. 2004). The cartridge was first conditioned with 6 ml of 10% MeOH in DCM, followed by 8 ml of 5% DCM in hexane. The 0.5 ml extract was loaded onto the cartridge and the fraction collected (using 8 ml of 5% DCM in hexane) contained all PCBs, OCs and PBDEs/BFRs of interest. The fraction was evaporated under a stream of N_2 to 1 mL (with rinsing), solvent exchanged into TMP and re-evaporated under nitrogen to around 250 µL. After quantitative transfer to a pre-weighed brown glass GC vial with insert and cap, the final sample fraction was then ready for GC-MS analysis. As described below, the fraction was injected two times, 1) OCs by GC-MS(EI) and 2) PCBs by GC-MS.

Section S5.4: Supplemental information on the compounds targeted in each POP analysis

Table S5.2: All compounds (PCB and OC pesticides) targeted for each individual predator marine mammal sample at both McGill University and Environment and Climate Change Canada. Only polar bears from 2012-2016 were analyzed at Environment and Climate Change Canada. An 'X' is used to indicate that a compound was analyzed at a specific location, and bolded values are used to indicate that they were analyzed at both locations. Only bolded compounds were included in further analyses.

Contaminant	McGill University Samples	Environment and Climate Change Canada Samples
Polychlorinated Biphenyls (PCBs)		
CB-16		X
CB-17	**X**	**X**
CB-18	**X**	**X**
CB-19		X
CB-22		X
CB-25		X
CB-28	**X**	**X**
CB-31	**X**	**X**
CB-33	**X**	**X**
CB-44	**X**	**X**
CB-49	**X**	**X**
CB-52	**X**	**X**
CB-56		X
CB-60		X
CB-66		X
CB-67		X
CB-70	**X**	**X**
CB-71		X
CB-74	**X**	**X**
CB-77		X
CB-81		X
CB-82	**X**	**X**
CB-87	**X**	**X**
CB-95	**X**	**X**
CB-97		X
CB-99	**X**	**X**
CB-101	**X**	**X**
CB-105	**X**	**X**
CB-110	**X**	**X**
CB-114		X
CB-118	**X**	**X**
CB-123		X
CB-126		X
CB-128	**X**	**X**

CB-132		**X**
CB-138	**X**	**X**
CB-141		X
CB-146		X
CB-146		X
CB-149	**X**	**X**
CB-151	**X**	**X**
CB-153	**X**	**X**
CB-156	**X**	**X**
CB-157		X
CB-158	**X**	**X**
CB-163		X
CB-167		X
CB-169	**X**	**X**
CB-170	**X**	**X**
CB-171	**X**	**X**
CB-173		X
CB-174		X
CB-177	**X**	**X**
CB-179		X
CB-180	**X**	**X**
CB-183	**X**	**X**
CB-185		X
CB-187	**X**	**X**
CB-189		X
CB-191	X	
CB-194	**X**	**X**
CB-195	**X**	**X**
CB-199	**X**	**X**
CB-203		**X**
CB-205	X	
CB-206		**X**
CB-208	X	
CB-209	**X**	**X**
Organochlorines (OCs)		
p,p'-DDT	**X**	**X**
p,p'-DDE	**X**	**X**
p,p'-DDD	**X**	**X**
Oxychlordane	**X**	**X**
***trans*-Chlordane**	**X**	**X**
cis-Chlordane	**X**	**X**
***trans*-Nonachlor**	**X**	**X**
cis-Nonachlor	**X**	**X**
Heptachlor Epoxide	**X**	**X**
α-Hexachlorocyclohexane	**X**	**X**

β-Hexachlorocyclohexane	**X**	**X**
γ-Hexachlorocyclohexane		X
1,2,4,5-Tetrachlorobenzene	**X**	**X**
1,2,3,4-Tetrachlorobenzene	**X**	**X**
Pentachlorobenzene	**X**	**X**
Hexachlorobenzene	**X**	**X**
Dieldrin	**X**	**X**
Mirex	**X**	**X**
Photomirex		X
Endosulfan sulfate	X	
Endosulfan II	X	
Octachlorostyrene		X

Section S5.5: Supplemental information on quality assurance/quality control in standard reference materials

Table S5.3: Analytical accuracy (calculated as [reported value in NIST SRM - value measured from our extraction]/ [reported value in NIST SRM] *100) for NIST standard reference material (SRM) 1945 organics in whale blubber (at McGill and at Environment and Climate Change Canada in the Letcher labs) and 1946 Lake Superior fish tissue included in each batch of killer whale, pilot whale, 2021 polar bear, and narwhal for polychlorinated biphenyls (PCB) and organochlorine (OC) pesticide analysis extracted at McGill University.

	PCB % Accuracy	**OC % Accuracy**
***SRM NIST 1945* at McGill University**		
Batch 1	12.5	13.7
Batch 2	17.4	18.1
Batch 3	14.9	16.3
Batch 4	0.6	7.1
Batch 5	36	36.2
Average (± SD)	16.3 ± 12.8	18.3 ± 10.9
SRM NIST 1945 at ECCC		
2012 Polar bear batch	2.1	10.0
2013 Polar bear batch	13.6	16.8
2014 Polar bear batch	11.2	12.5
2015 Polar bear batch	7.4	8.9
Average (± SD)	8.6 ± 5.0	12.1 ± 3.5
SRM NIST 1946		
Batch 1	40.2	5.7
Batch 2	4.1	4.9
Batch 3	22.6	22.3
Batch 4	24.3	24.4
Batch 5	42.5	9.9
Batch 6	18.5	9.7
Batch 7	5.0	19.7
Batch 8	12.8	13.6
Average (± SD)	20.6 ± 14.2	15.5 ± 6.4

Section S5.6: Supplemental information on Quality Assurance/Quality Control

Contaminant analysis: Accuracies of ΣPCBs and ΣOCs were calculated using either SRM NIST 1945 organics in whale blubber (Certificate of Analysis, 1945; Kucklick et al., 2010) or SRM NIST 1946 Lake Superior fish tissue (Certificate of Analysis, 1946). For SRM 1945, mean accuracies across all batches were 16.6 ± 9.8% and 19.0 ± 12.9%, for ΣPCBs and ΣOCs, respectively (Table S5.3). From SRM 1946, mean ΣPCBs and ΣOCs were 20.5 ± 13.4% and 14.6 ± 6.5%, respectively, across all batches (Table S5.3). Internal standard spikes showed recoveries for mass-labelled PCBs and ClBzs of 81.4 ± 16.4% and 62.3 ± 15.6%, respectively, across all batches (see table S5.4 for more information). The method limit of detection (MLoD) was set to 3 × the signal-to-noise ratio, and method limit of quantification (MLoQ) was set to 10 × the signal-to-noise ratio for each compound, and MLoD ranged from 0.1-3.6 ng/g and MLoQ ranged from 0.4-12.9 ng/g. Trace amounts of CBs 52, 151, 118, 153, 180, 138, and *p,p'*-DDE and *trans*-nonachlor (<0.88 ng/mL) were found in some blanks. However, these levels were more than ten times lower than the concentrations found in samples and thus black subtraction was not performed. For all samples, all individual OCs were detected, with the exception of methoxychlor and endosulfan II not being detected in >60% of samples, and as such, these were not included in further analyses. Due to lower recoveries of the ClBzs, these, but no other OCs, were recovery-corrected from mass labelled ClBz internal standards.

Table S5.4: Average recovery (and ranges) of mass-labelled internal standards from all spiked samples ran through the extraction method

Chemical Class/Compound	Averaged % Recovery
Organochlorines	
$^{13}C_6$-1,2,4,5-tetrachlorobenzene	65.1 (58.6-81.9)
$^{13}C_6$-1,2,4,5-pentachlorobenzene	58.8 (52.4-71.0)
$^{13}C_6$-1,2,4,5-hexachlorobenzene	72.1 (65.9-83.1)
Polychlorinated Biphenyls	
$^{13}C_{12}$-PCB-28	77.1 (74.1-82.1)
$^{13}C_{12}$-PCB-52	95.0 (84.2-101.5)
$^{13}C_{12}$-PCB-118	72.1 (68.5-98.2)
$^{13}C_{12}$-PCB-153	71.0 (59.8-95.6)
$^{13}C_{12}$-PCB-180	81.5 (66.1-93.0)
$^{13}C_{12}$-PCB-194	62.7 (49.1-78.2)

Fatty acids signature analysis: For quality assurance/control for FA signatures, this was reported previously for the 2012-2014 killer whales (Bourque et al., 2018), with SRM 1945 values averaging within 16 ± 0.21% of the published values (Kucklick et al., 2010). For all other SRM 1945 runs, our measurements averaged 14.0 ± 5.1% compared to published values (Kucklick et al., 2010) considering all 27 FAMEs. For RM 8037, our values averaged 18.0 ± 1.1% of the certified values for the 20 reported FAMEs (NIST Report of Investigation, 2020). For all duplicates, all FA proportions averaged 6.0 ± 1.4% of the values reported in corresponding samples, and thus, samples and their respective duplicate were averaged for each batch.

Section S5.7: Supplemental information on contaminant trends in each species per year

Table S5.5: ΣPolychlorinated biphenyls (ΣPCBs) and Σorganochlorine (ΣOC) pesticide comparison among different years in polar bear (Ursus maritimus), killer whale (Orcinus orca), long-finned pilot whale (Globicephala melas), and narwhal (Monodon monoceros). One-way analysis of variance (ANOVA) were used to test for differences among year, followed by post-hoc Tukey pairwise comparisons. Only p-values from ANOVAs among individual years are only shown

Species and years samples	**ΣPCBs**	**ΣDDTs**	**ΣCHLs**	**ΣClbzs**	**ΣHCHs**
Polar Bear (2012-2016, 2021)	*p= 0.066*	*p=0.51*	*p=0.28*	*p=0.33*	*p=0.49*
Pilot Whale (2016, 2018, 2021)	*p=0.31*	*p=0.62*	*p=0.11*	*p=0.78*	*p=0.27*
Killer Whale (2012-2014, 2021)	*p=0.13*	*p=0.78*	*p=0.61*	*p=0.83*	*p=0.39*
Narwhal (2015)	*NA*	*NA*	*NA*	*NA*	*NA*

Section S5.8: Supplemental information of the fatty acids included in dietary pattern analysis.

Table S5.6: All 69 fatty acids collected for each species and their mean relative proportion (in percentage). Each of the fatty acids is denoted by the nomenclature x:ynz, where x is the length of the carbon chain, y is the number of double bonds, and z is the position of the first double bond from the methyl ('n') end of the chain. A subset of 16 that were used in diet and modelling analyses are bolded. These fatty acids were selected because they were clearly present above detections limits (>0.1%; Pedro et al., 2020) across all killer whale (Orcinus orca), polar bear (Ursus maritimus), long-finned pilot whale (Globicephala melas), and narwhal (Monodon monoceros) and were also previously considered present in blubber/adipose through dietary intake and not through biosynthesis (Iverson et al., 2004).

Fatty Acid	Killer Whale	Narwhal	Pilot Whale	Polar Bear
8:0	0.01	0.02	0.01	0.01
10:0	0.09	0.13	0.04	0.00
12:0	0.79	0.82	0.29	0.04
13:0	0.08	0.05	0.04	0.02
iso14:0	0.53	0.20	0.11	0.04
14:0	8.71	5.88	6.49	3.22
14:1n9	0.45	0.67	0.18	0.06
14:1n7	0.36	0.51	0.13	0.04
14:1n5	2.79	1.86	1.26	0.58
iso15:0	1.56	1.09	0.56	0.31
anti15:0	0.25	0.14	0.11	0.07
15:0	1.03	0.33	0.47	0.23
15:1n8	0.03	0.02	0.02	0.01
15:1n6	0.13	0.08	0.06	0.04
iso16:0	1.13	0.34	0.38	0.11
16:0	7.89	7.96	10.18	6.60
16:1n11	1.25	1.60	0.46	0.22
16:1n9	1.51	1.53	1.36	0.45
16:1n7	17.91	19.50	13.35	8.96
7Me16:0	0.30	0.27	0.26	0.18
16:1n5	0.06	0.03	0.07	0.03
16:2n6	0.15	0.05	0.05	0.03
iso17:0	0.12	0.11	0.10	0.09
16:2n4	**0.42**	**0.24**	**0.47**	**0.15**
16:3n6	**0.53**	**0.41**	**0.28**	**0.29**
17:0	2.56	0.14	0.34	0.14
16:3n4	0.17	0.03	0.03	0.04
17:1	0.65	0.26	0.47	0.20
16:3n1	0.48	0.03	0.10	0.04
16:4n3	**0.15**	**0.12**	**0.23**	**0.14**

16:4n1	0.09	0.08	0.08	0.05
18:0	1.12	1.08	1.70	1.95
18:1n13	0.05	0.01	0.07	0.03
18:1n11	5.23	5.20	4.07	5.94
18:1n9	18.83	18.19	21.98	22.41
18:1n7	1.92	3.24	2.93	3.90
18:1n5	0.25	0.42	0.32	0.37
18:2D5,11	0.06	0.03	0.06	0.05
18:2n7	0.06	0.05	0.05	0.06
18:2n6	**0.17**	**1.15**	**1.32**	**1.75**
18:2n4	0.15	0.07	0.06	0.05
18:3n6	0.09	0.07	0.06	0.05
18:3n4	0.19	0.09	0.13	0.12
18:3n3	**4.53**	**0.46**	**0.86**	**0.62**
18:3n1	0.65	0.07	0.17	0.04
18:4n3	**0.72**	**0.54**	**0.50**	**0.90**
18:4n1	0.08	0.10	0.08	0.08
20:0	0.05	0.06	0.11	0.10
20:1n11	2.68	3.63	4.78	4.47
20:1n9	**2.97**	**8.18**	**6.98**	**13.72**
20:1n7	**0.05**	**0.42**	**0.32**	**0.70**
20:2n9	0.11	0.06	0.06	0.12
20:2n6	**0.10**	**0.23**	**0.25**	**0.30**
20:3n6	0.05	0.06	0.08	0.10
20:4n6	**0.21**	**0.20**	**0.29**	**0.17**
20:3n3	0.05	0.06	0.14	0.08
20:4n3	**0.46**	**0.33**	**0.49**	**0.45**
20:5n3	**1.07**	**2.53**	**1.90**	**1.88**
22:1n11	**2.23**	**4.31**	**6.59**	**4.34**
22:1n9	**0.12**	**0.63**	**0.65**	**0.92**
22:1n7	0.01	0.09	0.08	0.10
22:2n6	0.01	0.05	0.02	0.02
21:5n3	**0.09**	**0.09**	**0.11**	**0.34**
22:4n6	0.10	0.06	0.08	0.09
22:5n6	0.07	0.02	0.10	0.11
22:4n3	0.02	0.03	0.05	0.09
22:5n3	0.42	0.66	1.10	4.59
22:6n3	**1.08**	**1.87**	**3.26**	**6.46**
24:1n9	0.10	1.16	0.23	0.15

Table S5.7: Proportions of 16 major fatty acids (FAs) (mean and range) measured in killer whales (Orcinus orca), narwhal (Monodon monoceros), long-finned pilot whale (Globicephala melas), and polar bear (Ursus maritimus) individuals above nursing ages collected in East Greenland between 2012-2021. Significant differences from post hoc comparisons ($p<0.05$) are represented by different letters (a,b,c) next to the measurement.

Fatty Acid	Killer Whale	Narwhal	Pilot Whale	Polar Bear
16:2n4	0.32^{a} (0.27-0.54)	0.24^{b} (0.18-0.29)	0.43^{c} (0.09-0.66)	0.14^{d} (0.06-0.23)
16:3n6	0.54^{a} (0.37-0.66)	0.41^{b} (0.39-0.45)	0.27^{c} (0.14-0.37)	0.29^{c} (0.08-0.52)
16:4n3	0.16^{a} (0.12-0.24)	0.12^{b} (0.10-0.13)	0.22^{c} (0.06-0.29)	0.14^{ab} (0.08-0.20)
18:2n6	0.17^{a} (0.11-0.43)	1.15^{b} (0.57-1.51)	1.32^{b} (0.99-1.80)	1.75^{c} (1.51-2.09)
18:3n3	4.42^{a} (1.10-9.70)	0.46^{b} (0.37-0.57)	0.76^{c} (0.13-1.61)	0.63^{b} (0.37-0.90)
18:4n3	0.43^{a} (0.21-0.72)	0.54^{a} (0.38-0.69)	0.36^{a} (0.14-0.60)	0.89^{b} (0.23-2.02)
20:1n9	4.48^{a} (1.70-6.80)	8.18^{b} (5.53-13.13)	7.11^{b} (1.35-9.47)	13.57^{c} (7.56-20.46)
20:1n7	0.18^{a} (0.06-0.28)	0.42^{b} (0.27-0.80)	0.34^{b} (0.16-0.60)	0.73^{c} (0.61-1.14)
20:2n6	0.12^{a} (0.04-0.23)	0.23^{b} (0.14-0.29)	0.25^{b} (0.14-0.34)	0.29^{c} (0.23-0.390)
20:4n6	0.23^{a} (0.10-0.39)	0.20^{ab} (0.11-0.29)	0.27^{a} (0.12-0.46)	0.17^{b} (0.07-0.28)
20:4n3	0.29^{a} (0.12-0.47)	0.33^{a} (0.20-0.48)	0.42^{b} (0.16-0.59)	0.44^{b} (0.16-0.67)
20:5n3	1.29^{a} (0.51-2.53)	2.53^{b} (1.34-3.75)	1.64^{a} (0.68-3.77)	1.88^{a} (0.12-5.79)
22:1n11	2.09^{a} (0.58-6.80)	4.31^{b} (2.64-9.43)	6.69^{c} (0.70-11.04)	4.33^{b} (1.62-8.07)
22:1n9	0.26^{a} (0.12-0.44)	0.63^{b} (0.38-1.60)	0.69^{b} (0.16-1.32)	0.93^{c} (0.43-1.84)
21:5n3	0.13^{a} (0.05-0.52)	0.09^{a} (0.01-0.18)	0.10^{a} (0.03-0.17)	0.34^{b} (0.16-0.48)
22:6n3	1.81^{a} (0.33-3.18)	1.87^{a} (0.46-3.34)	3.09^{b} (0.91-5.5)	6.40^{c} (2.99-8.17)

Section S5.9: Supplemental information on dietary pattern comparison between ages

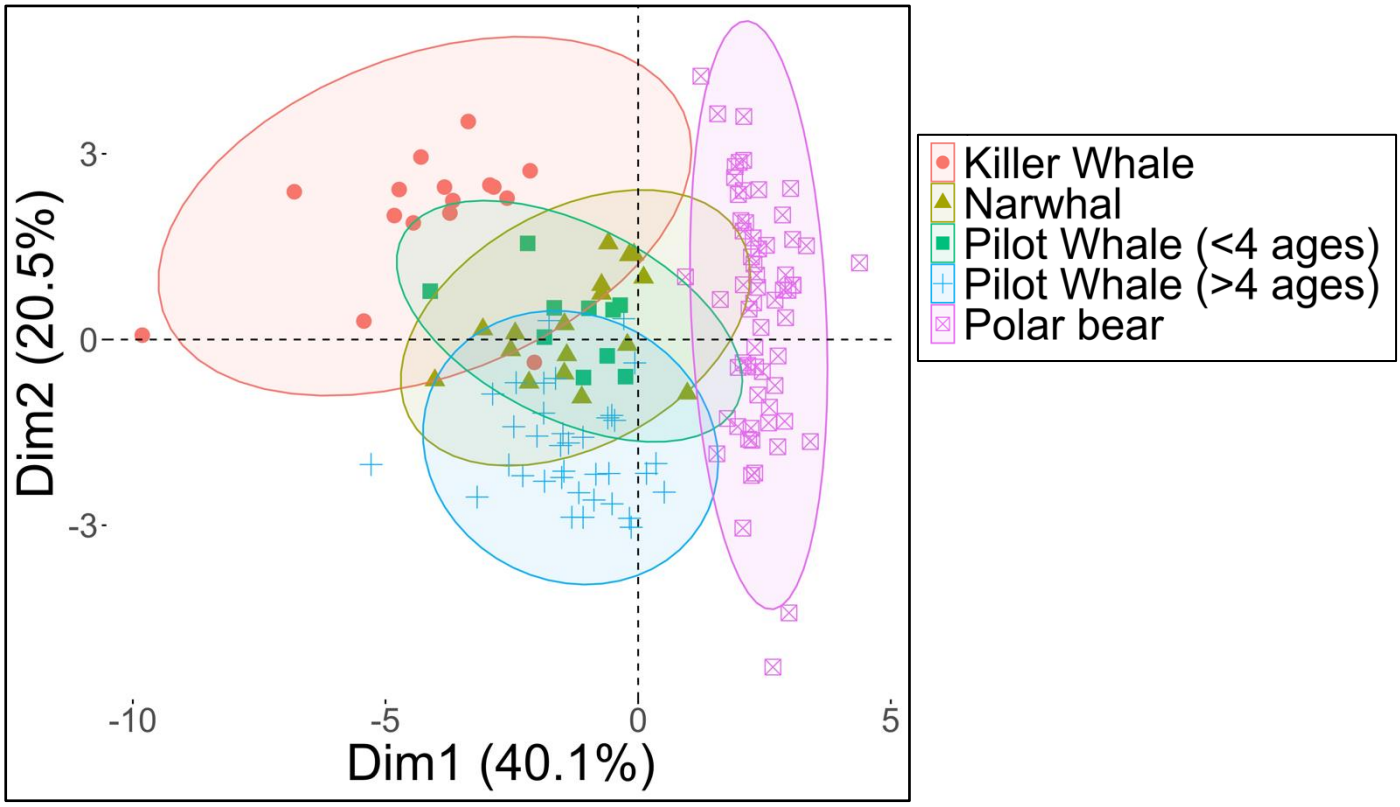

Figure S5.2: Principal components analysis (PCA) of 16 proportion dietary fatty acids in polar bear (*Ursus maritimus*), killer whale (*Orcinus orca*), long-finned pilot whale (*Globicephala melas)*, and narwhal (*Monodon monoceros*) with subadult pilot whales less than four years of age (who are likely nursing) included as a separate grouping. For killer whale and narwhal, age-specific data is not available, and no subadult FA profile in individuals are distinctly different. For polar bears, no samples were from polar bears of nursing ages. The first dimension of the PCA accounted for 40.1% of the total variation, and the second dimension accounted for 20.5%. Ellipses represent 90% confidence intervals. Due differences in pilot whale ages groups (between green squares and blue plus symbols), subadults less than 4 years of age were excluded from our analyses.

Section S5.10: Supplemental information on contaminant comparison among species

Table S5.8: Comparison of legacy contaminant levels for Σpolychlorinated biphenyls (ΣPCBs) and organochlorine (OC) pesticides, such as Σdichlorodiphenyltrichloroethanes (ΣDDTs), Σchlordanes (ΣCHLs), Σchlorobenzenes (ΣClBzs), Σhexachlorocyclohexanes (ΣHCHs), and Dieldrin in killer whales (*Orcinus orca*), narwhal (*Monodon monoceros*), long-finned pilot whale (*Globicephala melas*), and polar bear (*Ursus maritimus*). One-way analysis of variance (ANOVAs) with post-hoc Tukey pairwise comparisons were used to assess for statistical significance among species. Significant differences from post hoc comparisons ($p<0.05$) are represented by different letters (a,b,c) next to the measurement.

	Tooth Whales			Ursid
Contaminant	**Killer Whale (mg/kg lw)**	**Narwhal (mg/kg lw)**	**Pilot Whale (mg/kg lw)**	**Polar Bear (mg/kg lw)**
ΣPCBs	57.0^{a} (7.0-214)	2.57^{b} (0.7-8.7)	4.76^{b} (0.7-22.4)	12.69^{c} (1.8-54)
triPCBs	0.09^{a} (0.01-0.2)	0.03^{b} (0.01-0.1)	0.05^{b} (0.01-0.1)	$>0.01^{c}$
tetraPCBs	0.90^{a} (0.3-3.2)	0.30^{b} (0.04-1.3)	0.37^{b} (0.03-1.8)	0.02^{c} (0.01-0.03)
pentaPCBs	7.15^{a} (0.6-32.5)	0.70^{b} (0.1-2.7)	1.24^{b}(0.1-6.8)	0.74^{b} (0.2-3.2)
hexaPCBs	36.3^{a} (2.4-149)	1.10^{b} (0.2-3.8)	2.09^{b} (0.2-10.7)	5.11^{c} (1.1-16.5)
heptaPCBs	12.3^{a} (2.0-38.7)	0.33^{b} (0.1-0.8)	0.75^{b} (0.1-2.8)	5.42^{c} (0.5-28.8)
octaPCBs	0.24^{a} (0.01-0.5)	0.10^{a} (0.01-0.2)	0.24^{a} (0.1-0.6)	1.31^{b} (0.01-7.4)
decaPCB	0.06^{a} (0.01-0.7)	0.01^{b} (0.01-0.04)	$>0.01^{b}$	0.08^{a} (0.01-0.4)
ΣDDT	55.7^{a} (0.4-219)	2.10^{b} (0.2-5.1)	5.11^{b} (0.5-25.8)	0.28^{c} (0.03-2.0)
p,p'-DDT	2.56^{a} (0.01-9.3)	0.36^{b} (0.1-1.1)	0.50^{b} (0.1-1.9)	0.02^{c} (0.01-0.2)
p,p'-DDE	51.3^{a} (0.4-203)	1.34^{b} (0.1-5.1)	4.00^{b} (0.4-21.3)	0.23^{c} (0.01-1.7)
p,p'-DDD	1.81^{a} (0.01-6.1)	0.40^{b} (0.1-1.4)	0.62^{b} (0.1-2.6)	0.03^{c} (0.02-0.4)
DDE/DDT	18.6^{a} (10.2-45.1)	3.4^{b} (1.8-6.8)	7.2^{b} (4.0-11.6)	19.6^{a} (3.9-67.7)
ΣCHL	23.1^{a} (0.2-96.9)	0.30^{b} (0.03-1.2)	1.80^{b} (0.2-8.1)	1.73^{b} (0.3-6.5)
trans-Chlordane	0.27^{a} (0.01-1.1)	$>0.01^{b}$	$>0.01^{c}$	$>0.01^{c}$
cis-Chlordane	0.59^{a} (0.01-2.5)	0.05^{bc} (0.02-0.1)	0.17^{b} (0.03-0.6)	0.02^{c} (0.03-0.1)
trans-Nonachlor	13.7^{a} (0.1-55.6)	0.75^{b} (0.2-2.6)	1.02^{b} (0.1-4.9)	0.25^{c} (0.03-1.7)
cis-Nonachlor	1.67^{a} (0.01-6.3)	0.19^{b} (0.04-0.6)	0.31^{b} (0.04-1.3)	0.02^{c} (0.01-0.2)
Oxychlordane	6.57^{a} (3.1-29.5)	0.23^{b} (0.03-1.0)	0.16^{b} (0.01-0.8)	1.25^{c} (0.2-5.6)
Heptachlor Epoxide	2.04^{a} (0.01-8.2)	0.14^{bc} (0.02-0.6)	0.12^{b} (0.01-0.6)	0.20^{c} (0.03-0.3)
ΣClbz	0.65^{a} (0.01-2.2)	0.08^{b} (0.02-0.2)	0.28^{b} (0.03-0.8)	0.30^{b} (0.1-1.7)
ΣHCH	0.61^{a} (0.01-2.0)	0.96^{b} (0.3-2.5)	0.11^{b} (0.02-0.2)	0.23^{b} (0.01-0.6)
Dieldrin	3.52^{a} (0.03-15.5)	0.60^{b} (0.2-1.8)	0.69^{b} (0.2-2.4)	0.28^{b} (0.1-1.2)
Mirex	0.79^{a} (0.01-2.2)	0.02^{b} (0.01-0.04)	0.06^{b} (0.01-0.1)	0.03^{b} (0.01-0.3)

