

Movement ecology, diet, and contaminants: Establishing benchmarks for monitoring Arctic seabirds and their habitats in the face of environmental change

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LIST OF ABBREVIATIONS

AMAP	Arctic Monitoring and Assessment Programme
ANOVA	Analysis of Variance
CWS	Canadian Wildlife Service
DDE	Dichlorodiphenyldichloroethylene
DDT	Dichlorodiphenyltrichloroethane
ECCC	Environment and Climate Change Canada
ECSAS	Eastern Canada Seabirds at Sea
GLS	Geolocation sensor
GPS	Global Positioning System
HFR	Halogenated flame retardant
NSERC	Natural Sciences and Engineering Research Council
OC	Organochlorine
OPE	Organophosphate ester
OSPAR	Convention for the Protection of the Marine Environment of the North-East Atlantic
PBDE	Polybrominated diphenyl ether
PCB	Polychlorinated biphenyl
PCDD	Polychlorinated dibenzo-p-dioxin
PCDF	Polychlorinated dibenzofuran
PCN	Polychlorinated naphthalene
PDBE	Substituted diphenylamine antioxidant

PFAS	Per- and polyfluoroalkyl substance
POP	Persistent organic pollutant
PTT	Platform Transmitter Terminal
SD	Standard deviation
SDPA	Substituted diphenylamine antioxidant
SSM	State-space model
SST	Sea surface temperature
UHF	Ultra high frequency
UV	Ultraviolet

ABSTRACT

Birds have long been used as ecological indicators of environmental change. Seabirds, with their high trophic position, accessibility at central breeding locations, and ability to integrate signals across space and time, are particularly useful for monitoring changes in marine environments, especially in remote regions where in-depth ecological research can be logistically challenging. Indeed, long-term monitoring of seabirds has provided important insights on many pressing environmental threats, such as changes in ocean productivity, prey species distribution, and trends in pollution. However, knowledge on the ecology, movement, and threats to many seabird species remains limited, particularly in remote regions such as the Arctic. In this thesis, I examine how seabirds can be used as indicators of environmental change in the Arctic using multiple approaches, filling key knowledge gaps on the ecology of multiple Arctic-breeding seabirds. First, I examined the migratory movements of an Arctic-breeding generalist, the herring gull (*Larus smithsonianus*), and found that these birds exhibit high inter- and intra-individual variation in migration routes from the Canadian Arctic, but largely overwinter in the same area. This suggests that this population of herring gulls may be more susceptible to climate change impacts in their overwintering locations than during migration. Second, I expanded upon this work by examining individual repeatability in migration and overwintering strategies of another Arctic-breeding generalist species, the glaucous gull (*Larus hyperboreus*). Here, I found the first evidence of diverging migration in this species and show that wintering areas may shift due to changes in sea ice concentrations. These results indicate that this population may be flexible, at least in the short-term, to changes in climate throughout migration. Third, I used stomach content and stable isotope analyses to assess the diet of another Arctic-breeding gull, the black-legged

kittiwake (*Rissa tridactyla*). Here, I found that kittiwakes in the Canadian Arctic rely heavily on Arctic cod (*Boreogadus saida*), but that stomach content analyses may underestimate the number of soft-tissue organisms in the diet, such as invertebrates, which has implications for understanding how this species will be impacted by changes in food web structure. Next, I used a combination of new data and a review of historical work to assess plastic pollution ingestion in four Arctic-breeding seabird species. Here, I showed that plastic ingestion differs across species, regions, and time, but surface-feeding species consistently ingest more plastic than pursuit-diving species, emphasizing the importance of the northern fulmar (*Fulmarus glacialis*) as a monitoring tool for plastic ingestion in Canada and the Arctic. Finally, I reviewed how avian movements play a role in the source, transport, and fate of contaminants, and found that many studies did not consider tissue and contaminant turnover rates, tracking device resolution, and/or statistical power. Using this information, I provided key recommendations for future research in this field. Collectively, this research contributes to the understanding of the ecology of Arctic-breeding seabirds and can act as a benchmark for monitoring change in these species and the ecosystems they inhabit, in turn informing conservation, management, and policy in a rapidly changing climate.

RÉSUMÉ

Les oiseaux sont depuis longtemps utilisés comme indicateurs écologiques des changements environnementaux. Les oiseaux marins, grâce à leur haut niveau trophique, l'accessibilité de leur site de reproductions et leur capacité à intégrer des signaux dans l'espace et le temps, sont particulièrement utiles pour surveiller les changements dans les environnements marins, notamment dans les régions éloignées. En effet, la surveillance à long terme des oiseaux marins a fourni des informations importantes sur de nombreuses menaces environnementales pressantes, telles que les changements de productivité des océans, la distribution des espèces de proies, et les tendances en matière de pollution. Cependant, les connaissances sur l'écologie, les mouvements et les menaces qui pèsent sur de nombreuses espèces d'oiseaux marins restent limitées, en particulier dans les régions éloignées telles que l'Arctique. Dans cette thèse, j'examine comment les oiseaux marins peuvent être utilisés comme indicateurs de changements environnementaux dans l'Arctique en utilisant une approche multiple. Premièrement, j'ai examiné les mouvements migratoires d'un oiseau généraliste se reproduisant dans l'Arctique, le goéland argenté (*Larus smithsoniansus*). Ces oiseaux de l'Arctique canadien possèdent une grande variation inter- et intra-individuelle dans ces routes migratoires, mais hivernent en majorité dans la même zone. Cela suggère que cette population de goélands argentés pourrait être plus sensible aux impacts des changements climatiques dans leurs lieux d'hivernage que pendant la migration. Deuxièmement, j'ai examiné la répétabilité individuelle des stratégies migratoires et d'hivernage d'une autre espèce généraliste, le goéland bourgmestre (*Larus hyperboreus*). J'ai illustré pour la première fois une migration divergente chez cette espèce et que les zones d'hivernage peuvent varier à cause des changements dans les conditions de la banquise. Cela indique aussi que cette

population peut être flexible, au moins à court terme, aux changements climatiques tout au long de la migration. Troisièmement, j'ai utilisé le contenu de l'estomac et des analyses d'isotopes stables pour évaluer le régime alimentaire de la mouette tridactyle (*Rissa tridactyla*). J'ai constaté que les mouettes tridactyles de l'Arctique canadien se nourrissent essentiellement de morue Arctique (*Boreogadus saida*), mais que les analyses du contenu de l'estomac peuvent sous-estimer le nombre d'organismes à tissus mous dans leur régime alimentaire, notamment les invertébrés. Avec un réseau trophique en changement cause par les dérèglements climatiques, ces résultats amènent de nombreuses questions sur le comportement de cette espèce dans le futur. Ensuite, j'ai utilisé une combinaison de nouvelles données couplé aux informations historiques pour évaluer l'ingestion de pollution plastique chez quatre espèces d'oiseaux marins se reproduisant dans l'Arctique. J'ai montré que l'ingestion de plastique diffère selon les espèces, les régions, et le temps, mais que les espèces qui se nourrissent en surface ingèrent systématiquement plus de plastique que les espèces qui plongent. Cela souligne l'importance du fulmar boréal (*Fulmarus glacialis*) en tant qu'outil de surveillance de l'ingestion de plastique au Canada et dans l'Arctique. Finalement, j'ai examiné comment le mouvement des oiseaux joue un rôle dans la source, le transport, et le devenir des contaminants. J'ai constaté que de nombreuses études ne tenaient pas compte des taux de renouvellement des tissus et des contaminants, ainsi que de la résolution des dispositifs de géolocalisation de suivi et/ou de la puissance statistique. Cette thèse contribue à la compréhension de l'écologie des oiseaux marins se reproduisant dans l'Arctique et pourra servir de référence pour le suivi des changements chez ces espèces et dans les écosystèmes qu'elles habitent, afin d'éclairer la conservation, la gestion et la politique dans un climat en changements rapides.

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COVID-19 IMPACT STATEMENT

The COVID-19 pandemic had an impact on the scope and direction of this research. The original intention of this thesis was to assess the occurrence, transport, and fate of plastic pollution and plastic-related chemical contaminants in Arctic seabirds by: 1) quantifying plastics, organophosphate esters (OPEs) and UV-stabilizers in glaucous gulls and black-legged kittiwakes; 2) examining the maternal transfer of OPEs and UV-stabilizers to eggs; 3) linking the year-round movements of glaucous gulls and black-legged kittiwakes to levels of plastics, OPEs and UV-stabilizers; and 4) assessing the impacts of plastics, OPEs, and UV-stabilizers on oxidative stress of glaucous gulls and black-legged kittiwakes. This proposed work involved capturing, tagging, and sampling glaucous gulls from Coats Island (NU), Cambridge Bay (NU), and Prince Leopold Island (NU), and black-legged kittiwakes from the St. Lawrence Estuary (QC), Browne Island (NU), and Prince Leopold Island (NU) in Canada. In 2021, no fieldwork could be conducted at any of these sites as a result of COVID-19 travel restrictions. In 2022, it was still uncertain whether fieldwork should be conducted in the Canadian Arctic with the ongoing pandemic, thus the project was altered to focus on black-legged kittiwakes in the St. Lawrence Estuary, Canada, and Flatey, Iceland. While tracking devices were successfully deployed on black-legged kittiwakes at both of these sites in 2022, various factors inhibited their recapture. In 2023, the colony in the St. Lawrence Estuary (Île Laval) was completely deserted due to the presence of a red fox, while the colony on Flatey, Iceland, had considerably low reproductive success (very few birds on eggs), making recapture at these sites impossible. As a result of these challenges in the first three years of my degree, my supervisors and I decided to make the difficult decision to exclude these chapters from my thesis. Instead, we made use of existing data on Arctic seabirds

that were not previously analyzed or published. Specifically, we obtained data on herring gull and glaucous gull migration from multiple partners (Chapter 2 and 3, respectively), utilized samples collected from Inuit hunters in 2021 (when travel restrictions did not allow for travel to the Canadian Arctic) to examine diet and plastic pollution (Chapter 4 and 5, respectively), and conducted a literature review on spatial ecotoxicology (originally intended to be the literature review for this thesis prior to the change in subject; Chapter 6). Collectively, these chapters examine how gulls can be used as environmental indicators in a rapidly changing Arctic.

CONTRIBUTION OF AUTHORS

Chapter 2 is published in:

Baak J.E., Mallory M.L., Anderson C.M., Auger-Méthé M., Macdonald C.A., Janssen M.H., Gilchrist H.G., Provencher J.F., Gutowsky S.E. (2021). Inter-individual variation in the migratory behaviour of a generalist seabird, the herring gull (*Larus smithsonianus*), from the Canadian Arctic. *Animal Migration* 8(1): 144-155.
<https://doi.org/10.1515/ami-2020-0109>.

I developed the research question and study design under the guidance of Mark Mallory, Jennifer Provencher and Sarah Gutowsky. Fieldwork was conducted by the East Bay Migratory Birds Sanctuary Field Team, led by Christie MacDonald and Michael Janssen. Marie Auger-Méthé processed raw geolocation data. I conducted the spatial analysis with invaluable guidance and mentorship by Sarah Gutowsky. I created the data visualizations and drafted the manuscript. All authors contributed to previous versions of the manuscript and gave their final approval for publication. The Associate Editor of *Animal Migration*, Emily Cornelius Ruhs, and two anonymous reviewers provided insightful reviews of the manuscript. Funding was acquired by Grant Gilchrist and Mark Mallory.

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Chapter 4 is formatted for submission to Arctic Science as:

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I developed the research question and study design under the guidance of Kyle Elliott, Mark Mallory, and Jennifer Provencher. Carcass dissections were completed by myself and a team of graduate students, biologists, and volunteers at a dissection workshop at Acadia University. I dissected, identified, and counted all diet items in the gastrointestinal tract of black-legged kittiwakes. Stable isotope data were provided by Reid Smith, David Yurkowski, and Kevin Hedges. I analyzed the data, created the data visualizations, and drafted the manuscript. All authors contributed to previous versions of the manuscript. Funding was acquired by Jennifer Provencher and David Yurkowski.

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I developed the research question and study design under the guidance of Kyle Elliott, Mark Mallory and Jennifer Provencher. Carcass dissections were completed by myself and a team of graduate students, biologists, and volunteers at a dissection workshop at Acadia University. Kristine Hanifen, Shane Keegan, Mark Maddox and I dissected, identified, counted and measured all plastic pieces in the gastrointestinal tract of black-legged kittiwakes and black guillemots. I conducted the literature review, analyzed the data, created the data visualizations, and drafted the manuscript. All authors contributed to previous versions of the manuscript and gave their final approval for publication. The Editor in Chief of Marine Pollution Bulletin and two anonymous reviewers provided insightful reviews of the manuscript. Funding was acquired by Jennifer Provencher.

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I developed the research idea and study design under the guidance of Kyle Elliott, Mark Mallory, and Jennifer Provencher. I conducted the literature review, analyzed the data, created the data

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CONTRIBUTION TO ORIGINAL KNOWLEDGE

The Arctic is a vast and dynamic environment, which makes Arctic ecosystems and species within these ecosystems unique but logistically challenging to monitor. In this thesis, I analyze new information on seabird movement, diet, and contaminants, providing important benchmark data that can be used to monitor changes in Arctic seabirds and their habitats. Further, I emphasize how these studies can play an important role in our understanding of the threats that wildlife species continue to face in a rapidly changing Arctic.

Many Arctic-breeding seabirds spend only a small portion of their annual cycle in the North, thus the impacts of climate change and anthropogenic activities on Arctic-breeding populations may occur throughout migration. It is thus important to understand their movements to identify threats, inform conservation, and monitor changes in the marine environment. However, the non-breeding movements of many Arctic-breeding seabirds, particularly gulls, are not well understood. For example, while the migration of some gull species, such as herring gulls (*Larus smithsonianus*), has been assessed in the Canadian Arctic using tracking devices, analyses of within-population variation are scarce. Populations that exhibit individual variation in migration routes or wintering areas may be less sensitive to changes in the environment than those that specialize on certain regions or prey, thus knowledge on individual variation is crucial to

understand how these changes may impact populations as whole. In Chapter 2, I examined individual differences in the non-breeding movements of herring gulls in the Canadian Arctic and found that both migratory routes and stopover sites varied between and within individuals, but largely overlapped in their wintering area in the Gulf of Mexico. This suggests that this generalist species can make use of a variety of regions during migration but may be more susceptible to climate change impacts and anthropogenic activities in their wintering area.

Importantly, other gull species, such as glaucous gulls (*Larus hyperboreus*), have no published information on their non-breeding movements in the Arctic using tracking devices. This generalist predator has a diverse diet that includes small mammals, birds, fish, invertebrates, and anthropogenic debris, and as climate change impacts and anthropogenic activities increase, access to these resources may change, emphasizing the importance of understanding this species migration and habitat use. In Chapter 3, I present the migration and habitat use of glaucous gulls in the Arctic using tracking devices for the first time. I found the first evidence of a diverging migration strategy in glaucous gulls in the Arctic, where one migrated to the Sea of Okhotsk in the Pacific and the remainder wintered in the North Atlantic, but wintering range differed between years, likely because of changes in sea ice. As climate change impacts and anthropogenic activities continue to increase in the Arctic and worldwide, both Chapter 2 and 3 act as an important benchmark for monitoring changes in gull migration and how this may impact them in the Canadian Arctic.

Climate change may also alter seabird diet, which may have important implications on seabird health and reproduction. For example, in the European Arctic, diets of black-legged kittiwakes (*Rissa tridactyla*) have shifted from ice-associated Arctic cod to more open-water associated fish species over the past four decades. However, in Canada, knowledge on black-legged kittiwake diet is limited to few studies conducted 30-40 years ago. In Chapter 4, I examined black-legged kittiwake diet in two regions in the Canadian Arctic where diet has not been previously assessed. Using both stomach content and stable isotope analyses, I found that black-legged kittiwakes heavily rely on Arctic cod (*Boreogadus saida*) in the Canadian Arctic, which is similar to what has been reported in Europe for this species. This information can be used as a benchmark to monitor changes in Arctic cod distribution as well as black-legged kittiwake diet in the future. Additionally, I show that while black-legged kittiwakes do heavily consume cod, stomach content analysis may underestimate the amount of soft tissue prey in their diet, such as invertebrates, which emphasizes the importance of using multiple methods to assess diet in these regions, such as stable isotope analyses, faecal samples, and regurgitate samples, to better understand what these seabirds are eating and how this may shift in a changing climate.

Differences in diet and foraging ecology can impact the level of contaminants, such as plastic pollution, in these seabird species. In Canada, plastic pollution has been monitored in northern fulmars (*Fulmarus glacialis*), black-legged kittiwakes, thick-billed murres (*Uria lomvia*) and black guillemots (*Cepphus grylle*) for decades, but detailed analyses of the methodological, spatial, and temporal trends are lacking. In Chapter 5, I present new data and compare to historical work to inform future plastic ingestion monitoring in Canada. I determined that

regardless of the methods used to collect and process samples, northern fulmars continue to have higher levels of plastic ingestion than the other species in the Canadian Arctic, emphasizing their importance as a monitoring tool for plastic pollution in Canada. Moreover, I show a clear north-south gradient in plastic ingestion by this species, where fulmars in more southern regions generally have higher levels of plastic than in more northern regions, but plastic ingestion has increased at some Arctic colonies. This research shows that long-term monitoring programs provide important information on plastic pollution trends in these regions, but also highlights the importance of standardized collection, analysis, and reporting to better understand trends across regions and time.

Finally, collectively examining contaminants in, and the migration of, migratory birds can provide a better understanding of the potential source, transport, and fate of these contaminants. Historically, banding recoveries and stable isotope analyses have been used to assess the potential sources of contaminants to migratory birds, but these estimates are geographically coarse. In Chapter 6, I review for the first time how tracking devices have been increasingly used to assess the relationship between avian movements and contaminants. I found that while studies on the relationship between avian movements and contaminants are expanding, tracking methodology and contaminant analyses varied widely, and sample sizes were often low and/or studies did not statistically test the relationship between contaminant concentrations and tracking information. I identified important knowledge gaps on how movement plays a role in the source and transport of contaminants and provided detailed recommendations for future research on this relationship.

Together, these chapters offer valuable insights on the ecology of Arctic seabirds and the threats these they face in a rapidly changing Arctic. This research demonstrates how seabirds can be used as indicators of change in Arctic marine environments and serves as a benchmark for monitoring future change. As climate change impacts and anthropogenic activities continue to cause rapid, transformational changes in Arctic environments, research such as this can be used to inform the conservation planning and management of these Arctic-breeding seabird populations.

GENERAL INTRODUCTION

Birds have long been used as ecological indicators of environmental change (Leopold and Jones 1947; Cairns 1988; Little and Finger 1990; Canterbury et al. 2000; Piersma and Lindström 2004; Parsons et al. 2008). For example, in the 1930s and 1940s, Aldo Leopold noted that the early arrival of migratory birds denotes an early spring (Leopold and Jones 1947), and birds have been used to find and follow fish populations for centuries (Crawford and Shelton 1978; von Brandt et al. 2024). Using birds as tools to monitor ecosystem change is particularly pragmatic when monitoring the environment itself has more logistical challenges and/or higher financial costs. Seabirds, with their high trophic position, high nest site fidelity, and central-place foraging strategies, have been used as indicators of changes in the marine environment across the globe due to their accessibility at central breeding locations and because they integrate signals across space and time (Mallory et al. 2010b; Carravieri et al. 2013; Crawford et al. 2019; Thorne et al. 2021). In the Arctic, where research can be both financially and logistically challenging (Mallory et al. 2018), seabirds are increasingly used to monitor spatial and temporal changes in ocean productivity (Boersma 1978; Serratos et al. 2020), prey distribution (Crawford and Shelton 1978; Vihtakari et al. 2018; Crawford et al. 2019), pollution (Nettleship and Peakall 1987; Fort et al. 2014; Baak et al. 2020a) and more. For example, the black-legged kittiwake (*Rissa tridactyla*) is a ubiquitous, colonial-breeding gull that can be found across the Arctic and North Atlantic (Hatch et al. 2020), making it an excellent subject for monitoring trends across regions and time (Clairbaux et al. 2024). Contrary to diving birds, surface-feeding black-legged kittiwakes lack the flexibility of adjusting their foraging depth in response to changes in prey, which may make them more sensitive to environmental change. Indeed, four decades of monitoring of black-

legged kittiwake diet in the European Arctic revealed a shift from ice-associated prey to more southern, open-water associated prey, likely as a result of changes in sea ice (Vihtakari et al. 2018), and similar shifts have been reported for this species across three decades in the Pacific (Hatch 2013). This research emphasizes that long-term monitoring of indicator species can provide important insights on ecosystem shifts that may be otherwise challenging to monitor.

Importantly, some of the characteristics that make seabirds useful indicators, such as seasonal, predictable movements, central-place foraging strategies, and the return to a predictable breeding location that simplifies sampling, may also result in uncertainties in the information gained from monitoring them. Without an understanding of their movements, attributing a change in these birds to a change in the environment can be challenging. For example, contaminants, such as plastic pollution, may be acquired throughout migration (Robuck et al. 2022) and remain in the digestive system for months (Ryan 2015), thus it is important to consider where birds forage or migrate (i.e., where they may acquire these contaminants), to adequately understand levels and trends in the environment. However, knowledge on the ecology, movement, and threats to many seabird species remains limited, particularly in remote regions such as the Arctic.

The Arctic is warming much faster than the global average (AMAP 2021a), causing drastic changes in sea ice phenology and extent (Comiso et al. 2008; Cooley et al. 2020), temperature (Cote et al. 2021), weather (Knutson et al. 2010; McCrystall et al. 2021), prey availability (Perry et al. 2005), and pollution (Wit et al. 2022; Baak et al. 2023), which can impact seabird behaviour, reproduction, health, and more (e.g., Gaston et al. 2005; Descamps et al. 2017;

Amélineau et al. 2019). Importantly, Arctic seabirds are also threatened by overfishing, harvest, bycatch, pollution, disturbance, and more (CAFF 2008, 2019; Dias et al. 2019), which may have cumulative impacts on individuals or populations. As sea ice concentrations continue to decline, offering more opportunities for fishing, shipping and tourism activities in the north (Ng et al. 2018), these threats may be further exacerbated. Despite these pressing and growing issues, the impacts of such events on the health and behaviour of many Arctic seabird species are not well understood (Grémillet and Descamps 2023). Gaining a more comprehensive understanding of these shifts, including the impacts they may have on Arctic seabirds and the ecosystems they inhabit, will be crucial to inform conservation, management, and policy in the Arctic and across the globe.

In this thesis, I examine how seabirds, with an emphasis on colonial-breeding gulls, can be used as indicators of environmental change in the Arctic using a variety of approaches. In my first chapter, I review how studies on migration, stable isotopes, diet, and contaminants in seabirds can collectively be used to detect changes in the marine environment. In my second chapter, I examine the migratory movements of an Arctic-breeding generalist, the herring gull, to investigate the inter- and intra-individual variation in migration from the Canadian Arctic. In my third chapter, I expand upon this work by examining the migratory movements of another Arctic-breeding generalist species, the glaucous gull, to explore individual repeatability in migration and overwintering strategies over time. My fourth chapter examines the diet of a third Arctic-breeding gull species, the black-legged kittiwake, to better understand diet composition, how diet may differ between regions, and to obtain a benchmark for monitoring changes in diet as climate

change impacts increase in the Canadian Arctic. My fifth chapter uses a combination of new data and a review of historical work to assess plastic pollution in four Arctic-breeding seabird species to better understand trends across space and time. In my sixth chapter, I review how avian movements play a role in the source, transport, and fate of contaminants. Finally, I discuss how collectively, this research provides us with a better understanding of the ecology of these Arctic-breeding seabirds, with an emphasis on the importance of understanding seabird movements in the context of the health of the ecosystems they inhabit. Collectively, this research can act as a benchmark for monitoring change and can inform the conservation and management of these Arctic-breeding seabirds in a rapidly changing climate.

CHAPTER 1: LITERATURE REVIEW

This literature review will examine the broad question of how seabirds can be used as indicators of environmental change in the Arctic, with an emphasis on how distribution and movement play a role in understanding these shifts. Specifically, I review how studies on migration, stable isotopes, diet, and contaminants in seabirds can help us understand both the potential threats to seabirds themselves, as well as the broader changes in the ecosystems in which they inhabit (Figure 1.1). Finally, I highlight how, collectively, research on these topics can be used to conserve, manage, and create policy in the Arctic and across the globe.

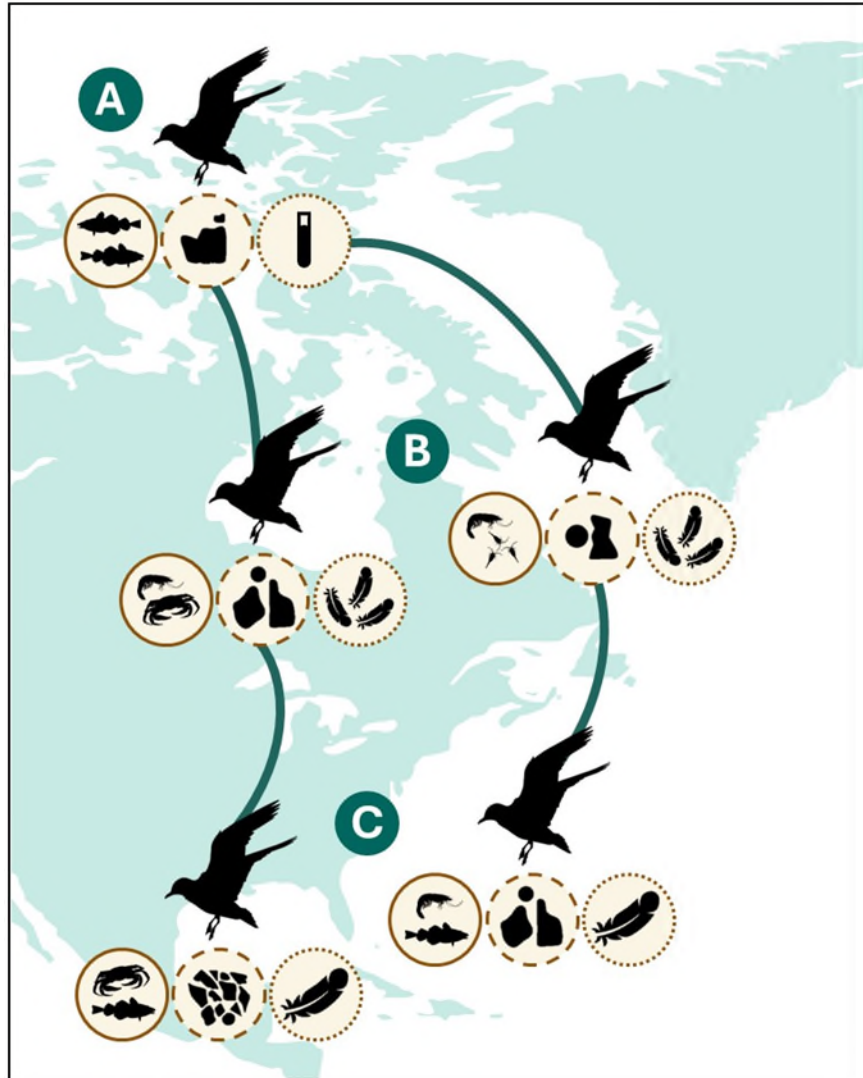


Figure 1.1: Schematic demonstrating the relationship between the different topics investigated in this literature review. Birds migrating from breeding sites (A) to stopover sites (B) and wintering areas (C) may take different routes throughout migration, resulting in differences in diet (circles with solid outline) and exposure to threats, such as contaminants (e.g., plastic pollution; circles with dashed outline). These differences can be studied by combining tracking information with stable isotope analyses of tissues developed at different times throughout the annual cycle (circles with dotted outline), such as blood to represent the breeding period (A), breast feathers to represent autumn (B) and secondary feathers to represent winter to spring (C). Note: tissue turnover rates may differ depending on the species and its moulting patterns, and feathers may not be useful for all contaminant types.

Migration

Each year, animals across the globe migrate following seasonal changes in their environments, such as changes in daylight (Bradshaw and Holzapfel 2007), temperature (Cattaneo and Peri 2016; Moore and Wesselbaum 2023), prey resources (Boyle et al. 2007), predation (Sabal et al. 2021), and competition (Cox 1968). The concept of bird migration began as early as the 4th century, where Greek philosopher Aristotle noted that certain bird species seemed to disappear and reappear with the changing seasons (Aristotle 350AD). These seasonal and predictable movements from one location to another likely evolved as a gradual extension of small annual movements to search for food as either climate, prey resources, predators, or parasites/disease changed throughout the year, such as glacial retreat and sea ice melt in the Arctic (Boyle et al. 2007; Salewski and Bruderer 2007; McKinnon et al. 2010; Møller and Szép 2011). Today, birds face a combination of natural, anthropogenic, and climate change-induced shifts in their environments that may alter the timing or availability of prey resources, and therefore must either adapt or face potential negative implications on health or reproduction, unless they have the inherent plasticity to accommodate these changes (Carey 2009; Whelan et al. 2022).

Birds have an inherent plasticity that allows them to respond dynamically to changes in their environment (Åkesson and Helm 2020). This is particularly evident in seabirds, which are intricately linked to the dynamic marine environment throughout their annual cycle (Grémillet and Boulinier 2009). Indeed, many seabird species exhibit remarkable plasticity in their nesting strategies, foraging strategies, and migratory movements as a result of seasonal changes in prey availability (Gulka and Davoren 2019), fluctuations in sea ice (Gutowsky et al. 2022), changes in

oceanic conditions (Patterson et al. 2022), and more. In the Arctic, seabirds face a unique set of challenges shaped by these dynamic environments. For example, many gull species exhibit a high degree of behavioral plasticity, adjusting their foraging strategies and migratory movements in response to change (Spencer et al. 2014; Descamps et al. 2017). The movements of Arctic seabirds can be used as valuable indicators of environmental variability and ecosystem health, where differences in movement ecology can provide insights on different parts of the environment (reviewed in Fiedler 2009). However, the movements of many Arctic-breeding seabirds, particularly gulls, are not well understood (Spencer et al. 2014; Gutowsky et al. 2020, 2021; Baak et al. 2021d).

Many Arctic-breeding gull species exhibit inter- or intra-individual variation in their migration strategies, where the area(s) of high importance to the population (i.e., where the population would be most at risk if an environmental change occurs), differs depending on the migratory strategies employed (Figure 1.2). For example, Thayer's gulls (*Larus glaucoides thayeri*) from the Canadian Arctic migrate across similar, overland routes, but exhibit high variability in overwintering areas and habitat use (Gutowsky et al. 2020). Contrastingly, herring gulls (*Larus smithsonianus*) and ivory gulls (*Pagophila eburnea*) from the Canadian Arctic exhibit high individual variation in migration routes, but generally overwinter in the same areas (Spencer et al. 2014, 2016; Baak et al. 2021c), suggesting that these populations may be more susceptible to environmental changes in their wintering areas than changes on their migration routes. Gulls can also exhibit diverging migration strategies, where birds from the same population migrate in different directions, overwintering in different areas (Baak et al. 2021d), or low variability in

migration, where birds migrate following relatively similar routes and overwinter in similar areas. For example, Sabine's gulls (*Xema sabini*) from a population in the Canadian Arctic showed high flexibility in migration routes between years, but birds generally made similar migratory decisions in the same years, and relied on the same staging and overwintering sites (Gutowsky et al. 2021). This suggests that, in a given year, this population may be more impacted following an environmental change in their stopover sites or overwintering areas than birds from a population that exhibits more variation in their migratory strategies (Figure 1.2). Thus, as the impacts of climate change and its associated threats may vary based on the ecology and life history of the species (Jenni and Kéry 2003), it is important to understand the migratory movements and connectivity of a species in a given region to monitor changes in these populations and inform conservation planning for habitat protection.

Scientific bird banding began in 1899 with the deployment of metal rings around European starlings (*Sturnus vulgaris*, Preuss 2001), allowing scientists to follow bird migrations at stopover or overwintering sites (von Lucanus 1919) and monitor changes over time (Clark et al. 2009; De Pascalis et al. 2020). For example, De Pascalis et al. (2020) analyzed over 30,000 band recoveries from a period of over 100 years to assess how space, time, and sources of threats may impact species according to their migration strategy, diet, and behaviour. Mortality rates were generally higher during migration and overwintering than during breeding, and in some species, mortality increased with the distance birds travelled during migration (De Pascalis et al. 2020). However, while band recoveries can provide important insights on trends and threats throughout migration, it is important to consider that recoveries are often biased towards accessible locations

or species with known migration routes. Thus, banding studies may not always detect important stopover sites or shifts in migratory movements, and resighting or recapture is difficult for birds at-sea or in remote regions (Table 1.1).

Biologging, the use of tracking devices that record information on the behaviour, movements, and/or environmental conditions of the bird being tracked, has been used to monitor bird movement for decades. The development of radiotelemetry allowed researchers to track individual birds through fixed antennas or by manually following individuals (e.g., Roy and Hart 1963; Henny and Blus 1986). This method can provide high-resolution information on migratory movements, and fixed antennas can provide opportunities for multi-year analyses of change. However, radiotelemetry is both resource- and time-intensive, as it often requires manual, ground-based or aircraft-based tracking. Moreover, similar to band recoveries, it is biased towards individuals that occur where they are expected to because tracking is limited by the locations of fixed antennas or the ability of researchers to follow an individual (Mech and Barber 2002). Indeed, Lamb et al. (2023) compared radiotelemetry data from a shorebird, the piping plover (*Charadrius melodus*), and a nearshore seabird, the common tern (*Sterna hirundo*), and showed that because terns use offshore migration routes and there are limited at-sea ground stations, detections were limited following the end of staging at known sites.

The development and miniaturization of remote-downloading devices revolutionized the approach to monitoring seabird movement by allowing researchers to obtain detailed information for birds that migrate at-sea or in remote locations. For example, satellite tags, which transmit

signals remotely, allow researchers to follow birds in real time. Jouventin and Weimerskirch (1990) were the first to track birds using these devices by following the offshore foraging patterns of wandering albatrosses (*Diomedea exulans*) in 1989. The initial large size of these devices, and the associated impacts on individual health (Barron et al. 2010; Vandenabeele et al. 2011), inhibited their use on small birds for many years, but recent technological advancements have increased our ability to deploy satellite tags on a wider range of birds (Bridge et al. 2011; Lahoz-Monfort and Magrath 2021).

Following this, light geolocation sensors, that use light levels to estimate location, were developed. These devices are relatively inexpensive, lightweight, and long-lasting (i.e., often have a battery life of up to three years) and have been used to demonstrate broad-scale trends in migratory movements. For example, Montevecchi et al. (2012) used a combination of satellite tags, light geolocation sensors, and global positioning systems (GPS) devices to track foraging and migration patterns of three seabird species in the North Atlantic to identify areas of importance for these populations. Multi-year data on these three species revealed foraging hotspots and indicated areas of risk due to climate and anthropogenic changes, emphasizing how these devices can be used to inform conservation and management (Montevecchi et al. 2012). However, birds carrying light geolocation sensors must be recaptured to obtain data, and these devices can have high error in location estimates (upwards of 400 km; Halpin et al. 2021), particularly around the spring and autumn equinoxes (Hill and Braune 2001), which may confound our ability to detect smaller scale changes in migratory behaviour with confidence. On the other hand, GPS devices, which use satellites to calculate positions within an accuracy of a

few metres, can detect more fine-scale changes in movement (e.g., landfill use; Langley et al. 2021), but generally have higher costs, larger sizes, and limited battery lifespan compared to other devices. Each of these devices can have multiple benefits and costs (Table 1.1), and the choice of which to use depends on the species, region, and ecological question.

Overall, the development and advancements of these technologies have allowed us to monitor changes in the movements of a variety of migratory birds, which can be used to better understand threats to these species and the environments in which they use. While the decision on which type of tracking device to use depends on a variety of factors, including the ecology of the species and the specific research question, each of these methods can be used to monitor changes in migratory movements as an indicator of environmental change. Despite this, tracking the migratory movements of many seabird species remains a challenge, particularly in remote regions where sites may not be accessible throughout the year or may be logistically challenging to reach. Indeed, we are only beginning to understand the movements of many Arctic-breeding seabird species, particularly gulls (Gutowsky et al. 2020, 2021; Baak et al. 2021d). Monitoring the movements of Arctic-breeding seabirds provides a unique opportunity to track environmental change while also monitoring how species may adapt to, or be impacted by, a rapidly changing Arctic.

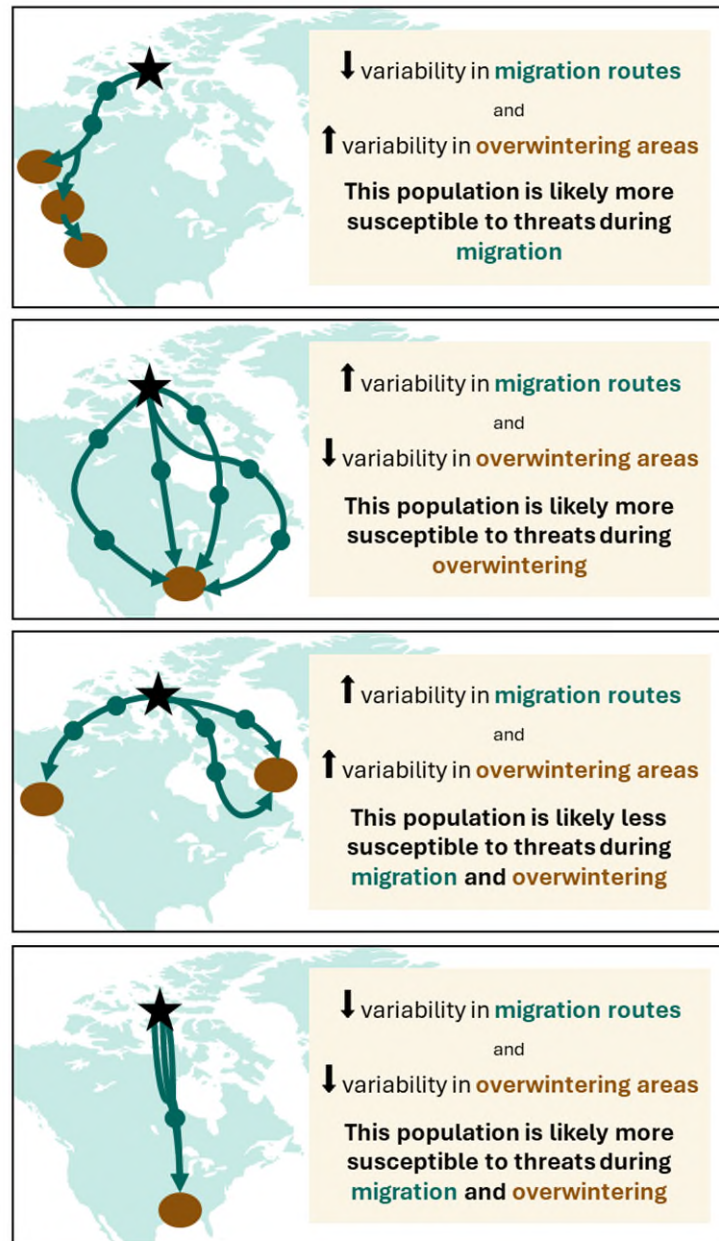


Figure 1.2: Examples of different migratory connectivity and how this may result in different impacts to the populations in the context of environmental change. A) Low variability in migratory routes but high variability in overwintering areas; B) High variability in migratory routes but low variability in overwintering areas; C) High variability in migration routes and high variability in overwintering areas; D) Low variability in migration routes and low variability in overwintering areas. Lines represent migration routes, blue circles represent stopover sites, brown ovals represent overwintering sites, and stars represent the colony of origin.

Table 1.1. Advantages and disadvantages of tracking methods to monitor bird migration.

Tracking method	Advantages	Disadvantages
Band recoveries	- Low cost - Lightweight - Exact information on start and end movements - Relatively easy to deploy on high number of individuals	- Recapture or resighting required, can be resource and time intensive - Biased towards accessible locations or species with known migration routes - Many species have low recovery rates - Can take many years to obtain sufficient data - Not ideal for birds at-sea or in remote regions
Stable isotope analyses	- Low cost - Can obtain multiple time points (tissues) from one sampling period - Multiple isotopes can be combined to increase spatial resolution	- Low spatial resolution - Lack of information on confounding variables for many species or regions (e.g., isotopic baselines, discrimination factors) - Turnover rates often unknown for metabolically active tissues - Requires that migrant moves between isotopically distinct landscapes
Radiotelemetry	- Relatively low cost	- Antennas often have low range

	- High spatial resolution if within range of transmission - Manual tracking provides opportunity to obtain additional information (e.g., behaviour, diet, habitat) - Inexpensive once ground station network is established	- Ground-based and aircraft-based tracking are resource and time intensive - Ground station networks can be costly to establish - Biased towards accessible locations, species with known migration routes, and location of ground stations - Not ideal for birds at-sea or in remote regions
Satellite tracking	- Low cost - High spatial resolution - Ability to transmit signals remotely - Ability to track birds in real time	- Many are large in size compared to other devices (can inhibit deployment on small birds) - If small, often provide few points due to battery capacity
Light geolocation	- Low cost - Lightweight - Long battery life - Interval between location points can be customized	- Recapture required - Low spatial resolution and high error in location estimates - No data during equinoxes or polar night - Not ideal for short-distance migrants - Biased to final capture population

Global positioning system (archival)	- High spatial resolution - Interval between location points can be customized	- Relatively large compared to other devices (can inhibit deployment on small birds) - Small devices have high costs and few location points - Limited battery life compared to other devices (but can be better than remote download or satellite GPS devices) - Recapture required
Global positioning system (remote download, satellite or base station)	- High spatial resolution - Ability to transmit signals remotely - Ability to track birds in real time - Ability to download data remotely for some devices - Interval between location points can be customized	- Relatively large size compared to other devices (can inhibit deployment on small birds) - Small devices have high costs and few location points - Limited battery life compared to other devices - Ground stations required for some devices

Stable isotopes

Isotopes are forms of elements with the same number of protons but a different number of neutrons, resulting in different atomic masses and properties (Herzog 2024). Stable isotopes are

non-radioactive, which generally do not spontaneously decay into other elements (i.e., remain stable; Herzog 2024). The ratio of stable isotopes comprising the element in an object (e.g., a body tissue) can thus provide valuable information about its origin and trophic interactions within an ecosystem. Stable isotopes are measured as isotopic deviations from certified standards using the following equation from Peterson and Fry (1987):

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

where δX represents the isotopic composition of the sample (e.g., ^{13}C or ^{15}N) and R is the corresponding ratio of heavy to light isotopes (e.g., $^{13}\text{C}/^{12}\text{C}$ or $^{15}\text{N}/^{14}\text{N}$), compared to an international standard. This equation expresses the isotopic composition in parts per thousand (per mil, ‰) relative to the standard.

As organisms consume and metabolize prey, incorporating the isotopes from their prey into their tissues, stable isotope signatures in the consumer will change (Hobson and Clark 1992a; Caut et al. 2009). This process, termed discrimination, represents the difference in isotopic composition between a predator and its prey, and thus varies between ecosystems, species, and even tissues. Indeed, discrimination can differ both between and within species, where distinct tissues will exhibit different discrimination factors as a result of differences in integration and turnover rates (Caut et al. 2009). For example, blood can have a turnover rate spanning days to weeks, whereas liver provides information integrated over the past week and muscle can provide information integrated over a several months (Hobson and Clark 1992a, 1992b; Hobson and Bond 2012; Vander Zanden et al. 2015). Moreover, feathers are metabolically inert at the time of growth, and thus retain the isotopic signatures at the time of incorporation into the tissue (Hobson and Clark

1992b). This emphasizes the importance of considering the appropriate discrimination factor for the tissue, species, and ecosystem in question.

Carbon ($\delta^{13}\text{C}$) and nitrogen ($\delta^{15}\text{N}$) isotopes change through the environment and food web and are therefore commonly used as biological tracers to monitor changes in ecological communities (Post 2002). Carbon isotopes largely reflect primary production at the base of the food web, which varies among habitats in a relatively predictable way (Peterson and Fry 1987). As such, these values can indicate differences in foraging location and habitat type. For example, in marine environments, more depleted $\delta^{13}\text{C}$ values, influenced by phytoplankton, generally indicate a diet derived from offshore, pelagic origins, whereas more enriched $\delta^{13}\text{C}$ values indicate inshore, benthic habitats (Peterson and Fry 1987; Hobson et al. 1994; Kelly 2000). However, slight discrimination occurs as carbon moves through food webs and ecosystems. These discrimination factors can range from approximately -0.4 to 2.6% , but vary by tissue, species, ecosystem and diet (Post 2002; Caut et al. 2009).

Nitrogen isotopes reflect the trophic position of an organism within the food web (Peterson and Fry 1987). Generally, organisms incorporate the isotopes of their prey into their tissues as they consume them, thus $\delta^{15}\text{N}$ increases between trophic levels in a relatively predictable and stepwise manner ($3-5\%$; Peterson and Fry 1987). Therefore, organisms at higher trophic levels generally have higher, or more enriched, $\delta^{15}\text{N}$ values, but these values can also be heavily influenced by baseline $\delta^{15}\text{N}$ in the environment (Peterson and Fry 1987; Bearhop et al. 2006). Stable nitrogen isotopes can therefore be used to determine the trophic position of the species in

question, but can also be used, along with or in addition to other isotopes, such as carbon, to identify previously unknown diet items (Hobson et al. 1994). Again, despite relatively predictable increase between trophic levels, these discrimination factors can also vary by tissue, species, ecosystem, and diet (Post 2002; Caut et al. 2009), emphasizing the importance of understanding both discrimination factors and environmental baselines in the context of the study system to make informed conclusions about migration and foraging patterns of the species in question.

Stable isotope analysis has been an important tool for understanding migration and foraging patterns for decades (Hobson and Wassenaar 2018), and can be used in conjunction with information on movement to interpret or confirm spatial differences. For example, in the early 2000s, Mehl et al. (2004) used a combination of stable isotopes and band recoveries to examine wintering areas of king eiders (*Somateria spectabilis*) breeding in the central Canadian Arctic, and found that while band recoveries suggested more eiders wintered in the east, stable isotopes revealed that two thirds to three quarters of the population wintered to the west. Stable isotope analyses can also be used to refine information from tracking data (Takahashi et al. 2015; Baak et al. 2021a). For instance, as light geolocation devices can have high latitudinal error (Halpin et al. 2021), stable isotopes can be used in conjunction with these studies to further refine important habitats (Baak et al. 2021a). St. John Glew et al. (2018) coupled light geolocation data with stable isotope analyses of feathers moulted at different times of the year in three seabird species, common murre (*Uria aalge*), razorbills (*Alca torda*), and Atlantic puffins (*Fratercula arctica*), to better understand foraging areas during moult. The authors demonstrated how the combination

of these methods can refine foraging areas and diet during moult, but also identify individual differences and flexibility in foraging behaviour at sensitive times in the annual cycle (St. John Glew et al. 2018). Importantly, one of the key components of this paper was having information on the isoscape in the North Sea, but this information is not available and/or difficult to obtain for many regions in the Arctic. Collectively, these studies demonstrate that, when used in conjunction with tracking information, stable isotopes can offer a powerful tool for monitoring trends in movement and foraging patterns over time, including refining important habitats for these birds.

Stable isotopes are also widely used to inform diet, offering insights into prey consumption that may be otherwise missed by conventional diet analyses methods. For instance, stomach content analyses are often biased towards indigestible, hard prey items (e.g., squid beaks or fish otoliths), because most soft-bodied organisms digest more quickly and are thus often undetected and/or underestimated (Barrett 2007). In these cases, stable isotopes can be used to supplement stomach content analyses to provide a better overall assessment of diet. For example, Gauthier et al. (2015) used a combination of bolus and stable isotope analyses to examine the diet of glaucous gulls from the Canadian Arctic, and found that stable isotope analyses revealed two to three times more aquatic prey in the diet than bolus analyses originally suggested.

Furthermore, stable isotopes can be used to examine trends in diet and contaminants over time. Indeed, sampling non-lethal tissues, such as blood or feathers, offers a unique opportunity to obtain repeated measures of isotopic signatures throughout the annual cycle. For example, Shoji

et al. (2021) examined changes in mercury concentrations in rhinoceros auklets (*Cerorhinca monocerata*) over time by sampling three tissues that represented different periods throughout the annual cycle: blood (current breeding season, “spring”), breast feathers (“winter”), and tail feathers (“autumn”). By comparing mercury concentrations to stable isotope analyses in the same tissues (trophic position and foraging habitat) and tracking data from the same birds (movement), the authors showed that these seabirds acquired mercury from multiple sources throughout their annual cycle (Shoji et al. 2021). This process allows researchers to identify potential sources of contaminants to seabirds themselves, while also providing key information on the spatial distribution of these contaminants in the environments in which they use.

Overall, isotopic signatures vary spatially and temporally due to a variety of factors, including tissues, species, ecosystems, and diet (Post 2002; Caut et al. 2009). This provides a unique challenge in interpreting results in the context of the study system (e.g., the need to consider discrimination factors), but also an opportunity to monitor changes in migration and foraging patterns over time. Notably, these methods are particularly valuable for gaining insights on the migration and foraging patterns of birds that we know relatively little about. For example, in the Canadian Arctic, it is both logistically and financially challenging to conduct long-term monitoring programs at seabird colonies (Mallory et al. 2018), thus the migration and foraging habits of many seabirds in the Canadian Arctic is not well understood (e.g., Hatch et al. 2020; Weiser and Gilchrist 2020), making it difficult to understand the changes in these birds and the ecosystems they inhabit. By correlating isotopic signatures with known migration routes or tracking data, we can refine specific habitats or regions where seabirds obtain their prey during

different phases of their annual cycle. This approach can provide a more holistic understanding of how diet influences movement patterns and habitat use throughout the annual cycle, which will be of increasing importance as climate change impacts and anthropogenic activities continue alter Arctic environments and the species that inhabit them.

Diet

As top predators, seabirds play an important role in regulating prey populations in the marine environment. For example, in years with less upwelling and thus reduced prey availability, common murre (*Uria aalge*) in California shifted from feeding on offshore rockfish (*Sebastes* sp.) to inshore northern anchovies (*Engraulis mordax*) and Chinook salmon (*Oncorhynchus tshawytscha*), causing significant declines in survival of the salmon population (Wells et al. 2017). This demonstrates that knowledge on seabird diet can provide insights on food web dynamics as well as the health of the marine environment. Importantly, there are various approaches to monitoring seabird diet, and the method used may influence our ability to evaluate spatial or temporal trends (Table 1.2).

Historically, seabird diet was assessed through visual observations of seabirds foraging at sea (e.g., Erwin 1977) or parents feeding chicks at colonies (e.g., Rowan 1952). For example, long-term monitoring of thick-billed murre delivering fish to nestlings in Hudson Bay, Canada, showed a decrease in ice-associated species, such as arctic cod, and an increase in more open water associated species, such as capelin (*Mallotus villosus*; Gaston et al. 2003; Gaston and Elliott 2014). These results suggested a shift in the relative abundance of these prey species in

Hudson Bay, likely due to declining sea ice concentrations (Gaston et al. 2003). While direct observations allow for repeated measured of individuals over time, data collection can be time consuming and is often limited to a short period in one location. More recently, videography and photography, such as trail cameras, have been used to record diet (e.g., Mosbech et al. 2017; Tengeres 2022), allowing researchers to monitor in locations and at scales that may not be otherwise feasible with direct observations (e.g., in multiple, remote areas for long periods of time). While data analysis of trail camera images can also be time-intensive, continued developments in artificial intelligence may improve this method over time (Bijl and Heltai 2022).

Stable isotope analysis is a relatively-non invasive method to obtain diet information across larger spatial or temporal scales. For example, Pratte et al. (2019) examined stable carbon ($\delta^{13}\text{C}$) and nitrogen ($\delta^{15}\text{N}$) in eggs of thick-billed murres, northern fulmars, glaucous gulls (*Larus hyperboreus*), and black-legged kittiwakes from the Canadian Arctic to assess how trophic ecology was influenced by sea ice conditions. Isotopic niches, or the range of isotopic values exhibited by these species, was broader in low-ice years for black-legged kittiwakes, glaucous gulls, and northern fulmars, suggesting that birds shifted to a more diverse diet in these years (Pratte et al. 2019). However, while stable isotope analysis can offer valuable insights on foraging habitat, trophic level, and community dynamics, these values provide a relatively coarse overview of diet. For example, stable isotopes can not be used to identify specific species nor determine the proportions of each species in the diet (Table 1.2). Therefore, integrating stable isotope analyses with other techniques, such as fatty acid analyses or stomach content analyses, can enhance our ability to understand shifts in food web dynamics in a changing Arctic.

Stomach content analyses, where stomach contents are either flushed (live birds) or dissected (dead birds), provide an opportunity to identify, age, sex, and/or determine the proportion of each species in the diet (e.g., Xavier et al. 2022). For example, Karnovsky et al. (2008) combined stable isotope analyses and stomach content analyses of black-legged kittiwakes, thick-billed murre, and dovekies (*Alle alle*) from the North Water Polynya to examine trends in diet across seasons. Diet shifted (e.g., dovekies shifted from consuming copepods in spring to consuming Arctic cod and amphipods in autumn), and stomach content analysis generally validated and enhanced stable isotope results. These results further reinforce the utility of combining multiple approaches to assess diet (Karnovsky et al. 2008). However, while stomach content analysis is a great way to obtain recent information on feeding events, it can be biased towards indigestible prey items (e.g., fish otoliths, squid beaks), and underestimate soft-bodied organisms (e.g., invertebrates; Table 1.2). Moreover, as this method is highly invasive (stomach flushing) or lethal (dissection), it is often not possible to obtain repeated measures of the same individual, making it difficult to assess trends.

Non-lethal sampling methods, such as regurgitates, boluses, or faeces, allow for repeated measures to assess dietary trends. For example, long-term monitoring of black-legged kittiwake regurgitates showed a shift from ice-associated prey to open water-associated prey across four decades, revealing a shift in prey composition as a result of changes in sea ice (Vihtakari et al. 2018). This demonstrates the value of using non-destructive sampling to monitor trends in diet as an indicator of environmental change. However, like stomach content analyses, regurgitates,

boluses, and faeces may be biased towards indigestible prey items (e.g., fish otoliths), and have high proportions of partially digested and/or unidentifiable prey items, which may lead to an underestimation of soft-bodied organisms (e.g., invertebrates) in the diet.

The development of DNA barcoding, where prey items are identified based on their DNA sequences, has revolutionized the information that can be gained from a diet sample. Indeed, this technique allows researchers to obtain detailed information on prey at the species and genetic level, including samples that may be partially digested or degraded. For example, Alonso et al. (2014) used DNA barcoding and stomach flushing to analyze the diet of Cory's shearwaters (*Calonectris diomedea*), and found that DNA barcoding captured prey species that are not often identified when visually inspecting stomach contents (e.g., juvenile cephalopods). However, DNA analyzed from stomach contents may contain DNA from both the prey of the bird and the prey of the prey, primers may be incorrect or not match the target DNA, and these analyses can only provide information on whether these species were present or not, thus potentially skewing results. Moreover, this method has high analysis costs, requiring highly specialized equipment and personnel, and therefore may not be suitable for large scale monitoring programs.

Biologging can provide high resolution data on a bird's foraging pattern, which can be used to infer prey distribution (e.g., Xavier et al. 2006). Prey items may be inferred from the variables recorded by the device (e.g., location, depth, temperature), making it difficult to make robust conclusions on diet composition, but this method can be used to monitor behavioural trends over time. For example, Eby et al. (2023) used three years of biologging data to examine changes in

foraging behaviour of thick-billed murres at two Arctic colonies. In low ice years, murres made more and shorter foraging trips, and had a lower nutritional state, suggesting lower prey availability in those years (Eby et al. 2023). In addition to sensors that obtain information on location, depth, and temperature, camera and video loggers can be used to monitor diet in more detail (Takahashi et al. 2008; Watanabe and Takahashi 2013). For example, Watanabe and Takahashi (2013) used video loggers to understand the diet and foraging behaviour of Adélie penguins (*Pygoscelis adeliae*) and showed temporal and spatial variability in the captures of krill, amphipods, and fish. These studies demonstrate that biologging can be used to monitor changes in diet and foraging behaviour, as well as to predict responses to environmental change.

Overall, while there are advantages and disadvantages to each method (Table 1.2), long-term monitoring of diet can provide important insights on changes in seabirds and the environments in which they inhabit. In addition, information on seabird diet can be used to understand the potential threats to these birds. For example, as seabird diet shifts due to changes in prey or the environment, the exposure to various threats, such as contaminants, may also shift (McKinney et al. 2009), emphasizing the importance of understanding diet in the context of multiple stressors, such as climate change and contaminants.

Table 1.2. Advantages and disadvantages of methods used to assess seabird diet.

Method	Advantages	Disadvantages
Direct observation	- High accuracy - Non-invasive - Repeated measures possible - Ability to determine prey composition/abundance - Direct observation provides opportunity to obtain additional information (e.g., behaviour, habitat)	- Time-intensive (both visual observations and trail camera analyses) - Data coverage limited to the time periods and locations of observations - Potential for observer bias - Not always possible to identify to species level, may underestimate small prey
Stable isotopes	- Integrated information over various spatial and temporal scales (tissue dependent) - Some samples are relatively non-invasive - Repeated measures possible - Offers insights into broader relationships (foraging habitat and trophic level)	- Not possible to identify prey to species level - Not possible to quantify proportion of each species in diet - Lack of information on confounding variables for many species or regions (e.g. isotopic baselines, discrimination factors) - Turnover rates often unknown for metabolically active tissues
Fatty acids	- Integrated information over various spatial and	- Fatty acid profiles can be influenced by metabolism

	temporal scales (tissue dependent)	and environmental factors in addition to diet
	- Some samples are relatively non-invasive	- Turnover rates often unknown for metabolically active tissues
	- Repeated measures possible	- Requires baseline data on the fatty acid composition of potential prey
Stomach content analysis	- High accuracy (contents unlikely to be missed)	- Prey may be partially digested or unidentifiable
	- Provides information on recent feeding events	- Bias towards indigestible prey items (e.g., fish otoliths, squid beaks)
	- Prey is often identifiable to species or another taxonomic level	- Lethal (dissections) or highly invasive (lavage) sampling
	- Can obtain information on age, sex, size, and more.	- Repeated measures often not possible
	- Ability to determine prey composition/abundance	
Regurgitate or bolus analysis	- Less invasive than stomach content analysis	- Prey may be partially digested or unidentifiable
	- Provides information on recent feeding events	- Often does not include entire stomach contents
	- Boluses often contain intact prey items that can be identified to species or another taxonomic level	- Boluses are biased towards indigestible prey items
	- Repeated measures possible	- Potential for external contamination if collected from the environment instead of the bird directly

Faecal analysis	- Non-invasive - Provides information on recent feeding events - Repeated measures possible	- Potential bias towards indigestible items - Potential for external contamination if collected from the environment instead of the bird directly
DNA analysis	- High resolution - Prey identifiable to species or genetic level - Can detect prey from partially digested or degraded samples - Ability to determine prey composition/abundance	- High cost (requires highly specialized equipment and personnel) - Potential for external contamination if collected from the environment
Biologging	- Provides high resolution data on behaviour - Repeated measures possible - Can be combined with other devices to obtain additional information (e.g., environmental variables)	- Prey items are inferred based on behaviour (time, location, depth) - Relatively invasive compared to other methods - Recapture required to retrieve data

Contaminants

Environmental contaminants, or chemicals that are either naturally or anthropogenically released into the environment, occur in marine environments from the Arctic (Vorkamp and Rigét 2014)

to the Antarctic (Bargagli 2008). For example, polychlorinated biphenyls (PCBs), a group of synthetic organic chemicals previously used in building materials and electrical equipment, have been reported in seawater as far as the North Pole (Sobek and Gustafsson 2004). Contaminants can reach these remote environments through a variety of processes, including atmospheric transport, riverine transport, oceanic transport, and biological transport, where they are then deposited into water, ice, and sediments (Schlosser et al. 1995; Macdonald et al. 2000; Semeena and Lammel 2005; Octaviani et al. 2015; Shoji et al. 2019). Once in the environment, these contaminants can enter and move through the food web, in plankton (Hallanger et al. 2011; Skogsberg et al. 2022), shrimp (Carlsson et al. 2016), fish (Rochman et al. 2014), marine mammals (Jepson et al. 2016), seabirds (Borgå et al. 2005) and more, and may have negative impacts on individuals or populations, such as altered metabolism, reduced reproductive success, and mortality (Letcher et al. 2010; McKinney et al. 2015; Dietz et al. 2019).