Section S5.11: Supplemental information on contaminant comparison by age class/sex group

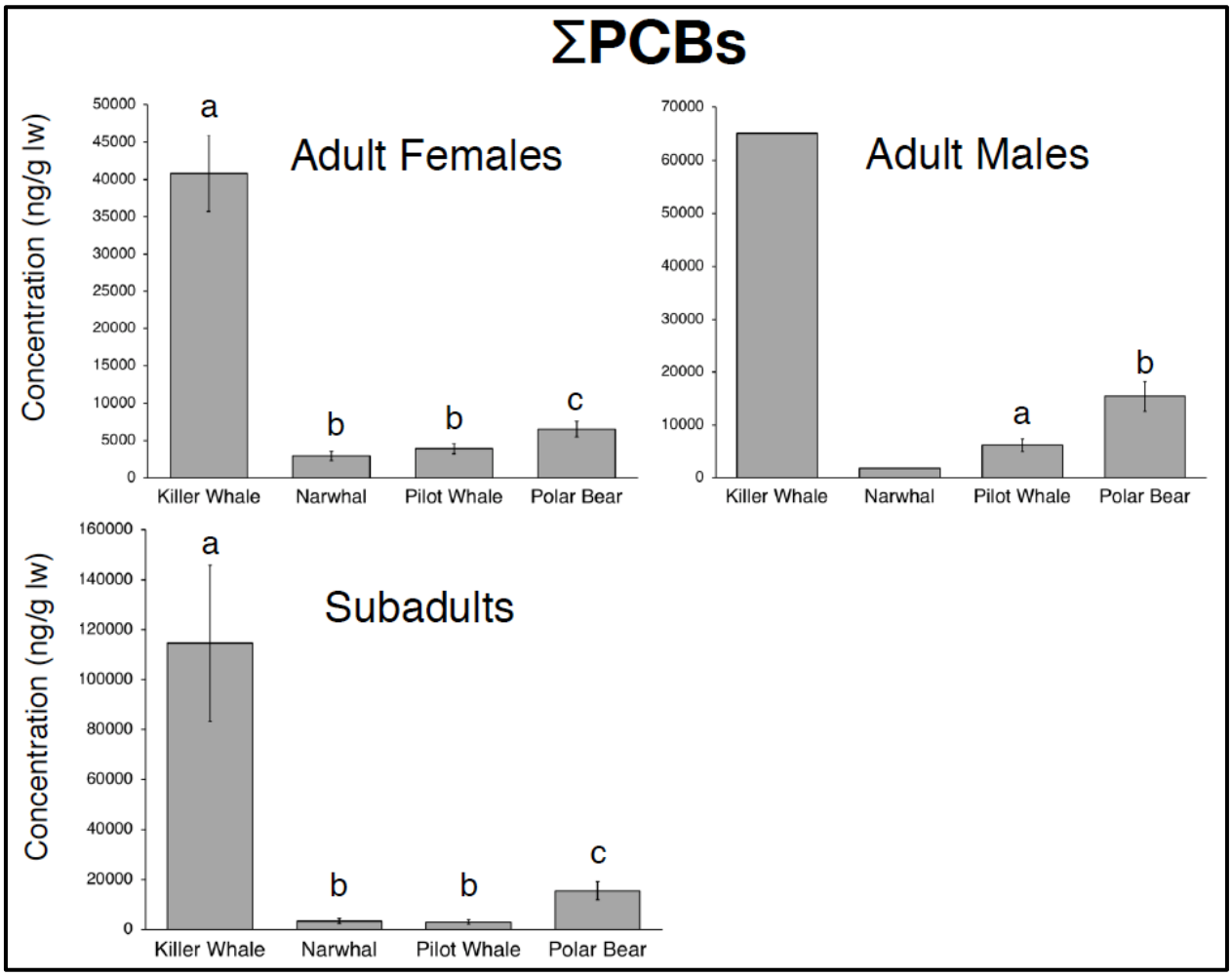

Figure S5.3: Comparison of legacy contaminant levels for Σpolychlorinated biphenyls (ΣPCBs) in killer whales (*Orcinus orca*), narwhal (*Monodon monoceros*), long-finned pilot whale (*Globicephala melas*), and polar bear (*Ursus maritimus*) grouped by age class/sex. One-way analysis of variance (ANOVAs) with post-hoc Tukey pairwise comparisons were used to assess for statistical significance among species using $p<0.05$. Significant differences are represented by different letters (a,b,c) above the measurement, except for adult male killer whales and narwhals were sample sizes were not large enough for statistical analyses. 19 killer whale (9 adult female, 2 adult males, 8 subadults), 15 narwhal (6 adult female, 2 adult males, 12 subadults), 46 pilot whale (15 adult female, 3 adult males, 10 subadults, 18 ND), and 60 polar bear (10 adult female, 23 adult males, 27 subadults) were sampled.

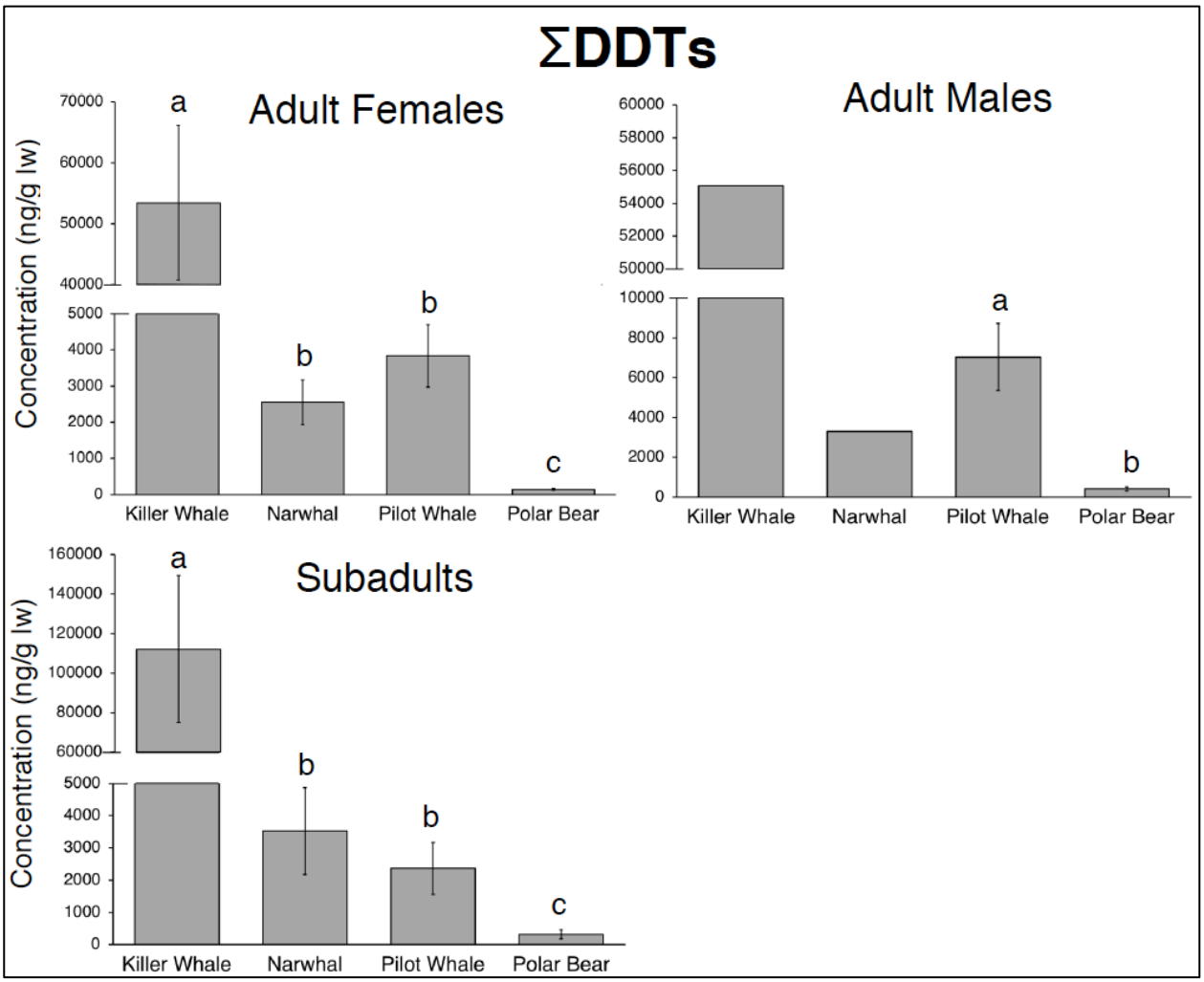

Figure S5.4: Comparison of legacy contaminant levels for Σdichlorodiphenyltrichloroethanes (ΣDDTs) in killer whales (Orcinus orca), narwhal (Monodon monoceros), long-finned pilot whale (Globicephala melas), and polar bear (Ursus maritimus) grouped by age class/sex. One-way analysis of variance (ANOVAs) with post-hoc Tukey pairwise comparisons were used to assess for statistical significance among species using $p<0.05$. Significant differences are represented by different letters (a,b,c) above the measurement, except for adult male killer whales and narwhals were sample sizes were not large enough for statistical analyses. 19 killer whale (9 adult female, 2 adult males, 8 subadults), 15 narwhal (6 adult female, 2 adult males, 12 subadults), 46 pilot whale (15 adult female, 3 adult males, 10 subadults, 18 ND), and 60 polar bear (10 adult female, 23 adult males, 27 subadults) were sampled.

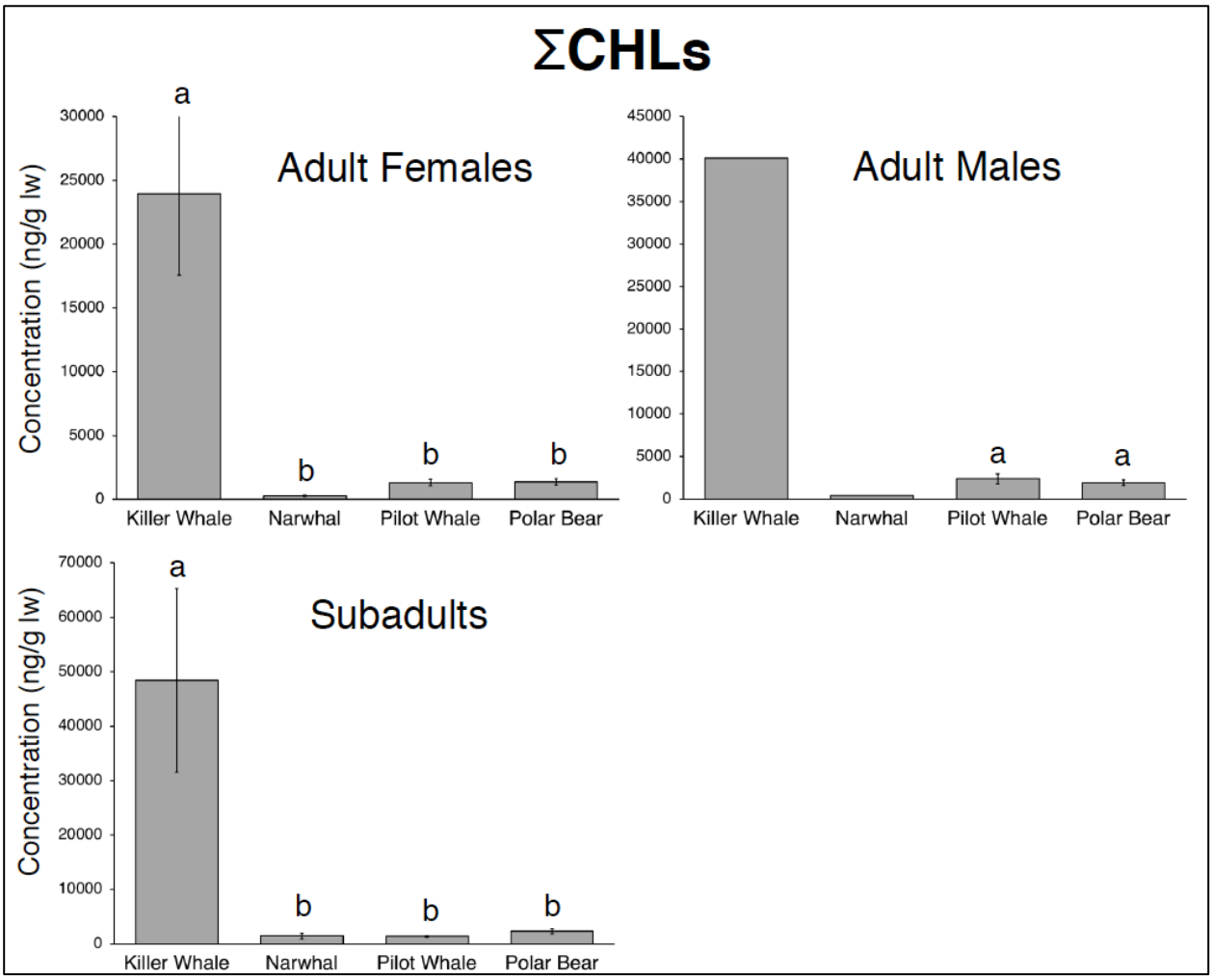

Figure S5.5: Comparison of legacy contaminant levels for Σchlordanes (ΣCHLs) in killer whales (*Orcinus orca*), narwhal (*Monodon monoceros*), long-finned pilot whale (*Globicephala melas*), and polar bear (*Ursus maritimus*) grouped by age class/sex. One-way analysis of variance (ANOVAs) with post-hoc Tukey pairwise comparisons were used to assess for statistical significance among species using $p<0.05$. Significant differences are represented by different letters (a,b,c) above the measurement, except for adult male killer whales and narwhals were sample sizes were not large enough for statistical analyses. 19 killer whale (9 adult female, 2 adult males, 8 subadults), 15 narwhal (6 adult female, 2 adult males, 12 subadults), 46 pilot whale (15 adult female, 3 adult males, 10 subadults, 18 ND), and 60 polar bear (10 adult female, 23 adult males, 27 subadults) were sampled.

Section S5.12: Supplemental information on metabolite/parent compound ratios

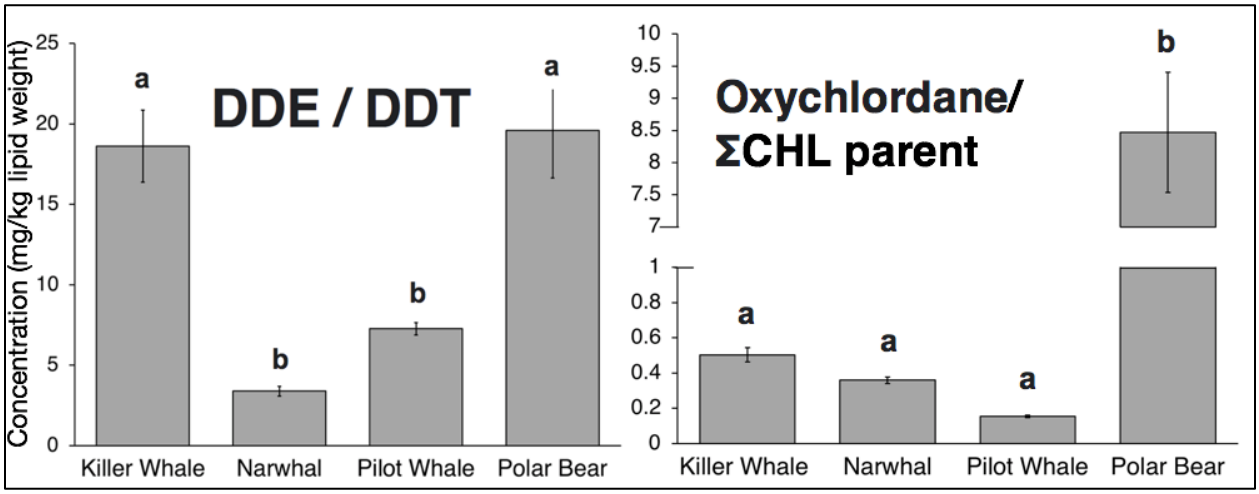

Figure S5.6: Comparison of legacy contaminant concentrations for summed dichlorodiphenyltrichloroethane (DDT) metabolite, DDE, over DDT (left) and summed chlordane (CHL) metabolites, oxychlordane and heptachlor epoxide, over parent compounds, chlordane and nonachlor (right), in killer whales (*Orcinus orca*), narwhal (*Monodon monoceros*), long-finned pilot whale (*Globicephala melas*), and polar bear (*Ursus maritimus*). One-way analysis of variance (ANOVAs) with post-hoc Tukey pairwise comparisons were used to assess for statistical significance among species using $p<0.05$. Significant differences are represented by different letters (a,b,c) above the measurement, except for adult male killer whales and narwhals were sample sizes were not large enough for statistical analyses.

Section S5.13: Supplemental information on fatty acid comparison among age class/sex grouping

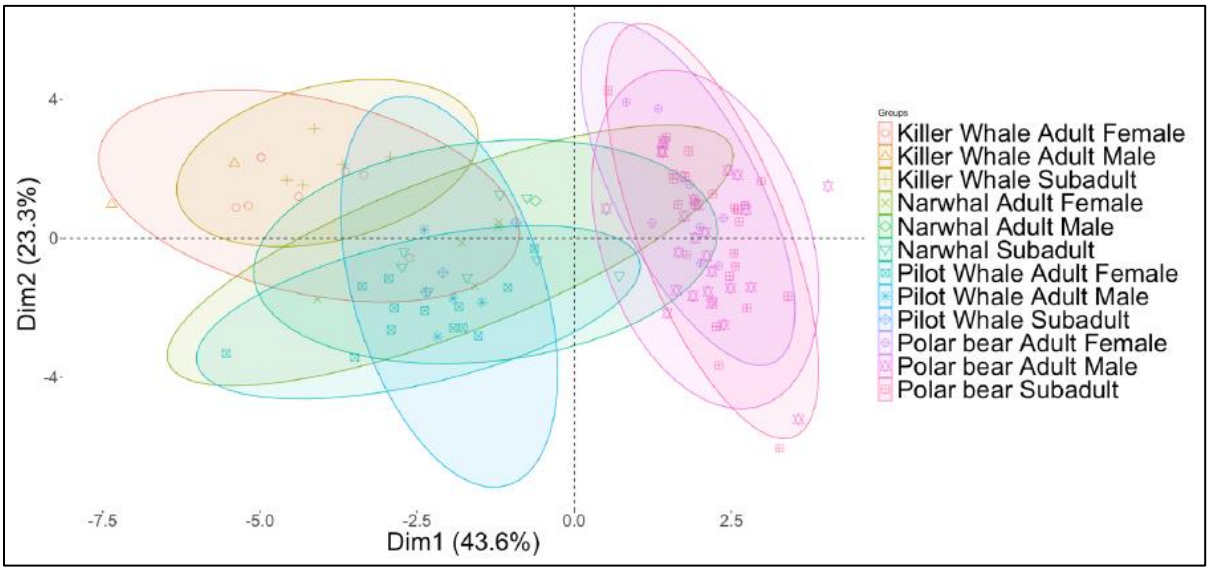

Figure S5.7: Principal components analysis (PCA) of 16 proportion dietary fatty acids in polar bear (Ursus maritimus), killer whale (Orcinus orca), long-finned pilot whale (Globicephala melas), and narwhal (Monodon monoceros) grouped by age class/sex. The first dimension of the PCA accounted for 43.6% of the total variation, and the second dimension accounted for 23.3%. Ellipses represent 90% confidence intervals.

Section S5.14: Supplemental information on dietary pattern principal component analysis axis three

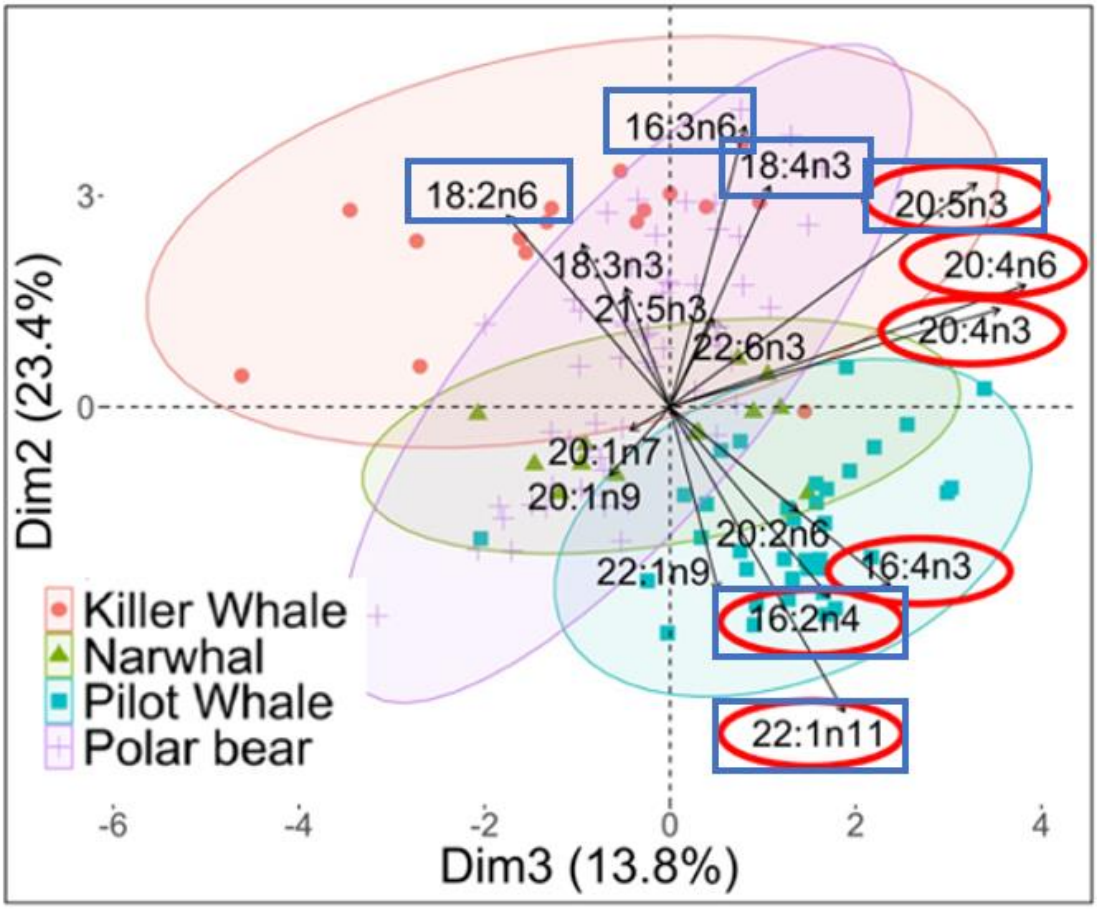

Figure S5.8: A: Principal component analysis (PCA) of the 16 highest proportion dietary fatty acids in killer whales (Orcinus orca), narwhal (Monodon monoceros), long-finned pilot whale (Globicephala melas), and polar bear (Ursus maritimus) on principal component axes one (PC2) and PC3. Ellipses represent 90% confidence intervals. Blue boxed FAs contributed to most of the variation of FA-PC2, while circled FAs in the red the ones contributed to most of the variation along FA-PC3.

Section S5.15: Supplemental information on dietary pattern on *Gonatus fabricii* prey species

Table S5.9: Proportions of 16 major fatty acids (FAs) measured in Gonatus fabricii collected in West Greenland

Fatty acid	*G. fabricii* 1	*G. fabricii* 2	Average
16:2n4	0.31	0.1345	0.22225
16:3n6	0.562	0.502	0.532
16:4n3	0.1555	0.07	0.11275
18:2n6	1.1235	0.9095	1.0165
18:3n3	0.5435	0.5	0.52175
18:4n3	4.2365	1.774	3.00525
20:1n9	16.569	9.7685	13.16875
20:1n7	0.355	0.522	0.4385
20:2n6	0.1765	0.4005	0.2885
20:4n6	0.251	0.4175	0.33425
20:4n3	0.395	0.384	0.3895
20:5n3	9.4805	11.259	10.36975
22:1n11	16.504	9.4595	12.98175
22:1n9	1.696	1.0355	1.36575
21:5n3	0.469	0.338	0.4035
22:6n3	8.5845	7.3595	7.972

Section S5.16: Supplemental information on contaminant modeling: full model information

Table S5.10: Best averaged model (all models averaged with AIC <2) of linear models for contaminant classes and individual contaminants/congeners in the blubber/adipose tissue of killer whales (Orcinus orca), narwhal (Monodon monoceros), long-finned pilot whale (Globicephala melas), and polar bear (Ursus maritimus) in east/southeast Greenland. Significant variables in each model are bolded, when confidence intervals did not cross zero. Squared semi-partial correlation coefficient are also reported to show the variance explained by each individual variable (given the influence of each other variable in the top model).