Importantly, many contaminants can persist in the environment for decades, and thus may have long-lasting effects on the wildlife within these environments. For example, dichlorodiphenyltrichloroethane (DDT), an insecticide used since the early 1940s, caused substantial population declines in birds of prey across North America, leading to its ban in much of the world in the early 1970s (Grier 1982; Best et al. 2010). However, DDT still persists in the environment today, even in remote regions such as the Arctic (Braune et al. 2019). Indeed, while some contaminants, such as DDT or PCBs, have declined over time in the Arctic (Muir and de Wit 2010) and the seabirds that inhabit it (Bianchini et al. 2022), others continue to increase. For example, despite being phased out in North America and Europe in the early 2000s, per- and

polyfluoroalkyl substances (PFASs) in northern fulmars and thick-billed murrelets from the Canadian Arctic are expected to continue to increase for years (Bianchini et al. 2022). Moreover, when these “legacy” contaminants are restricted or banned under international conventions (e.g., Stockholm Convention on Persistent Organic Pollutants; <http://www.pops.int>), they are often substituted by contaminants with similar characteristics that may pose similar risks, or “emerging” contaminants. As legacy and emerging contaminants continue to pose risks to ecosystems and the species that inhabit them, understanding the occurrence and trends of these contaminants will be of increasing importance, particularly in the face of a changing climate.

As climate change and anthropogenic activities continue to increase across the Arctic (Ng et al. 2018; AMAP 2021a), subsequently influencing contaminant levels in these environments (Svavarsson et al. 2021; Wit et al. 2022), it will be critical to monitor the source and fate of these contaminants. Consider sea ice, which can act as a sink for various contaminants, such as microplastics (Peeken et al. 2018). As these stores melt, these contaminants are released into the environment (Obbard et al. 2014; von Friesen et al. 2020) and may enter the food web, eventually magnifying in top predators, such as marine mammals and seabirds (McKinney et al. 2009; Braune et al. 2014). Moreover, with less sea ice or earlier ice breakup, more contaminated, transient, or sub-Arctic species may shift northward, potentially increasing contaminant concentrations in the predators that consume them (McKinney et al. 2009). Indeed, McKinney et al. (2009) showed that as polar bears (*Ursus maritimus*) shifted from ice-associated prey to open water-associated prey, brominated and chlorinated contaminants in these bears increased. Contrastingly, changes in sea ice may cause some seabirds to shift to more lower trophic level

prey, reducing concentrations of some contaminants (e.g., mercury in black-legged kittiwakes; Øverjordet et al. 2015). This emphasizes the importance of long-term monitoring of contaminants in Arctic seabirds to better understand the sources, effects, transports, and fates of contaminants in these ecosystems.

Monitoring contaminants in the Arctic marine environment can be challenging due to the logistical and financial demands of conducting research in these remote locations (Mallory et al. 2018). On account of these challenges, the Arctic Monitoring and Assessment Programme (AMAP) developed a suite of recommendations to prioritize monitoring various contaminants, including mercury (AMAP 2021b) and plastic pollution (AMAP 2021c; Provencher et al. 2022). In these reports, seabirds have been identified as one of the mechanisms to monitor change due to their high trophic position, long-lived nature, high nest site fidelity, and general accessibility in the north. For example, seabirds are the most widely studied animal group for plastic pollution in the Arctic (Bergmann et al. 2022), where over half of seabird species in the Arctic are reported to ingest plastic pollution to some degree (Baak et al. 2020a), making them a key component of trends monitoring in the north (Provencher et al. 2009; Baak et al. 2020b; Kühn et al. 2022). As a result of this, seabirds have been identified as a priority for immediate trend monitoring of plastic pollution in the Arctic (AMAP 2021c, 2021d).

Importantly, the same characteristics that make seabirds useful indicators of contaminants also make them susceptible to these contaminants. As top predators, contaminants can not only bioaccumulate in these long-lived organisms (Borgå et al. 2005), but also biomagnify up the food

web (Borgå et al. 2001; Fort et al. 2016). For example, Borgå et al. (2001) examined organochlorines (OCs) in a marine food web in the European Arctic, including crustaceans, copepods, euphausiids, amphipods, and fish (representing lower trophic levels), as well as seabirds (representing higher trophic levels). OC concentrations generally increased up the food web, biomagnifying in seabirds by one to three orders of magnitude (Borgå et al. 2001), which may impact stress, body condition, and more (Svendsen et al. 2018). However, this relationship differed based on the chemical compound and species examined (Borgå et al. 2001), underscoring the importance of studying the occurrence, source and fate of contaminants unique to each species and region.

Indeed, seabird species may vary in contaminant uptake due to a variety of factors, including differences in morphology, diet, foraging strategy, migratory movements, and more (Borgå et al. 2005; Poon et al. 2017; Baak et al. 2020a; Padula et al. 2020). Surface-feeding seabirds that feed at relatively high trophic levels, such as northern fulmars, are more susceptible to plastic ingestion than pursuit-diving seabirds, such as thick-billed murres (Poon et al. 2017). Similarly, seabirds that migrate to different areas may be exposed to different levels of contaminants. In one study, Leat et al. (2013) combined tracking data, stable isotope analyses, and contaminant analyses to investigate the impact of wintering area on OCs and polybrominated diphenyl ethers (PBDEs) in great skuas (*Stercorarius skua*) in the North Atlantic. The authors found that both wintering area and breeding site significantly influenced contaminant concentrations in these birds (Leat et al. 2013), emphasizing the importance of considering year-round movements in contaminant studies.

Many Arctic-breeding seabirds migrate long distances to more southern wintering areas, and thus may acquire contaminants from multiple sources throughout their annual cycle (Shoji et al. 2021). As birds move across this polluted landscape, many contaminants decrease in concentration with increasing latitude, such as plastic pollution (Kühn and van Franeker 2012; van Franeker and Law 2015), PCBs (Sobek and Gustafsson 2004), or mercury (Chételat et al. 2018). For example, Fort et al. (2014) combined tracking data and contaminant analyses to assess seasonal mercury contamination in dovekies, and found that dovekies were three and a half times more contaminated outside of the breeding season (i.e., in more southern regions during migration; Fort et al. 2014). By combining contaminant studies with tracking information, we can better understand how contaminant concentrations change throughout the annual cycle and identify potential sources of these contaminants in the marine environment and inform conservation, management, or policy decisions.

Informing conservation, management, and policy

Understanding movement, stable isotopes, diet, and contaminants in Arctic seabirds can help inform conservation strategies, management practices, and policy decisions both in the Arctic and worldwide. Indeed, information on seabird migration can identify important hotspots or areas of increased risk for these populations (Montevecchi et al. 2012; Wong et al. 2014; Yurkowski et al. 2019; Hindell et al. 2020), informing conservation efforts, such as the designation of protected areas. For example, Davies et al. (2021) analyzed over 1,500 tracks of 21 seabird species across over 50 colonies, identifying an extensive ($\sim 595,000 \text{ km}^2$) hotspot in

the North Atlantic, which informed the creation of the North Atlantic Current and Evlanov Seamount (NACES) Marine Protected Area (Davies et al. 2021a). Similarly, Augé et al. (2018) analyzed 750,000 tracking and at-sea observation locations for 33 species of seabirds and three species of pinnipeds across 17 years to establish the Marine Spatial Plan for the Falkland Islands.

In addition to helping delineate protected areas, tracking information can also help determine the effectiveness of existing protected areas (Handley et al. 2020; Arroyo et al. 2020). Arroyo et al. (2020) tracked Balearic shearwaters (*Puffinus mauretanicus*) over nine years to determine their use of a marine protected area in the Gulf of Cádiz, northeast Atlantic, and found that the protected area covered less than 40% of the key habitat for this endangered seabird. The authors suggested that previous data used to establish the boundary of this protected area were not sufficient (i.e., limited sampling years may fail to account for interannual variability in foraging areas; Arroyo et al. 2020). This underscores the importance of collecting long-term data to define marine protected areas, but also the utility of tracking data as a tool for adaptive management of conservation areas.

Tracking data can also be used to inform harvest management decisions, such as fishing regulations. For example, tracking data from albatrosses, petrels, penguins, and shags in South Georgia identified important foraging hotspots for Antarctic krill (*Euphausia superba*), informing the establishment the South Georgia and South Sandwich Islands Marine Protected Area, which is now closed to fishing for Antarctic krill during the breeding season of these species (Trathan et al. 2014; Hays et al. 2019). This demonstrates the value in integrating

tracking data with information on seabird ecology, such as diet, to identify areas of importance or risk to seabird populations.

Information on seabird diet can also help inform and evaluate the effectiveness of conservation measures, such as marine protected areas or fisheries closures (Xavier et al. 2007; Searle et al. 2023). Searle et al. (2023) analyzed 25 years of data from a forage fish fishery-seabird system in the North Sea to assess the efficacy of fisheries closures on the diet and reproductive success of black-legged kittiwakes, common guillemots, Atlantic puffins, and razorbills. The authors found that open sandeel (*Ammodytes* sp.) fisheries were associated with a decreased proportion of sandeel in the diet of kittiwakes, puffins, and razorbills, which led to reduced breeding success for kittiwakes that heavily rely on this species. Indeed, kittiwakes outside the fishery area did not experience the same declines, and following the closure, breeding success increased (although not to levels prior to the start of the fishery; Searle et al. 2023). Xavier et al. (2007) analyzed the diet of gray-headed (*Thalassarche chrysostoma*) and black-browed (*T. melanophry*) albatrosses and found that the current precautionary measures for squid fisheries (e.g., *Martialia hyadesii*) may be unnecessarily cautious in years of high squid availability and insufficient in years of low squid availability. These results demonstrate the utility of integrating multiple data sources to effectively evaluate conservation measures.

Movement studies have also been combined with contaminant studies to identify areas of risk for seabirds. For example, Bertram et al. (2022) combined light-level geolocators and mercury analysis in feathers moulted at different times of the year to assess the potential sources of

mercury in common terns (*Sterna hirundo*). The authors found that mercury concentrations significantly differed between wintering areas, but cautioned that these differences may also have resulted from differences in trophic positions at wintering areas, which can be inferred through diet or stable isotope analyses (Bertram et al. 2022). Similarly, Fort et al. (2014) used geolocators and mercury analysis to better understand mercury exposure in dovekeys throughout their annual cycle, and identified an important wintering area in the Northwest Atlantic that was associated with higher mercury concentrations in dovekeys. However, stomach content and stable isotope analyses showed that these birds also shifted from consuming copepods throughout breeding to krill in winter, which may also impact mercury concentrations (although this relationship was not tested; Fort et al. 2016). Studies that incorporate movement, diet, and contaminants in seabirds can provide a more holistic understanding of the potential sources, or areas of risk, to these birds. This information can then inform management and policy decisions for these Arctic-breeding populations, as well as for the contaminant groups assessed.

For a contaminant to be regulated or restricted under the Stockholm Convention, the chemical must persist in the environment, have the potential to bioaccumulate and cause harm in humans or wildlife, and have the ability to be transported long-range (The Stockholm Convention on Persistent Organic Pollutants 2001). Migratory birds can be used as a mechanism to monitor the transport of these contaminants in the environment (e.g., Bourdages et al. 2021; Geizer et al. 2021), as well as changes in contaminant levels in the environment over time. For example, Braune et al. (2015) monitored trends in PBDEs in the eggs of five seabird species in the Canadian Arctic and found that PBDEs in eggs increased from 1975 to 2003, followed by a rapid

decline consistent with the phase-out of these contaminants in the mid-2000s. However, the authors cautioned that concentrations in some species may have been influenced by European contaminants acquired at wintering grounds (Braune et al. 2015), again emphasizing the importance of considering seabird movement in contaminant monitoring programs.

Overall, this review emphasizes how studies on migration, stable isotopes, diet, and contaminants can be used individually, or in conjunction with each other, to better understand Arctic seabird ecology and the broader changes in the environments in which they use. Collectively, this information can be used to inform conservation, management, and policy in the Arctic and worldwide. In remote Arctic ecosystems that are otherwise challenging to monitor, utilising Arctic seabirds as indicators will be increasingly important, especially as climate change continues to cause rapid, transformational changes in these Arctic environments. Given the urgency of these changes, accelerating the development of policies that translate scientific findings into actionable measures is crucial. For example, fostering stronger collaborations between scientists and policymakers to bridge the gap between scientific knowledge and policy decisions (see Hughes et al. 2018), will help us towards conserving Arctic ecosystems, as well as the species that rely on them, in the face of accelerating change.

CHAPTER 2: INTER-INDIVIDUAL VARIATION IN THE MIGRATORY BEHAVIOUR OF A GENERALIST SEABIRD, THE HERRING GULL (*LARUS SMITHSONIANSUS*), FROM THE CANADIAN ARCTIC

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Abstract

The Arctic is warming three times faster than the rest of the globe, causing rapid transformational changes in Arctic ecosystems. As these changes increase, understanding seabird movements will be important for predicting how they respond to climate change, and thus how we plan for conservation. Moreover, as most Arctic-breeding seabirds only spend the breeding season in the Arctic, climate change may also affect them through habitat changes in their non-breeding range. We used Global Location Sensors (GLS) to provide new insights on the movement of Arctic-breeding herring gulls (*Larus smithsoniansus*) in North America. We tracked gulls that wintered in the Gulf of Mexico ($n = 7$) or the Great Lakes ($n = 1$), and found that migratory routes and stopover sites varied between individuals, and between southbound and northbound migration. This inter-individual variation suggests that herring gulls, as a generalist species, can make use of an array of regions during migration, but may be more susceptible to climate change impacts in their overwintering locations than during migration. However, due to our limited sample size, future, multi-year studies are recommended to better understand the impacts of climate change on this Arctic-breeding seabird.

Keywords

Animal movement; Climate change; geolocator; migration; seabirds

Introduction

Advancements in tracking technologies have facilitated new understanding of seabird movement patterns that were previously unknown, as seabirds spend most of their life at sea [1]. Such spatial information is crucial for our understanding of seabird ecology and life-history traits, and can be used to inform conservation [2]. Importantly, migration routes and wintering locations can vary among colonies and individuals within a population due to a multitude of factors, including genetics, natal colonies, competition and environmental stressors [3–8]. Thus, knowledge of both population and individual-level movements can provide important insights for conservation and management.

In the Arctic, ocean temperatures are warming three times faster than the rest of the globe, and Arctic ecosystems are experiencing rapid transformational changes [9]. Further, most Arctic-breeding seabirds spend only a portion of their annual cycle at high latitudes, thus climate change impacts are not localized and may occur across a broad range of important areas and habitats throughout migration. As these impacts continue to increase in frequency and intensity [9, 10], understanding seabird movements is critical both for conservation planning (e.g. understanding threats during the non-breeding period or informing marine protected areas) [2, 11] and predicting how marine fauna will respond to these environmental changes [12].

Despite the need for this information, the migratory movements of many Arctic-breeding seabirds, particularly gulls, are not well understood. Several studies have shown that Arctic-breeding gulls exhibit individual variation in migration routes and wintering areas but return to the same breeding sites each year [13–15]. Gulls that use a wide range of stopovers and wintering areas during migration may be less sensitive to certain stressors, such as habitat loss or climate change, than specialists that are constrained to a certain habitat or diet during migration [16]. Thus, understanding individual movements is integral to our understanding of how these stressors may impact the population as a whole.

American herring gulls (*Larus smithsoniansus*; hereafter herring gulls) are opportunistic seabirds that migrate both short and long-distances to diverse overwintering areas [17, 18]. As a generalist species, herring gulls can exploit resources in marine, freshwater, terrestrial and anthropogenic habitats [17, 19], and are thus distributed across inland and coastal areas across the northern hemisphere [20]. This flexibility allows herring gulls to thrive in a range of habitats and climatic conditions throughout their annual cycle, and as a result, provides a unique opportunity to monitor how individual generalists alter their migratory behaviour in an increasingly changing climate [9, 10].

Information on the migratory behaviour of Arctic-breeding herring gulls has only recently been revealed [17, 18]. Herring gulls from the Canadian Arctic exhibit variation in migration and habitat use among colonies, including relatively prominent migratory connectivity between regional colonies and specific wintering areas [17, 18]. For example, previous research indicates

that herring gulls from the eastern Canadian Arctic largely overwinter in the Gulf of Mexico, while gulls from the Great Lakes mostly remain in the Great Lakes region throughout the winter [17, 18]. Interestingly, individuals within these populations seemed to use different routes to reach their respective wintering areas [18], yet analyses of within-population variation are scarce. Here, we compare to, and expand upon, previous research [17, 18] by providing new insights on individual differences in migratory routes, stopover sites and overwintering areas of a herring gull population from the eastern Canadian Arctic. As generalist omnivores known for individual behavioral variation [20], we expected to observe considerable variation in migratory pathways and timing, as seen in ivory gull (*Pagophila eburnea*) [21] and long-tailed skua (*Stercorarius longicaudus*) migrations [14, 22], before arriving at the general wintering area. We then expected individuals from the same colony to converge in the same wintering areas, as reported in previous studies [17, 18].

Methods

Study Area

The East Bay (Qaqsauqtuuq) Migratory Birds Sanctuary (hereafter “East Bay”; 64°01 N, 81°47 W; Figure 2.1) where GLS tags were deployed is located on Southampton Island in Kivalliq Region, Nunavut, Canada. This sanctuary is an 112,811 ha area that supports a vast array of migratory Arctic breeding birds, including various species of gulls, ducks, geese and shorebirds. Several mammals, such as Arctic foxes (*Vulpes lagopus*) and polar bears (*Ursus maritimus*), also use the area [23–25] and take advantage of the abundance of seabird eggs and young as a food source [26]. Due to its importance as a nesting site for a variety of migratory birds, East Bay and

the surrounding area has been designated as an Important Bird Area [27], and listed as a key migratory bird terrestrial habitat site by the Canadian Wildlife Service [23]. The colony of herring gulls on Mitivik Island (Figure 2.1) in East Bay is small, approximately 15-20 breeding pairs and is thought to be stable (H.G. Gilchrist pers. comm) [28].

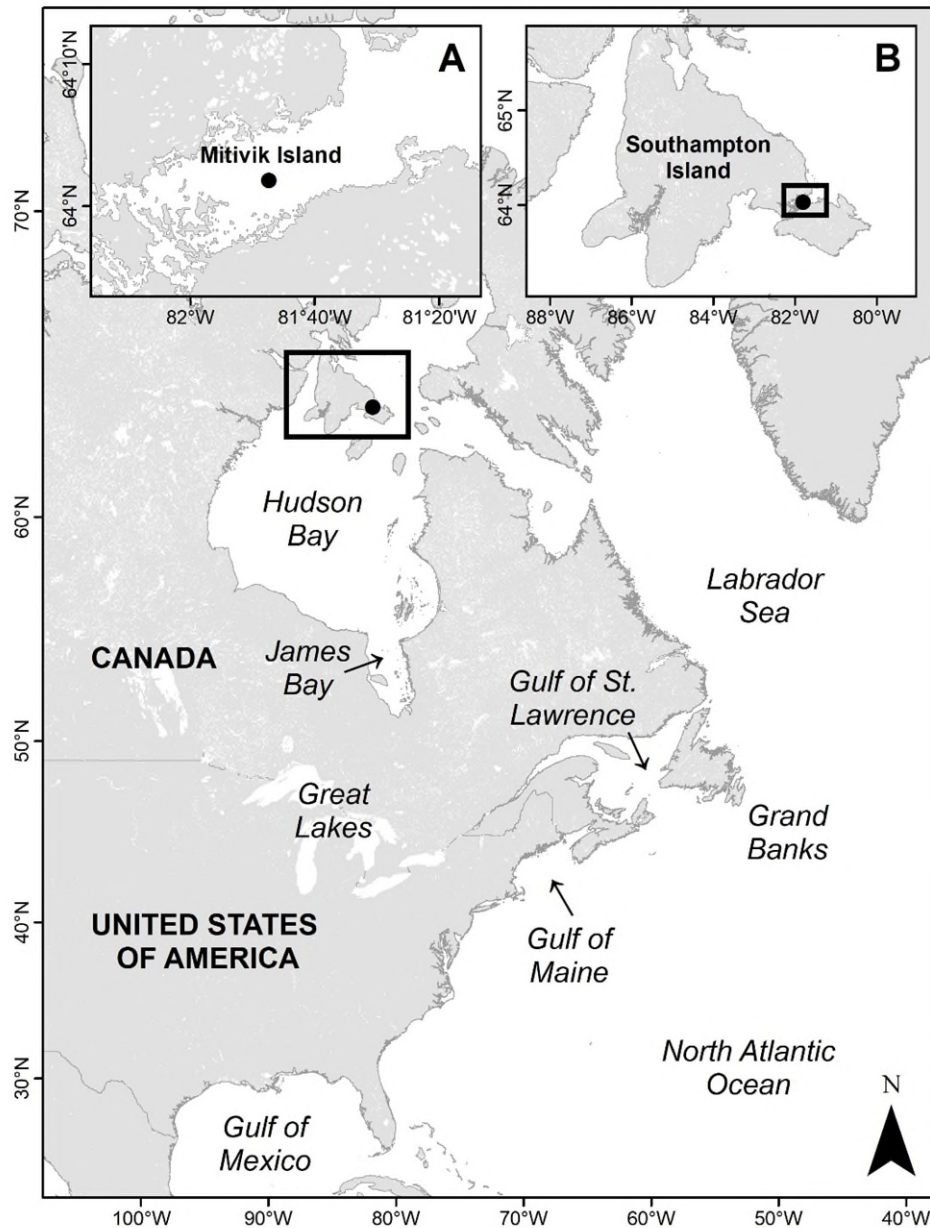


Figure 2.1: Location of Mitivik Island (A) in the East Bay Migratory Birds Sanctuary on Southampton Island (B) in Kivalliq Region, Nunavut, Canada, where GLS tags were deployed on herring gulls (*Larus smithsonianus*) from 2007 – 2008; 2009 – 2010, and 2010 – 2011.

Tag deployment and recapture

We captured adult herring gulls using a self-triggering wire mesh drop box trap over their nest in late-June or early July in 2007 ($n = 2$), 2009 ($n = 10$) and 2010 ($n = 15$). At the time of capture, we attached a stainless steel band to the right tarsus, a light level Global Location Sensor (GLS; Lotek LAT2500, 3.8 g, or LAT2900, 2.1 g) to the left tarsus and recorded mass (g) of the adult. GLS tags represented <1% of adult herring gull body mass, well under the recommended 3% maximum for seabirds [29]. The following year, we recaptured gulls as described above, removed the GLS and recorded mass (g) again.

Data processing

We downloaded data for the GLS units, and then processed and analyzed light-level data using R v 4.0.2 [30]. We restricted data to the known range of herring gulls [20], thus removing locations outside of 0°N – 72°N and 45°W – 130°W, and applied a speed filter of 100 km/h [31–37]. We segmented the time series of an individual when there were gaps >7 days and removed segments with <7 successive daily locations. We then used a state-space model (SSM) to model herring gull movement paths, which reduces location error (from approximately 200 km [29, 38], to 43 km [39]) and produces a single location estimate per 24 h [17, 40, 41]. The SSM did not predict locations for gaps >7 days, and we removed five birds that had partial tracks (i.e., large portions of southbound and/or northbound migration were missing). Based on visual inspection

of the SSM-locations, we removed data from one week before and three weeks after the vernal equinox and all data between May 31 and October 15 (which includes the autumnal equinox, June solstice and movements at the breeding colony) to exclude locations that cannot be accurately estimated at high latitudes [42, 43]. An additional two weeks of data before the vernal equinox were removed for one individual (gull 4) due to unrealistic movements.

Data analysis

We followed methods in Anderson et al. [18] to determine distance travelled per day (km/d), total distance traveled (km), travel speed (total distance travelled per travel day divided by the number of travel days; km/d), and the number and length of travel and stopover days. Briefly, locations were categorized as travel days if the bird moved > 75 km in a single day or $> 0.3^\circ$ latitude in the same direction for two of three successive days, and if not, locations were categorized as stopover days [18]. It is important to note that we present minimum values for the information we collected (e.g., distance travelled per day, total travel distance, stopover length), given the gaps in our data due to the fall and spring equinoxes. Individual birds are numbered (1 – 8) and the results for each individual are described by their number. We report means $\pm$ one standard deviation unless otherwise indicated.

Results

We recovered 13 of 27 loggers deployed (48%) and all deployments lasted one year. After data processing, we had complete tracks from 8 individuals (2007-2008: $n = 1$; 2009-2010: $n = 1$; 2010-2011: $n = 6$). All tracks start on October 15 (after the fall equinox) and end on May 31 (to

avoid localized movements around the colony before breeding), with a gap from March 13 to April 10 due to the spring equinox (February 27 to April 10 for gull 4). For gulls tagged from 2010-2011 ($n = 6$), mean mass did not significantly differ between tag deployment and recapture (paired t-test: $t_5 = 0.34$, $p = 0.75$).

Southbound migration and overwintering grounds

Due to the gap in data during the breeding season and fall equinox, we lacked southbound migration tracks for two birds (1, 6) that were already at their wintering grounds (Great Lakes: 1; Gulf of Mexico: 6) when tracks began. The remaining six birds (2 – 5, 7, 8) had partial routes (i.e., southbound migration began before or during the fall equinox, thus data at the beginning of southbound migration were missing). The gulls we tracked were either already located off the northeastern coast of the United States (US; gull 4), or were stopped on land in Québec near Hudson Bay (2, 3, 5) or in Hudson Bay/James Bay (7, 8; Figure 2.2a). After this stopover, the southbound migration routes of gulls diverged (estimated routes spread 2,300 km east to west), where gulls either travelled to locations off the coast of northeastern US (2), moved off the coast of northeastern Canada then the Gulf of Maine (7) before reaching their main wintering grounds in the Gulf of Mexico, or travelled directly to the Gulf of Mexico (3 – 5, 8), arriving in mid-November to mid-December. Gulls overwintered in the Gulf of Mexico for an average of 102 ± 29 days (range 48 to 143 days) with 2-10 travel days in between. The gull wintering in the Great Lakes (1) remained in this region for the duration of the wintering period before beginning northbound migration (Figure 2.2a).

Across the five gulls with partial tracks, the mean daily distance travelled during southbound migration was 113 ± 99 km/d (range 0 – 393 km) and the mean total distance travelled was 4833 ± 1753 km (range 1913 – 6998 km; Table 2.1). Mean travel speed was 183 ± 30 km/d (range 147 – 228 km/d). Mean stopover length was 15 ± 9 days (range 3 – 30 days; Table 2.1), whereas mean overwintering length was 109 ± 37 days (range 53 – 179 days; Table 2.2). During overwintering, the maximum daily distance travelled was 218 km.

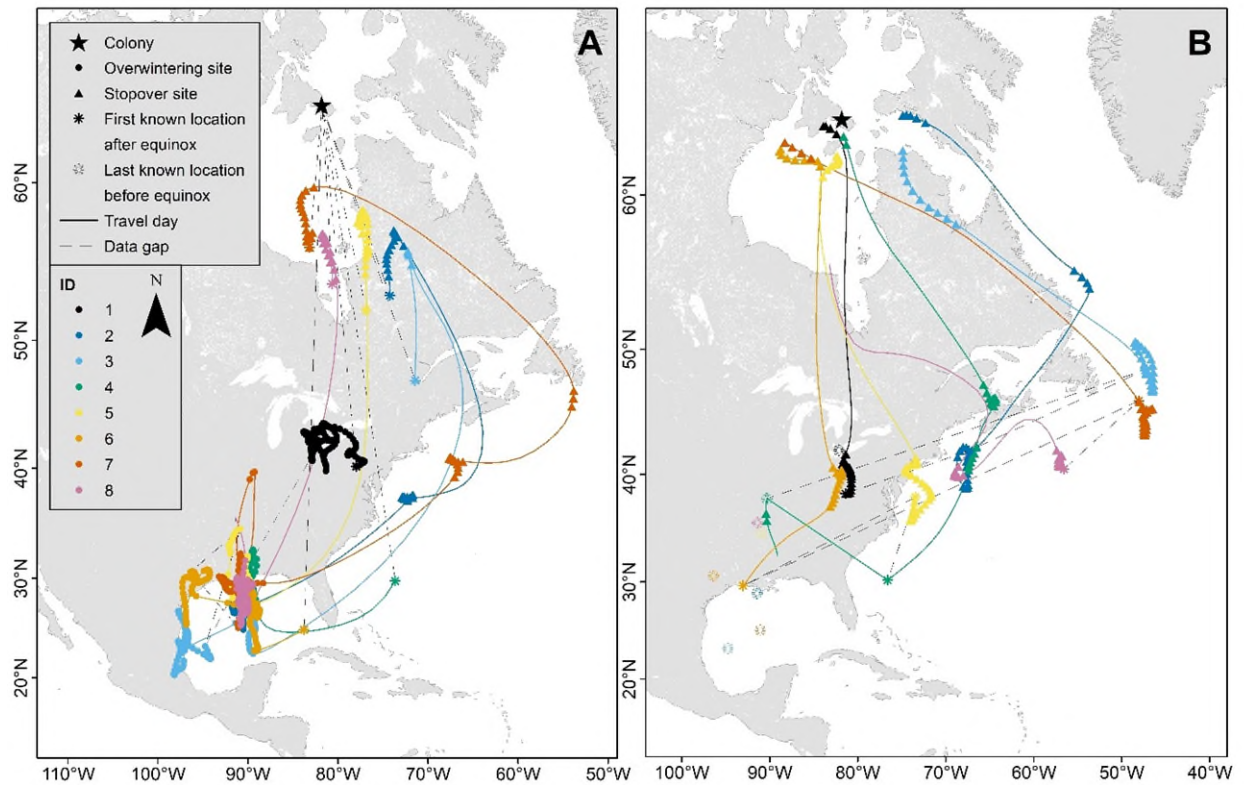


Figure 2.2: Southbound (A) and northbound (B) migration routes (lines), stopover sites (triangles) and overwintering sites (dots) predicted by state-space models of GLS-tracked herring gulls (*Larus smithsonianus*) from the East Bay Migratory Birds Sanctuary in Kivalliq Region, Nunavut, Canada in 2007 – 2008 (1); 2009 – 2010 (2); and 2010 – 2011 (3 – 8). Migration starts on October 15 (after the fall equinox) and ends on May 31 (to avoid localized movements around

the colony before breeding), with a gap from March 13 to April 10 (February 27 to April 10 for gull 4) due to the spring equinox.

Table 2.1: Summary of southbound and northbound migration routes of GLS-tracked herring gulls (*Larus smithsonianus*) from the East Bay Migratory Birds Sanctuary in Kivalliq, Nunavut, Canada during the 2007 – 2008, 2009 – 2010 and 2010 – 2011 non-breeding seasons. Migration starts on October 15 (after the fall equinox) and ends on May 31 (to avoid localized movements around the colony before breeding), with a gap from March 13 to April 10 (February 27 to April 10 for gull 4) due to the spring equinox.

Migration route	ID	Bird-year	Number of stopovers	Total number of stopover days	Mean $\pm$ SD stopover length (d)	Total distance traveled during stopover days (km)	Number of travel days	Mean $\pm$ SD distance traveled per day (km/d)	Total distance traveled during travel days (km)	Travel speed during travel days (km/d)
Southbound	1	2007-2008	NA	NA	NA	NA	NA	NA	NA	NA
	2	2009-2010	2	29	14.5 $\pm$ 2.12	916	29	97 $\pm$ 86	5609	212
	3	2010-2011	1	4	4 $\pm$ NA	171	30	170 $\pm$ 104	5769	187
	4	2010-2011	0	0	NA	2	13	147 $\pm$ 67	1913	147
	5	2010-2011	1	30	30 $\pm$ NA	780	19	96 $\pm$ 107	4691	206
	6	2010-2011	NA	NA	NA	NA	NA	NA	NA	NA
	7	2010-2011	3	39	13 $\pm$ 8.72	1213	35	95 $\pm$ 81	6998	165
	8	2010-2011	1	13	13 $\pm$ NA	609	15	144 $\pm$ 129	4021	228
Northbound	1	2007-2008	2	36	18 $\pm$ 19.80	726	15	61 $\pm$ 74	3499	185
	2	2009-2010	4	24	6.67 $\pm$ 3.79	1141	27	85 $\pm$ 46	6854	162
	3	2010-2011	2	38	19 $\pm$ 11.31	1713	13	70 $\pm$ 51	8423	516
	4	2010-2011	4	25	7.67 $\pm$ 6.66	965	35	87 $\pm$ 57	6689	164
	5	2010-2011	1	30	30 $\pm$ NA	780	19	96 $\pm$ 107	4691	206
	6	2010-2011	2	30	15 $\pm$ 8.49	986	21	88 $\pm$ 82	4800	182
	7	2010-2011	2	30	15 $\pm$ 15.56	999	21	79 $\pm$ 63	8354	350
	8	2010-2011	2	18	9 $\pm$ 4.24	601	33	88 $\pm$ 50	7469	208

Table 2.2: Summary of overwintering locations of GLS-tracked herring gulls (*Larus smithsonianus*) from the East Bay Migratory Birds Sanctuary in Kivalliq, Nunavut, Canada during the 2007 – 2008, 2009 – 2010 and 2010 – 2011 non-breeding seasons.

Migration starts on October 15 (after the fall equinox) and ends on May 31 (to avoid localized movements around the colony before breeding), with a gap from March 13 to April 10 (February 27 to April 10 for gull 4) due to the spring equinox.

ID	Bird-year	Overwinter location	Number of overwinter days	Number of travel days in between overwinter days	Mean ± SD distance traveled per day (km/d)	Total distance traveled (km) during overwinter
1	2007-2008	Great Lakes	179	0	24 ± 12	3579
2	2009-2010	Gulf of Mexico	89	0	26 ± 15	2329
3	2010-2011	Gulf of Mexico	100	10	39 ± 27	4301
4	2010-2011	Gulf of Mexico	109	4	33 ± 22	3680
5	2010-2011	Gulf of Mexico	95	3	29 ± 18	2844
6	2010-2011	Gulf of Mexico	135	12	33 ± 30	4800
7	2010-2011	Gulf of Mexico	53	20	62 ± 46	4559
8	2010-2011	Gulf of Mexico	112	7	29 ± 21	3401

Northbound migration

Due to the spring equinox, we lack data from March 13 to April 10 (February 27 to April 10 for gull 4), thus have partial northbound routes and duration for most individuals (i.e., northbound migration began during the spring equinox, thus data at the beginning of northbound migration are missing). The only gull with a full northbound migration track was the gull that overwintered in the Great Lakes (1; Figure 2.2b). It began northbound migration on May 14 and travelled across Canada and Hudson Bay for two weeks until returning to the colony in late May. Gulls that overwintered in the Gulf of Mexico had different northbound migration routes (Figure 2.2b), and stopped along the northeastern coast of the US (5), inland US (6), the Gulf of Maine (2, 4, 8), the Gulf of St. Lawrence (4), the Grand Banks (3, 7), and/or the Labrador Sea (2), before returning to colony in mid-late May. Overall, gulls used a combination of coastal and overland routes across northeastern Canada and US during northbound migration, diverging by up to 3,000 km east-west, and had limited overlap between routes and stopover sites.

Across all gulls, the mean daily travel distance recorded during northbound migration was 79 ± 63 km/d (range 2 – 295 km), while the mean minimum total travel distance was 6423 ± 1754 km (range 3499 – 8422 km), recognizing that these total travel distances are likely an underestimate as we lack data due to the spring equinox. Mean travel speed was 265 ± 120 km/d (range 154 – 516 km/d), and mean stopover length was 15 ± 10 days (range 2 – 32 days).

Comparison between southbound and northbound migration

Over the entire non-breeding period, gulls travelled an average total of $13,735 \pm 4269$ km (range 7078 – 19910 km), or 9293 ± 4229 km (range 2780 – 15719 km) during travel days only (not including local movements at stopovers and wintering areas). The mean daily travel distance during northbound migration was significantly lower than for southbound migration (paired t-test, $t_5=3.1$, $p=0.027$), and the mean minimum total travel distance was farther during northbound migration than southbound migration (paired t-test, $t_5=3.6$, $p=0.015$; Table 2.1). Mean travel speed was faster, but not significantly so, during northbound migration than southbound migration (paired t-test, $t_5=2.1$, $p=0.093$; similar results for non-parametric Wilcoxon test), and mean stopover length during northbound migration was similar to southbound migration (paired t-test, $t_4=0.3$, $p=0.811$; Table 2.1). Finally, migration routes and stopover sites varied considerably between individuals and between southbound and northbound migration (Figure 2.2). For example, both gull 2 and 3 took an overland route across northeastern Canada during southbound migration, then a coastal route along the northeastern United States to their wintering grounds in the Gulf of Mexico. However, on northbound migration, both individuals took a more eastern coastal route around the Grand Banks and Labrador Sea before returning to the colony. Moreover, some gulls that did not stop on the southeastern coast of North America during southbound migration, did so during northbound migration (e.g., 5, 8).

Discussion

This research provides new insights on individual differences in herring gull migration from the Canadian Arctic. Despite earlier work suggesting high migratory connectivity in herring gulls

[17, 18], we found that one gull migrated overland to winter in the Great Lakes, while the remainder migrated overland and then along the northeastern coast of North America to winter in the Gulf of Mexico, but migration routes and stopover sites differed markedly between individuals and between southbound and northbound migration. The majority of gulls wintered in the Gulf of Mexico, similar to other studies of the same population in 2008 and 2013 – 2015 [17, 18]. The Gulf of Mexico is a highly productive area as a result of upwelling and river inputs [44, 45], and therefore has an abundance of fish and invertebrate species [46]. Consequently, this region hosts a variety of passerines, waterfowl, seabirds and shorebirds during migration [47–49], including ring-billed (*Larus delawarensis*) [50] and herring gulls [51–53]. The Gulf of Mexico has high levels of fishing activity and includes some of the top fisheries in the United States [54, 55], thus herring gulls may also take advantage of discards from fishing vessels [56–58]. Compared to gulls from breeding colonies along the Atlantic Coast, Anderson et al. [17] showed that gulls from the Arctic spent proportionally more time at sea in the winter, presumably exploiting fisheries. However, herring gull diet during the non-breeding period is largely unknown, particularly in this region [52], thus future research on the non-breeding diet of herring gulls is encouraged.

Interestingly, one gull spent its entire overwintering period in the Great Lakes, which has been previously reported for one gull from this population through a band resighting [28], but has not been recorded in gulls tracked from this population [17, 18]. The Great Lakes is a stopover for many migratory birds [59] and also hosts herring gull populations year-round [51, 60]. This different overwintering location could be the result of movement between populations or

historical colonization from a Great Lakes colony [13], as herring gulls often move between colonies in this region and have low natal fidelity [20, 50]. However, it is also likely that herring gulls exhibit some year-to-year variation in overwintering areas [61], similar to other Arctic migrants such as the long-tailed skua [14]. However, we lack multi-year tracking data for these individuals to test wintering site fidelity, and thus additional tracking studies to examine year-to-year variation are recommended. Importantly, with trends of less severe winters (i.e., less ice and snow cover) [62, 63] in the Great Lakes region, this area may be an increasingly viable overwintering location for the Arctic-breeding component of the American herring gull population.

While some gulls took largely the same route for southbound and northbound migration, others took a more eastern, coastal route during northbound migration (Figure 2.2). Moreover, for all gulls with both southbound and northbound data, migration distances were longer on northbound than southbound migration. This is counter to general patterns observed for Thayer's (*Larus glaucoides thayeri*), Sabine's (*Xema sabini*) and ivory gulls breeding in the Canadian Arctic, which had relatively longer and slower fall migration, and shorter, quicker spring migration [15, 21, 64]. In all of those studies, however, breeding birds nested close to polynyas, areas of recurrent, predictable open water that provide access to potential food supplies early in the season [65]. In contrast, herring gulls at East Bay migrate across extensive, heavy pack ice [66] to arrive before their main food source arrives (other bird eggs from local eider and goose colonies), and they must forage in shifting pack ice and coastal leads while they set up their breeding territories (H.G. Gilchrist, unpubl. data). Hence, if gulls arrive too early and sea ice covers most foraging areas, they would have to rely on endogenous reserves, which could affect

reproduction [67]. Therefore, we speculate that annual variation in the phenology of sea ice break up constrains the timing of spring migration and arrival for herring gulls at this colony. Moreover, we note that while travelling longer distances can be more energetically costly, foraging along the coast might provide more predictable, high energy prey to increase energetic stores prior to breeding [18, 68]. It is also possible that gulls used this northbound route to take advantage of wind patterns [69–71], however, wind-driven flyways in the Gulf of Mexico and Atlantic Ocean seem to shift most migratory birds farther west in spring, not east [49, 72], thus this relationship merits further study. Given the expectations for increased variability or occurrence in strong storms and hurricanes in the North Atlantic [73, 74] and the accompanying strong winds which greatly influence seabird movement routes and energetic costs [75, 76], Arctic-breeding herring gulls using the southern coastal migration route may experience more storm events that could influence migratory patterns in the future. At the same time, if sea ice in Hudson Bay continues to break up earlier than in the past, we should expect herring gulls to respond by arriving earlier at the colony, a pattern observed at a nearby colony of thick-billed murres (*Uria lomvia*) [77].

Stopover sites also varied between individuals, and included areas throughout northeastern Canada and USA, including the Labrador Sea, Grand Banks and Gulf of Maine. The Labrador Sea is a hotspot for many fish, seabird and marine mammal species [78], including gulls [3, 11, 79–82]. Similarly, both the Grand Banks and Gulf of Maine, with high productivity levels [83, 84] and a variety of fish and invertebrate species [85–89], are large aggregation areas for many seabirds [90–92], including herring gulls [17, 18, 51]. The differences in stopover areas may be

partially explained by the flexible foraging behaviour of herring gulls as generalists [18, 20]. Previous reports of this breeding population showed no stopovers in the Labrador Sea and Grand Banks [18], which further emphasizes that this colony exhibits a wide range of individual behaviours, and possibly interannual variation for individuals.

Timing at overwintering and stopover sites also varied considerably; in fact, one gull was already at its wintering grounds when we started the tracking analysis in October. Herring gulls remained at wintering sites for an average of 109 days but wintering duration varied, similar to previous reports of this population and populations in more southern latitudes [17, 93]. However, due to missing data around the equinoxes, the duration of overwintering in our study is likely an underestimate. Stopovers also varied in length, but overall, herring gulls spent a relatively short time (mean 15 days for both southbound and northbound migration) at stopovers compared to overwintering sites, similar to more southern herring gull local populations [93]. In contrast, Sabine's gulls from northeast Greenland spent an average of 45 and 19 days at stopover sites during southbound and northbound migration, respectively [71]. These longer stops of Sabine's gulls are likely because trans-equatorial migrants have to refuel for longer periods to increase energetic stores for migration to more southern overwintering locations than those of the herring gulls. Indeed, Sabine's gulls migrated an average of 32,000 km total during the non-breeding period [71], whereas herring gulls in our study migrated an average of 9,000 km. Note that the migration distances in our study are likely an underestimate due to the data gap around the equinoxes; previous studies of this population estimate that herring gulls travel an average of 7361 km during southbound migration alone [18], compared to 4833 km in our study. Still, these

distances are much less than that of trans-equatorial migrants such as Sabine's gulls. Future research using higher resolution tracking devices, such as Global Positioning System (GPS) tags, would allow us to analyze migration timing and distances in more detail.

Overall, this inter-individual variation during migration, but relatively similar overwintering distribution, was expected based on previous findings from this population [17, 18] and the ability of herring gulls to exploit a variety of habitats during migration as a generalist species. This behaviour has also been reported in lesser black-backed gulls (*Larus fuscus*) from the Netherlands, where gulls used multiple migration routes but largely overwinter in the same region in Spain [94]. Interestingly, another similar-sized, Arctic-breeding generalist gull, the Thayer's gull, appears to use the opposite strategy; gulls tracked from the Canadian Arctic took similar routes on southbound migration but overwintered in different areas [15]. These contrasting strategies may impact these species in different ways in the face of a changing climate. For example, the strong inter-individual variation observed in herring gulls migrating to and from East Bay may benefit these gulls if prey abundance dramatically decreases in one stopover area, because only a portion of the overall colony would be affected. Importantly, because gulls from East Bay migrate to the same overwintering grounds (i.e., the Gulf of Mexico), they may be more vulnerable to climate change impacts than Thayer's gulls that overwinter in different regions. Indeed, in addition to the predicted increases in severe weather events along migration routes in the North Atlantic [73, 74], the Gulf of Mexico is predicted to experience increases in severe weather events and ocean temperatures [95] which can cause declines in fish and invertebrate populations [96, 97]. Moreover, an increase in storm

frequency and intensity can increase the risk of oil spills [98], making herring gulls that overwinter in this region vulnerable to a variety of climate change impacts. In contrast, in the Great Lakes region, productivity is expected to increase as snow and ice cover decrease [62, 63] and we know at least some of the East Bay herring gulls winter in this area. Thus, this region may become a more important overwintering location for Arctic-breeding gulls. Moreover, as herring gulls from East Bay spend the nonbreeding season in marine, freshwater and anthropogenic habitats [17], individuals may also be able to more easily adapt to new environments or exploit alternative food sources, such as fishing vessels [56–58] or other anthropogenic sources [19].

Conclusions

This research provides new insights on individual variation in herring gull migration from the Canadian Arctic. Herring gulls breeding at East Bay, Nunavut differed in their migration strategies, but largely overwintered in similar locations. This research shows that herring gulls, as an opportunistic species, are diverse in their migration strategies and make use of a suite of regions, but also highlights the importance of the Gulf of Mexico as a wintering area.

Consequently, these Arctic-breeding gulls may be less susceptible to climate change impacts during migration compared to more specialized Arctic seabirds, but may be more susceptible during overwintering as most gulls overwinter in the same region. This provides a unique opportunity to monitor how this generalist species will shift its migratory behaviour in the face of climate change. Future, multiyear studies [14] are recommended to better understand year-to-year variation and climate change impacts on the migratory behaviours of this Arctic-breeding seabird.

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LINKING STATEMENT

In Chapter 2, I examined the migratory movements of a herring gull population in the Canadian Arctic. Gulls showed both inter- and intra-individual differences in migration routes, demonstrating their ability to use a range of habitats throughout migration. However, these birds largely wintered in the same region, emphasizing that this population may be more susceptible to environmental changes on their breeding and wintering grounds than during migration. As climate change and anthropogenic activities increase in the Arctic and worldwide, other Arctic-breeding gull species may face similar challenges across their range. Although other gull species may also exhibit high individual variation, this can differ among species, regions, and years. Thus, information from one population or species cannot be readily applied to another, and multi-year data from the same individuals will be increasingly important to identify drivers of change. In Chapter 3, I expand upon this work by tracking the migration of another Arctic-breeding, generalist gull species, the glaucous gull. Here, I examined the variability, overlap and individual repeatability in glaucous gull migration and overwintering strategies across multiple years, as well as, for the first time, their habitat use and landfill use throughout migration.

CHAPTER 3: FIRST EVIDENCE OF DIVERGING MIGRATION AND OVERWINTERING STRATEGIES IN GLAUCOUS GULLS (*LARUS HYPERBOREUS*) FROM THE CANADIAN ARCTIC

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Abstract

Many seabird populations differ in their migration strategies, where individuals travel in different directions to separate wintering areas. These migratory strategies may expose individuals to

different threats, thus understanding migratory connectivity is crucial to assess risks to populations. Glaucous gulls (*Larus hyperboreus*) are generalist predators with flexible migratory behaviour that may alter these behaviours in response to climate change and anthropogenic activities, such as access to landfills, yet little is known about their migration. We deployed GPS and GLS tracking devices on glaucous gulls from Coats Island, Nunavut, Canada to obtain the first insights into their migration and habitat use outside of the breeding season. Gulls used two migration strategies during the non-breeding season, where one migrated as far as the Sea of Okhotsk in the Pacific and the remainder ($n = 7$) wintered in the North Atlantic. Gulls primarily overwintered in pelagic (56%) and coastal (38%) habitats. While in coastal habitats, one gull visited one landfill once, but visits increased with a 1 km and 3 km buffer, suggesting that urban glaucous gulls primarily used non-landfill habitats. This research can be used as a baseline to explore changes in migratory behaviour and inform future conservation of Arctic-breeding gulls.

Keywords

Animal movement; Habitat use; Geocator; Landfill; Seabirds

Introduction

Understanding seabird movement year-round is essential to understand life history, identify seabird hotspots and assess risks to seabird populations [1, 2]. Moreover, as migratory marine predators, seabirds can be used as indicators of biological changes in the marine environment [3]. Thus, knowledge on seabird migration and overwintering strategies can also inform conservation measures for the marine environment in which they use.

The development of miniature tracking devices, such as Global Positioning Systems (GPS) and solar Global Location Sensors (GLS), allows us to examine individual movements at finer scales to determine how seabirds use certain habitats during migration. Importantly, migration routes and habitat use can differ among individuals in a population [4–6], and populations can exhibit a migratory divide where individuals travel in different directions to multiple, distinct wintering areas [7]. Variation in migration routes and habitat use may expose seabirds to different risks, thus understanding migratory connectivity is crucial to assess threats to seabird populations. In the Arctic, seabirds are subject to a variety of threats, including anthropogenic stressors such as fishing activities, shipping activities and landfill use, as well as climate change [8, 9]. For example, changes in sea ice concentrations can influence seabird prey [10], migration strategies and habitat use [4, 11]. Indeed, as climate change impacts increase, both fish and seabird ranges are predicted to shift northward [10, 12], however, there remains a large knowledge gap in the migration strategies and habitat use of some Arctic gulls. To assess the impacts of climate change and inform marine protected areas in the Arctic, it is essential to have a baseline of how these indicator species use these regions.

Glaucous gulls (*Larus hyperboreus*) are circumpolar, generalist predators that breed along northern coasts in open tundra and coastal cliffs [13]. These large gulls have a diverse diet that includes fish, invertebrates, small mammals, bird eggs or chicks, and also anthropogenic debris [13]. This foraging behaviour may change in response to climate change and anthropogenic activities [13], such as changes in sea ice or access to landfills. Many gull species are known to

forage at landfills, which can provide an easy, energy-rich prey source that may benefit populations [14], but can also result in increased contaminant loads (e.g. halogenated flame retardants) [9, 15]. Though glaucous gulls have high contaminant loads in the Arctic [16, 17], and garbage has been found in their diet [14], there is little information on their migration and habitat use [13], making it difficult to understand where these gulls may acquire contaminants and how we can mitigate potential impacts on gull populations.

As climate change continues to alter the Arctic environment [18], and anthropogenic activities continue to increase [19], understanding seabird migration and habitat use will be increasingly important. We deployed GPS and GLS tags on glaucous gulls from Coats Island, Nunavut, Canada to provide the first insights on glaucous gull migration from the Arctic. Our objectives were to: 1) examine the variability, overlap and individual repeatability in migration and overwintering strategies of glaucous gulls from the Canadian Arctic; 2) examine the non-breeding habitat use of glaucous gulls from the Canadian Arctic; and 3) investigate the relationship between glaucous gull migration and landfill sites.

Methods

Study area

Akpatordjuark (Coats Island) is a 5,498 km² low-lying island situated in northern Hudson Bay, Nunavut, Canada (Figure 3.1; Francis 2015). This island is inhabited by a variety of seabird species, including approximately 2% (60,000) of Canada's thick-billed murre (*Uria lomvia*) population near Cape Pembroke (62°57' N, 82°00' W; Figure 3.1), Iceland gulls (*Larus glaucoides*;

50 pairs), glaucous gulls (30 pairs) and a variety of tundra-nesting shorebirds [21, 22]. This region has been identified as an Important Bird Area [23] and a key marine habitat site for migratory birds in Nunavut [24] and the Canadian Arctic [22].

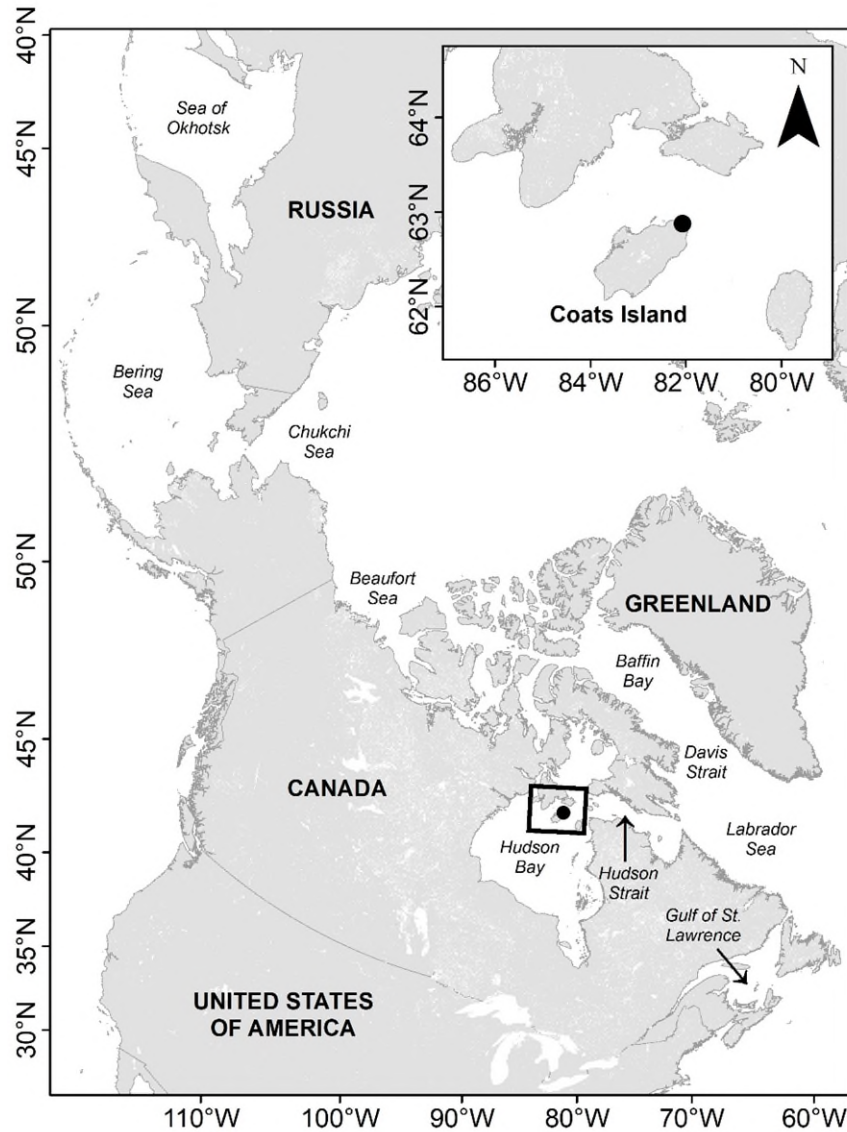


Figure 3.1: Study area of Coats Island (62°57' N, 82°00' W), Nunavut, Canada where glaucous gulls (*Larus hyperboreus*) were tracked during the 2017-2018 and 2018-2019 non-breeding seasons.

Tag deployment and recapture

Breeding glaucous gulls from Coats Island were captured on-nest using noose poles in 2017 and 2018. In July 2017, we deployed six GLS tags (MK3005, British Antarctic Survey) on gulls by attaching the tag to plastic leg bands using cable ties and super glue. GLS loggers collected light level data at 10-min intervals, wet/dry state was recorded at 3-sec intervals, and temperature data were recorded after 20-min of continuous wet state with repeated measurements every 4-hours. In June – August 2018, we captured gulls as above and deployed seven GPS loggers (4-Sterna and 3 Kite-M, Ecotone); devices were equipped with solar panels and UHF long-range download for retrieving data remotely. GPS loggers were attached using leg loop harnesses [25] made from Teflon ribbon (Bally Ribbon Mills). We programmed GPS devices to collect location fixes at 4-hour intervals throughout the non-breeding period. GLS-tagged gulls were recaptured on nest as above in June – July 2018/2019 (after 1 or 2 years) and tags were removed. GPS data were downloaded remotely the following breeding season. All individual glaucous gulls were numbered according to their band number.

GPS and GLS data analyses

For GLS data, we used the TwGeos package [26] to estimate twilights, with a light threshold of 15. We generated two location estimates per day using the probGLS package [27]. The probabilistic algorithm used a solar range of -10° to 3° ; 3°C maximum sea surface temperature (SST) difference; 0.5°C SST standard deviation; 2,000 particles, and 100 iterations. Random latitudes were generated for 21 days around the spring and fall equinoxes. We included a

movement model in location estimates based on available wet-dry sensor data with different movement rates for periods when the logger was dry (mean: 15 m/s, SD: 5 m/s, max: 25 m/s) or wet (mean: 1 m/s, SD: 1.3 m/s, max: 5 m/s). The temperature and wet/dry sensors of MK3005 loggers only recorded data for the first year of deployments; therefore, location estimates for 2018-2019 tracks were based only on light-level data.

We estimated migration timing by identifying preliminary ranges based on all locations for each individual in summer (Jun – Sep) and winter (Jan – Mar). Kernel density estimates were calculated for each individual in each winter with the `kernelUD` function in the `adehabitatHR` package [28] using a 5x5 km grid in Albers Equal Area projection and a smoothing parameter of 40 km. The 99th percentile of the utilization distribution was used to define a preliminary winter range. The start and end of fall migration period was defined as the last date each individual was within its summer range and the first date it arrived on its winter range. Likewise, timing of spring migration was defined as the last date each bird was within its winter range and the first date it arrived on its summer range.