Averaged Model (AIC_c <2)	*Parameter*	*Estimate*	*Confidence Interval*		R^2	*Semi-partial coefficient*^{2}
			2.50%	**97.5%**		
ΣPCBs~ Taxa + **FA-PC2** + **FA-PC3** + **sex/age class**	Taxa-ursid	0.10	0.01	0.20	0.38	0.07
	FA-PC2	0.04	<0.01	0.08		0.10
	FA-PC3	-0.12	-0.17	-0.06		0.18
	Adult males	0.19	0.02	0.39		0.02
ΣtriPCBs~ **Taxa** + **FA-PC2** + FA-PC3	Taxa-ursid	-0.01	-0.01	-0.01	0.53	0.50
	FA-PC2	<0.01	<0.01	<0.01		0.03
ΣtetraPCBs~ **Taxa + FA-PC2 + FA-PC3** + sex/age class	Taxa-ursid	-0.07	<-0.01	-0.13	0.57	0.51
	FA-PC2	0.01	<0.01	0.02		0.04
	FA-PC3	<-0.01	<-0.01	<-0.01		0.02
ΣpentaPCBs~ **Taxa +** FAPC2 + **FA-PC3** + sex/age class	Taxa-ursid	-0.21	-0.29	-0.13	0.27	0.22
	FA-PC3	-0.04	-0.07	-0.01		0.02
ΣhexaPCBs~ Taxa **+ FA-PC2** + **FA-PC3**	FA-PC2	0.04	0.01	0.07	0.21	0.05
	FA-PC3	-0.07	-0.14	-0.03		0.14
ΣheptaPCBs~ **Taxa** + FA-PC2 + **FA-PC3**	Taxa-ursid	0.07	0.06	0.34	0.24	0.08
	FA-PC3	-0.09	-0.14	-0.04		0.14
ΣoctaPCBs~ **Taxa** + **FA-PC2** + **FA-PC3**	Taxa-ursid	0.19	0.12	0.26	0.31	0.20
	FA-PC2	0.02	0.01	0.04		0.06
	FA-PC3	-0.03	-0.06	<-0.01		0.04
ΣdecaPCB~ **Taxa +** FA-PC2 + FA-PC3	Taxa-ursid	<0.01	<0.01	<0.01	0.08	0.04
ΣDDTs~ Taxa + **FA-PC2** + **FA-PC3**	Taxa-ursid	-0.82	-0.96	-0.67	0.60	0.53
	FA-PC2	0.07	0.03	0.11		0.06

	FA-PC3	-0.06	-0.11	<-0.01		0.02
DDT~ **Taxa** + **FA-PC2** + **FA-PC3**	Taxa-ursid	-0.27	-0.34	-0.21	0.52	0.44
	FA-PC2	0.03	0.02	0.05		0.04
	FA-PC3	-0.03	-0.05	-0.01		0.04
DDE~ **Taxa** + **FA-PC2** + FA-PC3	Taxa-ursid	-0.76	-0.91	-0.61	0.52	0.47
	FA-PC2	0.07	0.03	0.11		0.05
DDD~ **Taxa** + **FA-PC2** + **FA-PC3**	Taxa-ursid	-0.24	-0.29	-0.19	0.51	0.46
	FA-PC2	0.02	0.01	0.03		0.03
	FA-PC3	-0.02	-0.04	<-0.01		0.02
DDE/DDT~ **Taxa** + FA-PC2 + FA-PC3	Taxa-ursid	0.21	0.08	0.33	0.12	0.09
ΣCHLs~ Taxa + FA-PC2 + FA-PC3	Taxa-ursid	-0.28	-0.42	-0.14	0.27	0.14
	FA-PC2	0.04	0.01	0.08		0.05
	FA-PC3	-0.09	-0.14	-0.04		0.09
trans-Chlordane ~ **Taxa + FA-PC2 + FA-PC3**	Taxa-ursid	-0.06	-0.06	-0.02	0.26	0.14
	FA-PC2	0.01	<0.01	0.01		0.09
	FA-PC3	-0.01	-0.02	<-0.01		0.04
cis-Chlordane~ **Taxa + FA-PC2 +** FA-PC3	Taxa-ursid	-0.08	-0.11	-0.06	0.30	0.26
	FA-PC2	0.01	<0.01	0.02		0.04
trans-Nonachlor ~ **Taxa + FA-PC2 + FA-PC3**	Taxa-ursid	-0.46	-0.58	-0.34	0.46	0.36
	FA-PC2	0.06	<0.02	0.08		0.05
	FA-PC3	-0.06	-0.11	-0.02		0.05
cis-Nonachlor ~ **Taxa + FA-PC2 + FA-PC3**	Taxa-ursid	-0.19	-0.24	-0.14	0.45	0.36
	FA-PC2	0.02	0.01	0.04		0.06
	FA-PC3	-0.02	-0.04	<-0.01		0.03
Oxychlordane ~ **FA-PC2 + FA-PC3**	FA-PC2	0.03	0.01	0.06	0.21	0.06
	FA-PC3	-0.09	-0.13	-0.05		0.15
Heptachlor Epoxide ~ **Taxa + FA-PC2 + FA-PC3**	Taxa-ursid	-0.02	-0.17	-0.05	0.28	0.12
	FA-PC2	0.03	0.01	0.04		0.08
	FA-PC3	-0.04	-0.06	-0.02		0.08
ΣOxychlor/ΣChlordane ~ **Taxa +** FA-PC2 +	Taxa-ursid	0.81	0.71	0.91	0.64	0.61
FA-PC3+sex/age class	FA-PC3	-0.04	-0.08	-0.01		0.01
	Adult males	-0.19	-0.31	-0.06		0.01

ΣClbz~ Taxa + **FA-PC3** + sex/age class	FA-PC3	-0.02	-0.03	-0.01	0.09	0.07
ΣHCHs~ Taxa **+ FA-PC2 + FA-PC3**	FA-PC2	0.01	0.01	0.02	0.16	0.06
	FA-PC3	-0.02	-0.03	-0.01		0.11
Dieldrin~ **Taxa + FA-PC2 + FA-PC3**	Taxa-ursid	-0.22	-0.29	-0.15	0.37	0.29
	FA-PC2	0.02	<0.01	0.04		0.04
	FA-PC3	-0.03	-0.06	-0.01		0.04
Mirex~ **Taxa + FA-PC2 + FA-PC3**	Taxa-ursid	-0.05	-0.07	-0.03	0.33	0.19
	FA-PC2	<0.01	<0.01	0.01		0.06
	FA-PC3	-0.01	-0.02	<-0.01		0.08

Section S5.17: Supplemental information on contaminant modeling: FA-PC1 variable results

Table S5.11: Best averaged model (all models averaged with AIC <2) of linear models with FA-PC1 (instead of taxa) for contaminant classes and individual contaminants/congeners in the blubber/adipose tissue of killer whales (Orcinus orca), narwhal (Monodon monoceros), long-finned pilot whale (Globicephala melas), and polar bear (Ursus maritimus) in east/southeast Greenland. FA-PC1 was removed from other models due to high correlation with taxa (VIF>12). Significant variables in each model are bolded, when confidence intervals did not cross zero. Squared semi-partial correlation coefficient are also reported to show the variance explained by each individual variable (given the influence of each other variable in the top model).

Averaged Model (AIC_c <2)	***Parameter***	***Estimate***	***Confidence Interval***		***R^2***	***Semi-partial coefficient^2***
			2.50%	**97.5%**		
ΣPCBs~ FA-PC1 + **FA-PC2** + FA-PC3 + **sex/age class**	FA-PC1	0.03	0.01	0.05	0.41	0.07
	FA-PC2	0.04	<0.01	0.08		0.12
	Adult males	0.23	0.03	0.43		0.18
ΣtriPCBs~ **FA-PC1** + **FA-PC2** + FA-PC3	FA-PC1	<-0.01	<-0.01	<-0.01	0.56	0.52
	FA-PC2	<0.01	<0.01	<0.01		0.04
ΣtetraPCBs~ **FA-PC1 + FA-PC2** + sex/age class	FA-PC1	<-0.01	<-0.01	<-0.01	0.59	0.53
	FA-PC2	0.01	<0.01	0.02		0.04
	FA-PC3					0.02
ΣpentaPCBs~ **FA-PC1**+FA-PC2+FA-PC3+sex/age class	FA-PC1	-0.05	-0.06	-0.03	0.30	0.24
	FA-PC3					0.03
ΣhexaPCBs~ FA-PC1 **+ FA-PC2** + **FA-PC3**	FA-PC2	-0.03	-0.02	-0.04	0.25	0.08
	FA-PC3					0.16
ΣheptaPCBs~**FA-PC1**+FA-PC2+**FA-PC3**+sex/age class	FA-PC1	0.03	0.01	0.05	0.27	0.09
	FA-PC3					0.16
ΣoctaPCBs~ **FA-PC1**+**FA-PC2**+**FA-PC3**+sex/age class	FA-PC1	0.04	0.02	0.05	0.34	0.22
	FA-PC2	0.01	<0.01	0.03		0.08
	FA-PC3	-0.04	-0.07	-0.02		0.04
ΣdecaPCB~ **FA-PC1 +** FA-PC2 + FA-PC3	FA-PC1	<0.01	<0.01	<0.01	0.09	0.05
		<-0.01	<-0.01	<-0.01		
ΣDDTs~ FA-PC1 + **FA-PC2** + sex/age class	FA-PC1	-0.17	-0.19	-0.14	0.61	0.53
	FA-PC2	0.07	0.01	0.08		0.06
						0.02

DDT~ **FA-PC1** + **FA-PC2** + FA-PC3	FA-PC1	-0.05	-0.06	-0.04	0.54	0.46
	FA-PC2	0.02	0.01	0.04		0.04
						0.04
DDE~ **FA-PC1** + **FA-PC2**	FA-PC1	-0.16	-0.19	-0.13	0.55	0.50
	FA-PC2	0.04	0.01	0.08		0.05
DDD~ **FA-PC1** + **FA-PC2**	FA-PC1	-0.04	-0.05	-0.04	0.53	0.46
	FA-PC2	0.01	0.01	0.02		0.05
						0.02
DDE/DDT~ **FA-PC1** + FA-PC2 + FA-PC3	FA-PC1	0.03	<0.01	0.05	0.12	0.10
ΣCHLs~ **FA-PC1** + **FA-PC2** + **FA-PC3**	FA-PC1	-0.06	-0.09	-0.03	0.29	0.14
	FA-PC2	0.04	<0.01	0.07		0.03
	FA-PC3	-0.07	-0.12	-0.02		0.10
trans-Chlordane ~ **FA-PC1** + **FA-PC2** + FA-PC3	FA-PC1	-0.01	-0.01	<-0.01	0.29	0.14
	FA-PC2	0.01	<0.01	0.01		0.11
						0.04
cis-Chlordane~ **FA-PC1** + **FA-PC2** + FA-PC3	FA-PC1	-0.02	-0.02	-0.01	0.30	0.26
	FA-PC2	0.01	<0.01	0.01		0.04
trans-Nonachlor ~ **FA-PC1** + **FA-PC2** + FA-PC3	FA-PC1	-0.09	-0.11	-0.07	0.49	0.36
	FA-PC2	0.03	<0.01	0.07		0.08
						0.05
cis-Nonachlor ~ **FA-PC1** + **FA-PC2** + FA-PC3	FA-PC1	-0.04	-0.05	-0.03	0.45	0.36
	FA-PC2	0.02	<0.01	0.03		0.03
						0.06
Oxychlordane ~ **FA-PC2 + FA-PC3**	FA-PC2	0.04	0.01	0.07	0.22	0.07
	FA-PC3	-0.09	-0.13	-0.05		0.15
Heptachlor Epoxide ~ **FA-PC1 + FA-PC2 + FA-PC3**	FA-PC1	-0.02	-0.04	-0.01	0.28	0.12
	FA-PC2	0.02	0.01	0.04		0.08
	FA-PC3	-0.03	-0.05	-0.01		0.08
ΣOxychlor/ΣChlordane ~**FA-PC1+**FA-PC2+FA-PC3+**sex/age class**	FA-PC1	0.16	0.14	0.18	0.69	0.65
	Adult males	-0.17	-0.30	-0.05		0.03
						0.01
ΣClbz~ FA-PC1 + **FA-PC3** + **sex/age class**	FA-PC3	-0.02	-0.03	<-0.01	0.10	0.08

	Subadults	0.05	<0.01	0.10		
ΣHCHs~ FA-PC1 **+ FA-PC2 + FA-PC3**	FA-PC2	0.01	0.01	0.02	0.18	0.06
	FA-PC3	-0.02	-0.03	<-0.01		0.12
Dieldrin~ **FA-PC1 + FA-PC2 +** FA-PC3	FA-PC1	-0.22	-0.05	-0.03	0.44	0.34
	FA-PC2	0.02	<0.01	0.03		0.10
Mirex~ **FA-PC1 + FA-PC2 + FA-PC3**	FA-PC1	-0.01	-0.02	<-0.01	0.35	0.20
	FA-PC2	<0.01	<0.01	0.01		0.06
	FA-PC3	-0.01	-0.02	<-0.01		0.09

Section S5.18: Supplemental information on contaminant modeling: PCBs grouped by degree of chlorination

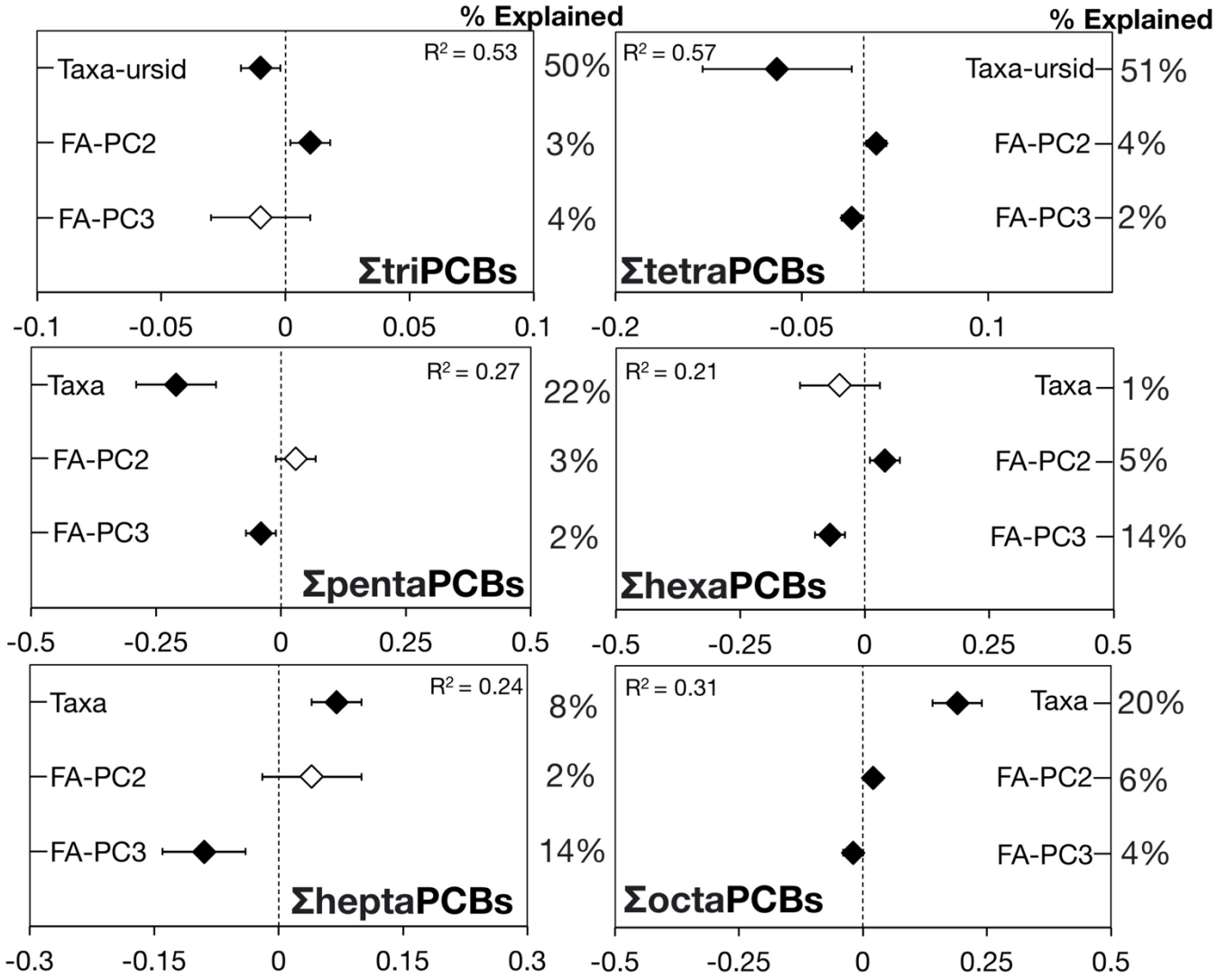

Figure S5.9: Confidence interval figures for top averaged models (AIC<2) for polychlorinated biphenyls (PCBs) grouped by degree of chlorination in killer whales (Orcinus orca), narwhal (Monodon monoceros), long-finned pilot whale (Globicephala melas), and polar bear (Ursus maritimus) collected between 2012-2021 in East Greenland. Significant (when confidence intervals do not cross zero) variables in top models are indicated by a black symbol (◆), while nonsignificant variables are white (◇).

CONNECTING TEXT

Chapter 5 discussed the use of FAs to explain interspecific differences in POP concentrations among marine mammals, where dietary FAs explained most of the variation (between 29-60%) for PCBs, DDTs, and CHLs among marine mammal species. However, a notable limitation when using FAs to examine dietary patterns in predators is due to large overlapping patterns among different prey items, often making it challenging to provide accurate diet estimates. For instance, large overlaps in FAs between narwhal and pilot whale in the PCA (**Figure 5.2**) may suggest similar diets, yet pilot whale likely feed on some subarctic fishes and squid (at least seasonally) while diets in narwhal consist of near-exclusively native Arctic species.

Instead, compound-specific isotope analysis of FAs (CSIA-FA) has been proposed to offer greater sensitivity than bulk stable isotopes or FA signatures alone in tracing feeding habits and assessing trophic transfer of contaminants. Although FA signatures may overlap or occur at similar proportions among different diet resources, individual FAs may still have distinct $\delta^{13}C$ values among prey. As such, using the same FA extracts from Chapter 5, Chapter 6 instead uses FA $\delta^{13}C$ values to assess variation in POP concentrations among killer whale, narwhal, pilot whale, and polar bear from East Greenland. To further investigate this approach, we also examine variability of FA $\delta^{13}C$ across an entire Arctic marine food web and explore the capacity of FA $\delta^{13}C$ to explain food web contaminant biomagnification. In comparison to FA proportions (from Chapter 5) and SI in bulk (whole) tissues (reported in Chapter 6), $\delta^{13}C$ values of some PUFAs may provide unique insights into lipophilic contaminant accumulation and biomagnification through food webs.

CHAPTER 6: THE POTENTIAL OF FATTY ACID CARBON ISOTOPES TO EXPLAIN CONTAMINANT ACCUMULATION AMONG SPECIES AND BIOMAGNIFICATION THROUGH FOOD WEBS

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6.1. ABSTRACT

Mercury (Hg) and persistent organic pollutant (POP) accumulation among species and biomagnification through food webs is typically assessed using stable isotopes of nitrogen ($\delta^{15}N$) and carbon ($\delta^{13}C$) in bulk (whole) tissues. Yet, bulk isotopic approaches have limitations, notably from the potential overlap of isotope values from different dietary sources and from spatial variation in source (baseline) signals due to environmental parameters such as water quality indices and seasonal nutrient availability. Here, we explore the potential of fatty acid carbon isotopes (FA $\delta^{13}C$) to (1) evaluate the trophic structure of a marine food web, (2) distinguish feeding patterns among four marine mammal consumers, (3) trace contaminant biomagnification through a food web, and (4) explain interspecific variation in contaminants among high-trophic position predators. In the Cumberland Sound (CS) food web of Nunavut, Canada, ranging from zooplankton to Greenland shark (*Somniosus microcephalus*), FA $\delta^{13}C$ values for the monounsaturated FAs, 20:1 and 22:1 isomers, did not vary across the food web, while the long-chain polyunsaturated FA, 22:6n3 showed $\delta^{13}C$ values that were enriched by ~1.5‰ with each trophic position. Values of $\delta^{13}C$ for shorter-chain and saturated FAs varied widely across this food web. In East Greenland (EG) marine mammals, FA $\delta^{13}C$ values were significantly higher in migratory sub-Arctic species relative to Arctic residents. Linear models using FA $\delta^{13}C$ as explanatory variables for contaminant concentrations demonstrated that baseline-corrected $\delta^{13}C$ values of certain dietary FAs explained more variation in POP concentrations than did bulk stable isotopes in EG marine mammals. However, bulk $\delta^{15}N$ better explained Hg variation in the CS food web. This study fully details the FA $\delta^{13}C$ instrumental methods, such that other researchers can test this novel approach on other species, locations, and food webs to further evaluate whether the $\delta^{13}C$ values of certain diet-derived FAs (18:3n3, 20:1,

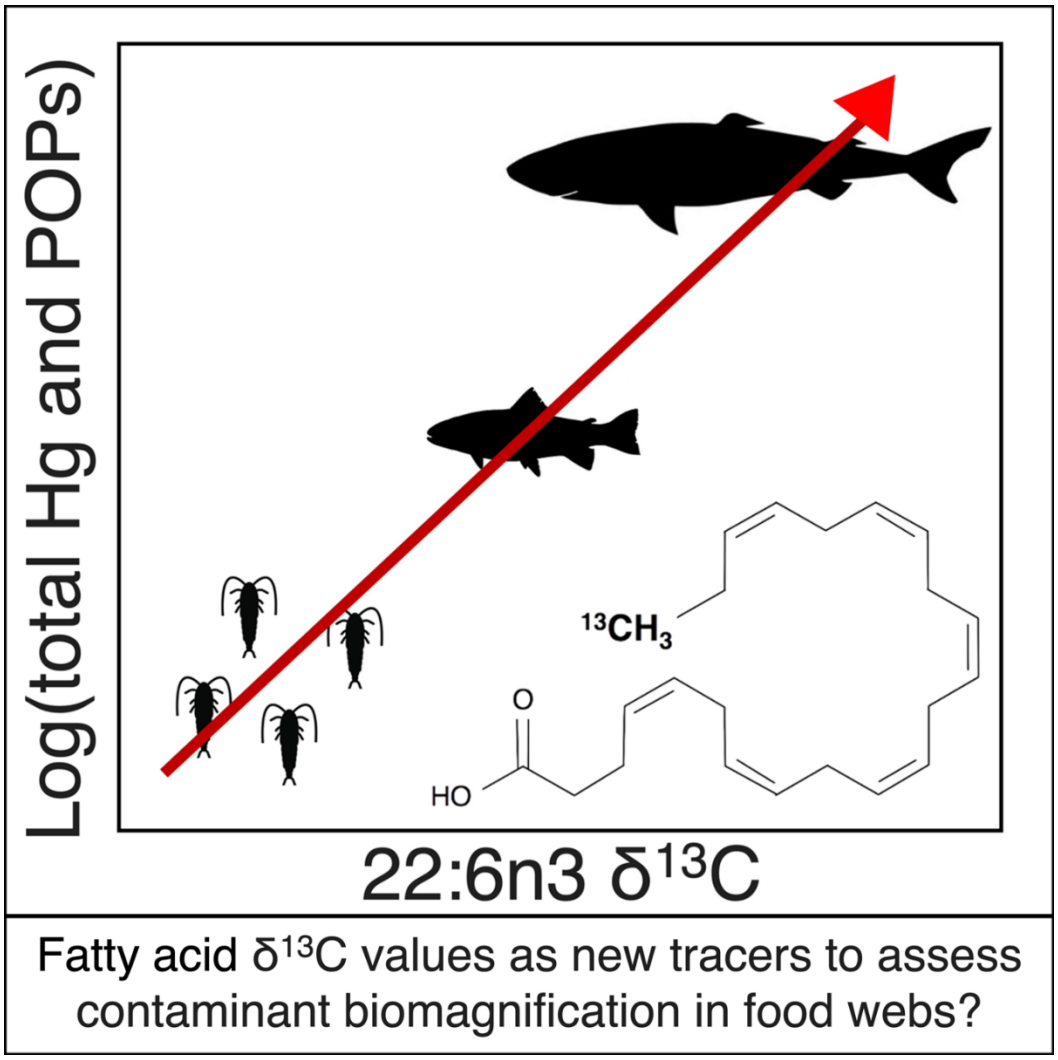
22:1, 22:6n3) consistently show limited or predictable trophic fractionation and may therefore be useful for assessing the accumulation and biomagnification of lipophilic contaminants, including POPs.

Keywords: *Greenland shark, polar bear, long-finned pilot whale, narwhal, killer whale, POPs, Hg*

Highlights

- $\delta^{13}C$ values of fatty acids (FAs) were measured in a marine food web and among marine mammals
- $\delta^{13}C$ values of nondietary FAs showed no clear patterns and widely varied among species
- The polyunsaturated FA (PUFA), 22:6n3, increased with trophic position in this food web
- 22:6n3 $\delta^{13}C$ was better correlated with contaminants in marine mammals than bulk $\delta^{15}N$
- Bulk $\delta^{15}N$ better explained Hg biomagnification than FA $\delta^{13}C$ across the food web

6.2. GRAPHICAL ABSTRACT



6.3. INTRODUCTION

Dietary accumulation and food web biomagnification of mercury (Hg) and persistent organic pollutants (POPs) are commonly assessed using stable nitrogen isotopes ($\delta^{15}N$) measured in bulk tissues (e.g. Hobson et al., 2002; Braune et al., 2005; Remili et al., 2021). Higher $\delta^{15}N$ values typically indicate higher trophic position as the lighter isotope (^{14}N) is more readily excreted, while more of the heavier isotope (^{15}N) is retained, resulting in higher in $^{15}N/^{14}N$ ($\delta^{15}N$) in consumers than in prey and increases in $\delta^{15}N$ of 2-4‰ with each trophic level in the food web (Nielsen et al., 2018). As Hg and legacy POPs biomagnify through marine food webs, simple linear regressions between contaminants and $\delta^{15}N$ in organisms are used to quantify trophic biomagnification, i.e., average changes in concentrations with trophic position (Fisk et al., 2002; Lavoie et al., 2013; Nielsen et al., 2018). Similarly, to assess POP and Hg accumulation in tissues, $\delta^{15}N$ or bulk $\delta^{15}N$-derived trophic position estimates are often included in linear regression models to determine how much variation in concentrations among species, locations, years of collection, and other variables is explained by differences in trophic position (Fisk et al., 2002; Newsome et al., 2010; Lavoie et al., 2013). Another commonly used stable isotope in trophic studies, carbon, $^{13}C/^{12}C$ ($\delta^{13}C$), shows less enrichment with trophic position, but instead is useful in evaluating feeding habitat in marine food webs (Fisk et al., 2002; Hobson et al., 2002). For instance, $\delta^{13}C$ is often used to test for differences in POP and Hg concentrations between benthic verses pelagic carbon sources (e.g., McKinney et al., 2012).

Although bulk stable isotopes are routinely used to assess feeding habits and patterns, this approach has some notable drawbacks. Bulk SI values at the base of food webs can vary widely across space and time (Goericke and Fry 1994), requiring an isotope “baseline” species to be selected among primary consumers to correct for differences in “isoscapes” that confound

interpretations of diet and food web variation (Post, 2002). However, there is currently widespread variation in selecting baselines and in the statistical approaches used to estimate trophic positions relative to the baseline among studies (Kjeldgaard et al., 2021). Furthermore, baseline values may not be entirely representative of omnivorous or highly mobile species feeding across different food webs and feeding habitats, making it difficult to characterize their feeding ecology from bulk SI alone (Jardine et al., 2006). Still, researchers often assess biomagnification of contaminants across food webs using bulk $\delta^{15}N$ (an estimated 88% of studies according to Elliott et al., 2021). Due to these drawbacks, alternative or complementary approaches have emerged, such as fatty acid (FA) signatures (i.e., proportional composition) that are similarly transferred from predator to prey with little or predictable modification (Budge et al., 2006). However, FAs patterns may overlap among different prey species, and they have rarely been used in assessments of contaminant accumulation and biomagnification (Pedersen et al., 2024a).

Compound-specific isotope analysis (CSIA) of individual biomolecules, such as amino acids (AAs; for $\delta^{15}N$ and/or $\delta^{13}C$ analysis, e.g., Matthews et al., 2024) and FAs (for $\delta^{13}C$ analysis alone as FAs do not contain nitrogen), is a recent approach that may offer greater sensitivity than bulk stable isotopes or FA proportions alone in tracing feeding habits and assessing trophic transfer of contaminants (Budge et al., 2008; Budge et al., 2011; McKinney et al., 2013; Elliot et al., 2021). Although bulk stable isotopes and FAs may overlap or occur at similar proportions among different diet resources, individual FAs may still have distinct $\delta^{13}C$ values among prey (Twining et al., 2020). Certain FAs, particularly the polyunsaturated FAs (PUFAs), have already been highlighted as potential trophic markers in CSIA-FA (Burian et al., 2020; Twinning et al., 2020), as PUFAs are important micronutrients that marine consumers show limited capacity to

synthesize *de novo* (Budge et al., 2006). The PUFAs are largely considered "dietary" FAs, as they may be directly deposited into fatty storage tissues following ingestion by consumers; nonetheless, slight modification in the carbon chains of dietary FAs may sometimes occur between ingestion and deposition in tissue (Iverson et al., 2004; Budge et al., 2006). As such, in the few controlled feeding trials to date on FA $\delta^{13}C$, which have focused largely on prey (e.g. phytoplankton and cyanobacteria) and low trophic-level consumers (e.g., zooplankton, fish), some investigated "dietary" FAs (in particular, 18:2n6, 18:3n3, 20:5n3, 22:6n3) showed little-to-no trophic fractionation (defined here as the difference in $\delta^{13}C$ or $\delta^{15}N$ values between predator and prey; Fujibayashi et al., 2016; Gladyshev et al., 2016; Burian et al., 2020). In contrast, these same studies have shown that the $\delta^{13}C$ of FAs that can largely be synthesized in consumers (i.e., saturated FAs [SFAs] and some shorter-chain monounsaturated FAs [MUFAs]) have showed wide and variable fractionation between prey and consumers, likely due to *de novo* synthesis of FAs from carbohydrates, chain desaturation/elongation, or catabolism of these FAs for energetic needs (Budge et al., 2011; Twining et al., 2020). In such reactions, FAs with more of the lighter ^{12}C react faster than those with more ^{13}C, resulting in the reactants (e.g., an 18 carbon-length SFA) showing higher $\delta^{13}C$ than the products (e.g., an 18 carbon-length MUFA from the desaturation of the SFA; Wada et al., 1991). Therefore, the $\delta^{13}C$ values of dietary PUFAs may instead be useful dietary tracers for assessing trophic transfer across food webs as they show low or predictable trophic fractionation (Fujibayashi et al., 2016; Burian et al., 2020).