To examine overlap within and between individual wintering areas, we recalculated kernel density estimates based on all wintering locations, using the method described above. Winter ranges were defined by the 90th percentile of the kernel density estimate. Overlap between pairs of individual utilization distributions was calculated using the Bhattacharyya's affinity method [29] with the 'adehabitatHR' package [28]. We report the mean, min and max overlap between all individuals using the same wintering area in 2018-2019. We also examined individual

consistency in wintering area by calculating overlap between the 2017-2018 and 2018-2019 wintering areas for individuals tracked over two non-breeding seasons.

Analyses were performed using R version 3.6.3 [30]. Unless otherwise noted, summary statistics in text are means $\pm$ standard deviations.

Habitat use

To determine habitat use, we classified GPS and GLS locations as either coastal, pelagic or inland. Due to the potential error of GLS tags (approximately 200 km) [31], we did not analyze habitat use in more depth. We obtained coastline shapefiles from the National Oceanic and Atmospheric Administration National Centers for Environmental Information (version 2.3.7, intermediate resolution) [32]. Locations were classified as coastal if they were ≤ 10 km inland to ≤ 50 km from the coastline, inland if they were > 10 km from the coastline inland and pelagic if they were > 50 km from the coastline to the sea [33]. Since GPS tags record three times more locations per day than GLS tags, and three birds had two bird-years (see Results), we averaged habitat use for each individual bird-year before calculating overall proportions of habitat use.

Landfill use

To assess if gulls used landfills during the non-breeding period, we excluded GLS-tracked gulls because GLS error is too high [31] to determine exact positions. We used the Intersect tool in ArcMap v. 10.7.1 [34] to determine if GPS positions intersected with landfill sites in Canada (polygon shapefile from the Government of Canada) [35]. Other bird species have been reported

to forage at landfills and rest near the landfill in between foraging bouts [36]. Thus, we also created a 1 km and 3 km buffer around each landfill site and repeated the above analyses to determine the number of times a gull falls within a landfill or landfill buffer during the non-breeding period.

Results

Migration and overwintering areas

We recovered GLS devices from three individuals (50% recapture rate), one in 2018 and two in 2019, for a total of 5 track years. All remaining GLS devices had either fallen off the leg bands or the individuals could not be recaptured in subsequent breeding seasons because they had moved to inaccessible breeding sites within the cliff colony. We downloaded GPS data from five individuals in 2019. The sixth gull returned to the colony in 2019 with the GPS unit still attached, but data could not be downloaded. One individual (134773232) was tracked using GLS in 2017-2018 and then GPS in 2018-2019.

Glaucous gulls used two distinct wintering areas, one in the northwest Atlantic and the second in the Sea of Okhotsk, Russia (Table 3.1, Figure 3.2). Six of the seven gulls wintered in the northwest Atlantic, ranging from the Gulf of St. Lawrence north to Davis Strait and east to southwest Greenland and the mid-Atlantic ridge. The one gull that wintered in the Sea of Okhotsk (134773232) returned there in both winters it was tracked.

Gulls used three migration corridors in fall and winter (Figure 3.2). An over land route between Southern Hudson Bay and the Gulf of Saint Lawrence was used for 30% of tracked migrations in

fall and 10% in spring. Hudson Strait was used on 50% of tracked migrations in fall and 60% in spring, although one individual using this route travelled partly over land through northeastern Canada. The gull that wintered in the Sea of Okhotsk travelled west overland following rivers until reaching the Beaufort Sea, then travelled along the coast of the Beaufort Sea until reaching the Bering Sea. Fall migrations (37 ± 26 days) were longer on average longer than spring migrations (12 ± 8 days), although both were highly variable (range 3 – 74 and 1 – 27 days, respectively; Table 3.1). The first fall migrant left in early October and the last migrant left at the end of December. Spring migrations began in mid-April and all birds had departed their wintering areas by the second week of May. On average, gulls spent 127 ± 15 days on their winter range (Table 3.1).

There was moderate overlap in wintering areas among those gulls that wintered in the North Atlantic during 2018-2019. On average, each wintering area overlapped with the wintering areas of four other gulls (range: 2 – 5). There was substantial variation in the degree of overlap across individuals; the mean amount of overlap among wintering areas was 18.4% (range: 0.0 – 70.0%). The highest overlap occurred for the three gulls that used the Gulf of St. Lawrence for part or all of the winter (Figure 3.3).

Three individuals were tracked over two years and showed different patterns of consistency in wintering distribution (Figure 3.3). The two gulls that wintered in the North Atlantic had limited overlap in their wintering areas between the two years (134773221: 2.0% and 134773235: 5.1%). Both gulls wintered farther north in 2018-2019 than they did in the previous winter. One gull

switched from spending the entire winter at sea in 2017-2018 to spending part of the winter inland in northeastern Canada in 2018-2019. The gull that wintered in the Sea of Okhotsk had significant overlap in its wintering home range between years (134773232: 78.1%). The datasets analyzed during the current study are available in the Movebank Data Repository (<https://doi.org/10.5441/001/1.tj948m64>; Baak et al., 2021).

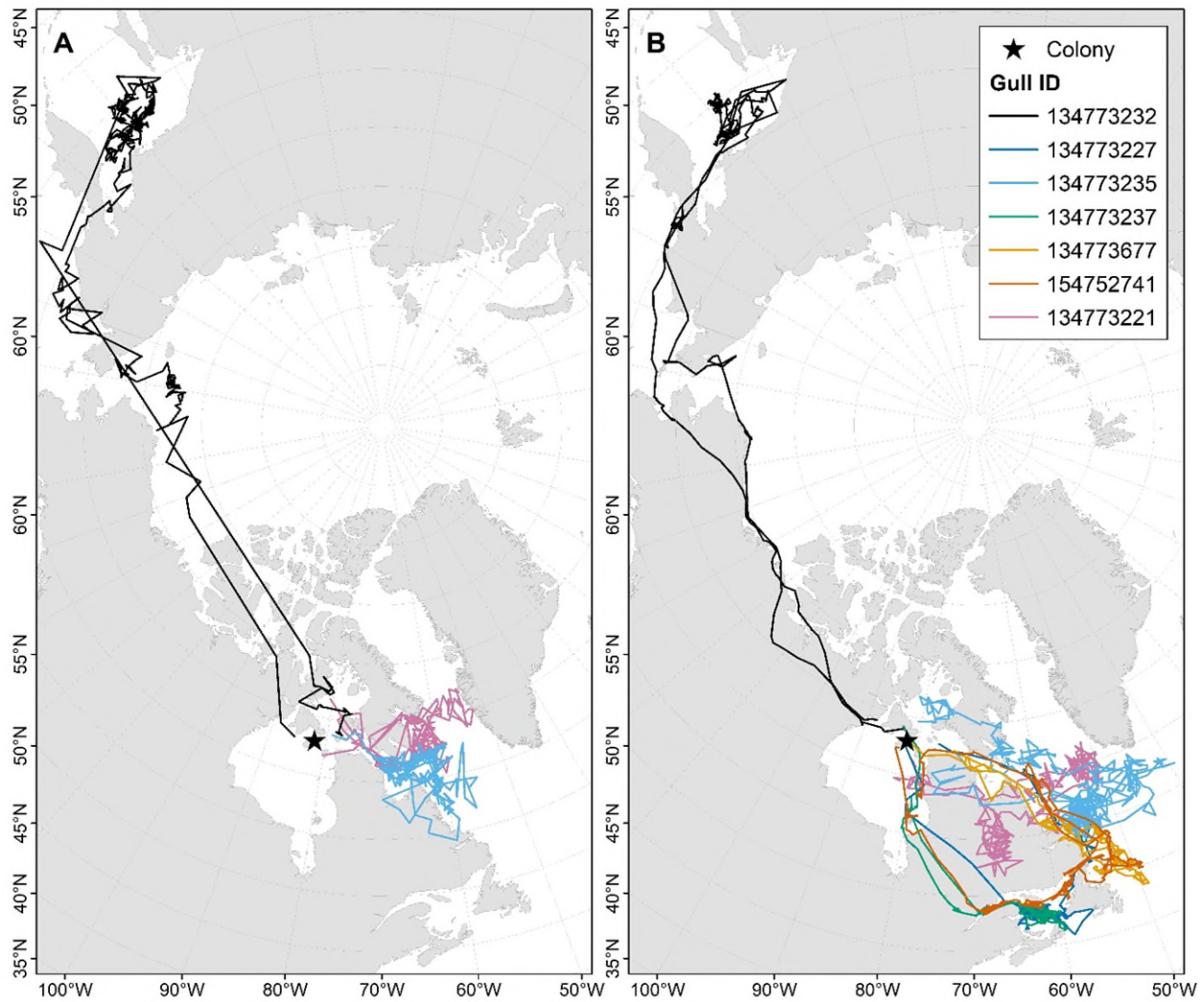


Figure 3.2: Migration routes of GPS- and GLS-tracked glaucous gulls (*Larus hyperboreus*) from Coats Island, Nunavut, Canada, during the non-breeding seasons in A) 2017-2018; and B) 2018-2019.

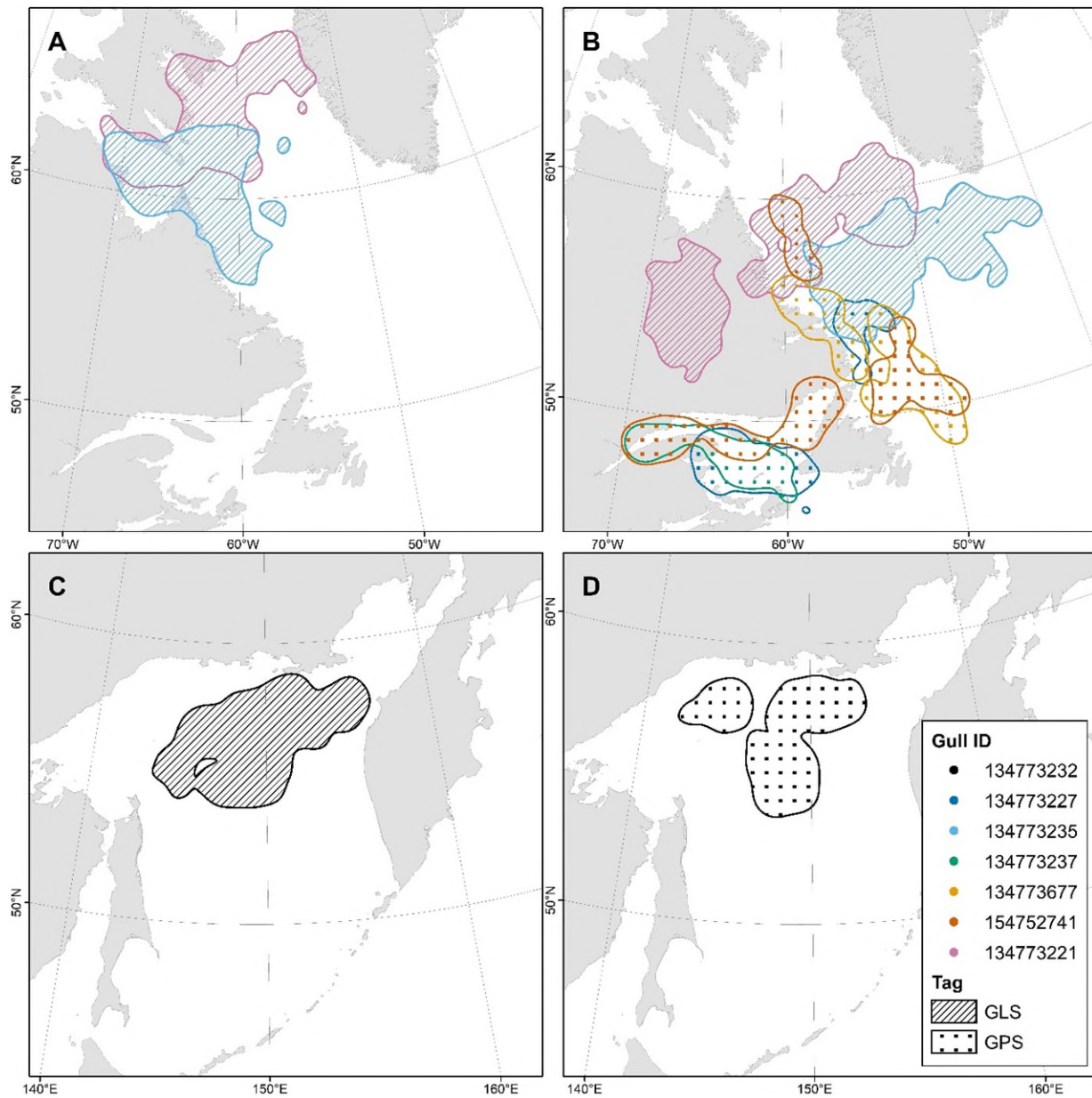


Figure 3.3: Wintering areas (90% utilization distributions) of GPS- and GLS-tracked glaucous gulls (*Larus hyperboreus*) from Coats Island, Nunavut, Canada, during the 2017-2018 (A and C) and 2018-2019 (B and D) non-breeding seasons.

Table 3.1: Migration summary for GPS- and GLS-tracked glaucous gulls (*Larus hyperboreus*) from Coats Island, Nunavut, Canada, during the 2017-2018 and 2018-2019 non-breeding seasons. Migration routes include Hudson Strait (HS), Southern Hudson Bay (SHB), and Beaufort Sea (BS). Wintering areas include the North Atlantic (NA) and the Sea of Okhotsk (SO).

Individual	Sex	Year	Tag type	Fall route	Fall start date	Fall end date	Fall duration (days)	Wintering area	Maximum distance (km)	Winter duration (days)	Spring route	Spring start	Spring end	Spring duration (days)
134773221	U	2017-2018	GLS	HS	2017-12-26	2017-12-29	3	NA	1,464	131	HS	2018-05-09	2018-05-15	6
		2018-2019	GLS	HS	2018-12-16	2018-12-27	11	NA	1,785	108	HS	2019-04-14	2019-04-22	8
134773227	M	2018-2019	GPS	SHB	2018-10-14	2018-12-27	74	NA	2,415	106	SHB	2019-04-12	2019-04-27	15
134773232	U	2017-2018	GLS	BS	2017-10-19	2017-12-17	59	SO	6,465	138	BS	2018-05-04	2018-05-31	27
		2018-2019	GPS	BS	2018-10-13	2018-11-28	46	SO	6,294	157	BS	2019-05-04	2019-05-24	20
134773235	U	2017-2018	GLS	HS	2017-12-20	2017-12-23	3	NA	1,599	124	HS	2018-04-26	2018-04-27	1
		2018-2019	GLS	HS	2018-11-10	2018-12-28	48	NA	2,430	118	HS	2019-04-25	2019-05-04	9
134773237	M	2018-2019	GPS	SHB	2018-10-06	2018-12-07	62	NA	2,324	129	SHB	2019-04-15	2019-04-23	8
134773677	M	2018-2019	GPS	HS	2018-11-16	2018-12-24	38	NA	2,588	124	HS	2019-04-27	2019-05-06	9
154752741	F	2018-2019	GPS	SHB	2018-11-13	2018-12-07	24	NA	2,457	139	HS	2019-04-25	2019-05-10	15

ern Hudson Bay (SHB), and Beaufort Sea (BS). Wintering areas include the North Atlantic (NA) and the Sea of Okhotsk (SO).

Habitat use

Across all individuals and bird-years, gulls were primarily associated with pelagic (56% of the non-breeding period) and coastal (38%) habitats, with limited use of inland areas (7%; Figure 3.4). The gull that wintered in the Sea of Okhotsk had the most positions in pelagic habitats, whereas the gull with the most positions inland (134773221) spent part of its overwintering period on land in northeastern Canada (see Figure 3.3). Finally, the three gulls with the most positions in coastal habitats (154752741, 134773237, 134773227) wintered in the Gulf of St. Lawrence (see Figure 3.2).

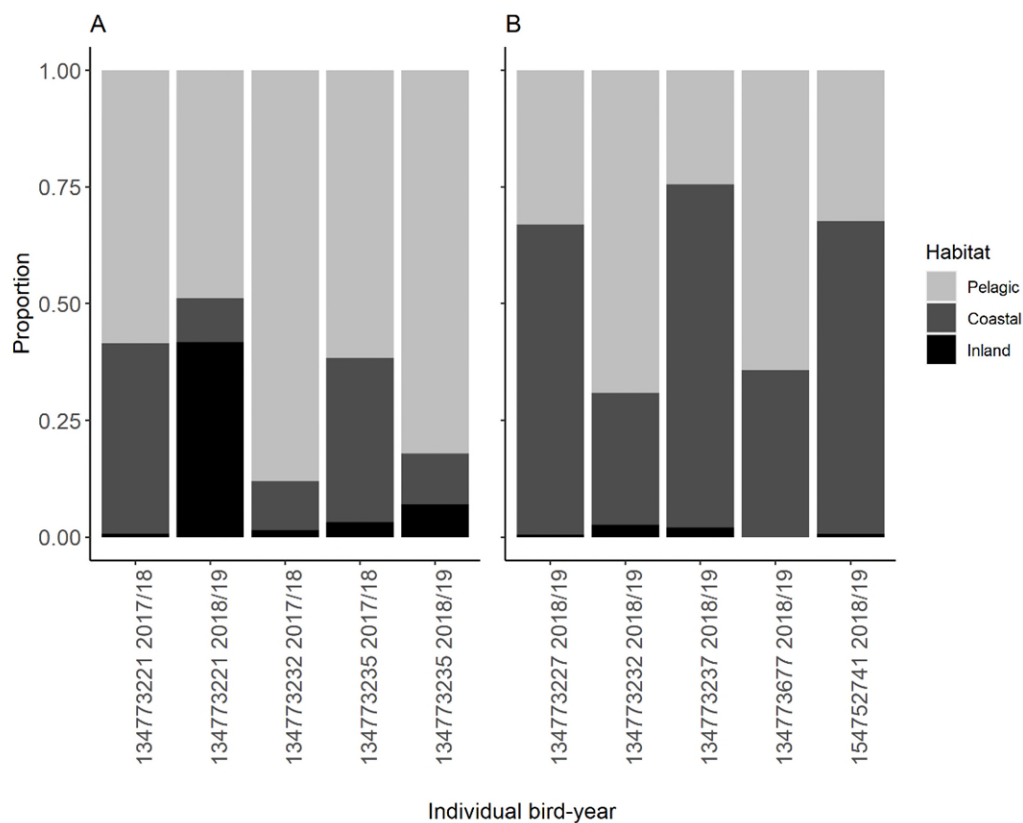


Figure 3.4: Habitat use of A) GLS- and B) GPS-tracked glaucous gulls (*Larus hyperboreus*) from Coats Island, Nunavut, Canada, during the 2017-2018 and 2018-2019 non-breeding seasons.

Landfill use

One gull (154752741) visited one landfill in Inukjuak (1 visit), Quebec, near the end of the non-breeding season (early May). When a 1 km buffer was created around each landfill, three individuals (154752741, 134773237, 134773227) visited a total of 16 landfill areas (229 total visits), with an average of 76.3 ± 84 visits per individual (range 21 – 173). The two most visited landfill areas (36 and 35 visits) were in Mantane, Quebec found within 2 km of the Gulf of St. Lawrence. Finally, when a 3 km buffer was created around each landfill, the three individuals visited a total of 18 landfill areas (654 total visits), with an average of 218 ± 176 visits per individual (range 105 – 421). Again, the two most visited landfill areas (115 and 80 visits) were in Mantane, Quebec.

Discussion

Migration and overwintering strategies

Our study reveals that glaucous gulls from the same nesting colony do not use the same migration and overwintering strategies during the non-breeding season. Wintering areas differed greatly in location, where one gull went as far as the Sea of Okhotsk in the Pacific and the remainder wintered in the North Atlantic. To our knowledge, this is the first study using tracking devices to examine the migration and overwintering strategies of glaucous gulls in the Canadian Arctic. Previous knowledge was primarily obtained from aerial or at-sea seabird

surveys, limited band recoveries and personal observations, which cannot be connected to a specific population and are mostly outdated or unpublished [13]. Thus, despite our small sample size, we provide key insights on the migratory connectivity of this Arctic-breeding seabird.

Gulls that wintered in the North Atlantic had two main overwintering strategies. Gulls either migrated through Hudson Strait or across Hudson Bay and northeastern Canada to waters in the Gulf of St. Lawrence or the Labrador Sea, respectively. The most common migratory route was through Hudson Strait and into Labrador Sea, which may be the result of the higher productivity levels in the Hudson Strait compared to Hudson Bay [37]; gulls likely chose this route following prey abundance. Indeed, both the Hudson Strait and Labrador Sea have been identified as important hotspots during the breeding and non-breeding seasons for a variety of seabird species [2], including black-legged kittiwakes (*Rissa tridactyla*) [38, 39], ivory gulls (*Pagophila eburnea*) [4] and Ross' gulls (*Rhodostethia rosea*) [40]. Thus, our data reinforce the importance of both of these regions for migratory seabirds.

While we only have multi-year tracks for three glaucous gulls, the overlap of overwintering locations of individuals between years differed among them. The gull that overwintered in the Sea of Okhotsk was remarkably consistent in its overwintering home range, whereas the two gulls that wintered in the North Atlantic wintered farther north in 2017-2018 than they did in 2018-2019. This could be the result of changes in sea ice, as the 2017-2018 non-breeding season was an abnormally low year for sea ice cover in the Labrador Sea [41]. This may have caused glaucous gulls to winter in more northern regions following ice-associated prey, such as Arctic

cod (*Boreogadus saida*) [13]. However, little is known about glaucous gull feeding ecology and ice association during the non-breeding season [13], thus these ideas merit further study. Collectively, these results suggest that Arctic-breeding glaucous gulls experience both inter- and intra-individual variation during the non-breeding period.

Arctic-breeding gulls can have high variation or strong fidelity in migration strategies and overwintering locations [5, 42, 43]. Davis et al. [7] recorded a similar migratory divide in Sabine's gulls (*Xema sabini*) from the Canadian High Arctic, where gulls also travelled to either the Pacific or Atlantic Ocean during migration. These divides can occur when there are multiple, suitable wintering areas that can be reached from a breeding colony with similar energetic costs [7, 44]. Individual differences that cause these divides may be attributed to a variety of factors, such as sex [6], movement between colonies, or historical colonization from multiple populations [7]. Therefore, whether migration strategies of individual glaucous gulls are flexible, or fixed and inherited, this migratory divide suggests that this population would be more resilient to different anthropogenic risks and changing conditions than specialist species that rely on a certain diet or habitat during the non-breeding period [45]. Our limited sample size inhibits further analysis of inter- and intra-individual variation, thus additional studies at this and other eastern Arctic colonies are encouraged to further our understanding of individual variation in migration and how this may impact the survival and/or breeding propensity of these Arctic-breeding gulls.

Habitat use

Glaucous gulls spent the majority of their overwinter period in pelagic and coastal habitats during the non-breeding period, consistent with other Arctic-breeding gulls [4, 7], where some also spend time inland, including in urban areas [5, 6]. Previous records [13], citizen science observations [46], and at-sea seabird surveys [47] of glaucous gulls from these regions are also in line with our findings, where glaucous gulls are primarily recorded in pelagic and coastal areas. Specifically, data from Eastern Canada Seabirds At Sea (ECSAS) surveys [47] on glaucous gull distribution during the non-breeding season are remarkably similar to that of our findings; glaucous gulls are primarily pelagic and coastal and concentrated in the North Atlantic (Figure 3.5), though these data are concentrated in the western Atlantic and are not available for Russia. Additionally, while our tracking data only include adult glaucous gulls that were breeding at the time of capture, ECSAS surveys include breeders, failed breeders and immature gulls, which suggests that glaucous gulls may have similar distribution among age classes. This would have important implications for juvenile survival and recruitment, thus this idea merits further research. Importantly, our data also highlight the use of other pelagic environments, such as the Sea of Okhotsk, which is not recorded in citizen science observations of this species [46]. This demonstrates that citizen science observations alone are not sufficient to estimate seabird abundance and distribution [48] and that tracking studies play an important role to generate information in marine habitats largely absent of human observers.

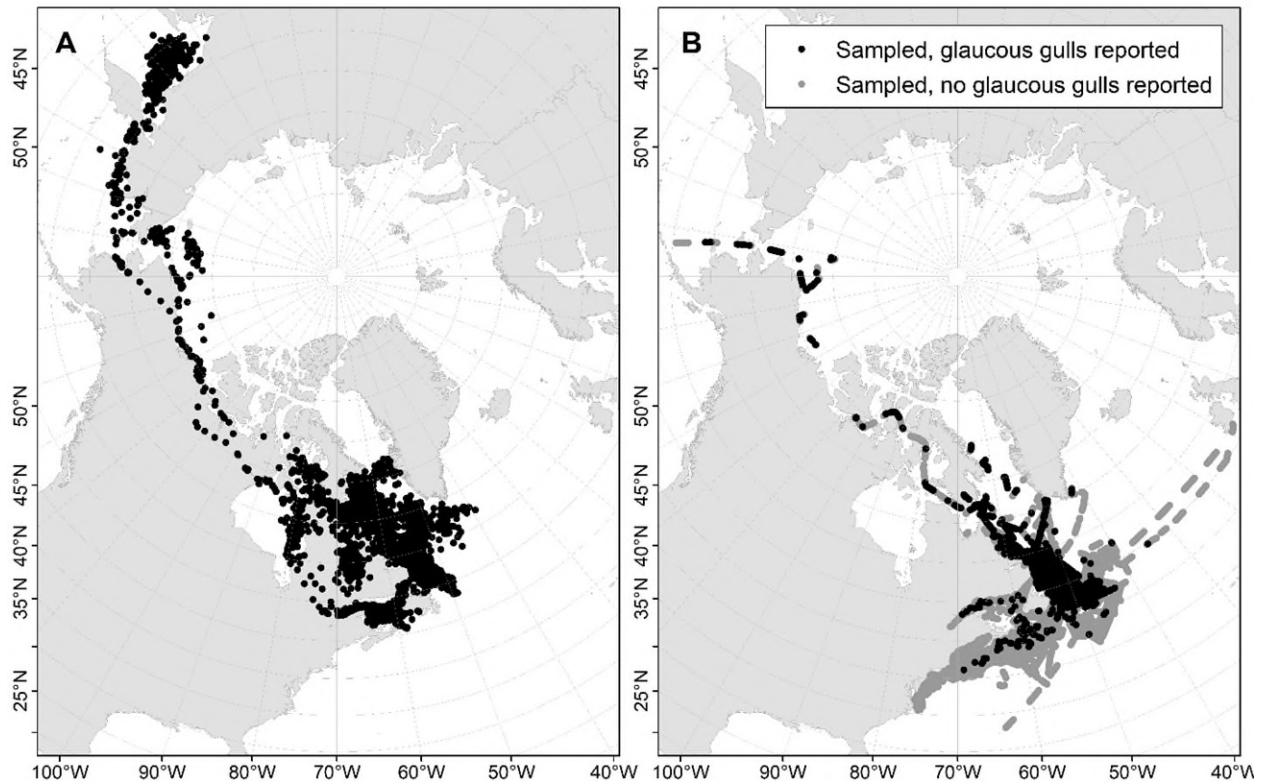


Figure 3.5: Comparison between A) GPS and GLS positions of glaucous gulls (*Larus hyperboreus*) from Coats Island, Nunavut, Canada, during the 2017-2018 and 2018-2019 non-breeding seasons; and B) Eastern Canada Seabirds at Sea (ECSAS) glaucous gull sightings and survey efforts during the non-breeding period (October to May) from 2006 – 2020.

Landfill use

While using coastal habitats, few glaucous gulls visited landfill sites in contrast to other gull species [15, 49, 50]. With no buffer around landfills, only one gull visited one landfill once. However, the number of gulls and visits per gull increased with the addition of both a 1 km and 3 km buffer. It is possible that the gulls foraged at a landfill and then moved outside of the landfill to rest, as bald eagles are often observed to do (*Haliaeetus leucocephalus*; Elliott et al. 2006),

however, these areas also host a variety of other anthropogenic features (e.g. residential areas, wastewater basins, fish-processing plants, other sources of food waste). Ring-billed gulls (*Larus delawarensis*) from Quebec, Canada have been reported to visit landfills near their colonies, but also other anthropogenic sources in these communities, including residential and industrial areas, wastewater basins and agricultural fields [15, 49]. Thus it is more likely that gulls are associating with urban areas in general, visiting a variety of anthropogenic sources that may include, but are not limited to, landfills. The landfill sites in Mantane, Quebec in the Gulf of St. Lawrence are in coastal areas, thus it is also likely that those gulls are foraging in coastal waters near communities and/or utilizing fishing vessels [13]. Importantly, communities are the main source of anthropogenic debris to the ocean [51], thus gulls foraging in these areas may still be at risk of exposure to anthropogenic debris and associated contaminants [49, 52]. Moreover, because glaucous gulls have a high trophic position in the food web, they may be exposed to additional contaminants through their diet. The occurrence of a migratory divide could benefit this population; the gulls that spend the majority of their winter in pelagic habitats (e.g. Sea of Okhotsk) with presumably less anthropogenic pollution sources will likely have less contaminant exposure than those who primarily associate with urban, coastal areas such as the Gulf of St. Lawrence. Therefore, future research dedicated to examining the relationship between gull movements, anthropogenic sources and contaminant levels is encouraged.

Conclusions

Climate change is an increasing threat to Arctic wildlife. As ocean temperatures warm and sea ice decreases, the distributions of seabirds and their prey are shifting [10, 12], and impacts on

seabirds and other marine mammals are now apparent (e.g. changes in phenology and reduced body condition) [53, 54]. Thus, understanding the migratory movements and overwintering patterns of seabirds is of increasing importance. This study can be used as an initial baseline for monitoring changes in the non-breeding distribution of glaucous gulls in the northern Canada, an area under significant threat to climate change [18]. This research further reinforces the importance of the Hudson Strait and Labrador Sea as biological hotspots for seabirds [2], and also highlights the importance of the Sea of Okhotsk as a wintering area for glaucous gulls breeding in the Canadian Arctic.