Some studies have characterized trophic fractionation of FA $\delta^{13}C$ in controlled-feeding experiments (e.g., Budge et al., 2011; Fujibayashi et al., 2016; Burian et al., 2020), but to our knowledge, variation in FA $\delta^{13}C$ values have not been explored across marine food webs or compared among mobile, higher-level consumers. Moreover, the utility of FA $\delta^{13}C$ to assess

trophic transfer of contaminants is essentially unknown. Although Budge et al. (2008) monitored FA $\delta^{13}C$ from primary producers to marine mammals in Barrow, Alaska to assess contribution of sea-ice algae to diets, only two FAs, 16:4n1 and 20:5n3, were monitored, and trophic fractionation across the entire food web was not analyzed or discussed. $\delta^{13}C$ values of some FAs (16:1n7, 18:4n3, 20:5n3, 22:6n3) were similarly monitored in invertebrates from the high Arctic (Kohlbach et al., 2016), but no higher trophic-level consumers were investigated. As such, the first objective of the present study is to 1) compare FA $\delta^{13}C$ values across a full marine food web in Cumberland Sound (CS; Nunavut, Canada) ranging from primary consumers to Greenland shark (*Somniosus microcephalus*), with existing bulk isotope and Hg concentration data (McKinney et al., 2012; McMeans et al., 2015). 2) We next investigate FA $\delta^{13}C$ variation among higher-level marine mammals in East Greenland (EG) including resident species, narwhal (*Monodon monoceros*) and polar bear (*Ursus maritimus*) and seasonal visitors, killer whale (*Orcinus orca*) and long-finned pilot whale (*Globicephala melas*). 3) Finally, we explore the utility of FA $\delta^{13}C$ in assessing biomagnification of Hg across the CS food web and in explaining interspecific variation of POPs among EG marine mammals. If certain FAs show consistent and predictable $\delta^{13}C$ trophic fractionation with increasing $\delta^{15}N$, then we predict that these FAs will explain variation in contaminant concentrations comparable to or better than bulk stable isotopes among high trophic-feeding consumers and across the food web.

6.4. METHODS

6.4.1. Sample Collection

All sampling information for the CS food web was previously described in McKinney et al. (2012) and McMeans et al. (2015; **Table 6.1**). In brief, all samples were collected between 2007-2009. Copepods (*Calanus hyperboreus*), Themisto (*Themisto libellula*, a carnivorous amphipod), shrimp (unidentified sp.), and red shrimp (*Lebbeus polaris*) were sampled whole by gill net, and multiple individuals (5-20) were pooled to obtain sufficient mass for Hg, bulk stable isotope, and FA analyses. Capelin (*Mallotus villosus*; n = 7) were collected via dip net, Arctic sculpin (*Myoxocephalus scorpiodies*; n = 7) were sampled by gill net, while Greenland halibut (*Reinhardtius hippoglossoides;* n = 6) and Greenland shark (n = 10) were collected via bottom long line. All samples in the CS food web were frozen at −80 °C in cryovials and kept frozen until FA analysis.

Table 6.1: Species, year of collection, and sample sizes analyzed in the present study from the Cumberland Sound food web and marine mammals in East Greenland.

Location	Species	Scientific Name	Year	Sample Size
Cumberland Sound	Copepods	*Calanus hyperboreus*	2008	1 (pool)
	Themisto	*Themisto libellula*	2008	3 (pools)
	Shrimp	Unidentified sp.	2008	1 (pool)
	Red shrimp	*Lebbeus polaris*	2008-2009	4 (pools)
	Capelin	*Mallotus villosus*	2008	7
	Arctic sculpin	*Myoxocephalus scorppiodies*	2008	7
	Greenland halibut	*Reinhardtius hippoglossoides*	2008-2009	6
	Greenland shark	*Somniosus microcephalus*	2007-2009	10
East Greenland	Killer whale	*Orcinus orca*	2012-2021	7
	Narwhal	*Monodon monoceros*	2015	15
	Long-finned pilot whale	*Globicephala melas*	2021	15
	Polar bear	*Ursus maritimus*	2021	15

The EG sample collection was reported previously in Pedersen et al. (2024a, b; **Table 6.1;** Table S6.1 for more detailed information). In brief, killer whale in 2012-2014 (n = 4) and 2021 (n = 3), narwhal in 2015 (n = 15), pilot whale in 2021 (n = 15), and polar bear in 2021 (n = 15) were opportunistically collected during subsistence harvests in Ittoqqortoormiit, Tasiilaq, and Kulusuk, Greenland. Full-blubber depth samples were collected from each whale and subcutaneous adipose was collected from each polar bear. Information on age class and sex determination is available in Pedersen et al. (2024a). All EG samples were stored at −20 °C until they arrived at McGill University, where they were then stored at −80 °C until time of analysis. Only the inner section was sampled from each large piece of blubber or adipose to avoid sample oxidation.

6.4.2. Bulk Stable Isotope Analysis

For the CS food web samples, bulk $\delta^{13}C$ and $\delta^{15}N$ for capelin, sculpin, halibut, and Greenland shark was reported in McKinney et al. (2012), while copepod, Themisto, and shrimp data was provided in McMeans et al. (2015). All samples were lipid-extracted, dried, and ground to a powder. Whole-body samples were used for copepods, Themisto, and shrimp, while muscle was used for the fish and Greenland shark. For the EG dataset, samples were not lipid-extracted, as differences in $\delta^{13}C$ between lipid- and nonlipid-extracted blubber samples is likely minimal (Land-Miller et al., 2023). The 2021 killer whale and all pilot whale and narwhal muscle samples were analyzed at McGill University as part of the current study, while bulk $\delta^{13}C$ and $\delta^{15}N$ data in muscle of narwhal were reported in Land-Miller et al. (2023). The remaining samples, 2012-2014 killer whale and 2021 polar bear muscle, were analyzed at the Center for Permafrost at the

University of Copenhagen, Denmark (see Supplemental Text #6.1 for more detailed stable isotope analysis information and QA/QC data).

6.4.3. Fatty Acid Carbon Isotope Analysis

FA signatures (from neutral lipids in triacyclglycerols; Budge et al., 2006) for all CS and EG samples were previously reported (McMeans et al., 2015, Pedersen et al., 2024a) from whole body samples (copepods, Themisto, shrimp, and red shrimp in CS), muscle samples (capelin, sculpin, halibut in CS), muscle, blood plasma, liver samples (Greenland shark in CS), and blubber/adipose samples (killer whale, narwhal, pilot whale, and polar bear in EG). In this study, the existing fatty acid methyl ester (FAME) derivative extracts, containing the antioxidant butylated hydroxytoluene (BHT) and stored at -80 °C prior to further analysis, were analyzed for FA $\delta^{13}C$ as previously described (McKinney et al., 2013) with minor modifications. In brief, the CS samples were run on a Trace GC Ultra coupled via a GC Combustion II/III Interface to a Delta V Advantage isotope ratio mass spectrometer (GC-C-IRMS; Thermo Scientific, Waltham, MA, USA) at the University of Windsor in 2011. The EG samples were run on a Thermo Scientific Trace GC 1310 coupled via a GC Isolink II to a Delta V Plus IRMS at McGill University in 2023. Injections were done in splitless mode to avoid fractionation in the inlet and at concentrations of 0.5 and 2.0 mg/mL total FAME. Running at two concentrations allowed us to check for reproducibility within samples, reduce peak co-elution that may occur at higher concentrations, and acquire more analyte peaks within the linear range of the IRMS (amplitude of ~600 to 6000mV at m/z 44 at University of Windsor and ~200-5500 mV at McGill University, see Figure S6.1 for more detailed information on linear ranges of the instrument). A DB-23 GC column (Agilent Technologies; 30 m, 0.25 mm i.d., 0.25 µm film thickness, Part #122-2332,

with 1 m deactivated fused silica guard column, Part #CP805310) was used to separate the FAMEs, with a ramping program as follows: initial temperature at 153°C for 2 mins, then increased at rate of 2.3°C/min until 174°C, held for 0.2 min, then a final ramp at a rate of 2.5 °C/min until 210°C and held for 6.27 min (total run time of 48 minutes). If mass 32 (O_2) was less than 5000 on the instrument, a two-hour oxidation was run on the instrument prior to sample analysis. An additional 18 second seed oxidization was also run prior to each individual sample injection. For the CS samples, five saturated FAME standards ([16:0 (#n16M), 18:0 (#n18M), 20:0 (#2), 20:0 (#x), and 24:0, ranging from −30.68‰ to −6.91‰; Schimmelmann Laboratories, Indiana University, Bloomington, IN, USA) were run weekly at dilutions of 125, 62.5, 31.25 and 7.81 μg/mL. For EG samples, five similar FAME standards ([16:0 (#n16M), 18:0 (#n18M), 20:0 (#21), 20:0 (#22) and 24:0, ranging from −30.43‰ to −10.50‰; Schimmelmann Laboratories, Indiana University, Bloomington, IN, USA) were also run weekly at 100, 50, 25,12.5, and 6.25 μg/mL dilutions to check the consistency of $\delta^{13}C$ values across concentrations. The median concentration standard in each lab (i.e., 31.25 and 25 μg/mL) was further run daily to make a calibration curve for our generated FAME $\delta^{13}C$ values versus the accepted FAME $\delta^{13}C$ values as reported by Schimmelmann Laboratories ($r^2 > 0.991$ and $r^2 > 0.996$ for CS and EG runs, respectively; see Figure S6.2 for an example calibration curve the EG dataset), which was then used to calculate the FAME $\delta^{13}C$ values of the samples. Only FAs that were well-separated and within the linear range for ≥ 80% of samples at one or both concentrations were reported for each dataset (see Table S2 for all FAs included). As a result, a total of 9 and 13 individual FAs or FA isomer groups were analyzed for the CS and EG sample sets, respectively, and example chromatograms are available in Figure S6.3 and S6.4 with retention times of each FA in Table S3. For both sample sets, 18:1 (consisting of 18:1n11, 18:1n9, 18:1n7, and 18:1n5), 20:1

(20:1n11, 20:1n9, and 20:1n7), and 22:1 (20:1n11, 20:1n9, and 20:1n7) isomers were each integrated as a single peak representing the $\delta^{13}C$ sum of each isomer group due to coelution of these isomers in each respective group at both concentrations. Duplicates of six random samples were run in the EG dataset, and all duplicates were <0.5‰ different for all FA analyzed; thus, duplicates were averaged. The U.S. National Institute of Standards and Technology (NIST) reference material RM 8037 krill oil was extracted and derivatized with each batch of samples and was used as an on-going precision check, as accepted FA $\delta^{13}C$ values for these reference materials do not currently exist (results from this study available in Table S64).

Values of $\delta^{13}C$ for the methanol used to derivatize the FAs to FAMEs in the CS dataset were determined by EA-IRMS (Environmental Isotope Labs, University of Waterloo, ON, Canada) using manual liquid injection (per McKinney et al., 2013). For the EG dataset, we pipetted an aliquot of the methanol directly onto a CO_2 absorbent material, EMAsorb (Isomass Scientific Inc, Calgary, Alberta, Canada, Part #B1117) inside a tin capsule and ran by EA-IRMS. Further information using this approach is available in the Supplemental Text #6.2. Mean $\delta^{13}C$ values for methanol used in the CS and EG datasets were -51.01 ± 0.80‰ and -41.60 ± 0.96‰, respectively. The $\delta^{13}C$ values for the methanol and FAME were then used to calculate FA $\delta^{13}C$ by the following mass balance equation: $(n + 1)\text{FAME-}\delta^{13}C = n(\text{FA-}\delta^{13}C) + \text{methanol-}\delta^{13}C$, where n = length of carbon chain.

6.4.4. Contaminant Analyses

Total Hg (THg) concentration data in muscle or whole-body tissues for CS food web samples was previously reported (McMeans et al., 2013; McMeans et al., 2015). For EG marine mammals, POP concentration data was also previously detailed (Pedersen et al., 2024a)

including polychlorinated biphenyls (PCBs) and organochlorine pesticides (e.g., dichlorodiphenyltrichloroethanes [DDTs] and chlordanes [CHLs]), using a modified QuEChERS (Quick, Easy, Cheap, Effective, Rugged, and Safe) method we developed (Pedersen et al., 2023; see Supplemental Text #6.3 for more detailed contaminant extraction and analysis information and QA/QC data).

6.4.5. Data Analysis

One-way ANOVAs and Tukey pairwise comparisons were used to test for differences in bulk isotopes and FA $\delta^{13}C$ values among species for the CS food web and the EG marine mammal datasets. We used the same approaches to test for differences in FA $\delta^{13}C$ values among three different Greenland shark tissues (i.e., muscle, liver, and blood plasma). Data were tested for normality prior to statistical analyses using Shapiro-Wilk tests, and all isotope data were normally distributed. We ran a principal component analysis (PCA) on each dataset to visualize variation in FA $\delta^{13}C$ values among species. To explore the possibility of FA $\delta^{13}C$ fractionation with increasing trophic position in each dataset, we generated Pearson correlations of individual FA $\delta^{13}C$ values with bulk $\delta^{15}N$.

For FAs that showed significant and positive correlations with $\delta^{15}N$, we averaged $\delta^{13}C$ of these FAs together, as mean values may provide better indices of stable isotope fractionation than using individual values (as seen in the CSIA analysis of other biomolecules; McMahon and Newsome, 2019; Elliot et al., 2021). Similarly, for FAs that showed no significant interspecific differences in $\delta^{13}C$ and that were not correlated with $\delta^{15}N$ in the CS food web (i.e., FA $\delta^{13}C$ values were conserved through the food web), we averaged these values together as they may provide information on baseline or "source" FA $\delta^{13}C$ values. As such, to correct for baseline or

"source" variation in some FAs that significantly increased with $\delta^{15}N$ (i.e., "trophic" FAs), we used the following equation:

Equation 1: $\text{FA } \delta^{13}C_{corrected} = \text{FA } \delta^{13}C_{Avg(trophic)} - \text{FA } \delta^{13}C_{Avg(source)}$

where $\text{FA } \delta^{13}C_{Avg(trophic)}$ represents the mean $\delta^{13}C$ values of FAs that showed significant, positive increases in the CS food web, and $\text{FA } \delta^{13}C_{Avg(source)}$ represents the mean $\delta^{13}C$ values of FAs that showed no significant differences among species and no significant differences with increasing $\delta^{15}N$ in the CS food web. It is important to note that this is an exploratory approach; the use of "trophic" and "source" FAs is entirely our shorthand, as FA $\delta^{13}C$ fractionation across food webs has not been explored previously. Nonetheless, similar methods have been used in the CSIA of other biomolecules for baseline or "source" corrections. For instance, average values of "trophic" AAs (like glutamic acid) are commonly baseline-corrected by subtracting values from "source" AAs (like phenylalanine; McMahon and Newsome, 2019; Elliot et al., 2021).

To test the ability of FA $\delta^{13}C$ to explain THg biomagnification through the CS food web and interspecific variation in POPs among higher-level marine species in EG, we first generated simple linear regressions of $\delta^{13}C$ values of individual FAs with strongly biomagnifying contaminant concentrations (THg in CS and CB-153 in EG). The same analyses were conducted using bulk $\delta^{15}N$ instead of FA $\delta^{13}C$ values to directly compare correlation coefficients. POP concentrations were lipid-normalized in the EG marine mammals, then concentrations from both datasets were $\log(x + 1)$ transformed to achieve normality, as confirmed by Shapiro-Wilk tests.

Furthermore, to test if FA $\delta^{13}C$ explained additional variation in contaminant concentrations beyond bulk SI in each dataset, we used generalized linear regression models with the following variables: FA $\delta^{13}C$ (of individuals FAs or $\text{FA } \delta^{13}C_{corrected}$, see equation above), age class/sex (i.e., adult male, adult female, and subadult for marine mammals in EG), and bulk $\delta^{13}C$

and $\delta^{15}N$. We used variance inflation factors (VIF) to assess multicollinearity among these variables with a cutoff of 5, and diagnostic plots were run for all models to ensure assumptions were met. We then tested every possible combination of variables for THg or CB-153 concentrations. The models were ranked using Akaike's information criterion (AIC) and then top (AIC < 2) models were averaged to produce the top average model for each contaminant class in each dataset. We also calculated the semi-partial correlation coefficient squared of each variable in top models, to determine the unique contribution of each variable (i.e., without the influence of any other variables; Eckardt and Mateu, 2021). All statistical analyses were conducted in R Studio (version 1.2.5042) and with α set to 0.05.

6.5. RESULTS AND DISCUSSION

6.5.1. Bulk SI and FA $\delta^{13}C$ variation in the Cumberland Sound food web

Muscle samples of Greenland shark, Greenland halibut, and sculpin showed the highest and similar bulk $\delta^{15}N$ (>16‰; *post-hoc* $p < 0.04$), while capelin muscle and red shrimp whole body were intermediate (~13-14‰), and values were significantly lower in whole body pooled samples of copepods, Themisto, and shrimp (<12‰; $p < 0.01$) (ANOVA $F_{4,23} = 52.66$, $p < 0.01$; Figure S6.5A; Table S6.5). Values for $\delta^{13}C$ were highest in red shrimp and sculpin (~-17-18‰), intermediate (~ -18‰) in Greenland shark and Greenland halibut, and lowest in capelin, shrimp, Themisto, and copepods (-19 to -20.5‰; Figure S56.A). The $\delta^{15}N$ results align with previously published diet assessments of Greenland shark in CS, where piscivorous fish, like sculpin and Greenland halibut were the most commonly observed diet items (McMeans et al., 2012), while capelin primarily feed at lower trophic positions on copepods (Ogloff et al., 2020). $\delta^{13}C$ values,

although still showing a 1-1.5‰ increase per trophic position across the entire food web, likely also indicate separation based on feeding habitat, among benthic (sculpin and red shrimp), benthopelagic (Greenland shark and Greenland halibut), and pelagic-feeding (capelin, copepods, and Themisto) species, where $\delta^{13}C$ values tend to be lower in pelagic and higher in benthic environments (Le Loc'h et al., 2008, but see also Szpak and Buckley, 2020).

The $\delta^{13}C$ of most FAs (i.e., 14:0, 16:0, 16:1n7, 18:0, 18:1, and 20:5n3) in CS showed no clear patterns across the food web and were not correlated with bulk $\delta^{15}N$ (Table S6.6), although they significantly differed among species (**Figure 6.1**; Table S6.5; ANOVA $F_{7,28} = 3.1$, $p < 0.01$) and clustered by species in the PCA (Figure S6A and B; comparisons between bulk SI, FA proportions, and FA $\delta^{13}C$ in the CS food web also available in Figure S6.7). Some *de novo* synthesis of the shorter-chain saturated FAs (SFAs; 14:0, 16:0, 18:0) and chain elongation and/or desaturation of MUFAs (e.g., 18:1 isomers) in consumers, including the fish species, is expected, however, it is likely more limited for the PUFA, 20:5n3, especially for species with high-fat and high PUFA diets (>30% of total calories from fat; Iverson et al., 2004; Budge et al., 2006; Tocher, 2003; Tocher, 2010). For example, desaturation of 16:0 and 18:0 to 16:1n7 and 18:1n9, respectively, is well-documented in teleost fishes and elasmobranchs (Tocher, 2010). *De novo* synthesis of some short-chain FAs from carbohydrates (e.g., 16:0 synthesis from enzyme pyruvate dehydrogenase and acetyl-CoA) in consumers typically results in FAs depleted in $\delta^{13}C$ between –6 to –8‰ (DeNiro and Epstein, 1977; Twining et al., 2020). Instead, fractionation from chain elongation and desaturation (e.g., 18:3n3 desaturation and elongation to 20:5n3) varies based on FA but can be up to ~2.6‰ (Menzel et al., 2017; Twining et al., 2020). As values varied only by up to ~2‰, interspecific variation for 14:0, 16:0, 16:1n7, 18:0, and 18:1 in the CS food web is likely largely from carbon chain elongation and/or desaturation from shorter

chain FAs, or in the case of MUFAs, from SFAs. As such, variation in $\delta^{13}C$ values for these FAs (i.e., 14:0, 16:0, 16:1n7, 18:0, and 18:1) that do not show any clear patterns with trophic position nor feeding habitat across the CS food web provides a substantial challenge for their use in diet tracing approaches, as supported by multiple controlled-feeding experiments (Bec et al., 2011; Budge et al., 2011; Fujibayashi et al., 2016; Burian et al., 2020) in which FA $\delta^{13}C$ values did not show clear patterns between diet and consumer.

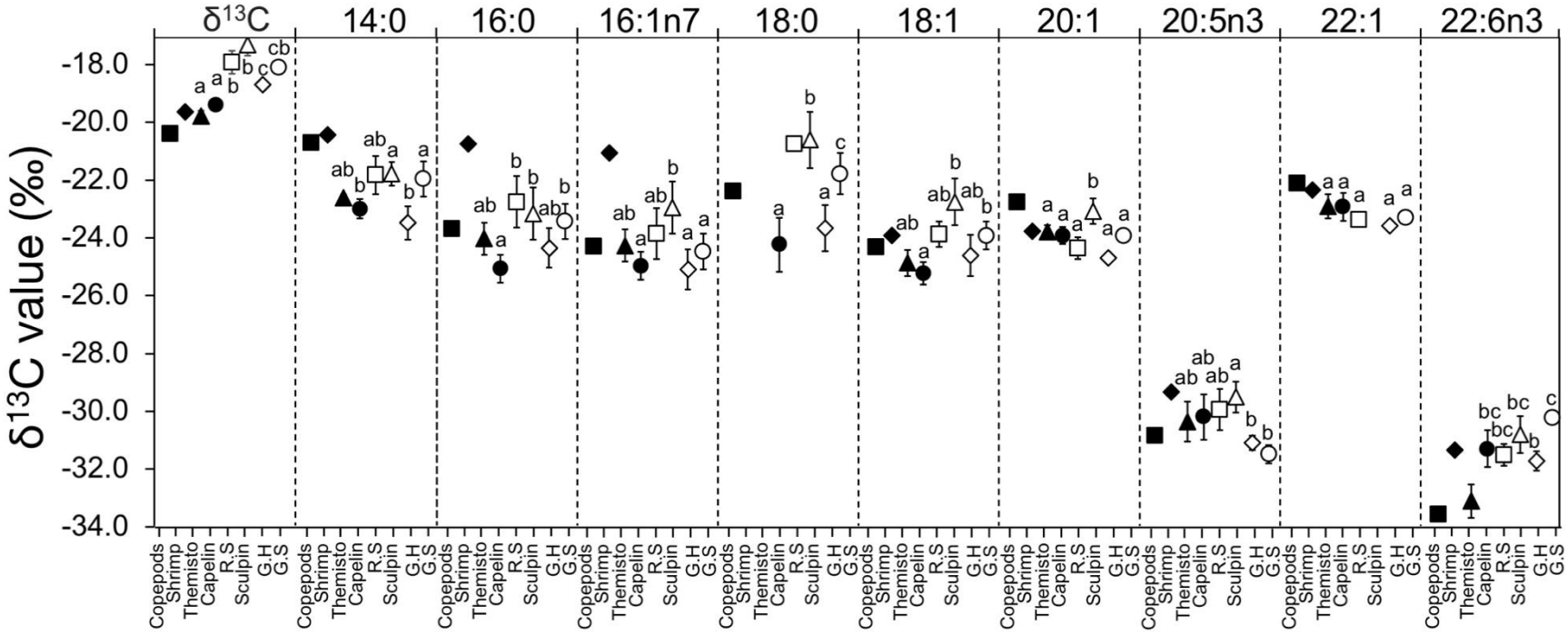


Figure 6.1: Bulk $\delta^{13}C$ values from lipid-extracted whole organism (copepods, shrimp, Themisto and red shrimp [R.S]) or muscle samples (capelin, sculpin, Greenland halibut [G.H], and Greenland Shark [G.S]) and individual fatty acid (FA) $\delta^{13}C$ values (‰) from lipid extracts of these same tissues for species in the Cumberland Sound (Nunavut, Canada) marine food web. One-way analysis of variance (ANOVAs) with *post-hoc* Tukey pairwise comparisons were used to assess for statistical differences in isotope values among species. Significant differences from *post hoc* comparisons ($p<0.05$) are represented by different letters (a,b,c) above the data points. Species in the Cumberland Sound food web are ordered by their $\delta^{15}N$ values.

Unlike these other FAs, the long-chain MUFA isomers 20:1 and 22:1 showed few or no significant differences among species, i.e., values were conserved across the CS food web (**Figure 6.1**). The 20:1 (20:1n11, 20:1n9, and 20:1n7) and 22:1 (22:1n11, 22:1n9, and 22:1n7) isomers are largely considered to be derived in consumers from their diet (Iverson et al., 2004; Budge et al., 2006). These long-chain MUFAs may be chain-elongated from 16:1 and 18:1 isomers into 20:1 and 22:1 isomers in lower order organisms at the base of food webs (Sargent et al., 1995), but fishes (Tocher, 2010), marine mammals, and seabirds are likely less capable of carrying out these processes, given already high levels of MUFAs in their diets (Budge et al., 2006). Consumer metabolism involving chain-shortening of 20:1 and 22:1 isomers into 18:1 isomers can occur (Norseth, 1979; Cooper et al., 2006), and that would explain higher deposition of 18:1 relative to 20:1 and 22:1 in marine mammal fat storage tissues (Iverson and Springer, 2002; Budge et al., 2004). However, while 18:1n9 isomers showed far higher proportions than any 20:1 and 22:1 isomers in grey seal (*Halichoerus grypus*) and harbor seal (*Phoca vitulina*) (Iverson et al., 2004), seabirds (Iverson and Springer, 2002), mink (*Mustela vison*) (Cooper et al., 2006), and toothed whales and polar bears being 5-10 times higher (Pedersen et al., 2024a), most of the 20:1 and 22:1 isomers (e.g., 20:1n9 and 22:1n11) were, instead, comparable or at even higher proportions than any 18:1 isomers in our studied Greenland shark and Greenland halibut in CS (McMeans et al., 2012). This may suggest limited chain-desaturation of these long-chain MUFAs in teleosts and elasmobranchs due to low activity of associated desaturase enzymes possibly due to high 18:1 levels from diet (as supported by similarly high 20:1 and 22:1 to 18:1 ratios in fishes reported elsewhere; Giraldo et al., 2018). Given this, and the consistent $\delta^{13}C$ values of these isomers across the food web, substantial *de novo* synthesis or chain-desaturation seems unlikely. Instead, 20:1 and 22:1 $\delta^{13}C$ values may be conserved throughout this food web

and directly deposited into consumer tissues with relatively high absorption efficiencies. If so, 20:1 and 22:1 $\delta^{13}C$ values could potentially be used as indicators of "source" or baseline food web values, akin to "source" amino acids (see section 2.3; Ramirez et al., 2021). Studies of other food webs and controlled-feeding experiments monitoring 20:1 or 22:1 fractionation between consumers and their diets, would be required to confirm this interpretation.