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LINKING STATEMENT

In Chapter 3, I examined the movements and habitat use of glaucous gulls from the Canadian Arctic throughout migration. Glaucous gulls from Coats Island exhibited a diverging migration strategy, where one bird wintered as far as the Sea of Okhotsk in Russia and the remainder wintered in the North Atlantic. Importantly, wintering areas differed between years, where gulls wintering in the North Atlantic shifted their wintering range between years, likely due to changes in sea ice concentration. As many Arctic-breeding gulls consume ice-associated prey, such as Arctic cod, information on diet is important to better understand both the changes in prey populations, as well as the potential implications of these changes on gull populations. Indeed, in the European Arctic, black-legged kittiwakes showed a clear shift from ice-associated fish species to more open-water associated species over the past few decades. However, in the Canadian Arctic, the diet of many Arctic-breeding gull species is unknown. To better monitor climate-induced shifts in prey species and the potential impacts this may have on their predators, information on diet of these indicator species is crucial. In Chapter 4, I used a combination of stable isotope analysis and stomach content analysis to assess the diet of black-legged kittiwakes in the Canadian Arctic to obtain a benchmark for monitoring future change.

CHAPTER 4: STABLE ISOTOPE AND STOMACH CONTENT ANALYSES REVEAL BLACK-LEGGED KITTIWAKES (*RISSA TRIDACTYLA*) HEAVILY RELY ON ARCTIC COD (*BOREOGADUS SAIDA*) IN THE CANADIAN ARCTIC

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Abstract

Ocean temperatures are rising faster in the Arctic than the rest of the globe, causing rapid declines in sea ice concentrations and changes in Arctic ecosystems. The diet of one of the Arctic's most abundant seabirds, the black-legged kittiwake (*Rissa tridactyla*), has been used as an indicator of these ecosystem changes in the European Arctic, yet little is known about their diet in the Canadian Arctic. We quantified the stomach contents of black-legged kittiwakes near Qikiqtarjuaq and Pond Inlet, Nunavut, in the Canadian Arctic, and assessed if stable carbon ($\delta^{13}\text{C}$) and nitrogen ($\delta^{15}\text{N}$) isotopes in the kittiwake livers differed from that of the dominant prey type in their diet. Based on stomach contents, prey type did not significantly differ between regions, and the dominant prey in both study areas was Arctic cod (*Boreogadus saida*). However, $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values of kittiwake liver were at a lower trophic level than that of Arctic cod muscle, after accounting for dietary discrimination. Thus, while black-legged kittiwakes do heavily consume Arctic cod, stomach content analysis may underestimate the number of soft tissue (i.e., more easily digested) prey species in their diet, such as invertebrates. Future research should include regurgitate samples, faecal samples, or stable isotope analyses of prey items, to better understand black-legged kittiwake diet in the Canadian Arctic in a manner that is not biased against soft parts. Nevertheless, this study provides important benchmark information for monitoring how climate change may impact these Arctic-breeding seabirds in Canada.

Keywords

Bioindicator; Canada; diet; gastrointestinal tract; seabirds

Introduction

Climate change impacts are accelerating across the world, causing increases in ocean temperatures, more frequent and intense extreme weather events, and rapid declines in sea ice concentrations (AMAP 2021). The Arctic is warming four times faster than the global average (Rantanen et al. 2022), causing substantial changes in Arctic ecosystems and adverse impacts on a variety of wildlife species. For example, early ice breakup and late ice formation (ACIA 2005; AMAP 2021), combined with a decrease in Arctic sea ice extent by over 30% since the late 1970s (Stroeve et al. 2012), has reduced important habitat and food sources for a variety of Arctic wildlife, including polar bears (*Ursus maritimus*), seals (e.g., *Pusa hispida*, *Erignathus barbatus*), walrus (*Odobenus rosmarus*), and many fish and seabird species (Descamps et al. 2017; Cote et al. 2021). As climate-induced changes continue to increase, potential mitigation solutions to expected conservation issues for Arctic wildlife will require an understanding of these changes and how they impact the wildlife that depend on these ecosystems.

Seabirds, due to their high trophic position and central-place foraging strategies, are highly sensitive to changes in the marine environment, making them useful indicators of environmental change (Parsons et al. 2008). Indeed, seabirds have been used across the Arctic to demonstrate changes in marine environments, such as warming ocean temperatures (Kuletz et al. 2020) and prey shifts (Provencher et al. 2012; Hatch 2013; Gaston and Elliott 2014; Vihtakari et al. 2018). As one of the most abundant seabird species in the North Atlantic and Arctic regions (IUCN 2018), black-legged kittiwakes (*Rissa tridactyla*; hereafter “kittiwakes”) have been used to monitor changes in marine environments for decades (Wanless et al. 2007a; Hatch 2013;

Vihtakari et al. 2018; Baak et al. 2024). Kittiwakes are primarily piscivorous, mainly feeding on fish such as Arctic cod (*Boreogadus saida*), capelin (*Mallotus villosus*), and sandlance (*Ammodytes dubius*), but can also consume amphipods, copepods, squid and more (Karnovsky et al. 2008; Lavoie et al. 2012; Hatch et al. 2020). Kittiwake diet can also exhibit spatial and temporal variation. For example, Vihtakari et al. (2018) monitored kittiwake diet in Svalbard across two decades and found that diet shifted from ice-associated Arctic species, such as Arctic cod and krill (*Thysanoessa inermis*), to more open water-associated Atlantic species, such as capelin and herring (*Clupea harengus*), coincident with changes in sea ice concentrations. This research shows how monitoring the diet of marine birds can allow us to detect changes in the marine environment, especially as such changes may also impact individual health and reproductive success (Hatch 2013).

Black-legged kittiwake populations are declining throughout most of their circumpolar range (Johansen et al. 2020). On a global scale, kittiwakes are listed on the International Union for Conservation of Nature Red List for Threatened Species as vulnerable and decreasing (IUCN 2018), however, estimates at the regional scale suggest some populations are more threatened than others. For example, in Svalbard and mainland Norway, kittiwakes are listed as near threatened and endangered, respectively (Baak et al. 2021), and populations are declining throughout their range in the European Arctic (besides Russia where populations are stable or slightly increasing; Johansen et al. 2020). Interestingly, while kittiwake populations have not been formally assessed by the Committee on the Status of Endangered Wildlife in Canada

(COSEWIC), intermittent population estimates suggest that kittiwake populations in the Canadian Arctic are increasing (e.g., Mallory et al. 2009; Gutowsky et al. 2022).

To understand why kittiwake populations are increasing in some regions but declining in others, knowledge on the ecological mechanisms that impact populations throughout their range, such as habitat loss, predation, competition, and food availability, is crucial. However, research on both the ecology and threats to kittiwake populations in Canada is extremely limited. For example, while there are increasing studies on kittiwake breeding success and the factors that influence this in Europe (e.g. Wanless et al. 2007; Frederiksen et al. 2007; Christensen-Dalsgaard et al. 2018), there are no detailed reports on the breeding biology of kittiwakes in Canada, and studies on variables that influence success, such as sea ice (Gutowsky et al. 2022) and diet (Gaston 1988; Karnovsky et al. 2008), are scarce. While stable isotope values and bolus samples suggest that kittiwakes in southeastern Canada primarily consume capelin and sandlance (Lavoie et al. 2012), their diet in the Canadian High Arctic seems to primarily consist of Arctic cod, but this is based on few studies with samples from the late 1980s and 1990s (Gaston 1988; Karnovsky et al. 2008; Matley et al. 2012). As warming ocean temperatures and decreasing sea ice concentrations continue to cause northward range shifts, such as with ice-associated Arctic cod (Vihtakari et al. 2018; Cote et al. 2021), it is crucial to obtain benchmark information for monitoring these changes across the Arctic, to understand how these shifts may impact Arctic wildlife species.

Stomach content analysis is a direct method to examine prey that were recently ingested.

However, soft-tissue organisms (e.g., krill or shrimp), can be digested more quickly than hard

fragments of organisms (e.g., exoskeletons or squid beaks) that can remain for a month or longer, causing a potential underestimation of soft-tissue species (Barrett et al. 2007). Over one third of seabirds collected at sea do not contain any prey items besides these hard fragments (RRV and G. L. Hunt, unpublished in Barrett et al. 2007). Moreover, birds collected at sea often have empty stomachs (Karnovsky et al. 2008). To address this issue, stable isotope analyses of seabird tissues, as well as potential prey items, can be used to further delineate diet composition. Stable carbon ($\delta^{13}\text{C}$) and nitrogen ($\delta^{15}\text{N}$) isotopes from animal tissues can provide insights on the dietary sources and trophic position of the individual, respectively, as these values change through the food web in a relatively predictable way (Hobson et al. 1994; Post 2002). $\delta^{15}\text{N}$ is associated with trophic position because of the large discrimination factor (3-5‰) that increases relatively predictably with trophic level, but these values can also be influenced by baseline $\delta^{15}\text{N}$ in the ecosystem (Peterson and Fry 1987). $\delta^{13}\text{C}$ values represent the carbon energy source of an organism's prey, where values are enriched in inshore habitats compared to offshore (pelagic) habitats due to inputs from rivers and terrestrial vegetation, upwelling, and benthic primary production, and thus inform foraging habitat (Peterson and Fry 1987). However, discrimination can occur as carbon propagates up the food webs, with the level of discrimination varying between species, diet, abundance of ice algae, and more (Post 2002; Caut et al. 2009).

The objective of this study was to assess the diet of black-legged kittiwakes on Baffin Island in the Canadian Arctic. To do this, we used a combination of stomach content analyses and stable isotope analyses from black-legged kittiwakes collected near Pond Inlet, Nunavut, and Qikiqtarjuaq, Nunavut. By combining information on stomach content and stable isotope

signatures, we can obtain a better understanding of the diet composition of black-legged kittiwakes in Qikiqtarjuaq and Pond Inlet as a benchmark for monitoring ecosystem change in these two study areas.

Methods

Black-legged kittiwakes were shot using a 12-gauge shotgun in areas where birds were actively feeding near Qikiqtarjuaq (n = 20) and Pond Inlet (n = 19), Nunavut, at the end of August, 2021 by Environment and Climate Change Canada and Inuit collaborators (Figure 4.1). The nearest colonies (i.e., likely breeding origin) for birds collected near Qikiqtarjuaq and Pond Inlet are Akpait and Cape Graham Moore, respectively. Upon collection, carcasses were frozen and shipped to Acadia University in Nova Scotia, Canada, for dissection. These samples were collected as a part of a long-term monitoring program and will be used in a suite of other studies (e.g., contaminant analyses; Baak et al. 2024). Unused portions of each specimen were stored in the National Wildlife Specimen Bank in Ontario, Canada for future research. During dissection, the gastrointestinal tract (proventriculus and gizzard) was removed, re-frozen and shipped to McGill University, Quebec, Canada, for dissection. Each gastrointestinal tract was slit longitudinally along the length of the tract and all contents were flushed into a glass beaker using tap water. Beaker contents were then separated into glass petri dishes, and all diet items visible to the naked eye were removed and preserved in 70% isopropyl alcohol (Gall et al. 2006; Palm et al. 2012) until identification and measurements.

Sagittal otoliths were photographed and identified to species following Campana (2004), and then length (measured along an axis parallel to the sulcus) and width were measured (mm) using the software ImageJ (<https://imagej.net/ij/>). Fragmented otolith pieces were matched with their other halves when possible, and if not, length was estimated using the known width in the following equation (Campana 2004):

$$Otolith\ length = (2.8481 \times otolith\ width) - 0.9768$$

Otoliths that were of the same species and within 0.2 mm length of each other were then paired (i.e., concluded to be from the same fish). The minimum number of fish in each stomach was then calculated as the number of matched otolith pairs plus the number of unmatched individual otoliths (Provencher et al. 2012). Finally, fish length was estimated for Arctic cod following Bradstreet (1980), using the average otolith length for each pair in the following formula:

$$Fish\ length = (20.86 \times otolith\ length) + 19.33$$

For all other prey species (i.e., invertebrates), samples were identified to the lowest taxonomic level possible. To avoid an overestimation of invertebrate species, we counted the number of whole invertebrates and/or the number of heads to provide a minimum abundance for each sample (Provencher et al. 2012).

To corroborate the stomach content analysis results, we also examined stable carbon ($\delta^{13}\text{C}$) and nitrogen ($\delta^{15}\text{N}$) values in liver tissue of black-legged kittiwakes from both study areas. Livers were removed at the time of dissection and sent to the National Wildlife Research Centre in Ottawa, Canada. There, samples were homogenized using chemically cleaned (triple hexane and acetone rinsed) Polytron shafts (SOP-TP-PROC-07I), then frozen at -40°C until freeze drying.

Stable isotopes were analyzed at the Ján Veizer Stable Isotope Laboratory at Ottawa University (<https://www.uottawa.ca/research-innovation/isotope/services>). Finally, we obtained stable isotope values for black-legged kittiwake livers from Pond Inlet in 2018 for temporal comparisons (Provencher et al. 2020).

In addition to kittiwake samples, we examined $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values of various potential prey species from Pond Inlet, Nunavut to further assess kittiwake diet. Details on sample collection can be found in Dupuis-Smith et al. unpubl. Briefly, benthic fishes and invertebrates were collected in Eclipse Sound using a Campelen 1200 research trawl on the MV Nuliajuk from August 3-13, 2019. The bottom trawl was towed for 15 min on bottom at 2-3 knots, and specimens were frozen at -20°C until processed. Fish muscle, decapod abdomens and whole amphipods, mysids, and gastropods were collected for stable isotope analysis. Samples were freeze dried for 48h at -50°C , then subsequently lipid extracted using 2:1 chloroform methanol. For details on stable isotope analysis and accuracy/precision metrics, see Dupuis-Smith et al. unpubl.

To ensure we only included stable isotope values for relevant prey species, we removed all species not known to be ingested by kittiwakes in the Arctic as well as any species with a sample size < 5 . The following species were included in this analysis based on previous records for black-legged kittiwake diet (e.g., Lønne and Gabrielsen 1992; Weslawski et al. 1994; Harris and Wanless 1997; Karnovsky et al. 2008; Vihtakari et al. 2018): Arctic cod, bigeye sculpin (*Triglops nybelini*), Atlantic poacher (*Leptagonus decagonus*), daubed shanny (*Leptoclinus maculatus*),

Doubleline eelpout (*Lycodes eudipleurostictus*), Arctic eelpout (*L. reticulatus*), and longear eelpout (*L. seminudus*), Boreomysis sp., crimson pasiphaeid (*Pasiphaea tarda*), northern prawn (*Pandalus borealis*), and *Themisto libellula*. Finally, three eelpout species (*Lycodes eudipleurostictus*, *L. reticulatus*, and *L. seminudus*) were evaluated a priori and grouped together, as both $\delta^{13}\text{C}$ (Welch's ANOVA; $F_{2,8.87} = 1.842$, $p = 0.21$) and $\delta^{15}\text{N}$ ($F_{2,8.69} = 3.91$, $p = 0.06$) values did not significantly differ between species. To compare stable isotope values between kittiwakes and their prey, we adjusted kittiwake liver isotope values using discrimination factors of -0.4‰ and 2.7‰ for $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$, respectively (Hobson 1993) and a lipid correction factor of 0.61‰ for $\delta^{13}\text{C}$ (Kojadinovic et al. 2008).

All statistical analyses were conducted in RStudio 1.3.1073 (R Core Team 2022). For stomach content analyses, we used unpaired t-tests to determine if number, occurrence, and size of prey species differed between study areas. For stable isotope analyses, we also used unpaired t-tests to examine differences between study areas or years. We considered results as significant if $p \leq 0.05$; means are presented ± 1 standard deviation (SD). As predator stable isotope space did not overlap with prey stable isotope space after correcting for discrimination, suggesting some prey were missing or there were spatial changes in isoscapes between predator and prey, we were unable to run formal mixing models (Phillips et al. 2014; Polito et al. 2019).

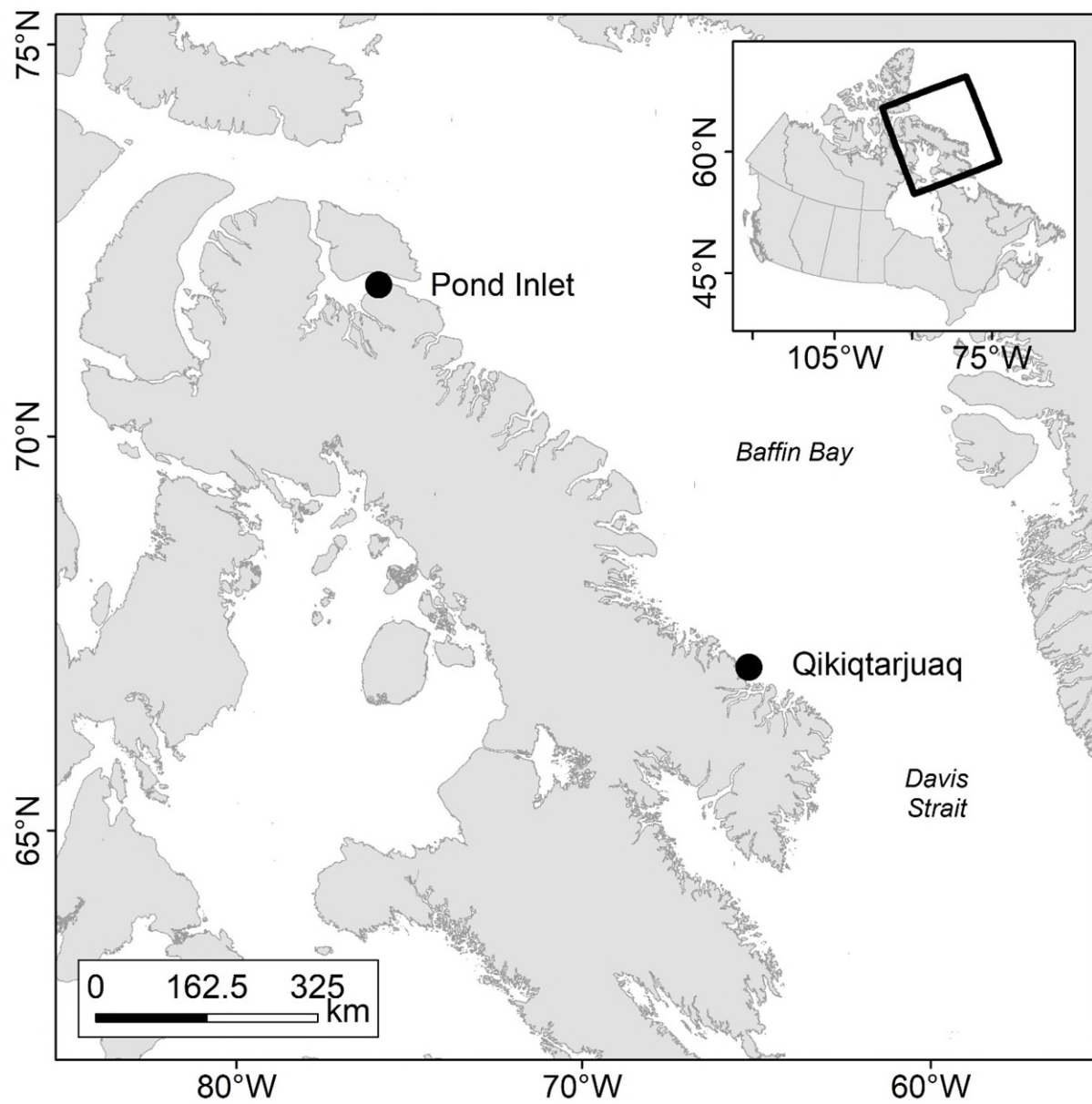


Figure 4.1: Locations of collections of black-legged kittiwakes (*Rissa tridactyla*) from Qikiqtarjuaq ($n = 20$) and Pond Inlet ($n = 19$), Nunavut, Canada in 2021.

Results

Stomach content analysis

Thirty-nine black-legged kittiwakes were dissected for prey items; four had no apparent gut content (11%; three from Qikiqtarjuaq and one from Pond Inlet). In kittiwakes with prey items present, most prey were digested and could not be identified. Arctic cod was the most prevalent identifiable prey species, dominating the diet composition across both study areas (99% of total prey items; Table 4.1, Figure 4.2), with an average of 7 ± 5 cod per stomach. Other prey included Arctic char (*Salvelinus alpinus*), shrimp (*Pandalus borealis*) and euphausiids (*Euphausiidae* spp.), but together, these made up only 1% of black-legged kittiwake stomach content by number.

As there were only two invertebrate samples and one fish otolith that was not Arctic cod, our sample sizes of kittiwake prey were too small to test for differences among species. The frequency of occurrence of Arctic cod did not differ between Qikiqtarjuaq (99%) and Pond Inlet (98%; unpaired t-test: $t_{32} = 1.00$, $p = 0.32$). Similarly, there was no difference in the number of Arctic cod between study areas (Qikiqtarjuaq: 137; Pond Inlet: 112; unpaired t-test: $t_{37} = -0.57$, $p = 0.57$). The length and width of Arctic cod otoliths ranged from 1.72 to 7.05 mm (mean 3.73 ± 1.05) and 0.76 to 3.05 mm (1.72 ± 0.41 mm) in Qikiqtarjuaq and Pond Inlet, respectively, and did not differ between study areas (Figure 2; unpaired t-test: $t_{267} = 1.86$, $p = 0.06$). Similarly, mean estimated fish length was 98.8 ± 23.2 mm (55.2 – 166.0 mm) and did not differ between study areas (Table 4.1, Figure 4.2; unpaired t-test: $t_{174} = 1.66$, $p = 0.10$).

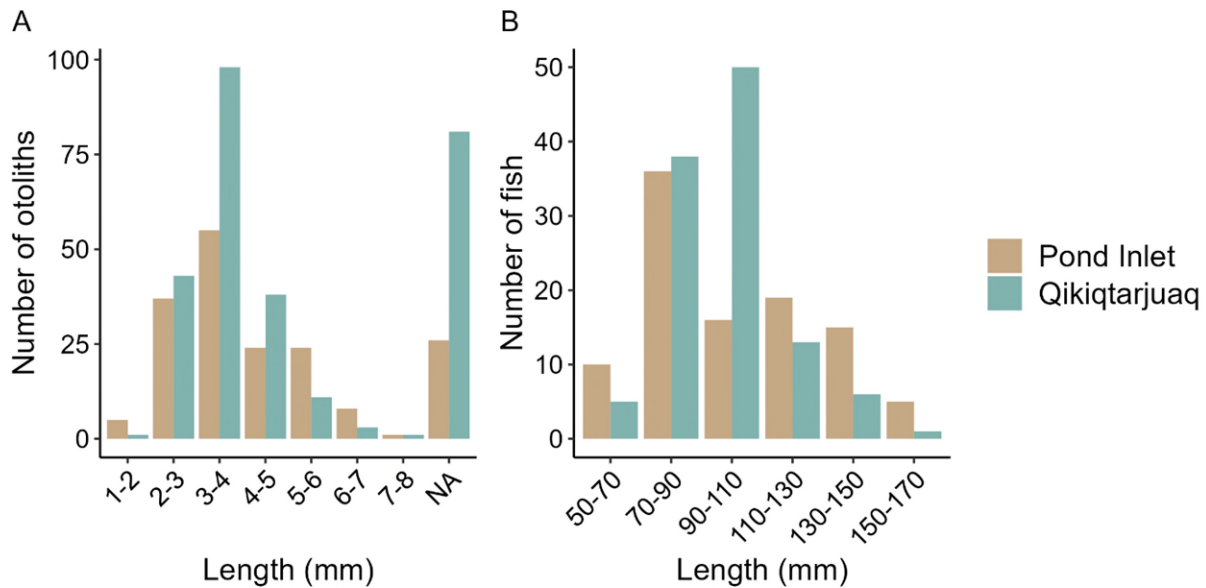


Figure 4.2: Arctic cod (*Boreogadus saida*) otolith length (A) and estimated fish length (B) from gastrointestinal tracts of black-legged kittiwakes (*Rissa tridactyla*) collected in Qikiqtarjuaq ($n = 20$) and Pond Inlet ($n = 19$), Nunavut, Canada in 2021. Otoliths of length NA represent fragmented otoliths where length could not be estimated.

Table 4.1: Diet composition from stomach content analysis of black-legged kittiwakes (*Rissa tridactyla*) from Qikiqtarjuaq ($n = 20$) and Pond Inlet ($n = 19$), Nunavut, Canada in 2021.

Region	Species	Total number	Percent	Mean $\pm$ SD (range) number per bird	Mean $\pm$ SD (range) estimated fish length (mm)
Qikiqtarjuaq	Arctic cod (<i>Boreogadus saida</i>)	137	99	8.06 $\pm$ 5.17 (0-18)	93.3 $\pm$ 18.6 (61.3-164.0)
	<i>Euphausiidae</i> spp.	1	1	1 $\pm$ NA (0-1)	-

Pond Inlet	Arctic cod (<i>Boreogadus saida</i>)	112	98	6.22 ± 4.73 (0-19)	102.0 ± 27.2 (55.2-166.0)
	Arctic char (<i>Salvelinus alpinus</i>)	1	1	1 ± NA (0-1)	-
	Northern prawn (<i>Pandalus borealis</i>)	1	1	1 ± NA (0-1)	-

Stable isotope analysis

Stable isotope values ($\delta^{13}\text{C}$ and $\delta^{15}\text{N}$) from black-legged kittiwake livers in Qikiqtarjuaq and Pond Inlet are presented in Table 4.2 and Figure 4.3. For carbon, mean $\delta^{13}\text{C}$ was $-21.0 \pm 0.4\text{‰}$ in 2021 across study areas (this study) and $-21.1 \pm 0.3\text{‰}$ in 2018 in Qikiqtarjuaq (Provencher et al. 2020). For nitrogen, mean $\delta^{15}\text{N}$ was $15.9 \pm 0.5\text{‰}$ in 2021 (this study) and $16.4 \pm 0.5\text{‰}$ in 2018 (Provencher et al. 2020). There were no significant differences in liver $\delta^{13}\text{C}$ (unpaired t-test: $t_{36} = -1.01$, $p = 0.32$) or $\delta^{15}\text{N}$ ($t_{33} = 0.50$, $p = 0.62$) between study areas in 2021. In Qikiqtarjuaq, there were no significant differences in $\delta^{13}\text{C}$ between 2018 and 2021 ($t_{38} = -1.50$, $p = 0.14$), however $\delta^{15}\text{N}$ values were significantly higher in 2018 than in 2021 ($t_{37} = 3.05$, $p = 0.004$).

Stable isotope values for fish and invertebrates are presented in Table 4.2 and Figure 4.4. For fish, $\delta^{13}\text{C}$ ranged from -21.3 to -17.4‰ (mean: $-19.3 \pm 1.3\text{‰}$) and $\delta^{15}\text{N}$ ranged from 13.8 to 18.7‰ (mean: $16.0 \pm 1.2\text{‰}$). For invertebrates, $\delta^{13}\text{C}$ ranged from -21.7 to -18.0‰ (mean: $-20.1 \pm 0.9\text{‰}$) and $\delta^{15}\text{N}$ ranged from 10.4 to 16.1‰ (mean: $13.3 \pm 1.6\text{‰}$; Table 2).

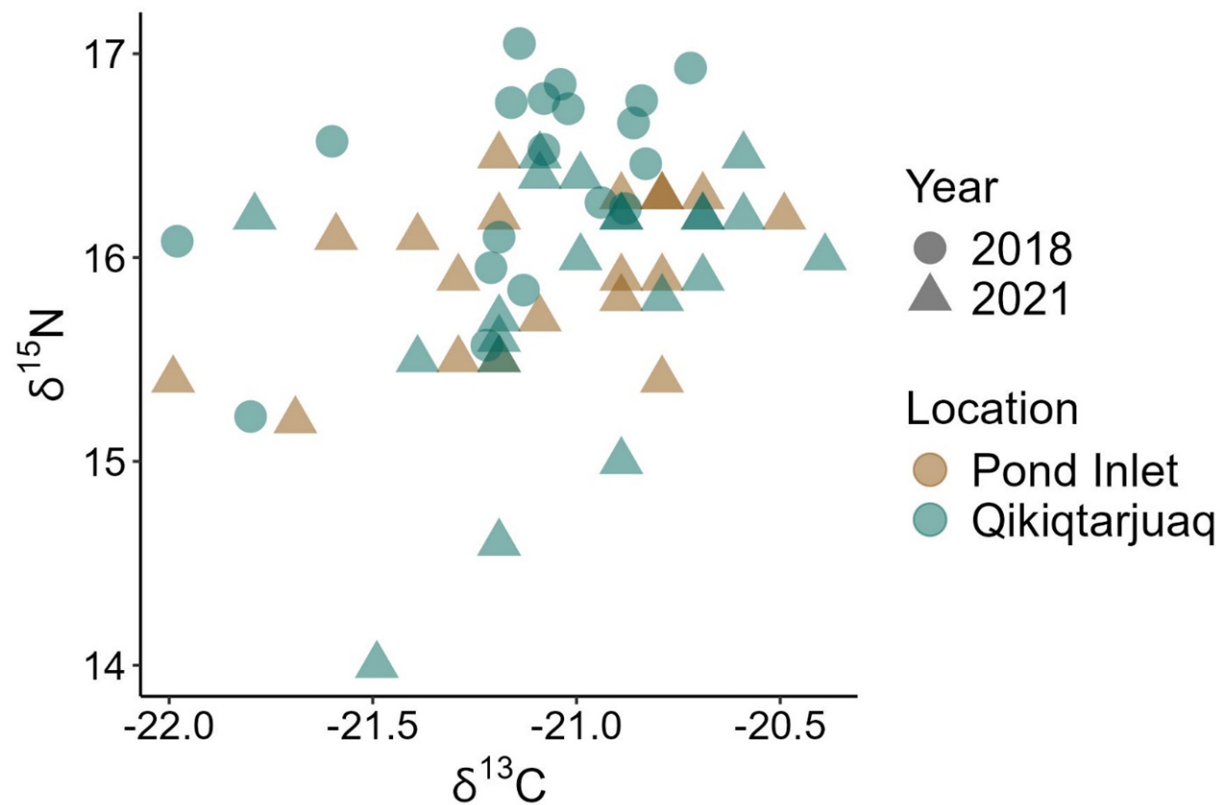


Figure 4.3: Relationship between stable carbon ($\delta^{13}\text{C}$) and stable nitrogen ($\delta^{15}\text{N}$) isotope values (‰; non-adjusted) from black-legged kittiwake (*Rissa tridactyla*) liver from Pond Inlet and Qikiqtarjuaq, Nunavut, in 2018 and 2021. Black-legged kittiwake livers were lipid-corrected following Kojadinovic et al. (2008).