One FA, 22:6n3, showed significant, positive correlations with bulk $\delta^{15}N$ across the CS food web, and was significantly higher in Greenland shark (-30.40 ± 0.23‰), and lower in Themisto (-33.40 ± 0.77‰), than all other species (**Figure 6.1** and **Figure 6.2**; Table S6.5; Table S6.6). 22:6n3 is considered to be nearly exclusively of dietary origin in marine predators (Iverson et al., 2004). Synthesis of 22:6n3 occurs via chain-elongation and desaturation of 18:3n3 from Δ6 and Δ5 desaturases, and although this process does occur in some consumers (Hastings et al., 2001), it is generally limited in top marine predators (Budge et al., 2006). Although the $\delta^{13}C$ values of 18:3n3 were below the linear range for most CS samples, multiple controlled-feeding experiments have shown relatively consistent fractionation of 18:3n3 from diet to consumers, including in *Daphnia* (Bec et al., 2011; Gladyshev et al., 2016) and eider duck (*Polysticta stelleri* and *Somateria fischeri*; Budge et al., 2011). Biosynthesis of 18:3n3 in consumers is not possible in vertebrates due to their lack of Δ12 and Δ15 desaturates (Tocher, 2010), so values in consumers may be consistent with those in their diet (Fujibayashi et al., 2016). Nonetheless, 18:3n3 fractionation may instead result from catabolism for energy prior to deposition in tissues if there is dietary excess of these FAs (Budge et al., 2006; Budge et al., 2011). More rapid catabolism of isotopically lighter 18:3n3 (or any FA) should result in the remaining 18:3n3 that is deposited in lipid storage tissues showing higher $\delta^{13}C$ values than diet. For example, in experimentally fed eider, diets with an excess of 18:3n3 showed higher $\delta^{13}C$ of

18:3n3 by ~2‰ in eider than in the diet; however, when fed a diet with minimal 18:3n3, no net fractionation was observed (Budge et al., 2011). It was hypothesized that 18:3n3 had fallen below a minimum dietary threshold, suppressing the use of this FA for energetic needs. Similarly, 22:6n3 may be in excess in our studied Greenland shark and fish species, resulting in catabolism for energy prior to deposition in tissues. This is consistent with 22:6n3 $\delta^{13}C$ values being higher in the fishes than in the lower trophic level organisms, whereas if 22:6n3 was being formed to any substantial extent from chain-elongation and desaturation of 18:3n3 in the fishes, it would be expected that the $\delta^{13}C$ values would be lower than in the diet (at least if the 18:3n3 and 22:6n3 $\delta^{13}C$ values of the diet were similar). Further controlled feeding experiments, especially involving higher-level consumers, are required to improve these interpretations of FA-specific $\delta^{13}C$ fractionation in natural food webs.

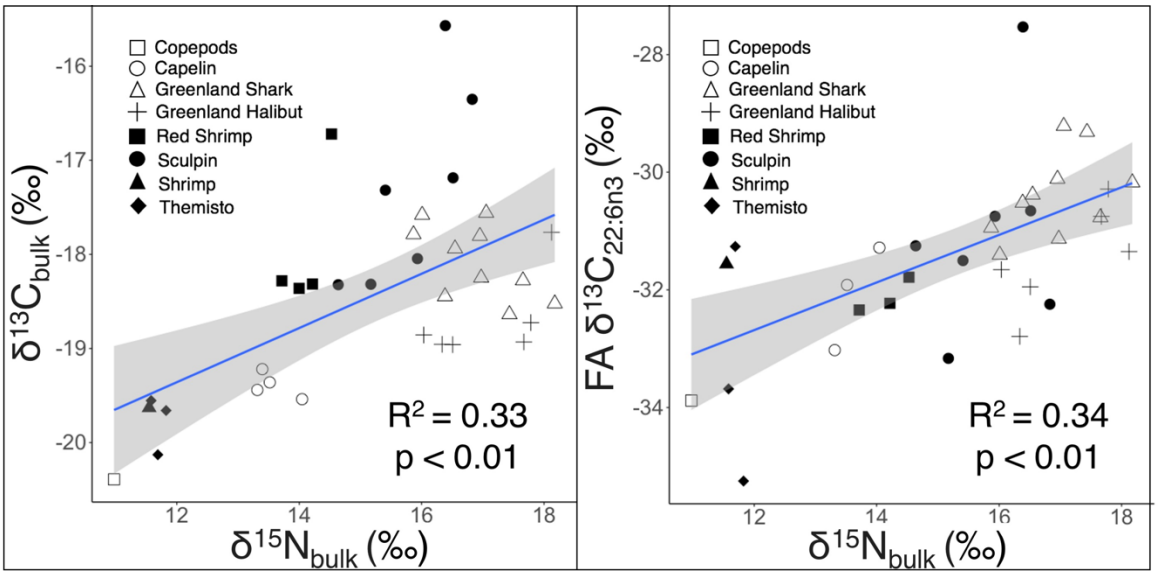


Figure 6.2: Linear correlations between bulk $\delta^{13}C$ and $\delta^{13}C$ values of 22:6n3 (FA $\delta^{13}C_{22:6n3}$) with bulk $\delta^{15}N$ (both in ‰) in a Cumberland Sound, Nunavut, Canada food web.

FA $\delta^{13}C$ values also varied based on tissue/matrix-type in Greenland shark (ANOVA $p < 0.01$), where most FAs (14:0, 16:1n7, 18:0, 20:1, 20:5n3, 22:1, and 22:6n3) were significantly higher in liver and muscle compared to blood plasma, i.e., liver = muscle > blood plasma (Table S6.7). The FAs, 14:0, 16:0, 16:1n7, 18:0, 20:1, and 22:6n3 also showed no significant differences between Greenland shark blood plasma and the sharks' primary diet item, Greenland halibut, while 20:5n3 and 22:1 instead were not significantly different between Greenland shark liver and muscle and halibut (Table S6.7). In the eider study, FA $\delta^{13}C$ values for 18:0, 18:1, and 18:2n6 in blood serum were also more similar to the values in diet compared to those in adipose tissues (Budge et al., 2011). However, the eiders were fasted prior to blood sampling, likely resulting in fractionation from both FA mobilization from adipose to the blood and from catabolism for energy (Stevens, 1996; Price, 2010). Instead, similar values between blood plasma and Greenland shark diet may suggest that fractionation is instead occurring prior to deposition in tissues, and likely a result of catabolism for energy when FAs, like 22:6n3, are in excess. That is, there should be more of isotopically lighter 22:6n3 in blood used for energy, leaving greater proportion of isotopically heavier 22:6n3 for deposition in muscle and liver tissues. Non-significantly different $\delta^{13}C$ values between shark muscle and Greenland halibut for 22:1 and 20:5n3 may further support direct assimilation of these FAs into tissues from diet (i.e., not used for energy at least in these predators), especially as *de novo* synthesis and chain modifications to these longer-chain FAs in these upper trophic level consumers is likely limited (Budge et al., 2006). However, given limited information on the nutritional status of these individuals, it is difficult to draw more robust conclusions, as periods of fasting may affect $\delta^{13}C$ fractionation and remobilization into blood (Budge et al., 2011). Future controlled-feeding experiments in higher-

levels consumers should seek to monitor FA $\delta^{13}C$ values among multiple tissue types to gain further insight into the mechanisms of tissue-specific and FA-specific fractionation.

6.5.2. Bulk SI and FA $\delta^{13}C$ variation in East Greenland marine mammals

Mean muscle bulk $\delta^{15}N$ values varied among EG marine mammal species, with significance of polar bear (17.76 ± 0.33‰) > killer whale (14.92 ± 0.78‰) = narwhal (14.37 ± 0.57‰) > pilot whale (11.19 ± 0.39‰; Table S6.8; Figure S6.5B). Values of bulk $\delta^{13}C$ were more similar across species, although killer whale (-19.02 ± 0.31‰) and pilot whale (-19.86 ± 0.57‰) showed significantly higher levels than narwhal (-20.60 ± 0.44‰), while polar bear were more intermediate (-20.03 ± 0.57‰; Table S6.8). The $\delta^{15}N$ results align with previous feeding assessments including quantitative fatty acid signature analysis (QFASA)-estimates showing high trophic position-feeding in polar bear (McKinney et al., 2013) and killer whale (Remili et al., 2022), with diets nearly exclusively of marine mammals. Some killer whale likely still feed to a lesser extent on fishes based on QFASA (Remili et al., 2022) and recent AA CSIA assessments (Matthews et al., 2024), which may explain their relatively lower $\delta^{15}N$ values than polar bear. In comparison, narwhal and pilot whale feed at lower trophic positions on fish and/or invertebrates, e.g. squid, octopus (Garde et al., 2022; Heide-Jørgensen et al., 2023; Pedersen et al., 2024a). However, as killer whale and pilot whale are increasingly moving farther north and are present in East Greenland mainly during the late summer months (Higdon et al., 2014; Heide-Jørgensen et al., 2023), variations in baseline SI values due to eutrophication and primary production between them and the Arctic-endemic narwhal and polar bear likely also influences interspecific variation in bulk SI values.

The FA $\delta^{13}C$ values also significantly differed among EG species (ANOVA $F_{3,38} = 9.4$, $p < 0.02$) (**Figure 6.3;** Table S6.8) and clustered by species in the PCA, although pilot whale and killer whale showed substantial overlap (Figure S6C and D). An additional five fatty acids compared to the CS food web (18:2n6, 18:3n3, 18:4n3, 20:4n3, and 22:5n3) were also in the linear range of the instrument and thus included in this analysis (see Table S6.8 and Figure S6.8). Results for *post-hoc* Tukey pairwise comparisons for most FA $\delta^{13}C$ showed similar patterns among species as the bulk $\delta^{13}C$, where significance trends were: killer whale = pilot whale > polar bear = narwhal (**Figure 6.3**; Table S6.8) for 14:0, 16:0, 18:0, 18:1, 20:1, and 22:6n3. However, for the FAs 16:1n7, 18:2n6; 18:4n3, 20:4n3, 20:5n3, 22:1; and 22:5n3, polar bear showed intermediate values that were more similar to pilot whale and killer whale. Interspecific variation in these FA $\delta^{13}C$ values is likely similar to the causes of observed variation in bulk $\delta^{13}C$, i.e., large differences in baseline SI values related to feeding in different food webs that also vary by latitude. As lower latitude environments tend to show enriched baseline $\delta^{13}C$ values relative to those at higher latitudes (Rau et al., 1982; Goericke and Fry, 1994), higher $\delta^{13}C$ values in killer whale and pilot whale likely result from seasonal feeding at sub-Arctic latitudes (Matthews et al., 2024). Both species also show similar bulk $\delta^{13}C$ values to fin whale (*Balaenoptera physalus*) skin samples from the North Atlantic (-18.7 ± 0.4‰; Das et al., 2017). Furthermore, as $\delta^{13}C$ values of all reported FAs from ice-associated algae showed significantly higher values than pelagic algae sampled from the high Arctic (Kohlbach et al., 2016), higher values in pelagic-feeding killer whale and pilot whale than ice-associated narwhal further suggest alternative explanations for wide interspecific variation in values, namely latitudinal-based differences. Similarly, differences in baseline $\delta^{13}C$ may impact variation in values between benthic-feeding narwhal and the pelagic-feeding species, as benthic environments tend to show

higher $\delta^{13}C$ values than pelagic environments. Previous studies have also indicated similarly distinct bulk $\delta^{13}C$ values between Arctic and sub-Arctic consumers. For example, multiple sub-Arctic-feeding pinnipeds and cetaceans (including pilot whale) showed significantly higher bulk $\delta^{13}C$ values compared to Arctic ringed seal (*Pusa hispida*), walrus (*Odobenus rosmarus*), and narwhal (Land-Miller et al., 2023). Overlap in polar bear bulk $\delta^{13}C$ and some dietary FA $\delta^{13}C$ (e.g., 20:5n3 and 22:1) with pilot whale and killer whale may indicate higher instances of feeding on seasonally present sub-Arctic species (i.e., increased harp/hooded seal (*Pagophilus groenlandicus*/*Cystophora cristata*) consumption as documented in East Greenland; McKinney et al., 2013), while narwhal diet likely mostly still consists of native Arctic species (Garde et al., 2022). Furthermore, distinct differences in $\delta^{13}C$ values of 20:5n3 were used to distinguish between ice-associated and pelagic diets (Budge et al., 2008), and significant differences in 20:5n3 values between narwhal and the other two cetaceans (while values in polar bear were intermediate) may suggest more ice-associated diets in narwhal and potentially shifts to more open-water prey in polar bear (as reported elsewhere; McKinney et al., 2009).

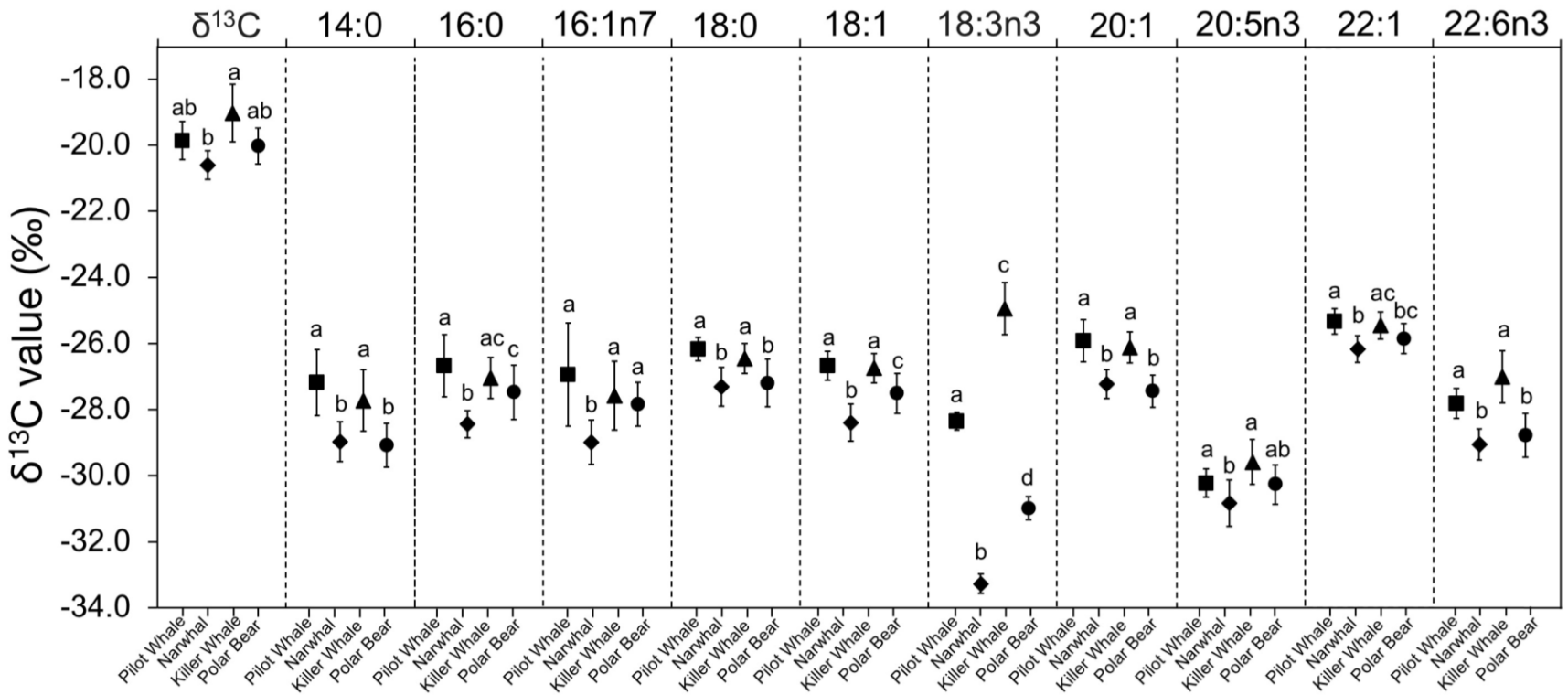


Figure 6.3: Bulk $\delta^{13}C$ from non-lipid extracted blubber samples from marine mammals (long-finned pilot whale, narwhal, killer whale, and polar) blubber samples from East Greenland and individual fatty acid (FA) $\delta^{13}C$ values (‰) from lipid extracts of these same tissues. One-way analysis of variance (ANOVAs) with post-hoc Tukey pairwise comparisons were used to assess for statistical differences in isotope values among species. Significant differences from post hoc comparisons ($p<0.05$) are represented by different letters (a,b,c) above the data points. Species are ordered by their $\delta^{15}N$ values.

The $\delta^{13}C$ values of the dietary FAs, 18:3n3 and 22:6n3, showed weak but significant positive correlations ($R^2 < 0.15$, $p < 0.04$; Table S6) with bulk $\delta^{15}N$ values, while trends were not significant for all other FAs ($R^2 < 0.14$, $p > 0.03$), although results should be interpreted cautiously with just four species included here. Variation in 18:3n3 also showed more variation among species than all other FAs, with values in killer whale > pilot whale > polar bear > narwhal (**Figure 6.3**). The 22:6n3 results are similar to those in the CS food web, where 22:6n3 values increased significantly with $\delta^{15}N$, which may similarly indicate catabolism for energy when 22:6n3 is in excess (as also reported in Budge et al., 2011 for 18:3n3). Synthesis of 22:6n3 from 18:3n3 or 20:5n3 is also unlikely to occur due to the consumption of high fat diets, e.g. >50% of diet from fat in polar bear (Stirling and McEwan, 1975; Budge et al., 2006; McKinney et al., 2013). Still, variation in $\delta^{13}C$ values of these FAs is likely also related to feeding at different latitudes, making it difficult to accurately compare values and to determine causes for wide interspecific variation without baseline corrections.

6.5.3. Using FA $\delta^{13}C$ to trace contaminant accumulation

Both the CS and EG datasets showed significant, positive correlations of 22:6n3 $\delta^{13}C$ values with THg concentrations (in CS) or with CB-153 concentrations (in EG) ($R^2 < 0.20$, $p = 0.01$; **Figure 6.4;** Table S6.9), but no other FA $\delta^{13}C$ were significantly correlated with the contaminant concentrations in both datasets. The 22:6n3 $\delta^{13}C$ values were also associated with $\delta^{15}N$ in both datasets (see section 3.1 and 3.2; Table S6.6). Additionally, the dietary FAs, 18:3n3, 18:4n3, and 22:5n3 showed significant correlations with CB-153 in the EG marine mammals ($R^2 < 0.33$, $p < 0.01$; Table S6.9), but note that these FAs were too low to acquire reliable $\delta^{13}C$

values for in the CS food web samples. We therefore cautiously suggest that the long-chain PUFAs (e.g., 18:3n3 and 22:6n3), which are considered to be dietary FAs, may be most suitable to trace contaminant accumulation across food webs, among species and over time, especially compared to shorter chain SFAs and MUFAs with a known potential for *de novo* synthesis.

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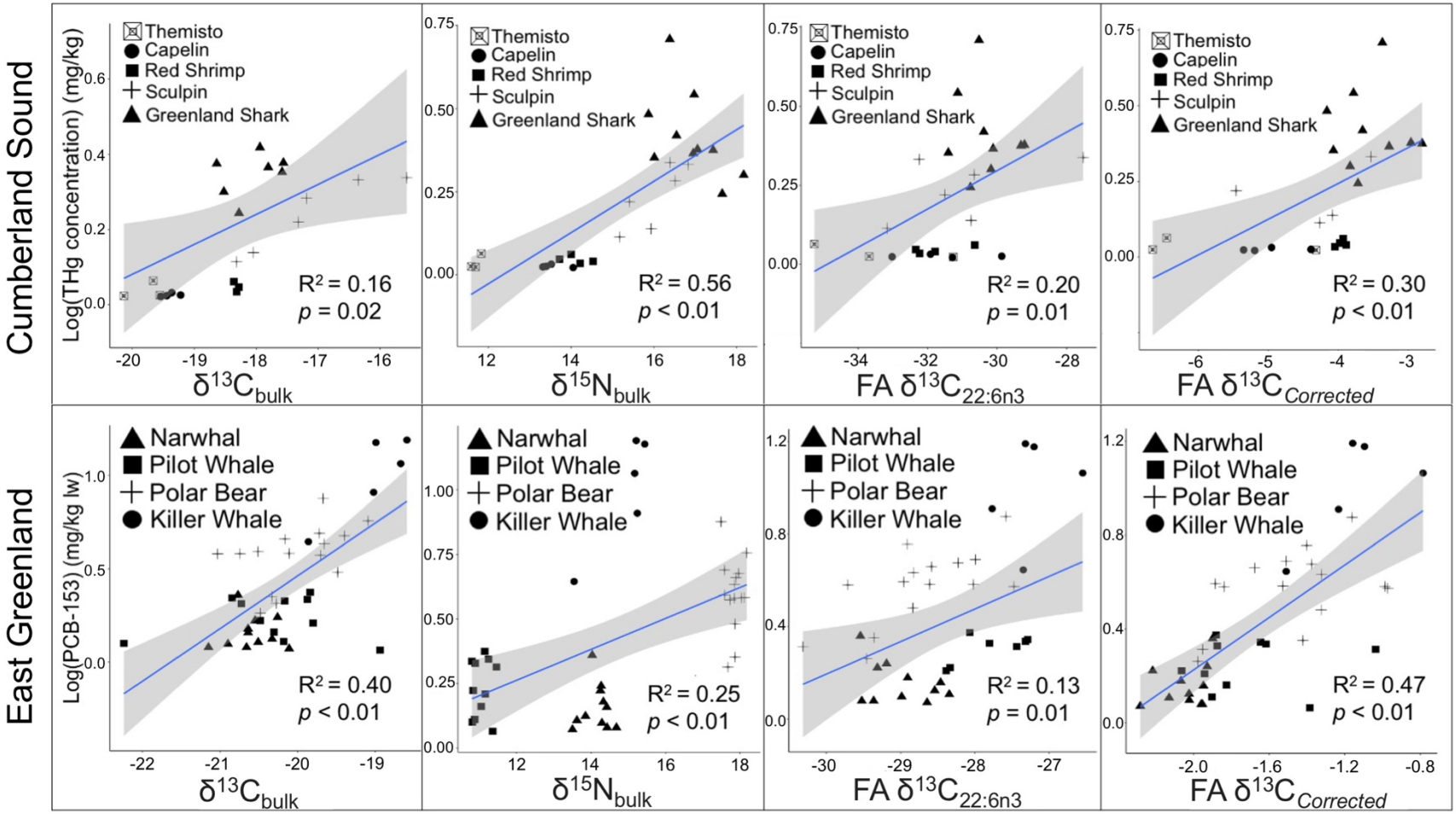

Figure 6.4: Log-linear correlations between bulk $\delta^{13}C$, bulk $\delta^{15}N$, $\delta^{13}C$ values of 22:6n3 (FA $\delta^{13}C_{22:6n3}$), or $\delta^{13}C$ values of "source"-corrected mean "trophic" FAs (FA $\delta^{13}C_{Corrected}$) (all in ‰) and total Hg (THg in dry weight in a Cumberland Sound, Nunavut, Canada food web; top panels) or PCB-153 concentrations in lipid weight (among marine mammals in East Greenland; bottom panels).

For the trophic-associated FAs, 18:3n3 (only measured in EG) and 22:6n3 (in both datasets), we further calculated $\delta^{13}C$ values "corrected" for source variation using mean $\delta^{13}C$ values of 20:1 and 22:1 (see equation 1). In this exploratory analysis, 18:3n3 and 22:6n3 were selected as "trophic" FAs as they were significantly correlated with $\delta^{15}N$ (and trophic position) in both datasets, while 20:1 and 22:1 were selected as "source" FAs as they showed almost no significant differences among any species of the CS dataset (i.e., values are largely conserved and these FAs may be directly deposited in tissues from prey without any modifications or use for energy; **Figures 6.1 and 6.2**). Instead, 20:1 and 22:1 values in EG were more likely distinct among Arctic and subarctic species due to latitudinal differences, while, in comparison, most species in the CS food web are resident (i.e., nonmigratory) species likely feeding at similar isoscapes. This approach is exploratory, and results should be interpreted cautiously until further studies across other food webs and from controlled feeding trials are performed. That said, "corrected" values showed significant positive correlations with THg in the CS ($R^2 = 0.30$; $p < 0.01$) and with CB-153 in the EG datasets ($R^2 = 0.47$; $p < 0.01$; **Figure 6.4**). However, to make a directly comparable dataset to CS in EG, we also calculated "corrected" values using 22:6n3 alone (i.e., without 18:3n3) and these values were also significant ($R^2 = 0.27$; $p < 0.01$), but explained less variation than when using mean values of 18:3n3 and 22:6n3. As the $\delta^{13}C_{Corrected}$ (using both 18:3n3 and 22:6n3 as "trophic"-associated FAs, and 20:1 and 22:1 as "source" FAs, see section 3.1) values showed higher R^2 than all other variables in EG, this suggests that 1) certain FAs like 20:1 and 22:1 may be conserved from diet to consumer and thus reflect baseline $\delta^{13}C$ values and 2) "source" corrections analogous to what has been proposed for AA $\delta^{15}N$ may better predict legacy POP concentrations than individual FA $\delta^{13}C$ values for mobile, higher-order

consumers may feed within multiple food webs, as supported elsewhere for AAs (e.g., Elliot et al., 2021).

To determine the unique contribution of bulk SI and FA $\delta^{13}C$ values in explaining contaminant variation in each dataset, we used generalized linear models with six variables, FA $\delta^{13}C_{22:6n3}$, FA $\delta^{13}C_{Corrected}$, bulk $\delta^{13}C$, bulk $\delta^{15}N$ for both datasets, and additionally included age class/sex and FA $\delta^{13}C_{18:3n3}$ for the EG dataset. Strong correlations between FA $\delta^{13}C_{22:6n3}$, FA $\delta^{13}C_{18:3n3}$, and FA $\delta^{13}C_{Corrected}$ were indicated by the VIF analysis (VIF > 5), though, so we removed FA $\delta^{13}C_{18:3n3}$ and FA $\delta^{13}C_{22:6n3}$ from our models, as regardless of which variable was included in the model, they showed similar results (e.g., Table S6.10 shows results for FA $\delta^{13}C_{22:6n3}$).

In CS, the top models (using AIC < 2) only included bulk $\delta^{13}C$ and $\delta^{15}N$, suggesting that bulk SI values are better suited than FA $\delta^{13}C$ values for assessing THg biomagnification in the food web. This model explained 65% of the variation among species, with only $\delta^{15}N$ being significant (confidence internals not overlapping zero; **Figure 6.5**). Squared semi-partial correlation coefficients for each variable showed that $\delta^{15}N$ explained nearly all of the variation in this model at 52%, while $\delta^{13}C$ explained ~5%. Although, if other potential "trophic" FAs, like 18:3n3, were able to be included in calculations, we cannot rule out the possibility that FA $\delta^{13}C_{Corrected}$ would explain more of contaminant variation, as seen in the EG dataset (**Figure 6.5**). Still, $\delta^{15}N$ alone explained a large and significant amount of variation in this model, possibly indicating that FA $\delta^{13}C$ are not as useful as bulk SI for tracing THg bioaccumulation across food webs.

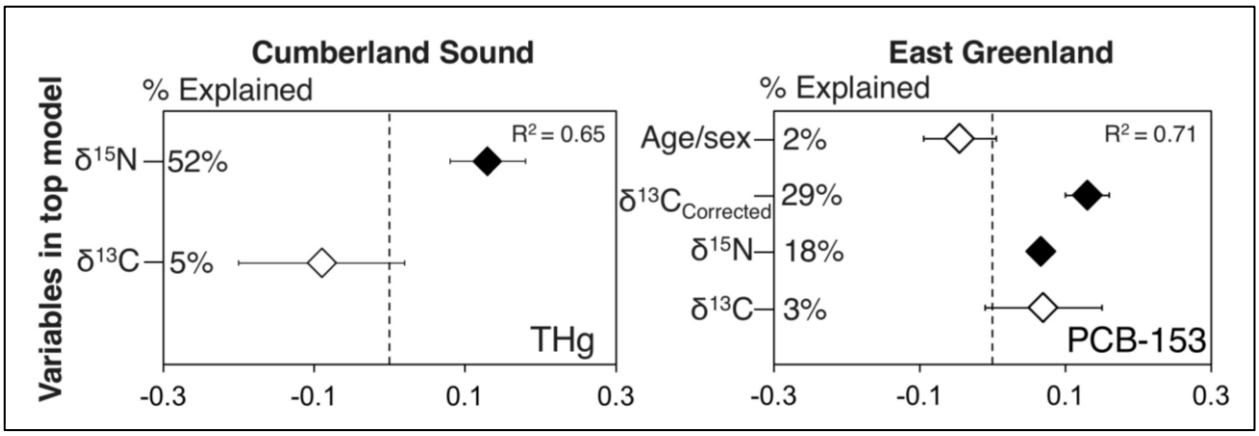

Figure 6.5: Confidence interval figures for top averaged models (AIC < 2) for total Hg (THg) concentrations analyzed in a Cumberland Sound, Nunavut, Canada food web (left panel) and PCB-153 blubber concentrations analyzed in multiple predator marine mammals in East Greenland. $\delta^{13}C$ and $\delta^{15}N$ represent bulk values in samples, while $\delta^{13}C_{22:6n3}$ represents $\delta^{13}C$ mean values of baseline-corrected "trophic" fatty acids. Significant (when confidence intervals do not cross zero) variables in top models are indicated by a black symbol (◆), while nonsignificant variables are white (⋄). Percent explained by each variable, from squared semi-partial correlation coefficients, is next to each variable.

In comparison, baseline "corrected" FA $\delta^{13}C$ values, in combination with bulk $\delta^{15}N$, seem to better explain interspecific variation in blubber legacy POP concentrations among marine mammals. The top average model for CB-153 in EG marine mammals explained 71% of the variation. It included all four variables, but only FA $\delta^{13}C_{Corrected}$ and $\delta^{15}N$ were significant. The FA $\delta^{13}C_{Corrected}$ values explained most of the variation at 29%, while $\delta^{15}N$ explained less at ~18%. Models for ΣPCB, ΣDDT, and ΣCHL concentrations showed similar results with only $\delta^{15}N$ and FA $\delta^{13}C_{Corrected}$ as significant variables in top models, and R^2 ranged from 47-62% (Table S6.11). As these EG marine mammals represent highly mobile organisms and likely occupy different food webs seasonally, some dietary FAs and their $\delta^{13}C$ values likely provide higher resolution insights into trophic transfer than bulk SI alone, at least those that are not baseline corrected. Wide differences in baseline values among sub-Arctic-feeding killer whale and pilot whale and Arctic-feeding polar bear and narwhal are likely obscuring the detection of diet patterns from non-baseline-corrected bulk SI (see section 6.2.2.). Furthermore, in marine

mammals with specialized fatty storage tissues (i.e., blubber or adipose), FA $\delta^{13}C$ may better reflect variation in lipophilic contaminants, like POPs, as they are sampled within the same tissues and likely better reflect lipophilic contaminant dynamics in food webs, while bulk SI in protein-rich muscle or liver may be more suitable to monitor proteinophilic contaminant accumulation. However, if bulk SI were instead sampled in the same tissue as where POPs accumulate in marine mammals (i.e., blubber), they may better reflect concentrations, although SI analysis in blubber is far less commonly performed than in muscle or skin as lipids contain little nitrogen required for $\delta^{15}N$ analysis (Groß et al., 2021).

Multiple previous studies have also detailed limitations of bulk SIs in explaining dietary patterns and/or contaminant variation in mobile top predators. For example, in multiple mobile pelagic predators, striped marlin (*Kajikia audax*), blue marlin (*Makaira nigricans*), and common dolphinfish (*Coryphaena hippurus*), bulk SI demonstrated limited utility in distinguishing among prey species, while FA proportions instead distinguished prey groups with higher resolution (Young et al., 2018). Similarly, in transient North Pacific killer whales, SI from skin lacked sufficient resolution to distinguish intraspecific differences in diet, while FAs and POPs were more strongly associated with one another (Herman et al., 2005). Furthermore, in an Arctic food web consisting of seabirds, Arctic fish, and invertebrates, bulk $\delta^{15}N$ alone led to inaccurate trophic biomagnification factors of legacy POPs (Elliot et al., 2021). Using the same EG samples as the present study, we (Pedersen et al., 2024a) also previously showed that FA proportions from a PCA explained a similar amount of CB-153 variation (~28%) as FA $\delta^{13}C$ values (29%) among these marine mammals, while bulk $\delta^{15}N$ explained less than 18%. However, results from these FA proportions and their $\delta^{13}C$ values (i.e., between Pedersen et al., 2024a and the current study) are likely not directly comparable as different FAs are included in each analysis and only

select $\delta^{13}C$ values of some FAs are likely useful to trace trophic transfer (see Figure S6.7). Still, as baseline corrections are typically required to perform when analyzing bulk SI, FA proportions and their $\delta^{13}C$ values may inherently provide higher resolution insights into the trophic transfer of contaminants in these mobile marine predators as they may provide both source and trophic information in the same analysis. As bulk SI currently lack standardization in methods to determine baseline, it has been suggested that CSIA of AA or even FA may serve as suitable alternatives in providing higher resolution and baseline-corrected trophic assessments (Twining et al., 2020; Kjeldgaard et al., 2021; Matthews et al., 2024).

These results also align with previously published AA CSIA assessments, where some $\delta^{15}N$ values of some AAs show 1) wide variation in values between prey and consumers, 2) consistent trophic enrichment, or 3) nonsignificant differences in marine food webs and in controlled-feeding experiments. For example, some AAs like glycine and serine are challenging to classify as "trophic" or "source" markers, as trophic fractionation is typically wide and variable, similar to most FAs likely derived from biosynthesis across the CS food web (e.g., 14:0, 16:0, 16:1n7, 18:0, and 18:1; McMahon and McCarthy, 2016). However, other AAs like glutamic acid (and likely others) are often enriched in marine food webs as a result of fractionation during the formation of other biomolecules via transamination and deamination (McClelland and Montoya, 2002; Chikaraishi et al., 2009; McMahon and McCarthy, 2016). Phenylalanine, instead, is largely conserved in marine food webs and often used to baseline-correct AA-based tropic position estimates (although which AAs should be identified as "source" or "trophic" markers at upper trophic positions is currently under investigation; see Elliot et al., 2021 and Matthews et al., 2024). $\delta^{13}C$ values of 22:6n3 may show similar consistent or predictable fractionation across marine food webs due to endogenous processes (e.g., catabolism

for energy, *de novo* synthesis of other biomolecules, etc.), and thus FA CSIA, like AA CSIA, holds promise as a new and useful tracer of trophic structure and contaminant biomagnification in food webs.

CSIA-FA is a relatively new and underused approach to studying trophic ecology and contaminant bioaccumulation and biomagnification. As such, the trophic fractionation of FA $\delta^{13}C$ and associations with contaminant accumulation is currently exploratory, especially in studies of higher-order wildlife species. Similar to AA CSIA, further investigation in diverse marine food web studies is required to confirm or refute whether the patterns of some FAs apparently showing consistent trophic fractionation (like 22:6n3 and, potentially, 18:3n3), and others having $\delta^{13}C$ values that are largely conserved (like 20:1 and 22:1 isomers), holds across other locations and ecosystem types. Although controlled-feeding experiments are ideal to identify "trophic" and "source" FAs, they are difficult, if not impossible, to conduct on cetaceans and across full marine food webs. Unknown factors beyond those previously discussed likely also impact trophic fractionation for some FAs, especially as the diet-, tissue-, species-, and FA-specific trophic fractionation are still not well-understood (Twining et al., 2020). Here, we present the first information on $\delta^{13}C$ patterns for multiple FAs across an entire marine food web and find that FA $\delta^{13}C$ of known dietary origin show promise in assessing trophic relationships and contaminant trophic transfer. Further characterization of FA $\delta^{13}C$ in controlled-feeding experiments on higher-order organisms and across other freshwater, marine, and terrestrial food webs is warranted to enhance our understanding of their applicability in assessing trophic roles and contaminant dynamics.

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6.8. SUPPORTING INFORMATION

Table S6.1: Biological data (Age class and sex) for each sample analyzed in the Cumberland Sound food web, and from toothed whale/ursid individual from East Greenland and collected from 2012 to 2021that were used in current study.

Species	ID	Sex	Age/Age Class	Year Collected	Location
Killer whale	48335	female	adult	2012	Tasiilaq
	48736	female	adult	2013	Tasiilaq
	48733	female	adult	2013	Kulusuk
	35143	female	adult	2013	Kulusuk
	GL-01	male	adult	2021	Ittoqqortoormitt
	GL-03	female	adult	2021	Ittoqqortoormitt
	64752	female	adult	2021	Kulusuk
Narwhal	53802	female	adult	2015	Gaasefjord
	53812	male	adult	2015	Gaasefjord
	53823	male	subadult	2015	Gaasefjord
	58324	male	subadult	2015	Gaasefjord
	53825	female	subadult	2015	Gaasefjord
	53835	female	adult	2015	Gaasefjord
	53839	female	subadult	2015	Gaasefjord
	53840	male	subadult	2015	Gaasefjord
	53834	male	subadult	2015	Gaasefjord
	53801	female	adult	2015	Gaasefjord
	53845	female	subadult	2015	Gaasefjord
	53811	female	adult	2015	Gaasefjord
	53842	female	adult	2015	Gaasefjord
	53844	female	adult	2015	Gaasefjord
	53846	female	subadult	2015	Gaasefjord
Pilot Whale	64702	female	adult	2021	Tasiilaq
	64703	female	adult	2021	Tasiilaq
	64705	female	adult	2021	Tasiilaq
	64709	male	subadult	2021	Tasiilaq
	64710	female	subadult	2021	Tasiilaq
	64711	female	adult	2021	Kulusuk
	64712	male	adult	2021	Tasiilaq
	64714	female	adult	2021	Tasiilaq
	64720	male	adult	2021	Kulusuk
	64721	female	adult	2021	Kulusuk

	64722	male	subadult	2021	Kulusuk
	64723	female	subadult	2021	Tasiilaq
	64724	male	subadult	2021	Tasiilaq
	64727	male	subadult	2021	Tasiilaq
	64728	female	subadult	2021	Tasiilaq
Polar Bear	61866	male	subadult	2021	Ittoqqortoormitt
	61867	female	adult	2021	Ittoqqortoormitt
	61868	female	subadult	2021	Ittoqqortoormitt
	61869	female	adult	2021	Ittoqqortoormitt
	61870	female	adult	2021	Ittoqqortoormitt
	61871	male	adult	2021	Ittoqqortoormitt
	61872	female	subadult	2021	Ittoqqortoormitt
	61873	male	adult	2021	Ittoqqortoormitt
	61874	male	adult	2021	Ittoqqortoormitt
	61875	female	adult	2021	Ittoqqortoormitt
	61876	female	subadult	2021	Ittoqqortoormitt
	61877	male	subadult	2021	Ittoqqortoormitt
	61878	female	subadult	2021	Ittoqqortoormitt
	61879	male	adult	2021	Ittoqqortoormitt
	61880	male	adult	2021	Ittoqqortoormitt

Supplemental Text #6.1 on Stable Isotope Analysis

All Cumberland Sound samples were analyzed on an elemental analyzed coupled to an isotope ratio mass spectrometer (Delta V Advantage). Trophic position was calculated in consumers using $\delta^{15}N$ relative to copepods and a constant 3.8‰ trophic enrichment factor. All QA/QC data is available in McMeans et al. (2015).

In EG, all narwhal muscle $\delta^{13}C$ and $\delta^{15}N$ data is reported in Land-Miller et al. (2023). All 2021 killer whale and pilot whale muscle samples were analyzed at McGill University. In brief, all muscle samples were non-lipid extracted, and ~0.4 g of tissue was weighed, cut into small pieces, and dried in an oven overnight at 80°C (Barrow et al. 2008). Samples were then ground using a glass mortar, then 1.2 mg of each powdered sample was weighed in a tin capsule and analyzed on a Thermo Scientific EA Isolink Flash Elemental Analyzer paired with a Delta V Plus Isotope Ratio Mass Spectrometer (IRMS). Values were calibrated against reference materials from the United States Geological Survey (USGS; USGS40, USGS41a) and International Atomic Energy Agency (IAEA; IAEA-N-2), and accuracy was determined using standards USGS88 and USGS89. Standard deviation of both USGS standards was 0.13‰ for carbon and 0.28‰ for nitrogen. Accuracy was 0.02 ± 0.01‰ for carbon and 0.02 ± 0.005‰ for nitrogen. The remaining samples (2012-2013 killer whale and 2021 polar bear muscle) were analyzed at the Center for Permafrost at the University of Copenhagen, Denmark and were also non-lipid extracted. These samples were analyzed using an elemental analyzer paired with IRMS (Finnigan MAT Delta PLUS, Thermo Scientific). IAEA sucrose and ammonium sulfate standards were used for calibration, and analytical precision was <0.1‰ standard deviation. Trophic position could not be estimated as no baseline organisms were collected

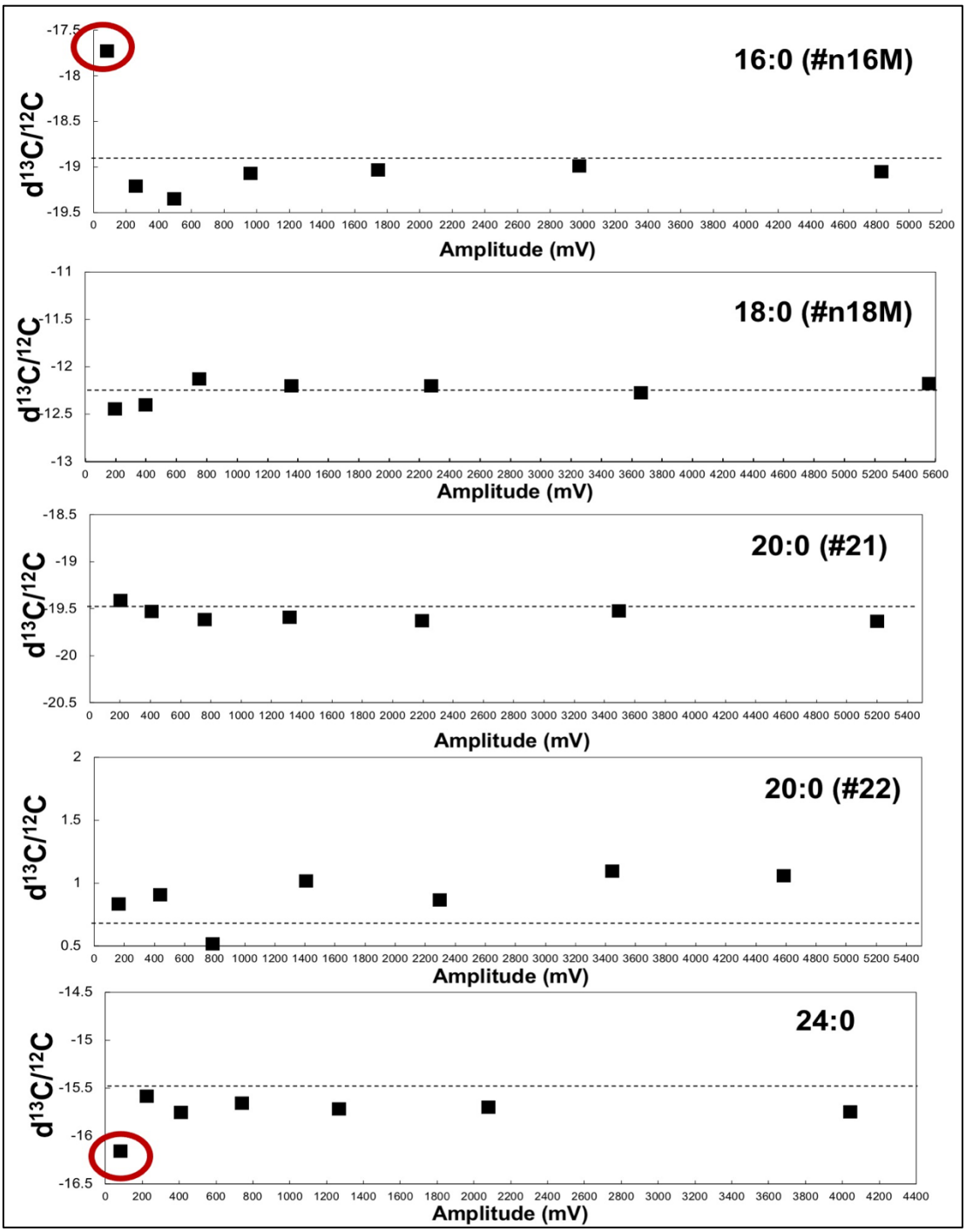

Figure S6.1: $\delta^{13}C$ values ‰ and amplitudes for FAME standards, 16:0 (#n16M), 18:0 (#n18M), 20:0 (#21), 20:0 (#22) and 24:0 at seven concentrations, 3.12, 6.25, 12.5, 25, 50, 100, and 200 µg/mL dilutions to check the consistency of values across concentrations. Dotted lines represent accepted values. Concentrations with amplitudes lower than 200 mV (red circles) showed wider variability in $\delta^{13}C$ values and were not included in analysis. We also determined sufficient values up to peaks with 5500 mV amplitude, and larger peaks tended to show significant fronting (see Figure S3). Thus, we determined the linear range of our instrument to be ~200-5500 mV.

Table S6.2: All fatty acids in the Cumberland Sound, Nunavut, Canada food web and East Greenland datasets that were quantified for $\delta^{13}C$. These FAs were well-separated and within linear range for ≥ 80% of samples from each dataset. X signifies that the fatty acid was analyzed in this dataset.

Fatty Acid	Cumberland Sound	East Greenland
14:0	**X**	**X**
16:0	**X**	**X**
16:1n7	**X**	**X**
18:0	**X**	**X**
18:1n11	**X** (as 18:1)	**X** (as 18:1)
18:1n9		
18:1n7		
18:1n5		
18:2n6		**X**
18:3n3		**X**
20:1n11	**X** (as 20:1)	**X** (as 20:1)
20:1n9		
20:1n7		
20:4n3		**X**
20:5n3	**X**	**X**
22:1n11	**X** (as 22:1)	**X** (as 22:1)
22:1n9		
22:1n7		
22:5n3		**X**
22:6n3	**X**	**X**

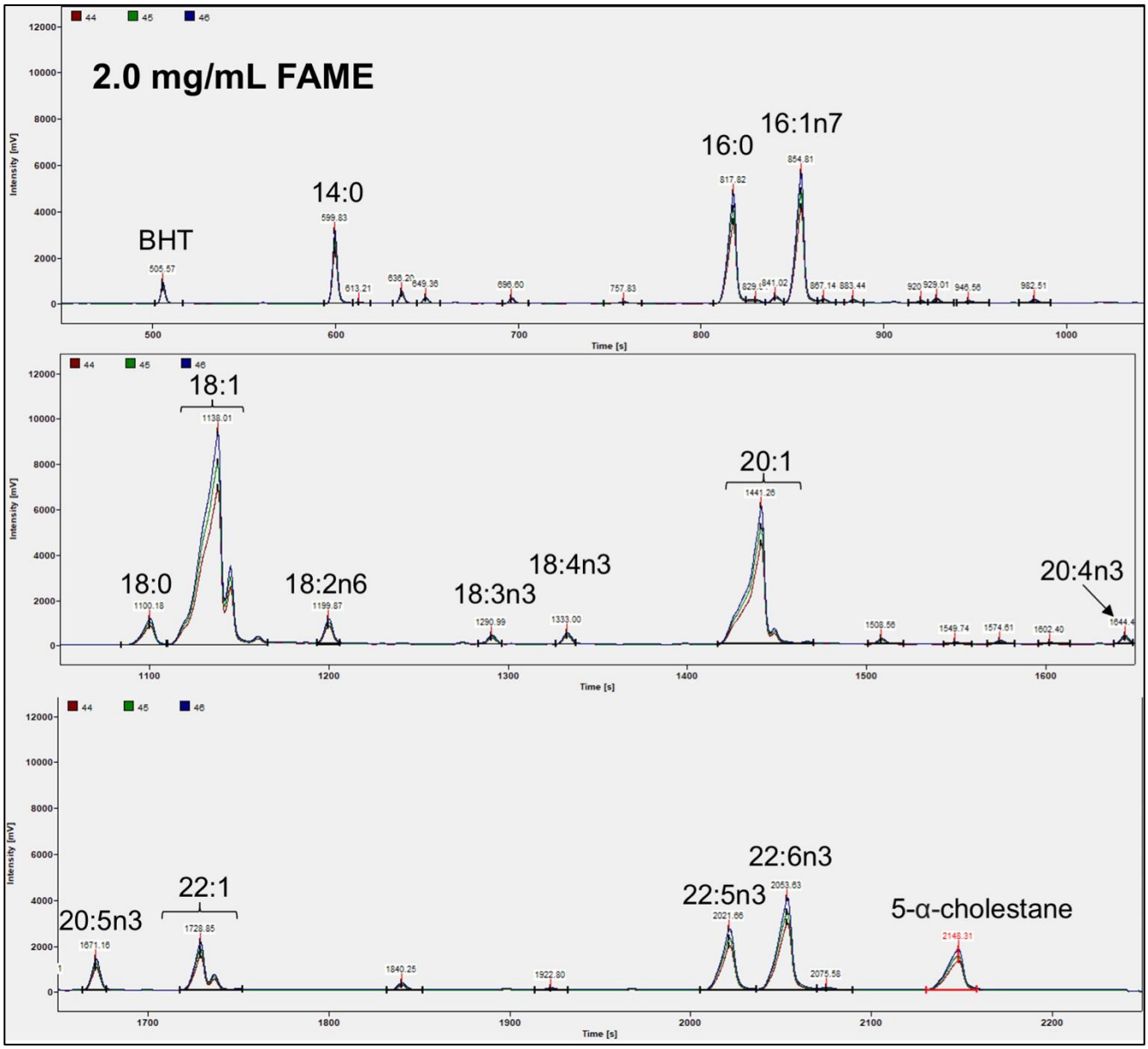

Figure S6.2: Example chromatogram in a fatty acid methyl ether (FAME) extract in polar bear adipose at 2.0 mg/mL concentrations with labelled peaks for each individual FA. Only peaks with the linear range of the instrument (200-5500 mV for peak amplitude) were included in analyses. For peaks larger than this, they were often in the linear range at the lower 0.5 mg/ml concentration that was run (see Figure S3).

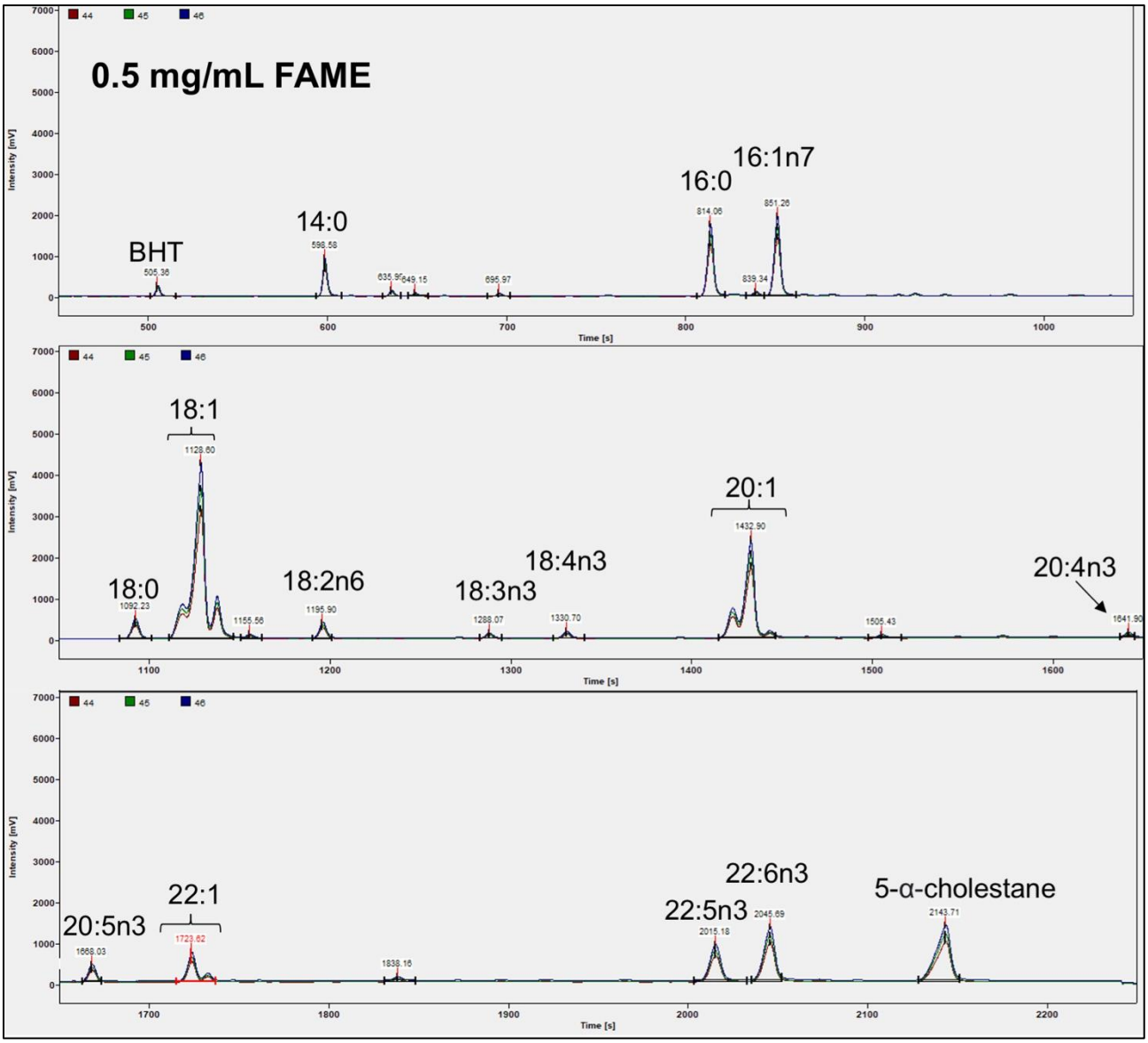

Figure S6.3: Example chromatogram in a fatty acid methyl ether (FAME) extract in polar bear adipose at the lower concentrations at 0.5 mg/mL with labelled peaks for each individual FA. Only peaks with the linear range of the instrument (200-5500 mV) were included in analyses. If peaks from both concentrations were both within the linear range (and showed very similar $\delta^{13}C$ values), they were averaged together.

Table S6.3: Retention times of fatty acids in blubber/adipose samples ran on the GC-IRMS. Full chromatograms available in Figure S6.2 and S6.3.

Fatty Acid	Retention Time (s)
BHT	506
14:0	603
16:0	816
16:1n7	850
18:0	1093
18:1	1128
18:2n6	1204
18:3n3	1289
18:4n3	1332
20:1	1442
20:4n3	1647
20:5n3	1668
22:1	1723
22:5n3	2013
22:6n3	2043

Table S6.4: Mean (+/- standard deviation) values of carbon isotopes of individual fatty acids in the U.S. National Institute of Standards and Technology (NIST) standard reference material RM 8037 krill oil. No accepted values currently exist for carbon isotopes in these reference materials.