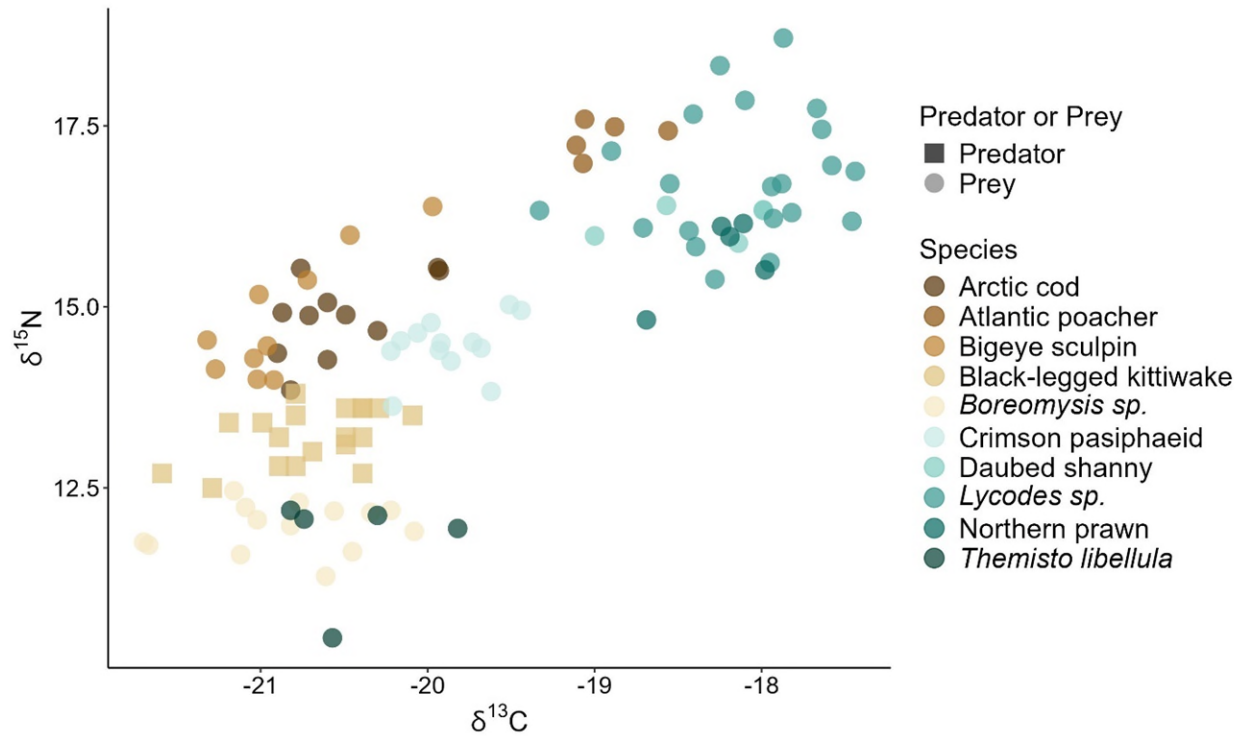


Figure 4.4: Relationship between stable carbon ($\delta^{13}\text{C}$) and stable nitrogen ($\delta^{15}\text{N}$) isotope values (‰) from black-legged kittiwake (*Rissa tridactyla*) livers and their potential prey from Pond Inlet, Nunavut, in 2021 (black-legged kittiwakes) and 2019 (all other species). Black-legged kittiwake livers were adjusted using discrimination factors of -0.4‰ and 2.7‰ for $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$, respectively (Hobson 1993) and lipid-corrected following Kojadinovic et al. (2008).

Table 4.2: Mean $\pm$ standard deviation (SD) and range of $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values (‰; non-adjusted) of black-legged kittiwake (*Rissa tridactyla*) liver and its prey sampled from Pond Inlet and Qikiqtarjuaq, Nunavut, in 2018, 2019 and/or 2021. Black-legged kittiwake livers were lipid-corrected following Kojadinovic et al. (2008).

Location	Year	Species	<i>n</i>	$\delta^{13}\text{C}$	$\delta^{15}\text{N}$	Source
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Qikiqtarjuaq	2021	Black-legged kittiwake	21	-21.0 ± 0.3 (-21.8, -20.4)	15.8 ± 0.6 (14.0, 16.5)	This study
	2018		19	-21.1 ± 0.3 (-22.0, -20.7)	16.4 ± 0.5 (15.2, 17.0)	Provencher et al. (2020)
Pond Inlet	2021	Black-legged kittiwake	19	-21.1 ± 0.4 (-22.0, -20.5)	15.9 ± 0.4 (15.2, 16.5)	This study
	2019	Arctic cod	11	-20.5 ± 0.3 (-20.9, -19.9)	14.9 ± 0.5 (13.8, 15.5)	Dupuis-Smith et al. unpubl.
		Atlantic poacher	5	-18.9 ± 0.2 (-19.1, -18.6)	17.3 ± 0.2 (17, 17.6)	Dupuis-Smith et al. unpubl.
		Bigeye sculpin	10	-20.9 ± 0.4 (-21.3, -20)	14.8 ± 0.9 (14, 16.4)	Dupuis-Smith et al. unpubl.
		<i>Boreomysis sp.</i>	14	-20.8 ± 0.5 (-21.7, -20.1)	12 ± 0.3 (11.3, 12.5)	Dupuis-Smith et al. unpubl.
		Crimson pasiphaeid	13	-19.9 ± 0.3 (-20.2, -19.4)	14.5 ± 0.4 (13.6, 15)	Dupuis-Smith et al. unpubl.
		Daubed shanny	5	-18.3 ± 0.4 (-19, -18)	16.2 ± 0.2 (15.9, 16.4)	Dupuis-Smith et al. unpubl.
		<i>Lycodes sp.</i>	21	-18.1 ± 0.5 (-19.3, -17.4)	16.8 ± 0.9 (15.4, 18.7)	Dupuis-Smith et al. unpubl.
		Northern prawn	5	-18.2 ± 0.3 (-18.7, -18)	15.7 ± 0.6 (14.8, 16.1)	Dupuis-Smith et al. unpubl.
		<i>Themisto libellula</i>	5	-20.4 ± 0.4 (-20.8, -19.8)	11.8 ± 0.7 (10.4, 12.2)	Dupuis-Smith et al. unpubl.

Discussion

Based on stomach content analysis alone, black-legged kittiwake diet in the Canadian Arctic was dominated by Arctic cod, as expected based on other regions in the Arctic (Gaston 1988; Dahl et al. 2003; Matley et al. 2012; Vihtakari et al. 2018). Indeed, black-legged kittiwakes are opportunistic piscivores, generally taking the most abundant schooling prey (Hatch et al. 2020), and Arctic cod is one of the most abundant pelagic fishes in the Canadian Arctic Archipelago (Darnis et al. 2012; LeBlanc et al. 2020). These results differ from those observed in kittiwakes in the southern portion of their range, where birds primarily consumed open water-associated fishes, such as capelin and sandlance (Lavoie et al. 2012), reinforcing the importance of Arctic cod in the diet of Arctic-breeding black-legged kittiwakes (Gaston 1988; Matley et al. 2012; Vihtakari et al. 2018), but also illustrating the adaptive nature of this species across its breeding range.

Our findings were consistent with some of the earlier studies from the Canadian Arctic (Gaston 1988; Matley et al. 2012). For example, approximately 40 years prior to our study, on Hantzsch Island, Nunavut, Gaston (1988) found a 97% occurrence of fishes (Arctic cod and snailfishes) in kittiwake regurgitates, with lower proportions of crustaceans, molluscs, and annelids. These results are not directly comparable, however, as stomach content samples may be more biased towards hard-bodied organisms than regurgitate analyses (Barrett et al. 2007), and Hantzsch Island is located in the low Arctic, approximately 600-1300 km south of Qikiqtarjuaq and Pond Inlet, respectively, which may influence species composition (Provencher et al. 2012). However, observational studies of kittiwakes at-sea in the High Arctic near Cornwallis Island, Nunavut,

also suggest that kittiwakes rely heavily on Arctic cod when foraging (Matley et al. 2012). Interestingly, Karnovsky et al. (2008) found a higher proportion of the amphipod *T. libellula* compared to Arctic cod in kittiwake stomachs collected from the North Water Polynya (located in northern Baffin Bay, between Devon/Ellesmere Islands and Greenland) in the summer and fall, but this relationship was reversed in spring. Our samples were collected at the end of the breeding period, thus while it is possible that the high occurrence of Arctic cod results from kittiwakes trying to increase their energetic stores prior to migration, this may also reflect the availability of Arctic prey at these sites at that time of year.

Importantly, differences in the digestive rate of hard prey items (e.g., otoliths) compared to soft-bodied organisms (e.g., invertebrates) likely impacts the estimates of the proportions of prey items in the diet (Iverson et al. 2007). Indeed, only two soft-bodied organisms were identified in stomach samples; one northern prawn and one Euphausiidae species. Moreover, four stomachs had no apparent gut content and of the remainder, most contents were heavily digested. Thus, while it was evident during dissection that kittiwakes consumed invertebrate species (e.g., many invertebrate legs were present), it was not possible to identify these to a reasonable taxonomic level. Karnovsky et al. (2008) examined three seabird species in the North Water Polynya and noted similar issues, where 25% of birds had empty stomachs. This reinforces the need to assess kittiwake diet using additional methods, such as stable isotope analysis.

Stable carbon values were relatively depleted in kittiwake livers in 2021 ($-21.0 \pm 0.4\text{‰}$) and 2018 ($-21.1 \pm 0.3\text{‰}$; Provencher et al. 2020) compared to kittiwake muscles from western

Greenland in 2003 ($-19.5 \pm 0.4\text{‰}$; Linnebjerg et al. 2016) and the North Water Polynya in 1998-1999 ($19.3 \pm 0.1\text{‰}$; Hobson et al. 2002; Karnovsky et al. 2008). In terms of predator and prey relationships, kittiwakes were more depleted in $\delta^{13}\text{C}$ than their potential prey items (Figure 4.4). While it is possible that there are invertebrates with more depleted $\delta^{13}\text{C}$ values that we are missing in this analysis, these differences may result from spatial differences in sampling locations of the birds and their prey (i.e., sampling pelagic-feeding kittiwakes versus benthic fishes and invertebrates) or differences in prey among these regions.

Stable nitrogen values in kittiwake livers were slightly higher in 2018 than 2021, but were generally similar to kittiwake livers from Lancaster Sound, Nunavut in 1988 and 1999 (mean $16.6 \pm 1.0\text{‰}$, but values also varied between years; Hobson 1993). Interestingly, $\delta^{15}\text{N}$ values in kittiwake muscle from the North Water Polynya ($13.7 \pm 0.2\text{‰}$; Hobson et al. 2002) and western Greenland ($12.1 \pm 0.8\text{‰}$, Linnebjerg et al. 2016) were markedly lower than that of liver in this study, suggesting that birds in these regions may be consuming more lower trophic level prey. Again, as the turnover rate for liver is shorter than that of muscle, $\delta^{15}\text{N}$ values are expected to be higher in liver, thus comparisons between these tissues should be interpreted with caution (Hobson 1993). Despite this, while stomach content analyses from our study and previous studies in Canada (e.g., Gaston 1988; Karnovsky et al. 2008) indicate a predominantly Arctic cod diet, stable isotope results suggest the consumption of other, lower trophic level prey.

Black-legged kittiwakes are known to eat a variety of prey species at the surface, including amphipods, copepods, and pteropods (Karnovsky et al. 2008; Vihtakari et al. 2018). Indeed, early

research from Lancaster Sound suggested that amphipods contributed 50 to 80% of kittiwake diet (Hobson 1993), thus it is likely that invertebrates play more of a role in kittiwake diet composition than stomach content analyses suggest. Other surface-feeding seabirds in the Canadian Arctic, such as northern fulmars (*Fulmarus glacialis*), have also been reported to consume high levels of invertebrates during the breeding season (Mallory et al. 2010). These soft-bodied organisms can digest easily (i.e., may be underrepresented in stomach content analyses) and were not captured in the benthic trawls in this study, but may influence carbon or nitrogen signatures in birds if they are consumed in large quantities. For example, the consumption of copepods (e.g., *Calanus spp.*) and pteropods (e.g., *Limacina spp.*) could result in lower $\delta^{15}\text{N}$ values that ultimately decrease the overall trophic level of the bird (Dahl et al. 2003; Linnebjerg et al. 2016). Future work should therefore attempt to examine the occurrence of soft-bodied organisms that may be underrepresented in stomach samples.

The differences in diet between stomach content and stable isotope values may result from a variety of factors. First, most stomachs contained only indigestible, hard prey items (e.g., otoliths, other bones, rocks), which may lead to an underestimation of invertebrate species (Jackson and Ryan 1986; Hilton et al. 2000; Barrett et al. 2007). Indeed, birds were collected actively foraging at sea, thus it is possible that birds were searching for prey but had not recently ingested any, or had recently regurgitated either prior to sampling or upon death (Barrett et al. 2007). Second, stable isotope values can vary temporally and spatially due to changes in water temperature (Bloomfield et al. 2011), nutrient availability (Pastor et al. 2013), prey sources and more (Hobson 1993; Karnovsky et al. 2008; Mallory et al. 2010). Temporally, $\delta^{15}\text{N}$ values in

kittiwake livers differed between years in Qikiqtarjuaq, similar to earlier records in Lancaster Sound (Hobson 1993). As there is high inter-year variability in sea ice concentrations in the waters around Pond Inlet and in Lancaster Sound in general (Pratte et al. 2019; Gutowsky et al. 2022), differences in isotopic signatures could result from the differences in sampling years between predator and prey. Spatially, comparing pelagic, surface-feeding kittiwakes to benthic invertebrates is difficult because carbon is generally more depleted in offshore, deeper waters (Peterson and Fry 1987), thus future studies should aim to collect predator and prey samples from the same area at the same time of year. Finally, there are both inter- and intraspecific differences in discrimination factors among species and tissues, which are heavily influenced by prey sources and environmental conditions. Here, we corrected stable isotope values for black-legged kittiwake livers using an average discrimination factor for a related species, the ring-billed gull (*Larus delawarensis*; Hobson 1993). In addition to being from a different species, these samples were from juveniles collected in the western Canadian Arctic in the late 1980s, and thus may vary due to differences in diet, time and space (Hobson 1993; Hatch et al. 2020; Pollet et al. 2020).

Despite these limitations, stomach content analyses suggested that black-legged kittiwakes in the Canadian Arctic rely on Arctic cod, consistent with other studies in the Canadian (Gaston 1988; Matley et al. 2012) and European Arctic (Mehlum and Gabrielsen 1993; Weslawski et al. 1994; Barrett 1996; Vihtakari et al. 2018). Arctic cod mainly feed on sea-ice algae, copepods and/or amphipods near ice edges, and are therefore highly dependent on sea ice in the early stages of their life (i.e., spring to summer; Bouchard et al. 2016). As juveniles, they transition to feeding in

surface waters until the fall, eventually moving to deeper waters, segregated by size, for the winter (Geoffroy et al. 2016, 2023; LeBlanc et al. 2020). Black-legged kittiwakes in this study generally consumed cod ranging from 55 to 166 mm, indicative of juvenile to age-1+ fish typically found in surface or shallow waters (Geoffroy et al. 2023), consistent with kittiwakes from other regions in the Arctic (Springer et al. 1984; Bouchard et al. 2016). As the Arctic cod sampled from benthic trawls would have primarily been older individuals in more benthic habitats, future research on potential prey items collected near the surface is encouraged.

As rising sea surface temperatures and rapid declines in sea ice continue to alter Arctic ecosystems, cod populations may decline and/or shift northward, replaced by more sub-Arctic fish species such as capelin and sandlance (Steiner et al. 2019; Cote et al. 2021). This shift in prey has already been observed in kittiwakes in the European Arctic (Vihtakari et al. 2018) as well as thick-billed murres (*Uria lomvia*) in the Canadian Arctic (Gaston et al. 2003), with possible negative implications for breeding success and survival in these populations. While the Canadian High Arctic has not yet experienced large declines in sea ice concentrations (Gutowsky et al. 2022), coastal sea ice loss is projected to be higher in more northern communities (including Pond Inlet; Cooley et al. 2020). The cumulative impacts of ocean warming, sea ice declines, and freshwater inputs (e.g., glacial runoff) in this region may lead to shifts in prey, increased competition, and new predators for Arctic cod (Geoffroy et al. 2023). These changes may have substantial impacts on Arctic cod populations in this area (Geoffroy et al. 2023), and in turn, impact the marine predators that rely on them (Gaston et al. 2003; Matley et al. 2012), particularly in regions where sympatrically breeding species rely on the same prey sources. For

example, both northern fulmars (Mallory et al. 2010) and thick-billed murre (Provencher et al. 2012) in the Canadian Arctic also consume relatively high proportions of Arctic cod. As these species breed sympatrically with black-legged kittiwakes near both Qikiqtarjuaq and Pond Inlet (Mallory et al. 2019), shifts in the distribution or abundance of Arctic cod may have broader implications for this trophic community as a whole.

Overall, we found that black-legged kittiwakes in the Canadian Arctic rely heavily on Arctic cod as a key prey item, but that stomach content analysis likely underestimates other important prey species, such as marine invertebrates. Indeed, the mismatch between the stable isotope values of the birds and the fish species suggests a high consumption of invertebrates that was not captured in stomach content analyses. Future research should therefore use a combination of methods, such as regurgitates, faecal samples, and DNA barcoding, stable isotope analysis, and/or stomach content analysis, to consider potential biases in methodology, but also potential spatial and temporal effects of Arctic sea ice phenology (Mallory et al. 2010). This study provides an important benchmark for monitoring changes in black-legged kittiwake diet in a rapidly changing Arctic. As the ongoing decline of sea ice across the Arctic reshapes prey distribution and increases pressures on sympatrically breeding seabirds, a comprehensive understanding the diet of Arctic seabirds will be crucial in interpreting shifts in the marine environment and assessing consequential impacts on these Arctic-breeding species.

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LINKING STATEMENT

Understanding seabird diet can provide important information on a variety of threats and how this may impact seabird health. For example, shifts in prey species may influence stress, energetics, or contaminant concentrations. In Chapter 4, I examined diet in black-legged kittiwakes to better understand what these gulls are consuming in the Canadian Arctic and how this may change as climate change impacts increase in this region. Black-legged kittiwakes heavily rely on Arctic cod, but that stomach content analysis may underestimate the number of soft-bodied organisms that this species may consume. As ocean temperatures continue to increase in the Arctic, consequently reducing sea ice concentrations, black-legged kittiwakes may shift to more open-water associated prey as ice-associated species shift northward. In addition to the potential implications these changes may have on individual health or reproduction, these shifts may inadvertently increase exposure to other threats, such as plastic pollution and chemical contaminants. In Chapter 5, I expand on this research by dissecting the birds from the previous chapter for plastic pollution. Here, I present new data and review historical information on plastic ingestion by four seabird species in Canada: northern fulmars, black-legged kittiwakes, thick-billed murres and black guillemots. I provide insights on the methodological, spatial, and temporal trends in plastic ingestion by these species across Canada. By monitoring changes in diet and other threats, such as plastic pollution, we can better understand the potential cumulative impacts of these threats on Arctic seabird populations.

CHAPTER 5: DECADES OF MONITORING PLASTIC POLLUTION IN SEABIRDS IN CANADA: SPATIAL, TEMPORAL AND METHODOLOGICAL INSIGHTS

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Abstract

Plastic ingestion by seabirds is an increasing issue worldwide, yet species can vary in ingestion based on ecological and morphological differences. This provokes the ecological question of which species are better suited to monitor plastic ingestion across regions and time. In Canada, we examined plastic ingestion in sympatric northern fulmars (*Fulmarus glacialis*), black-legged kittiwakes (*Rissa tridactyla*), thick-billed murres (*Uria lomvia*), and black guillemots (*Cepphus grylle*). Here, we present new data and compare to historical work to inform plastic pollution monitoring in Canada. In 2021, 62% of fulmars, 7% of kittiwakes and 7% of murres contained plastic, whereas guillemots had no pieces >1 mm. Regardless of the methods used to collect and process samples, fulmars continue to have low levels of ingestion compared to the European Arctic, but high levels compared to other species in the Canadian Arctic, emphasizing their continued utility as a monitoring tool for plastic pollution in Canada.

Keywords

Arctic; bioindicator; long-term monitoring; plastic ingestion; standardized; trends

Highlights

- We review data and present new data on plastics in four seabird species in Canada.
- Plastic ingestion appears to be stable in kittiwakes, murres and guillemots.
- Plastic ingestion by fulmars increased at two colonies, but remains stable in others.
- Fulmars exhibit a north-south plastic gradient, with lower ingestion in the north.
- Continued higher plastics in fulmars underscores their utility as a monitoring tool.

Introduction

Plastic pollution is an increasing and widespread issue worldwide, including in remote areas with less human activity, such as the Arctic (Bergmann et al., 2022), which is already under severe threat due to changes in climate (AMAP, 2021). Indeed, plastic pollution has been found across the Arctic environment, including seawater (Huntington et al., 2020; Morgana et al., 2018), the sea floor (Tekman et al., 2017), beaches (Pollet et al., 2023), snow (Bergmann et al., 2019), and sea ice (Peeken et al., 2018). Once in the environment, plastic pollution can be ingested by biota, and has been reported in various Arctic species, including zooplankton (Huntington et al., 2020), invertebrates (Fang et al., 2018), fish (Kühn et al., 2018; Morgana et al., 2018), marine mammals (Moore et al., 2021) and seabirds (Baak et al., 2020a). Due to their high trophic position, sensitivity to changes in the marine environment, and accessibility at central breeding colonies, seabirds are often used as indicators of ecosystem health (Parsons et al., 2008), and consequently, are one of the most widely studied animal groups for plastic pollution in the Arctic and across the globe (Bergmann et al., 2022). Over half of seabird species both worldwide (Kühn and van Franeker, 2020) and in the Arctic (Baak et al., 2020a) are reported to have ingested plastic debris, and multiple regions have developed monitoring programs to examine trends in plastic pollution ingestion by seabirds. For example, northern fulmars (*Fulmarus glacialis*) are used as indicators of plastic pollution across northern waters (van Franeker et al., 2011), including the Arctic, due to their widespread distribution and susceptibility to plastic ingestion (e.g., Environment and Climate Change Canada, 2020; Kühn et al., 2022). Indeed, multiple regions have co-developed harmonized protocols to collect, analyze and report plastic pollution ingestion in this species (Baak et al., 2021; OSPAR, 2015; Provencher et al., 2019; van Franeker et al., 2021).

Despite the development of various protocols to collect, analyze and report plastic ingestion by seabirds, methods have not always been consistent across the Arctic. Indeed, Baak et al. (2020a) found that less than one third of studies used methods that would allow plastic ingestion to be compared quantitatively across regions and time. For example, samples may be collected from beached birds (e.g., Avery-Gomm et al., 2012), bycatch birds (e.g., Mallory et al., 2006) or birds sacrificed for scientific research (e.g., Poon et al., 2017), and may be processed using standardized methods (e.g., flushing stomach contents over a 1 mm sieve to ensure plastic pieces are not missed; Hanifen et al. this issue) or not (e.g., directly examining stomach contents in a petri dish; Byers et al., 2010; Mallory, 2008). Additionally, many studies had small sample sizes or did not report key metrics, such as the minimum size of plastics detected (Baak et al., 2020a), making it difficult to compare plastic ingestion in seabirds across various spatial and temporal scales. As declines in sea ice increase opportunities for more shipping, fisheries and tourism activities in the north, plastic pollution in the Arctic will continue to increase, highlighting the importance of using seabirds as a tool to monitor the spatial and temporal trends of this environmental pollutant.

Importantly, plastic ingestion by seabirds can vary based on various ecological and morphological differences. For example, surface-feeding seabirds, such as northern fulmars (hereafter “fulmars”) and black-legged kittiwakes (*Rissa tridactyla*; “kittiwakes”), are more susceptible to plastic ingestion than pursuit-diving seabirds, such as thick-billed murres (*Uria lomvia*; “murres”) and black guillemots (*Cepphus grylle*; “guillemots”), as plastic pollution

generally concentrates on the ocean's surface (Egger et al., 2022) or on the sea floor (Choy et al., 2019). Moreover, morphological differences, such as the relative ability (kittiwakes) or inability (fulmars) to regurgitate indigestible prey items (e.g., bones), may also result in differences in plastic pollution accumulation in birds (Poon et al., 2017). Procellariiformes, an order of pelagic seabirds that includes fulmars, albatrosses, shearwaters and petrels, generally have the highest levels of plastic ingestion globally due to their foraging ecology, range and diet (Roman et al., 2019). This prompts the ecological question of which species are better suited for monitoring plastic pollution ingestion across regions and time.

Canada is one of the leading Arctic states in monitoring plastic pollution ingestion by seabirds, with over 16 sites examined in the Canadian Arctic (Baak et al., 2020a), and various long-term studies in other regions of the country (e.g., murre in Newfoundland; Bond et al., 2013). The first report of plastic pollution ingestion by seabirds in the Canadian Arctic was in 1978 (M.S.W. Bradstreet, unpubl. data in Day et al., 1985), and there are now over four decades of plastic ingestion data across the country (e.g., Baak et al., 2020b; Bond et al., 2013; Day et al., 1985; Mallory, 2008; Poon et al., 2017; Provencher et al., 2014). Indeed, in 2017, the Canadian government dedicated funding to monitor plastic ingestion by seabirds, focusing on four key seabird species: fulmars, kittiwakes, murre and guillemots. These species were selected in part due to their ecological and morphological differences, but also their accessibility in some of the more logistically challenging landscapes in Canada (i.e., the High Arctic; Mallory et al., 2018). In 2020, the fulmar was officially designated as an indicator of plastic pollution in Canada by the federal government (Environment and Climate Change Canada, 2020), following similar actions

pursuant to the Convention for the Protection of the Marine Environment of the North-East Atlantic (OSPAR) in Europe (Kühn et al., 2022). Both of these programs share a similar target of >10% of fulmars containing >0.1 g of plastic pollution (Environment and Climate Change Canada, 2020; Kühn et al., 2022). To work towards meeting this target, long-term monitoring of plastic ingestion by fulmars and other seabirds is required to inform policy decisions on plastic pollution in Canada and across the globe (Linnebjerg et al., 2021).

Currently, there are nine sites across Canada with multi-year data on plastic ingestion by fulmars, kittiwakes, murre, or guillemots (Figure 5.1). There is a need to provide data and evidence on plastic pollution trends in the marine environment in relation to the ongoing development of plastic pollution reduction policies. This includes understanding how different species are affected by plastic pollution over time, across sites, and in relation to each other as bioindicators are considered for monitoring trends. Here, we present new data and summarize previous research on plastic ingestion by these four seabird species in Canada to: 1) highlight temporal, spatial and methodological trends; and 2) inform future plastic pollution monitoring in Canada and worldwide.