Fatty Acid	Rm 8037 (in ‰)
14:0	-34.10 ± 0.35
16:0	-32.90 ± 0.30
16:1n7	-34.29 ± 0.20
18:0	-30.76 ± 0.18
18:1	-33.19 ± 0.32
18:2n6	-36.07 ± 0.32
18:3n3	-35.76 ± 0.29
20:1	-32.41 ± 0.49
20:4n3	-34.32 ± 0.52
20:5n3	-34.73 ± 0.27
22:1	-32.30 ± 0.40
22:5n3	NA
22:6n3	-33.00 ± 0.23

Supplemental Text #6.2 on $\delta^{13}C$ for the methanol using EMAsorb

EMAsorb (part number B1117) was purchased from Isomass Scientific Inc, Calgary, Alberta, Canada. A 3 μL aliquot of methanol (with the same lot # that was used to derivative FAs) was pipetted onto one individual piece or "rock" of EMAsorb, which was then immediately placed inside a tin capsule and wrapped. To avoid any residual CO_2 absorption in the laboratory setting, the methanol-EMAsorb was ran on the EA-IRMS on the same day it was prepared. Eight runs of methanol from Fisher Scientific lot #221044 showed a mean $\delta^{13}C$ value of -31.30 ± 0.80‰, while eight runs of methanol from Fisher Scientific lot #202389 showed mean values of -41.60 ± 0.96‰. Given the low standard deviations and distinct difference in values among lot #s, this method of using EMAsorb to determine $\delta^{13}C$ values of methanol is likely sufficient (and also simple and inexpensive to perform) for future studies of FA $\delta^{13}C$ that are measure as FAME $\delta^{13}C$.

Supplemental Text #6.3 on Contaminant Extraction and Analysis

For the CS food web, all Hg concentration data (in muscle or whole-body tissues) is available in McMeans et al., (2013) and McMeans et al. (2015). In brief, total mercury (THg) concentrations were determined via atomic absorption spectrometry on a DMA-80 Direct Mercury Analyzer (Milestone Inc, Shelton, CT, USA) at the University of Windsor, Ontario, Canada. This system requires no sample pre-processing. Only Greenland shark muscle tissue (i.e. not liver or blood plasma) was analyzed for THg. However, due to a lack of available sample remaining for Greenland halibut, copepods, and shrimp, THg concentrations were unable to be measured for these species. See McMeans et al. (2015) for detailed QA/QC information.

In EG, all POP concentration data is detailed in Pedersen et al. (2024). In brief, all blubber/adipose samples were analyzed for polychlorinated biphenyls (PCBs) and organochlorine pesticides (e.g., dichlorodiphenyltrichloroethanes [DDTS] and chlordanes [CHLs]) and extracted using a QuEChERS (Quick, Easy, Cheap, Effective, Rugged, and Safe) method that we previously developed (Pedersen et al., 2023) at McGill University. Extracts were monitored on an Agilent 7820A gas chromatograph with mass spectrometer (GC–MS) (Agilent Technologies, Santa Clara, CA, USA). See Pedersen et al. (2024) for detailed QA/QC information.

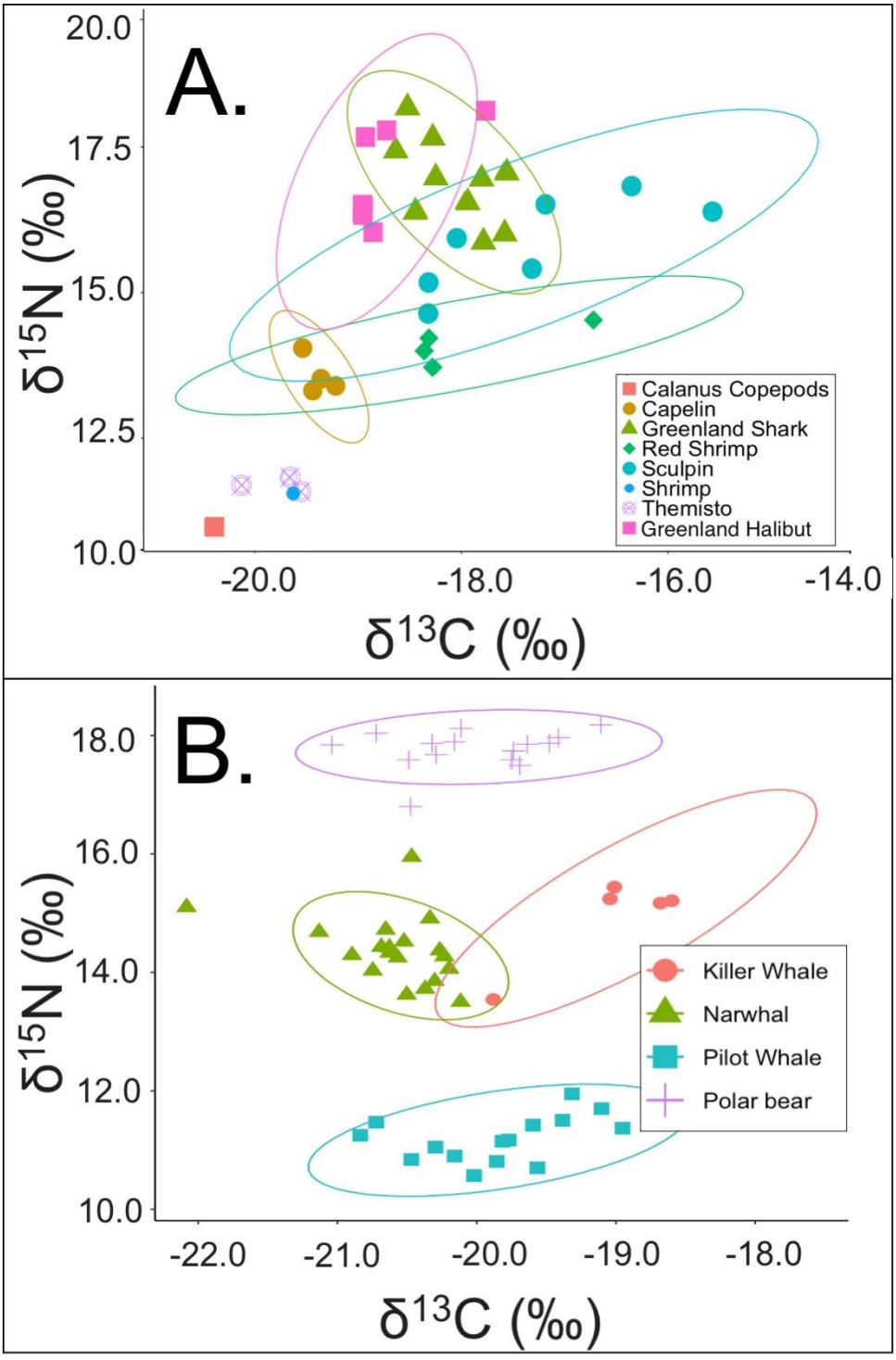

Figure S6.4: Isotopic biplot of A) species from the Cumberland Sound food web and B) predator species from East Greenland for bulk $\delta^{13}C$ and $\delta^{15}N$ (in ‰). Cumberland Sound data was subset from McKinney et al. (2012) and McMeans et al. (2015).

Table S6.5: $\delta^{13}C$ values of individual fatty acids (FAs) and bulk $\delta^{13}C$ and $\delta^{15}N$ (in ‰) analyzed in multiple species in a Cumberland Sound food web. One-way analysis of variance (ANOVAs) with post-hoc Tukey pairwise comparisons were used to assess for statistical significance among species. Significant differences from post hoc comparisons ($p<0.05$) are represented by different letters (a,b,c) next to the measurement.

Fatty Acid	Copepods	Shrimp	Themisto	Capelin	Red Shrimp	Sculpin	Greenland Halibut	Greenland Shark
14:0	-22.75	-22.48	-22.67 ± 0.06^{ab}	-23.04 ± 0.16^{b}	-21.87 ± 0.33^{ab}	-21.83 ± 0.15^{a}	-23.53 ± 0.22^{b}	-22.02 ± 0.19^{a}
16:0	-23.66	-20.73	-24.01 ± 0.32^{ab}	-25.06 ± 0.24^{a}	-22.74 ± 0.44^{ab}	-23.15 ± 0.34^{a}	-24.33 ± 0.28^{ab}	-23.41 ± 0.19^{a}
16:1n7	-24.34	-19.11	-24.31 ± 0.46^{ab}	-25.01 ± 0.32^{a}	-23.90 ± 0.40^{ab}	-23.00 ± 0.31^{b}	-25.14 ± 0.28^{a}	-24.52 ± 0.18^{a}
18:0	-22.37	NA	NA	-24.22 ± 0.47^{a}	-20.72	-20.57 ± 0.37^{b}	-23.64 ± 0.33^{a}	-21.75 ± 0.23^{c}
18:1	-24.35	-23.94	-24.90 ± 0.26^{ab}	-25.27 ± 0.19^{a}	-23.91 ± 0.22^{ab}	-22.78 ± 0.31^{b}	-23.64 ± 0.29^{ab}	-23.95 ± 0.16^{b}
20:1	-23.47	-23.78	-23.80 ± 0.22^{a}	-23.93 ± 0.30^{a}	-24.38 ± 0.37^{a}	-23.08 ± 0.45^{b}	-24.70 ± 0.14^{a}	-23.93 ± 0.16^{a}
20:5n3	-30.89	-29.36	-30.41 ± 0.70^{ab}	-30.24 ± 0.79^{ab}	-29.98 ± 0.72^{ab}	-29.55 ± 0.53^{a}	-31.15 ± 0.28^{b}	-31.54 ± 0.32^{b}
22:1	-23.08	-22.33	-22.90 ± 0.42^{a}	-22.91 ± 0.48^{a}	-23.36 ± 0.26^{a}	NA	-23.57 ± 0.04^{a}	-23.29 ± 0.17^{a}
22:6n3	-33.88	-31.56	-33.40 ± 0.77^{a}	-31.52 ± 0.66^{bc}	-31.75 ± 0.39^{bc}	-31.01 ± 0.67^{bc}	-31.96 ± 0.36^{b}	-30.40 ± 0.23^{c}
Bulk $\delta^{13}C$	-20.39	-19.63	-19.78 ± 0.12^{a}	-19.39 ± 0.33^{ab}	-17.92 ± 0.34^{c}	-17.30 ± 1.40^{c}	-18.70 ± 0.88^{bc}	-18.08 ± 0.73^{c}
Bulk $\delta^{15}N$	10.97	11.55	11.70 ± 0.31^{a}	13.57 ± 0.13^{b}	14.11 ± 0.80^{b}	16.27 ± 1.04^{c}	17.08 ± 0.47^{c}	16.90 ± 0.40^{c}

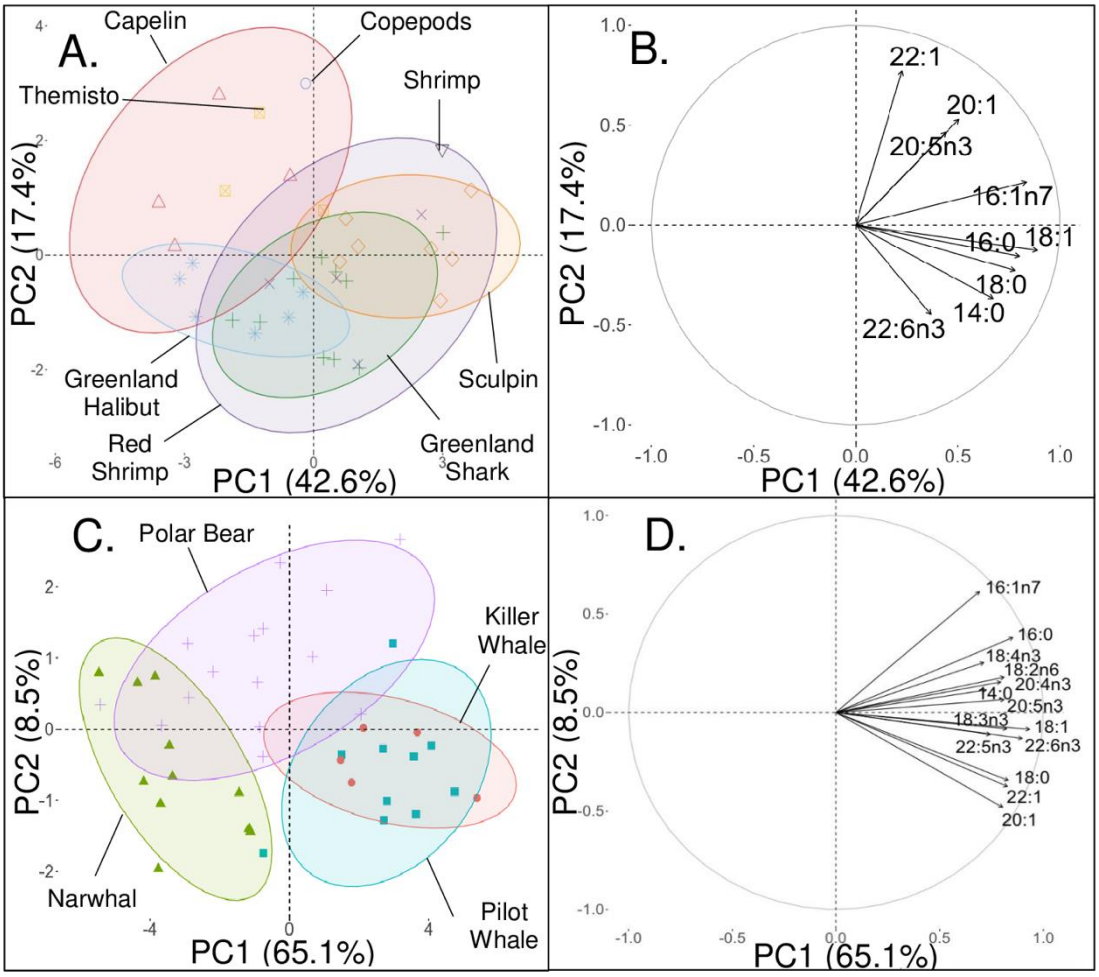

Figure S6.5: A: Principal component analysis all $\delta^{13}C$ values (‰) of individual fatty acids (FAs) in (A) species in a Cumberland Sound, Nunuvat, Canada food web and (C) among marine mammal blubber samples collected from East Greenland. Variable correlation plots of all FAs are shown for (B) Cumberland Sound samples and (D) East Greenland samples. Ellipses represent 90 % confidence intervals.

Table S6.6: Results from linear correlations for bulk $\delta^{13}C$ and for $\delta^{13}C$-FAs against bulk $\delta^{15}N$ values in a Cumberland Sound, Nunavut, Canada food web and in multiple blubber samples from marine mammals in East Greenland. Bolded values indicate significant trends ($p < 0.05$).

	Cumberland Sound		**East Greenland**	
Fatty Acid	**R^2**	***p* value**	**R^2**	***p* value**
14:0	0.11	$p > 0.05$	0.10	$p > 0.05$
16:0	0.01	$p > 0.05$	0.01	$p > 0.05$
16:1n7	0.04	$p > 0.05$	0.01	$p > 0.05$
18:0	0.02	$p > 0.05$	0.13	$p > 0.05$
18:1	0.11	$p > 0.05$	0.09	$p > 0.05$
18:2n6	NA	NA	0.05	$p > 0.05$
18:3n3	NA	NA	**0.10**	**$p = 0.04$**
18:4n3	NA	NA	0.01	$p > 0.05$
20:1	0.03	$p > 0.05$	0.10	$p > 0.05$
20:4n3	NA	NA	0.04	$p > 0.05$
20:5n3	0.06	$p > 0.05$	0.01	$p > 0.05$
22:1	0.10	$p > 0.05$	0.15	$p > 0.05$
22:5n3	NA	NA	0.04	$p > 0.05$
22:6n3	**0.34**	**$p < 0.001$**	**0.15**	**$p = 0.01$**
Bulk $\delta^{13}C$	**0.33**	**$p < 0.001$**	0.05	$p > 0.05$

Table S6.7: $\delta^{13}C$ values (in ‰) of individual fatty acids (FAs) analyzed in multiple Greenland shark (GS) tissues from Cumberland Sound, Nunavut, Canada. The primary diet item of GS, Greenland Halibut was also included for comparison. One-way analysis of variance (ANOVAs) with post-hoc Tukey pairwise comparisons were used to assess for statistical significance among species. Significant differences from post hoc comparisons ($p<0.05$) are represented by different letters (a,b,c) next to the measurement.

Fatty Acid	GS Muscle	GS Liver	GS Blood plasma	Greenland Halibut
14:0	-22.02 ± 0.19^{a}	NA	-23.57 ± 0.16^{b}	-23.53 ± 0.22^{b}
16:0	-23.41 ± 0.19^{a}	-24.07 ± 0.25^{b}	-24.21 ± 0.28^{b}	-24.33 ± 0.28^{b}
16:1n7	-24.52 ± 0.18^{a}	-24.60 ± 0.31^{a}	-25.59 ± 0.26^{b}	-25.14 ± 0.28^{b}
18:0	-21.75 ± 0.23^{a}	-21.89 ± 0.03^{a}	-23.08 ± 0.31^{b}	-23.64 ± 0.33^{b}
18:1	-23.95 ± 0.16^{ab}	-24.24 ± 0.10^{a}	-23.89 ± 0.21^{a}	-23.64 ± 0.29^{b}
20:1	-23.93 ± 0.16^{a}	-23.97 ± 0.11^{a}	-24.87 ± 0.20^{b}	-24.70 ± 0.14^{b}
20:5n3	-31.54 ± 0.32^{a}	-31.36 ± 0.44^{a}	-32.34 ± 0.29^{b}	-31.15 ± 0.28^{a}
22:1	-23.29 ± 0.17^{a}	-23.56 ± 0.13^{a}	-24.42 ± 0.18^{b}	-23.57 ± 0.04^{a}
22:6n3	-30.40 ± 0.23^{a}	-30.29 ± 0.19^{a}	-31.63 ± 0.27^{b}	-31.96 ± 0.36^{b}

Table S6.8: Blubber $\delta^{13}C$ values (in ‰) of individual fatty acids (FAs) and bulk $\delta^{13}C$ and $\delta^{15}N$ for marine mammals sampled from East Greenland. One-way analysis of variance (ANOVAs) with post-hoc Tukey pairwise comparisons were used to assess for significant differences among species. Significant differences from post hoc comparisons ($p<0.05$) are represented by different letters (a,b,c) next to the measurement.

Fatty Acid	Killer Whale	Pilot Whale	Narwhal	Polar Bear
14:0	-27.65 ± 0.25^{a}	-27.10 ± 0.26^{a}	-28.91 ± 0.16^{b}	-29.02 ± 0.24^{b}
16:0	-26.97 ± 0.31^{ab}	-26.59 ± 0.25^{b}	-28.38 ± 0.11^{c}	-27.41 ± 0.16^{a}
16:1n7	-27.48 ± 0.25^{ab}	-26.84 ± 0.41^{a}	-28.91 ± 0.18^{c}	-27.75 ± 0.27^{bc}
18:0	-26.42 ± 0.27^{a}	-26.14 ± 0.09^{a}	-27.28 ± 0.15^{b}	-27.16 ± 0.12^{b}
18:1	-26.70 ± 0.23^{a}	-26.63 ± 0.11^{a}	-28.36 ± 0.15^{b}	-27.47 ± 0.12^{c}
18:2n6	-32.81 ± 0.23^{a}	-30.95 ± 0.43^{a}	-35.74 ± 0.30^{b}	-32.78 ± 0.31^{a}
18:3n3	-26.16 ± 0.85^{a}	-29.82 ± 0.29^{b}	-35.13 ± 0.32^{c}	-32.65 ± 0.38^{c}
18:4n3	-32.24 ± 0.25^{a}	-31.98 ± 0.15^{a}	-35.54 ± 0.16^{b}	-32.94 ± 0.32^{a}
20:1	-26.07 ± 0.18^{a}	-25.87 ± 0.17^{a}	-27.19 ± 0.11^{b}	-27.40 ± 0.12^{b}
20:4n3	-30.59 ± 0.08^{a}	-30.59 ± 0.09^{a}	-32.91 ± 0.12^{b}	-31.53 ± 0.17^{b}
20:5n3	-29.53 ± 0.22^{a}	-30.17 ± 0.11^{a}	-30.78 ± 0.18^{b}	-30.21 ± 0.17^{ab}
22:1	-25.41 ± 0.17^{ab}	-25.29 ± 0.10^{a}	-26.13 ± 0.10^{c}	-25.81 ± 0.11^{bc}
22:5n3	-27.30 ± 0.31^{a}	-28.21 ± 0.15^{ab}	-28.76 ± 0.14^{c}	-28.66 ± 0.13^{bc}
22:6n3	-26.95 ± 0.25^{a}	-27.76 ± 0.12^{a}	-29.01 ± 0.12^{b}	-28.73 ± 0.20^{b}
$\delta^{15}N$	14.92 ± 0.78^{a}	11.19 ± 0.39^{b}	14.37 ± 0.57^{a}	17.76 ± 0.33^{c}
$\delta^{13}C$	-19.02 ± 0.31^{a}	-19.86 ± 0.57^{a}	-20.60 ± 0.44^{b}	-20.03 ± 0.57^{ab}

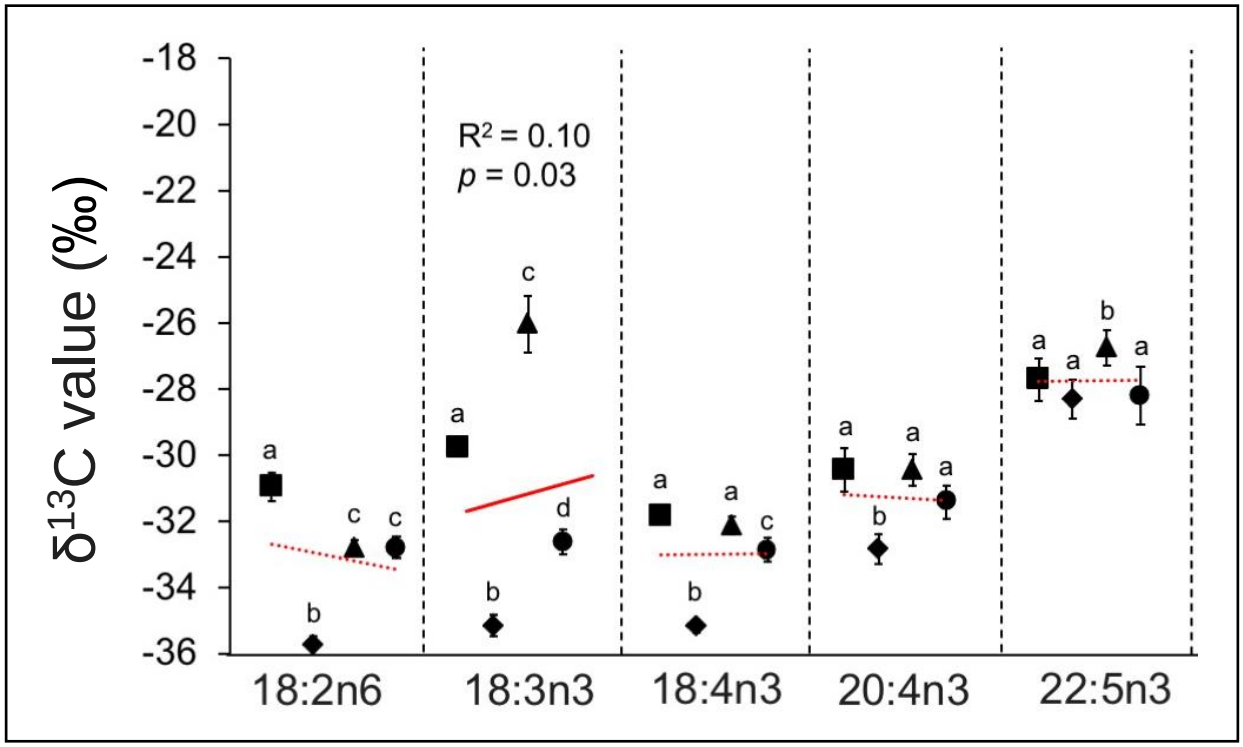

Figure S6.6: Additional individual fatty acid (FA) $\delta^{13}C$ values (in ‰) from non-lipid extracted blubber samples from marine mammals (long-finned pilot whale, narwhal, killer whale, and polar) blubber samples. These FAs were not extracted in the Cumberland Sound food web samples but were within the linear range of East Greenland samples and thus were included in the analyses. One-way analysis of variance (ANOVAs) with *post-hoc* Tukey pairwise comparisons were used to assess for statistical differences in isotope values among species. Significant differences from *post hoc* comparisons ($p<0.05$) are represented by different letters (a,b,c) above the data points. Species are ordered by their $\delta^{15}N$ values and linear correlations are plotted against $\delta^{15}N$ (plotted with a red line only when significant)

Table S6.9: Results from linear correlations for δ^{13}C-FAs (in ‰) against 1) log(total mercury) (THg mg/kg in dry weight) in a Cumberland, Nunavut, Canada food web and 2) log(PCB-153 mg/kg in lipid weight) (the PCB congener at the highest concentrations) in multiple blubber samples from marine mammals in East Greenland. Bolded values indicate significant trends ($p < 0.05$).

	Cumberland Sound		**East Greenland**	
Fatty Acid	**R^2**	***p* value**	**R^2**	***p* value**
14:0	0.05	$p > 0.05$	0.01	$p > 0.05$
16:0	0.01	$p > 0.05$	0.10	$p > 0.05$
16:1n7	0.03	$p > 0.05$	0.02	$p > 0.05$
18:0	0.10	$p > 0.05$	0.01	$p > 0.05$
18:1	0.14	$p > 0.05$	0.15	$p > 0.05$
18:2n6	NA	NA	0.05	$p > 0.05$
18:3n3	NA	NA	**0.33**	***p* < 0.01**
18:4n3	NA	NA	**0.23**	***p* < 0.01**
20:1	0.01	$p > 0.05$	0.01	$p > 0.05$
20:4n3	NA	NA	0.04	$p > 0.05$
20:5n3	0.05	$p > 0.05$	**0.09**	***p* < 0.01**
22:1	0.01	$p > 0.05$	0.06	$p > 0.05$
22:5n3	NA	NA	**0.12**	***p* < 0.01**
22:6n3	**0.20**	***p* = 0.01**	**0.13**	***p* < 0.01**

Table S6.20: Top averaged model (all models averaged with AIC <2) of linear models with FA $\delta^{13}C_{22:6n3}$ (instead of FA $\delta^{13}C_{Corrected}$) and total mercury (THg) in the Cumberland Sound food web and for persistent organic pollutants (POPs) among marine mammals in East Greenland. Significant variables in each model are bolded, when confidence intervals did not cross zero. Squared semi-partial correlation coefficient are also reported to show the variance explained by each individual variable (given without the influence of other variables in the top model).

Averaged Model (AIC_c <2)	***Parameter***	***Estimate***	***Confidence Interval***		***R^2***	***Semi-partial coefficient^2***
			2.50%	**97.5%**		
CS: THg ~ $\delta^{13}C$ + **$\delta^{15}N$**	$\delta^{15}N$	0.13	0.07	0.18	0.65	0.52
EG: ΣPCBs~ $\delta^{13}C$ + $\delta^{15}N$ + FA $\delta^{13}C_{22:6n3}$ + age/sex	$\delta^{13}C$	0.15	0.03	0.27	0.56	0.13
	$\delta^{15}N$	0.06	0.02	0.09		0.06
	FA $\delta^{13}C_{22:6n3}$	0.19	0.08	0.31		0.20
	Adult-males	-0.09	-0.17	> -0.01		0.03
EG: PCB-153~ $\delta^{13}C$ + $\delta^{15}N$ + FA $\delta^{13}C_{22:6n3}$ + age/sex	$\delta^{13}C$	0.13	0.05	0.21	0.65	0.12
	$\delta^{15}N$	0.08	0.05	0.10		0.18
	FA $\delta^{13}C_{22:6n3}$	0.13	0.10	0.25		0.25
	Adult-males	-0.05	-0.11	> -0.01		0.03
EG: ΣDDTs~ $\delta^{13}C$ + **$\delta^{15}N$** + FA $\delta^{13}C_{22:6n3}$ + age/sex	$\delta^{13}C$	0.31	0.12	0.49	0.45	0.26
	$\delta^{15}N$	-0.10	-0.14	-0.05		0.18
EG: ΣCHLs~ $\delta^{13}C$ + $\delta^{15}N$ + FA $\delta^{13}C_{22:6n3}$ + age/sex	$\delta^{13}C$	0.22	0.08	0.36	0.38	0.13

Table S6.11: Top averaged model (all models averaged with AIC <2) of linear models with FA $\delta^{13}C_{Corrected}$ and total mercury (THg) in the Cumberland Sound food web and for persistent organic pollutants (POPs) among marine mammals in East Greenland. Significant variables in each model are bolded, when confidence intervals did not cross zero. Squared semi-partial correlation coefficient are also reported to show the variance explained by each individual variable (given without the influence of other variables in the top model).

Averaged Model (AIC_c <2)	***Parameter***	***Estimate***	***Confidence Interval***		***R^2***	***Semi-partial coefficient²***
			2.50%	**97.5%**		
CS: THg ~ $\delta^{13}C$ + **$\delta^{15}N$**	$\delta^{15}N$	0.13	0.07	0.18	0.65	0.52
EG: ΣPCBs~ $\delta^{13}C$ + **$\delta^{15}N$** + **FA $\delta^{13}C_{Corrected}$** + age/sex	$\delta^{15}N$	0.05	0.02	0.07	0.62	0.28
	FA $\delta^{13}C_{Corrected}$	0.15	0.09	0.21		0.13
EG: PCB-153~ $\delta^{13}C$ + **$\delta^{15}N$** + **FA $\delta^{13}C_{Corrected}$** + age/sex	$\delta^{15}N$	0.07	0.05	0.08	0.71	0.29
	FA $\delta^{13}C_{Corrected}$	0.13	0.09	0.17		0.18
EG: ΣDDTs~ $\delta^{13}C$ + **$\delta^{15}N$** + **FA $\delta^{13}C_{Corrected}$** + age/sex	$\delta^{15}N$	-0.06	-0.11	-0.02	0.54	0.15
	FA $\delta^{13}C_{Corrected}$	0.17	0.07	0.26		0.15
EG: ΣCHLs~ $\delta^{13}C$ + $\delta^{15}N$ + **FA $\delta^{13}C_{Corrected}$** + age/sex	FA $\delta^{13}C_{Corrected}$	0.12	0.05	0.19	0.47	0.26

CHAPTER 7: COMPREHENSIVE SCHOLARLY DISCUSSION

7.1. NEW APPROACHES TO ASSESS CONTAMINANTS IN NORTHERN MARINE MAMMALS

7.1.1. Using QuEChERS to extract legacy POPs from marine mammal blubber

The QuEChERS extraction, as developed in Chapter 3, was used to a successfully extract a wide variety of lipophilic contaminants in marine mammal blubber including an extensive suite of legacy POPs (e.g, PCBs, and OC pesticides like DDTS, CHLs, HCHs, ClBzs) and nontarget/suspect screened contaminants, mostly PRCs (see in Chapter 4). Although most legacy POPs showed acceptable accuracy and precision through the developed method (Table 3.1), this approach has some limitations. For example, recoveries of some highly chlorinated PCBs, including nona- and deca-chlorinated congers (e.g., PCB-206 and 209) were less than 50%. As these congeners are generally more hydrophobic than lower chlorinated congers and with logK_{ow} > 7.9 (Ballschmiter et al., 2005), a significant fraction likely remained in the lipid pellet following the initial liquid-liquid extraction. In comparison, phthalate recoveries from internal standard-matrix spikes in Chapter 4 varied based on individual compound. Phthalates generally show increasing hydrophobicity with increasing chain length (Ellington, 1999), and, therefore, our results showed higher recoveries for longer-chain phthalates. For example, shorter-chained dimethyl and diethyl phthalate (logK_{ow} = 1.61 and 2.38, respectively), showed low recoveries at 25.4 ± 10.2% and 49.5 ± 11.2%, while recoveries for dicyclohexyl phthalate (logK_{ow} = ~6.3) were significantly higher at 81.3 ± 10.2% (Table S4.5; Ballschmiter et al., 2005). However, diisobutyl phthalate (logK_{ow} = ~4.6) showed similarly high recoveries at 79.1 ± 11.2%, suggesting that the QuEChERS method may be sufficient in extracting chemicals with logK_{ow} > 4.5. As bioaccumulative organic contaminants are typically defined as those with a logK_{ow} > 5

(Geyer et al., 2000), the QuEChERS extraction should ideally extract most of analytes of interest in fatty matrices, although recovery-correction may be necessary for very hydrophobic (e.g., $\log K_{ow} > 7.5$) or more hydrophilic chemicals (e.g., $\log K_{ow} < 4$).

Future research groups, especially those without preexisting instrumentation required by current-use methods, should seek to implement this QuEChERS-based approach for the routine analysis of legacy POPs and CEACs. Although current-use methods show acceptable and reproducible results, QuEChERS offer a lower cost, faster, and effective alternative method for the analysis of legacy POPs in marine mammal blubber and adipose tissues. For instance, ongoing legacy and emerging contaminant monitoring through NCP and AMAP can employ a QuEChERS-based approach for blubber and adipose samples going forward in other marine mammal species with lesser-known POP concentrations across the Arctic (e.g., blue whale [*Balaenoptera musculus*], fin whales [*Balaenoptera physalus*], and bowhead whales [*Balaen mysticetus*]) and in other locations. In addition, NCP contaminating monitoring in marine mammal blubber occurs biennially (i.e., every other year) using current-use approaches, and QuEChERS, as an alternative, lower cost, more accessible method, could be implemented instead to provide annual data, also providing greater statistical power to assess temporal trends. However, prior the routine usage of QuEChERS across a wide variety of tissues and biological tissues for routine analyses, further investigation in diverse marine mammal tissues across different Arctic regions is also warranted.

Similar QuEChERS approaches could be applied to other upper-trophic level species with high fat content tissues, including piscivorous fish and sea birds in the Arctic; and, less clean-up steps are likely required here (e.g., only one EMR-lipid cartridge), as these tissues are far less fatty than marine mammal blubber (e.g., less than 20% lipid content; Venugopal and

Shahidi, 1996). Still, few studies to date have employed a similar QuEChERS approach for contaminant analysis in any Arctic top predator species, although a recent study monitored phthalate concentrations in common bottlenose dolphin (*Tursiops truncatus*) and short-finned pilot whale (*Globicephala macrorhynchus*) blubber using a modified QuEChERS extraction (Sambolino et al., 2024). As such, the implementation of QuEChERS in other marine mammal species is warranted and would allow for a better understanding of the benefits and limitations from adopting this method for more routine contaminant analyses by marine mammal monitoring programs.

Modified QuEChERS methods could similarly be employed to measure POP exposure to human populations in the Arctic. Inuit municipalities in East Greenland, in particular, recently showed sufficiently high concentrations of POPs, PFAS, and MeHg, which were associated with high marine mammal consumption of killer whale and polar bear; Long et al., 2023). Due to ethical considerations, blood, instead of lipid, is primarily sampled in humans instead, and a multitude of previous studies have detailed potentially less costly and more accessible QuEChERS approaches to measure legacy POPs in blood (e.g., Lee et al., 2020; Rial-Berriel et al., 2020; Manz et al., 2022). Although legacy POP concentrations have shown declining trends over 30 years of biomonitoring in humans, CEACs and unregulated PFAS are instead showing increases in some Inuit populations (Palaniswamy et al., 2024). As such, QuEChERS approaches should allow for faster, less costly, and more accessible contaminant analysis and to continue the biomonitoring in Inuit populations in the Arctic, who have previously shown some of the highest concentrations reported in humans globally (Long et al., 2023).

7.1.1. Nontarget and suspect screening to monitor emerging contaminant concentrations

A nontarget/suspect screening workflow was developed for the analysis of "unknown" contaminants in marine mammal blubber and adipose tissues, as described in Chapter 4, and the potential presence of at least 138 unique, never-before-screened compounds in killer whale, pilot whale, and narwhal was identified. However, as mass-labelled standards were unavailable for the majority of these compounds, the presence of only 5 compounds was confirmed. As such, further investigation into these remaining 133 compounds is warranted.

Although some biogenic compounds (e.g., fatty acids) are present on the list, the majority consists of CEACs. For example, the suspect screening workflow showed a >80% match to the library database for the UV stabilizers, UV-320 and UV-329 (Table S4.6). UV stabilizers are commonly added to plastic polymers to prevent photodegradation, yet some compounds, particularly UV-328 (not identified in our samples), show POP-like properties and a potential for long-range transport (Khare et al., 2023). UV-328 is now regulated under Annex A (Elimination) of the Stockholm Convention (**Table 2.2**), while UV-320 was recently added to the European REACH list of substances of very high concern due to its PBT properties, and UV-329 is currently under investigation for regulation (ECHA, 2023). UV stabilizers, including UV-329, were also recently detected in seabirds and ringed seal liver in the Canadian Arctic (Lu et al., 2019). Additionally, triclosan, an HPV and commercially used chlorinated antimicrobial chemical (Weatherly and Gosse, 2017), was detected in blubber samples in the present study with a mean 99.7% matching score. Triclosan exposures have been associated with reproductive and developmental defects, carcinogenicity, and an endocrine disrupting potential (Weatherly and Gosse, 2017), and triclosan was also recently detected in Arctic marine zooplankton

(Sørensen et al., 2023). As such, chemical standards should be used to confirm the presence of these toxic compounds.

Overall, the vast number of other chemicals on this list represent a potential for widespread exposure to "unknown" and toxic chemicals in Arctic marine mammals. More than 100 other chemicals of emerging concern are still potentially present and at unknown concentrations, including other phthalates (e.g., Diethyl terephthalate), synthetic dyes (e.g., Sudan III and Malachite Green), surfactants (e.g., Surfonyl 104), parabens (Butyl 4-hydroxybenzoate), and other antioxidants and their metabolites (e.g., Ethanox 702, PEP 36, Irganox 1010 and 1076 metabolites). In addition, recent evidence has suggested that the majority of PRCs (> 75%; Wagner et al., 2024) lack basic toxicity information, including for some of the many tentatively identified chemicals from Chapter 4. However, toxicity of some confirmed compounds, like Irganox 1010 and dioctyl sebacate, is likely relatively low; yet, further investigation is required to detail concentrations in marine mammals and if they exceed suggested nontoxic thresholds (Wagner et al., 2024). As such, this work largely indicates that the magnitude of CEAC accumulation in marine mammals is poorly understood, and further nontarget/suspect approaches are required to better characterize the extent of this "unknown" chemical exposure.

Modifications to the nontarget/suspect workflow and chemical extraction can be made in future research to screen for other compounds of potential interest. For example, the QuEChERS method, developed for the analysis of strictly hydrophobic chemicals, can be modified for analysis of more polar compounds in other tissues. Similar QuEChERS methods have been previously developed for pesticide analysis in liver and muscle of livestock (i.e., cow, chicken pigs) and piscivorous fish, using PSA cartridges, $MgSO_4$, and acetonitrile as the extraction

solvent (Hamamoto et al., 2017; Baesu et al., 2021). Therefore, these approaches could be adapted for use in marine mammal liver and muscle for the suspect screening of less hydrophobic chemicals including PFAS, some phthalates, PPCPs, bisphenols, and some HNPs. Furthermore, QuEChERS methods could be modified to extract and monitor concentration of lipophilic PCB and DDT metabolites, like OH- and $MeSO_2$-PCBs and DDTs (although targeted with GC- electron capture negative ion (ECNI) is often used to instead monitor these metabolites instead, e.g., Letcher et al., 2008).

Further suspect screening studies should also use different library database than those employed in the present study. Although the *Extractable & Leachables* PCDL contains >1,000 PRCs and was modified to include >100 additional CEACs, other chemicals not included in the library are still likely present in these samples. For example, BFRs in killer whale blubber from Norway (e.g, pentabromotoluene and hexabromobenzene; Andvik et al., 2021), chlorinated paraffins in gray and harbor seal blubber from the Baltic Sea (de Witt et al., 2020), emerging PFAS in polar bear liver from East Greenland (e.g., chlorinated polyfluoroalkyl ether sulfonic acid [F-53B]; Gebbink et al., 2016), and PCNs in polar bear liver from Hudson Bay, Canada (Letcher et al., 2018) were all recently detected, yet none of these compounds were present in our library database. Still, this study represents the first nontarget study on narwhal, long-finned pilot whale, and killer whale, and further applications can be used to screen for additional "unknown" chemicals in other marine mammal species, across different regions, and in other tissues, using different library databases.

7.2. NEW APPROACHES TO ASSESS CONTAMINANT ACCUMULATION VIA DIET IN NORTHERN MARINE PREDATORS

7.2.1. Using fatty acid signatures to assess contaminant variation among top marine mammals

Although FAs have been widely used to provide insight into diets of marine mammals in the Arctic (Thiemann et al., 2009), they have rarely been used to assess the accumulation of contaminants from diet. Bulk SI alone were used to assess trophic transfer of PCBs and DDTs through a marine food web to ringed seal and polar bear in the North Water Polynya (Hobson et al., 2002). Bulk $\delta^{15}N$ and $\delta^{13}C$ were also used to assess intraspecific variation of PCBs in southern resident killer whale (Krahn et al., 2007). Similarly, bulk SI were used to determine diet type and differences in PCBs among Icelandic killer whales (Remili et al., 2021). However, more recently, studies have increasingly included FAs in dietary assessments to complement (or even substitute) bulk SI to assess contaminant variation in marine mammals. For example, QFASA-based diet estimates largely explained POP variation among killer whale samples throughout the North Atlantic (Remili et al., 2023a). Similarly, FAs were used to complement bulk SI, and both were included in linear models to assess differences in legacy POPs and PFAS between sub-Arctic and Arctic ringed seal (Facciola et al., 2022).

FAs have also not yet, to my knowledge, been used to assess interspecific differences in nontarget screened contaminants, including CEACs. Nontarget screened contaminant data from chapter 4 was not added into Chapter 5 models, as concentration data was missing for most compounds (and for those with concentration data, only a few individuals showed concentrations above detection limits). Furthermore, some contaminants, like organophosphate flame retardants and pesticides (like chlorpyrifos) and their metabolites, may show differences in concentrations among the same studied species as Chapter 5 due to functional loss of genes like PON1 in cetaceans (responsible for detoxifying organophosphate metabolites; Meyer et al., 2019). As such, future studies should also seek to use similar approaches as Chapter 5 to test how dietary

patterns from FAs influence interspecific differences in CEAC concentrations, relative to the influence of biological differences in xenobiotic biotransformation capacities.

Still, FA signatures may provide higher resolution insights than bulk SI into the accumulation of contaminants and variation among mobile predator species. As bulk SI data (from Chapter 6) was not discussed throughout Chapter 5, direct comparisons between these two diet tracing methods are further discussed here. For PCB-153, FA-PC1 and FA-PC2 explained a combined 38% of the variation in concentrations among the studied marine mammal species (**Figure 5.3**), while bulk $\delta^{15}N$ explained less than 18% (**Figure 6.3**). All other contaminants showed similar trends, with FA PC axes combined explaining 60% of the variation for DDTs and 27% for CHLs, while $\delta^{15}N$ explained 15% and 5%, respectively. As pilot whale and killer whale represent migratory species that are likely only present in the Arctic seasonally, part of the reason that FA better explain contaminant variation is that baseline differences in bulk SI values based on geographic location are likely obscuring detection of dietary pattern based on $\delta^{15}N$. However, an additional reason why FA proportions explain more variation is likely simply that they are more variables (i.e., > 10 individual dietary FAs used) to capture interspecific differences in contaminant concentrations, as a single variable (i.e., bulk 8IN) in a model is likely insufficient to describe complex food web dynamics alone (as also seen in AA CSIA; Elliot et al., 2021). If the $\delta^{15}N$ and $\delta^{13}C$ were baseline-corrected, they may explain a significantly higher amount of the variation in models; however, baseline corrections using lower trophic position organisms is likely still not possible for these highly mobile mammals, especially as the habitat range of these individuals is largely unknown (and sampling across most of the North Atlantic is not feasible). As such, alternative approaches that do not require baseline corrections,

such as FA signatures or even FA or AA CSIA, may be more suitable approaches to assess dietary patterns in highly mobile marine predators.

7.2.2. Using fatty acid carbon isotopes to trace contaminant accumulation among predators and through food webs

Similar to FA proportions, FA carbon isotopes may provide new, potentially higher resolution insights than bulk SI into the trophic transfer of POPs and Hg in marine food webs. As discussed in Chapter 6, although bulk $\delta^{15}N$ explained most of the variation for THg in the CS food web, "source"-corrected FA $\delta^{13}C$ values instead explained more variation in POPs among EG marine mammals. Bulk SI likely explained far less variation in EG due to wide differences in baseline $\delta^{13}C$ and $\delta^{15}N$ values between native Artic species and migratory sub-Arctic species.

As bulk SI currently lack standardization in methods to determine baseline, it has been suggested that CSIA of FA or AA may serve as suitable alternatives in baseline-corrected trophic assessments (Twining et al., 2020; Kjeldgaard et al., 2021). Our approach to assess trophic structure using FA $\delta^{13}C$ is largely based on approaches used for AA, where controlled-feeding experiments from phytoplankton to zooplankton and fish originally were used to provide baseline-corrected trophic position estimates using "trophic" and "source" AAs (e.g, glutamic acid [glu] and phenylamine [phe], respectively; Chikaraishi et al., 2009). This approach was further investigated for its use in upper-trophic level consumers, including beluga whale and bowhead whale (Matthews et al., 2020; Matthews et al., 2024), and applied to assess the magnification of POPs and Hg to seabirds (Elliot et al., 2021). Although this AA approach requires further controlled diet studies prior to its widespread application in cetaceans and other marine predators (Matthews et al., 2020), it holds promise as an additional tool to assess trophic

structure and biomagnification of contaminants to top marine consumers. In comparison, although a multitude of controlled-feeding experiments have similarly identified some potentially trophic-associated FAs (e.g., 18:3n3 and 22:6n3) and some FAs that vary minimally or predictably with trophic position (Bec et al., 2011; Budge et al., 2011; Fujibayashi et al., 2016), our study is the first to date to monitor FA $\delta^{13}C$ values in high trophic level consumers and through a marine food web.

Similar to AA, controlled-feeding studies in higher-level consumers are required to gain insight into the utility of FA $\delta^{13}C$ to assess the bioaccumulation and trophic transfer of contaminants. For example, captive feeding trials in harbor seal were previously conducted to investigate QFASA applications in blubber (Nordstrom et al., 2008) and bulk SI discrimination factors in blood (Zhao et al., 2006). Samples of archived blubber from deceased, captive killer whale housed at SeaWorld were also used to assess FA stratification (Bourque et al., 2018) and the application of QFASA in killer whale blubber (Remili et al., 2022). Although controlled-feeding experiments in marine mammals are costly and difficult to perform, FA $\delta^{13}C$ values acquired using nonlethal sampling techniques including biopsies and blood sampling in marine predator consumers and their prey items would provide valuable insights into the trophic fractionation of FA $\delta^{13}C$. These controlled feeding experiments could provide crucial evidence regarding FA-specific fractionation and confirm whether some FAs from prey are directly deposited without modification into blubber (like potentially 20:1 and 22:1 isomers) and if some are enriched and used for energy when in dietary excess (like 22:6n3). Additionally, if species are fasted during these feeding trials (i.e., FAs like 22:6n3 no longer in excess), dietary FAs may show no differences in values between predator and prey (see Budge et al., 2012). Although multiple controlled-feeding experiments in lower trophic level consumers have been

investigated, FA *de novo* synthesis and chain elongation/desaturation reactions are limited at upper trophic level consumers, likely making these results not directly comparable to marine mammals. Overall, as multiple factors including periods of fasting, unknown diet items, and tissue- and species-specific trophic fractionation likely impact our findings from Chapter 6, further characterization of FA $\delta^{13}C$ in controlled-feeding experiments is still crucial to enhance our understanding of their applicability in assessing trophic roles and contaminant dynamics.

7.3. FURTHER APPLICATIONS

This thesis provides useful methodological advancements for the screening of organic contaminants in marine mammals that should be employed by routine contaminant monitoring programs. For instance, AMAP-funded work has detailed concentrations of legacy POPs in East Greenland polar bear for several decades (1983-2013; Dietz et al., 2013), and, in Chapter 5, we provide further contaminant data in this same population from more recent years using our developed QuEChERS-based approach. As samples extracted using current-use methods show very similar values to those extracted using QuEChERS (**Figure 3.2**), further core monitoring efforts by NCP and AMAP in marine mammals should adopt our newly developed methodology to reduce costs. Furthermore, any cost savings could be directly allocated towards other projects, including the nontarget/suspect screening of CEACs, following AMAPs call for the development of more nontarget approaches (AMAP, 2020). For an interlaboratory comparison, SRM NIST 1945 or 1946 can also be extracted along samples to demonstrate reproducibility of the procedure among labs. Furthermore, mass-labelled standards should be purchased for all confirmed compounds from Chapter 4 to better assess actual concentrations and whether they exceed expected toxicity thresholds, if available. Further implementation of these newly

developed approaches is also warranted across marine mammals where recent POP and emerging contaminant concentrations are less studied, including pilot whale and narwhal sampled elsewhere in the Arctic.

Further application of FAs and their stable carbon isotopes should also be used by routine monitoring programs to assess the accumulation of contaminants from diet. For instance, FA signatures should be routinely collected to investigate contaminant trends in diverse marine mammal populations across the Arctic, without the need for baseline corrections. However, further investigation into the utility of FA carbon isotopes to assess contaminant accumulation is required prior to its routine usage.

The application of these methods is also crucial to assess climate change-driven alterations in POP and CEAC exposure in Arctic marine mammals. Climate change, in general, impacts multiple physical, biological, and ecological processes that influence accumulation in food webs (Borgå et al., 2022). For example, increases in temperature can increase mobilization and long-range transport of contaminants from primary sources and remobilization from secondary sources (e.g., permafrost; Borgå et al., 2022). The Arctic is also estimated to be warming two to three times faster than the rest of the world, largely impacting sea ice extent, age and thickness, lengths of ice seasons, glacial presence, snow cover, and permafrost (AMAP, 2020). As many Arctic species, like polar bear, are reliant on sea ice for access to food, earlier sea break-up and longer ice-free seasons have been associated with changes in contaminant exposure. For instance, in the southern Beaufort Sea, polar bear are spending extended periods of time and feeding onshore (e.g., on bowhead whale remains and even sea birds and their eggs), corresponding with lower POP concentrations (McKinney et al., 2017). However, reductions in sea ice extent also reduce polar bear access to high-quality prey and may cause greater energy

expenditure as they move longer distances to find prey (Borgå et al., 2022). Longer periods of fasting and increased energy expenditure are also associated with decreases in body condition, lower fat reserves, and mobilization of contaminants from fat to the blood (Obbard et al., 2016).

Climate change is also shifting the global redistribution of species towards cooler regions, including the Arctic, that is impacting species interactions and contaminant exposures. For instance, our studied killer whale (across all four results chapters) are presumed to be mostly consuming fish in the North Atlantic; however, as they follow prey towards the Arctic in areas such as East Greenland, killer whale have access to higher trophic level (and far more contaminated) prey like harp, hooded, and ringed seal (Pedro et al., 2017; Borgå et al., 2022). In fact, killer whale in East Greenland were previously estimated to show order of magnitude higher concentrations than fish-feeding killer whale in the Faroe Islands (Pedro et al., 2017). Increased polar bear consumption of subarctic seal and decreases in endemic ringed seal in East Greenland was also previously reported (McKinney et al., 2009; McKinney et al., 2013), which may be associated with increases in POPs. Climate change-driven impacts on contaminant exposure are currently well documented across numerous international assessments (e.g., AMAP, 2020), and it is imperative that researchers have suitable and accessible approaches, such as QuEChERS coupled with nontarget screening, to monitor temporal trends of POPs and CEACs on an annual basis.

By using QuEChERS to monitor annual POP concentrations and FA signatures to assess POP accumulation in the same marine mammal blubber/adipose tissues, these new techniques may also reduce the unexplained interannual variation from core monitoring programs and increase the statistical power to detect temporal changes in contaminant concentrations and monitor the impacts of climate change. For instance, temporal trends in POP concentrations from

AMAP reported that long-term time series in POP data was only able to detect annual changes in concentrations in 12% of the entire dataset (Riget et al., 2019). As the number of years is proportional to the statistical power of the time series, the remaining 88% was reported to require additional years of data collection to fulfill statistical requirements (Riget et al., 2019). As such, the routine application of alternative, more accessible methods like QuEChERS on an annual basis could increase the statistical power of future temporal data series to detect interannual changes in POP concentrations. Similarly, QuEChERS and FA approaches could be implemented on archived samples not yet reported in Riget et al. (2019), if available. Although other studies on temporal trends have shown general decreases in most POPs across the Arctic, widespread, current-day unintentional production of some POPs like PCBs, HCB, and HCBD by signatory nations of the Stockholm Convention threatens further long-range transport to the Arctic and accumulation in food webs (Wania and McLachlan, 2024). Especially as climate change-driven ecological process are currently (and will continue to) largely influence POP and CEAC exposures in marine mammals and in Arctic marine food webs (Borgå et al., 2022), it is essential that studies possess adequate statistical power to determine long term changes in contaminant patterns, and the routine implementation of these newly developed approaches can help ensure this.

CHAPTER 8: CONCLUSIONS

This doctoral thesis develops and implements multiple new methodologies to: 1) improve the screening of environmental contaminants in marine mammals and 2) provide new insights into contaminant accumulation using new dietary tracers in multiple northern marine predator species. Chapter 3 discusses the development of a new QuEChERS approach to monitor legacy POPs in marine mammal blubber. This method helps overcome several of the challenges of current-use methods, enabling contaminants analysis to be conducted with lower costs, in shorter time frames, and using less toxic solvents, and thus supporting the principle of green analytical chemistry. Chapter 4 further improves contaminant monitoring efforts in marine mammals through the development of a nontarget/suspect screening approach to identify "unknown" and never-before-screened contaminants of potential concern. Multiple PRCs were detected, and further work is required to detail concentrations and confirm if they exceed expected nontoxic thresholds. Lastly, Chapter 5 and 6 implement new dietary tracers using FAs and their stable carbon isotopes to assess contaminant accumulation in top marine predators. Compared to bulk SI, FA proportions and their $\delta^{13}C$ values likely provide higher resolution insights into the trophic transfer of contaminants without the need for baseline corrections in highly mobile marine predators. However, controlled-feeding experiments in higher-trophic level consumers in warranted to further assess the applicability of FA $\delta^{13}C$ in assessing trophic structure and contaminant dynamics. This work has now provided future researchers with new tools to 1) better characterize the magnitude of legacy and emerging contaminant exposures and 2) enhance our understanding of the accumulation of contaminants from diet in some of the most threatened marine mammal populations globally.

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