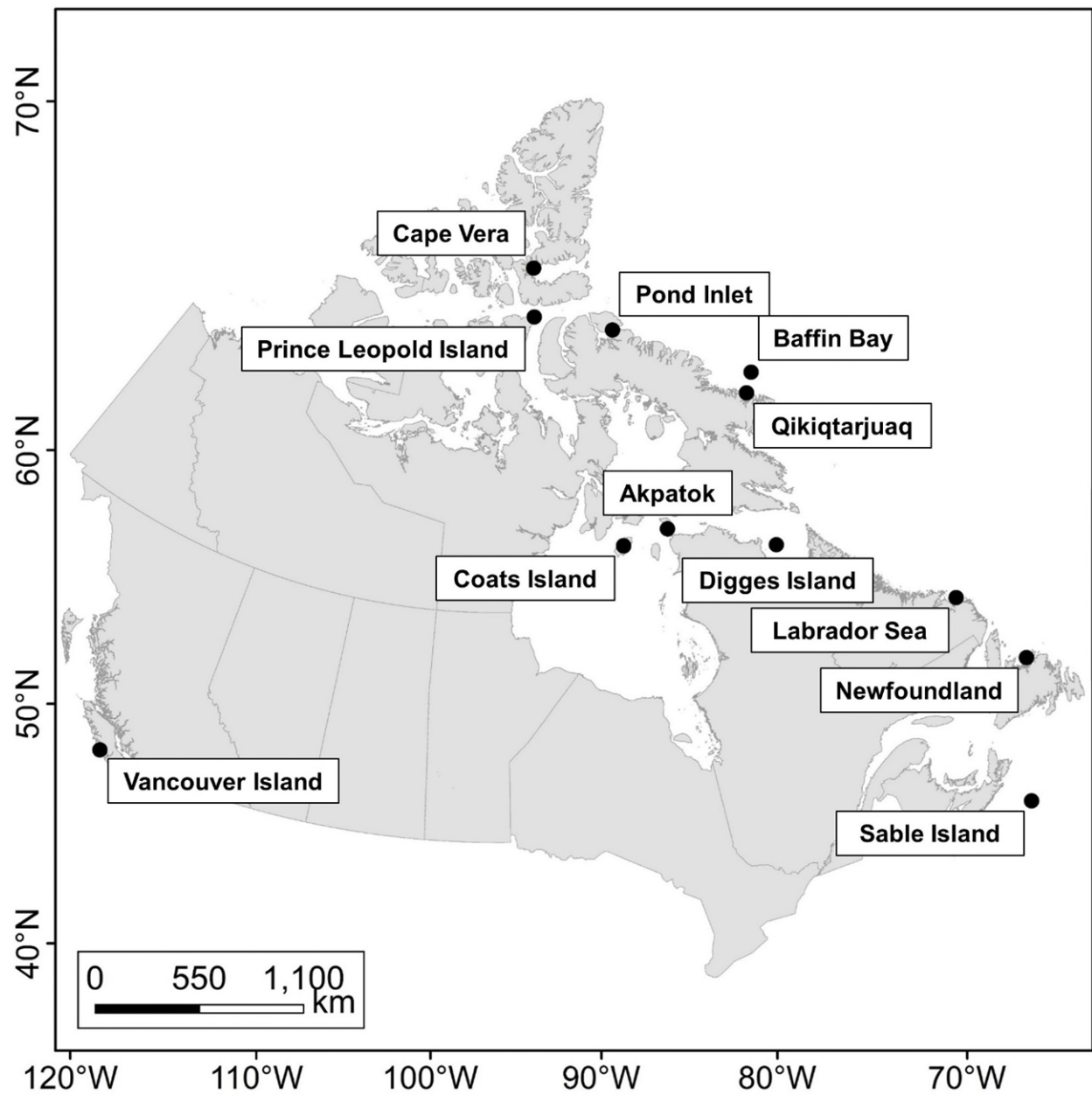


Figure 5.1: Locations of sampling sites for northern fulmars (*Fulmarus glacialis*), black-legged kittiwakes (*Rissa tridactyla*), thick-billed murres (*Uria lomvia*), and black guillemots (*Cepphus grylle*) sampled for plastic pollution monitoring in Canada from 1978 to 2022.

Methods

New information on plastic ingestion

Black-legged kittiwakes and black guillemots were collected using a 12-gauge shotgun by Inuit hunters in areas where birds were actively feeding during the breeding season in 2021 near Qikiqtarjuaq, Nunavut (kittiwakes: $n = 20$; guillemots: $n = 29$), and Pond Inlet, Nunavut (kittiwakes: $n = 19$; guillemots: $n = 1$; Table 5.1; Figure 5.1). As only one black guillemot was collected in Pond Inlet in 2021, Inuit hunters returned in 2022 and captured an additional 21 guillemots using the same methods. All collections were carried out under the necessary territorial (Government of Nunavut; 2021-041, 2022-033) and federal (ECCC; SC-NR-2021-NU-003 and MM-NR-2021-NU-006) collection and research permits. Upon collection, carcasses were frozen and shipped to Acadia University in Nova Scotia, Canada, where the gastrointestinal tract (proventriculus and gizzard) was removed for analysis. These samples were collected as a part of a long-term monitoring program and will be used in a suite of other studies (e.g., diet analyses, other contaminant analyses, etc.) and unused portions of each specimen were stored in the National Wildlife Specimen Bank in Ontario, Canada for future research. Additionally, in 2008, five black-legged kittiwakes breeding on Prince Leopold Island were captured with a noose pole and euthanized via cervical dislocation (Table 5.1; Figure 5.1). Carcasses were frozen and shipped to the Nunavut Arctic College, where gastrointestinal tracts were removed, re-frozen, and shipped to Acadia University for analysis of plastic pollution. For all samples, each gastrointestinal tract was slit longitudinally then flushed over a 1 mm sieve, where all plastic items were removed and confirmed under a light microscope. Plastic pieces were then identified,

measured and analyzed following standardized methods for data collection, analysis and reporting (Baak et al., 2021; Provencher et al., 2019, 2017; van Franeker et al., 2011).

Table 5.1: Locations, sample years, sample sizes (*n*) and frequency of occurrence (FO) of plastic pollution in northern fulmars (*Fulmarus glacialis*), black-legged kittiwakes (*Rissa tridactyla*), thick-billed murres (*Uria lomvia*), and black guillemots (*Cepphus grylle*) in Canada from 1978 to 2022.

Species	Location	Sample year	<i>n</i>	FO	Source
Northern fulmar	Vancouver Island	2009-2010	36	97	Avery-Gomm et al. 2012*
	Cape Vera	1980-1984	233	0	Byers et al. 2010
		2003-2004	102	31	Mallory 2008
	Baffin Bay	2002	42	36	Mallory et al. 2006
	Labrador Sea	2014	39	64	Avery-Gomm et al. 2018
		2015	31	97	Avery-Gomm et al. 2018
	Pond Inlet	1978-1979	214	40	M.S.W. Bradstreet unpub. in Day et al., 1985
		2021	29	62	Hanifen et al., <i>this issue</i>
	Prince Leopold Island	2008	10	80	Provencher et al. 2009
		2013	9	89	Poon et al. 2017
	Qikiqtarjuaq	2008	15	87	Provencher et al. 2009
		2018	29	72	Baak et al. 2020b
		2021	29	62	Hanifen et al., <i>this issue</i>
	Sable Island	2001	1	100	Bond et al. 2014
		2002	1	100	Bond et al. 2014

		2003	1	100	Bond et al. 2014
		2004	13	100	Bond et al. 2014
		2005	37	95	Bond et al. 2014
		2006	12	100	Bond et al. 2014
		2007	32	81	Bond et al. 2014
		2008	15	87	Bond et al. 2014
		2009	21	95	Bond et al. 2014
		2010	7	100	Bond et al. 2014
		2011	32	97	Bond et al. 2014
		2012	4	100	Bond et al. 2014
		2022	3	100	Hanifen et al., <i>this issue</i>
Black-legged kittiwake	Pond Inlet	1978-1979	50	12	M.S.W. Bradstreet unpub. In Day et al. 1985
		2021	19	0	This study
	Prince Leopold Island	2008	5	20	This study
		2013	11	9	Poon et al. 2017
	Qikiqtarjuaq	2018	20	15	Baak et al. 2020b
		2021	20	15	This study
Thick-billed murre	Akpatok	2008	31	23	Provencher et al. 2010
	Coats Island	2006	16	0	Provencher et al. 2014
		2007	25	4	Provencher et al. 2010
	Digges Sound	2008	30	17	Provencher et al. 2010
		2009	61	7	Provencher et al. 2010
	Newfoundland	1985-1986	1249	8	Bond et al. 2013*
		1996-1997	310	5	Bond et al. 2013*

		2005	11	0	Provencher et al. 2014
		2006	15	0	Provencher et al. 2014
		2011-2012	32	10	Bond et al. 2013*
	Pond Inlet	1978-1979	283	1	M.S.W. Bradstreet unpub. In Day et al. 1985
		2021	21	10	Maddox et al., <i>this issue</i>
	Prince Leopold Island	2008	50	0	Provencher et al. 2010†
		2013	10	0	Poon et al. 2017
	Qikiqtarjuaq	2007	30	2	Provencher et al., 2010
		2008	20	0	Provencher et al., 2010
		2018	30	0	Baak et al. 2020b
		2021	22	5	Maddox et al., <i>this issue</i>
Black	Cape Vera	1980-1984	45	0	Byers et al. 2010
guillemot					
	Pond Inlet	2021	1	0	This study
		2022	21	0	This study
	Prince Leopold Island	2013	3	0	Poon et al. 2017
	Qikiqtarjuaq	2018	30	0	Baak et al. 2020b
		2021	29	0	This study

*Data from outside of the breeding season.

†Data from outside of the breeding season not included from this study.

Statistical analysis

In addition to the above samples, we obtained historical data from previous published research (Table 5.1) on plastic ingestion by fulmars, kittiwakes, murre and guillemots to examine spatial

and temporal trends in plastic ingestion across Canada. All statistical analyses were conducted in RStudio 1.3.1073 (R Core Team, 2022). We used Fisher's Exact Tests to determine if the frequency of occurrence of plastic ingestion differed between species and/or years. If previously published data were analyzed for temporal trends, we report that test result here and cite the manuscript accordingly. We considered significance at $p \leq 0.05$ and means are presented ± 1 standard deviation (SD).

Results

New information on plastic ingestion

In 2008, one of five (20%) kittiwakes contained plastic (Table 5.1). That individual contained two pieces of plastic >1 mm in size (Table 5.2). Both pieces were user plastics (fragments), where one was green and the other was an off/white-clear colour. In 2021, 62% of fulmars and 7% of murre from Qikiqtarjuaq and Pond Inlet contained plastic (Table 5.1), and details on these species are published elsewhere (Hanifen et al., this issue; Maddox et al., this issue). There were no plastics found in guillemots from Qikiqtarjuaq in 2021, or Pond Inlet in 2021 or 2022. Similarly, there were no plastics found in kittiwakes from Pond Inlet in 2021, but 15% of kittiwakes from Qikiqtarjuaq contained plastics in 2021 (Table 5.1). Of these, individuals contained a range of one to four pieces of plastic >1 mm in size (Table 5.2), but one individual had approximately 17 plastic pieces that were <1 mm in size (potentially one large piece that was ground up in the gizzard). All plastic pieces from all individuals were fragments of off/white-clear colour. In 2021, the frequency of occurrence of plastic ingestion by fulmars was significantly higher than kittiwakes, murre and guillemots in Qikiqtarjuaq (Fisher's Exact Test

for multiple comparisons; all $p > 0.02$) and kittiwakes and murre in Pond Inlet (all $p > 0.001$; black guillemots not assessed due to limited sample size).

Methodological differences

We reviewed 16 studies on plastic ingestion by fulmars, kittiwakes, murre and guillemots in Canada (17 including the results presented in this study), where 74% of samples for a given species, region and year were collected by sacrificing birds, 24% (three studies) were collected from beaches and 2% (one study) was bycatch. Standardized methods for examining plastic ingestion by seabirds recommend the use of a 1 mm sieve in sample processing to ensure plastic pieces are not missed and a light microscope to confirm potential plastic pieces (e.g., Provencher et al., 2017; van Franeker et al., 2011), unless plastic pieces are <1 mm in size, where polymer identification is recommended (not considered in this study). Of the 17 studies (57 sample groups for a given species, region, and year), 54% used a 1 mm sieve in sample processing, 12% did not, and the remainder were unknown, where 15 sample groups referenced standardized methods in their study but did not indicate whether this specific method was used, and the remainder (4 sample groups) did not cite standardized methods. If we consider citations of these protocols as confirmation that a sieve was used, the total number of sample groups processed using a sieve increases to 46 (81%). Forty percent of sample groups that contained plastic pieces were confirmed using a microscope, while the remainder were not. Generally, more recent studies include the use of these recommended methods, whereas earlier studies do not. For example, the average sample year for sample groups where sieves were used during processing was 2015 (± 6 years), whereas the average sample year was 1987 (± 11 years) for sample groups where sieves were not used. Importantly, all studies from 2017 onwards reported using standard recommended methods.

Trends in plastic ingestion

Black guillemots have been assessed for plastic pollution across four regions in Arctic Canada (Qikiqtarjuaq, Pond Inlet, Prince Leopold Island and Cape Vera). Plastic pollution >1 mm in size has not been detected in guillemots in Canada to date, thus below we limit the discussion on temporal trends in plastic ingestion to fulmars, kittiwakes and murre.

Northern fulmars have been sampled across eight regions in Canada, where the overall mean frequency of occurrence of plastic was 48% (± 50) but ranged from 0 to 100% (Figure 2.2). Of these eight sites, five had multiple years of data that allowed us to assess temporal trends in plastic ingestion (Baffin Bay and Vancouver Island could not be assessed due to single time points or limited sample sizes). Frequency of plastic ingestion was stable in the Labrador Sea (Avery-Gomm et al., 2018; 2014-2015), Prince Leopold Island (Poon et al., 2017; 2008-2013), Qikiqtarjuaq (Fisher's Exact Test, $p = 0.09$; 2008-2021) and Sable Island ($p = 0.21$; 2001-2022), but increased at Cape Vera ($p < 0.001$; 1980-2004) and Pond Inlet ($p = 0.04$; 1978-2021).

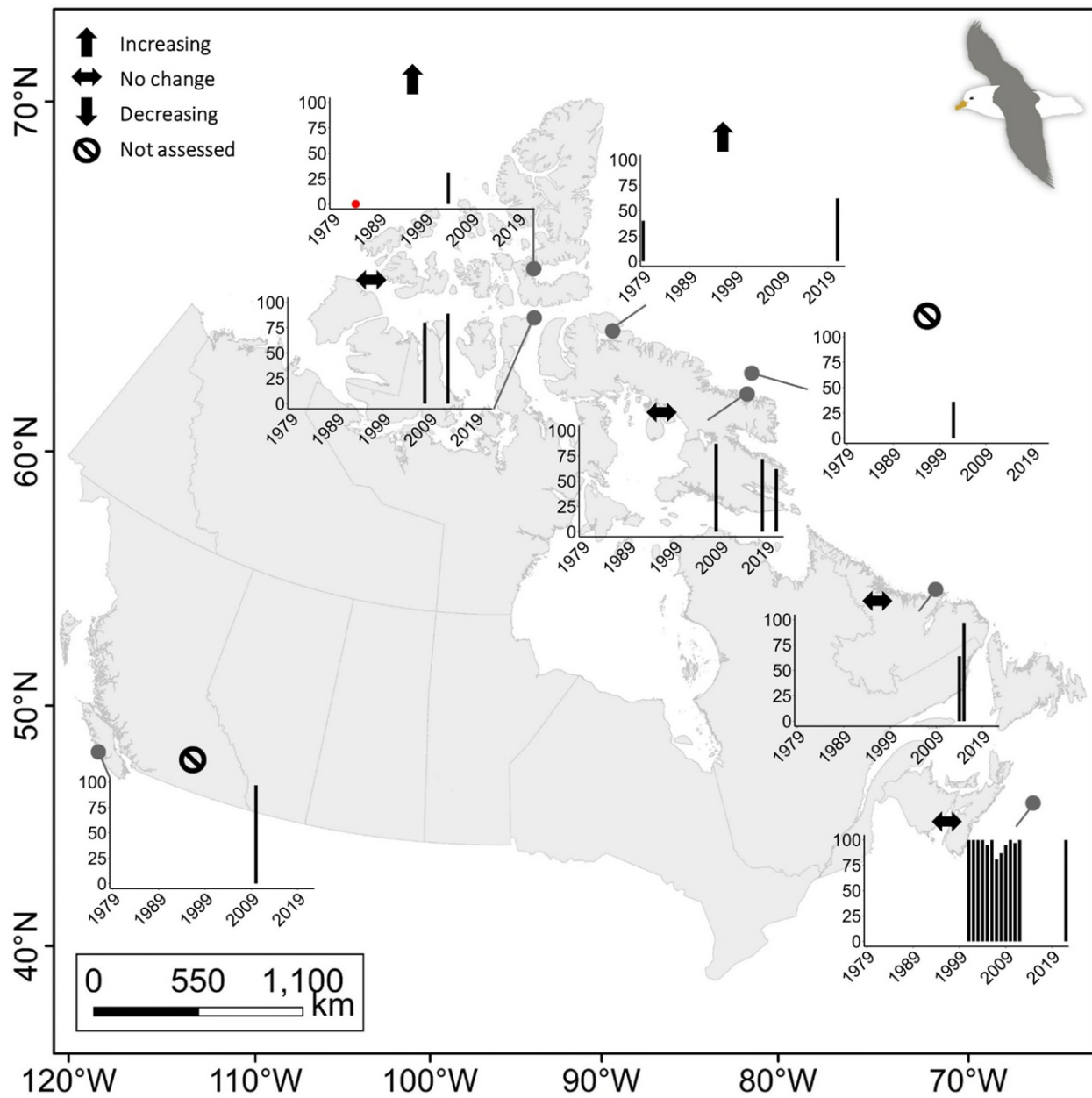


Figure 2.2: Average frequency of occurrence (%) and trend of plastic ingestion by northern fulmars (*Fulmarus glacialis*) across Canada. Red circles indicate a frequency of occurrence of zero in that year.

Black-legged kittiwakes have only been sampled across three regions in the Canadian Arctic, and the mean frequency of occurrence of plastic ingestion is 10% (± 31 ; range 0-20%; Figure 5.3). Frequency of plastic ingestion in Qikiqtarjuaq (Fisher's Exact Test; $p = 1.0$), Pond Inlet ($p = 0.18$) and Prince Leopold Island ($p = 0.33$) appeared to be stable between 2018-2021, 1978-2021, and 2008-2013, respectively.

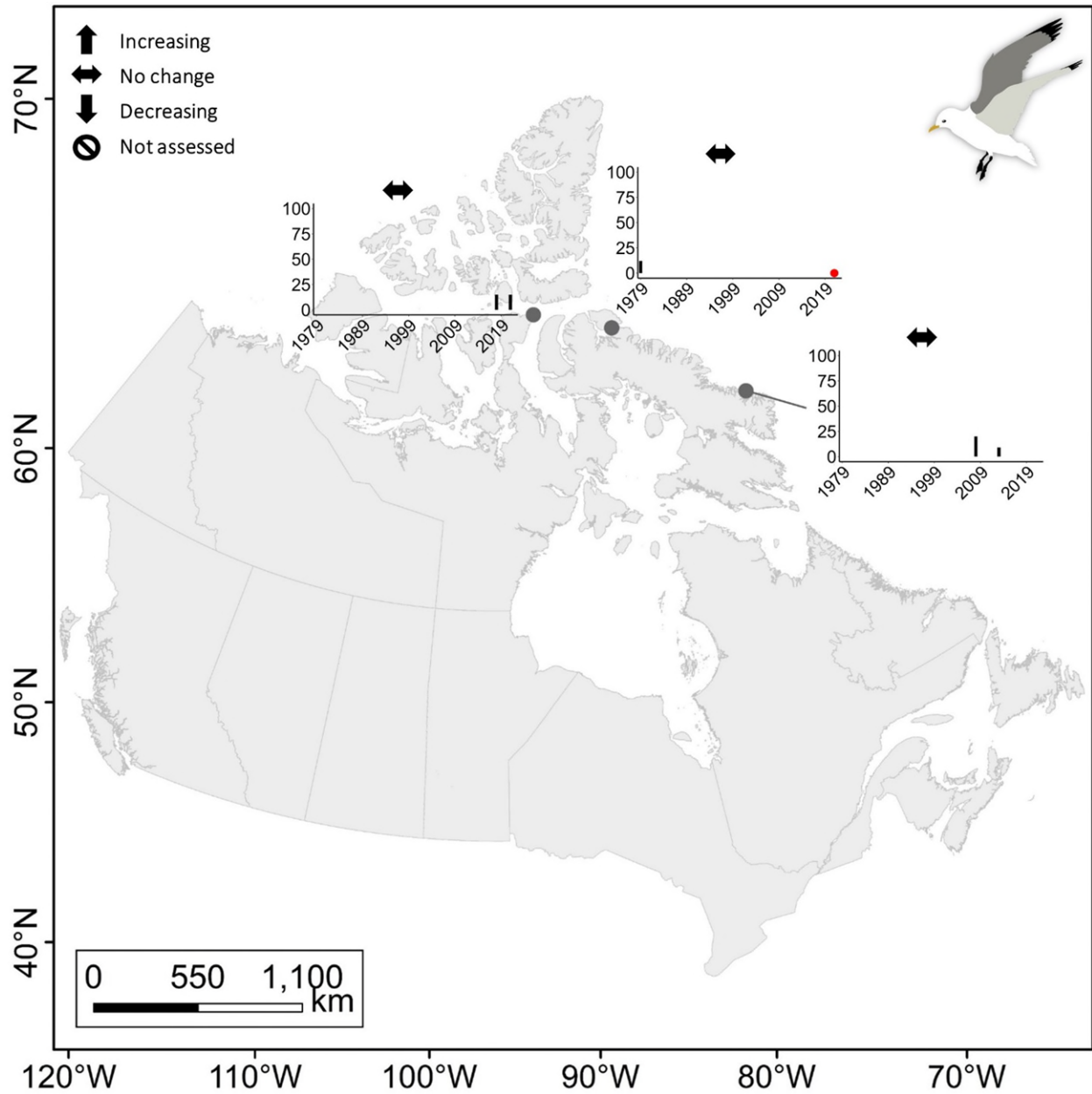


Figure 5.3: Average frequency of occurrence (%) and trend of plastic ingestion by black-legged kittiwakes (*Rissa tridactyla*) across Canada. Red circles indicate a frequency of occurrence of zero in that year.

Thick-billed murres have been sampled across eight regions in Canada, with an overall mean frequency of occurrence of 6% (± 24 , range 0-23%; Figure 5.4). While two sites could not be assessed for temporal trends (Akpatok and Labrador Sea), plastic pollution was generally stable in Qikiqtarjuaq (Maddox et al., this issue; 2007-2021), Prince Leopold Island (Poon et al., 2017; 2008-2013), Coats Island (Fisher's Exact Test; $p = 1.0$; 2006-2007), Digges Island ($p = 0.14$) and Newfoundland ($p = 0.25$; 1986-2012), but increased in Pond Inlet ($p = 0.02$; 1978-2021).

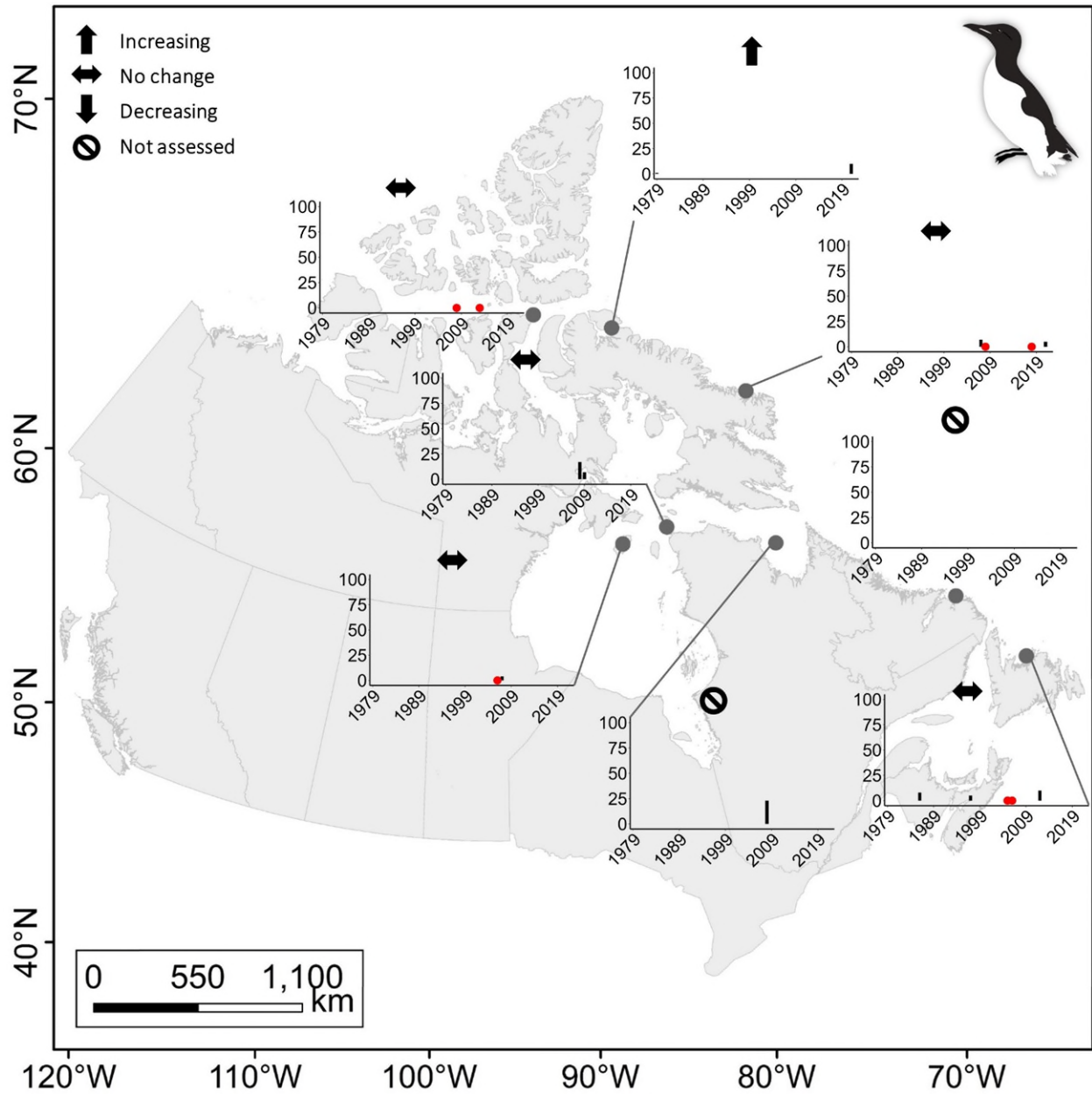


Figure 5.4: Average frequency of occurrence (%) and trend of plastic ingestion by thick-billed murre (*Uria lomvia*) across Canada. Red circles indicate a frequency of occurrence of zero in that year.

Discussion

We reviewed 16 studies on plastic ingestion by fulmars, kittiwakes, murres and guillemots in Canada, and presented new data on plastic ingestion by kittiwakes and guillemots. Our goal was to summarize the state of biomonitoring of plastic pollution in Canada, as indexed by plastic ingestion by four seabird species that differ in foraging strategies and feeding locations.

Monitoring of plastic pollution in other wildlife species is still in its infancy in Canada; relatively recent papers are presenting the first efforts to detect plastic debris in a few wildlife species, including waterfowl (English et al., 2015; Holland et al., 2016), seals (Bourdages et al., 2020) and whales (Moore et al., 2021). By comparison, seabird species have a more robust history of plastic research in Canada (Baak et al., 2020a; Provencher et al., 2015), and as we summarize here, seabirds have been monitored for several decades, albeit intermittently (and perhaps even “unintentionally”; Day et al., 1985), where some locations have only been sampled once (e.g., Vancouver Island). Nevertheless, seabirds provide our best biotic tool for examining plastic pollution trends temporally and, at least at present, spatially in Canada, particularly in the Arctic. Looking back over several decades in Arctic Canada, our results from 2021 were similar to previous years (e.g., Baak et al., 2020b; Poon et al., 2017), where some surface-feeding species (fulmars) contained more plastic than pursuit-diving species (murres and guillemots). Below, we consider the influence of differences in methodology and discuss trends in plastic ingestion by seabirds in Canada across species, regions, and time.

Methodological insights

The discussion on the importance of consistent or standardized methods in sample collection, processing and analysis is well documented (e.g., Avery-Gomm et al., 2016; Baak et al., 2020a; Poon et al., 2017; Provencher et al., 2019, 2017), and there have been both national (Provencher et al., 2015) and international (Baak et al., 2021; Kühn et al., 2022) efforts in the Arctic to standardize methods to allow for comparisons of plastic ingestion across species, regions and time. For example, differences in sample collection, such as beached birds or birds sacrificed for research, may result in differences in plastic ingestion, as body condition may be related to plastic ingestion (Charlton-Howard et al., 2023; Lavers et al., 2014; Ryan, 1987). This highlights the importance of either using consistent collection methods in long-term monitoring programs, or including the sampling method as a factor in analyses to ensure results are comparable over time. In Canada, most birds (74%) were sacrificed for plastic pollution research, while bycatch birds have only been used in one study (Mallory et al., 2006), and beached birds have only been collected in more southern regions of Canada (Vancouver Island and Sable Island). This was expected, as the vast, mostly uninhabited areas of the Canadian Arctic make it difficult to find beached birds, particularly in a timely manner before scavengers remove carcasses or decomposition deleteriously influences their use for plastic ingestion or other contaminants research (Pagel et al., 2012). Thus, most seabird samples from the Canadian Arctic are collected for plastic pollution research as well as a suite of other studies (other contaminant studies, diet studies, stable isotope analyses; e.g., Sühring et al., 2022). While the method of sample collection is often not a choice, as long as it is documented and considered in analyses, it may be possible to detect general trends across species, space or time.

Sample processing methods can also influence the detection of plastic pollution in a species. For example, Avery-Gomm et al. (2016) and Fife et al. (2015) both examined plastic ingestion by beached dovekies (*Alle alle*) from nearby areas (350 km apart) in Newfoundland at the same time of year, but plastic ingestion was more than twice as high in Avery-Gomm et al. (2016). Avery-Gomm et al. (2016) suggested that this difference may be a result of differences in sample processing, where they examined both the proventriculus and gizzard for plastic ingestion and processed samples over a 1 mm sieve (following standardized guidelines; OSPAR, 2015), whereas Fife et al. (2015) only examined the gizzard and did not rinse samples over a sieve. Indeed, studies have shown that plastic pollution can differ between the proventriculus and gizzard (e.g., Terepocki et al., 2017), and many monitoring programs recommend the use of a 1 mm sieve to ensure plastic pieces are not missed during processing (e.g., Provencher et al., 2017; van Franeker et al., 2011). In Canada, over half of samples were processed using a sieve and 40% were confirmed under a microscope, although since 2017, all studies used these standard procedures. Generally, the use of these methods seemed to increase over time, suggesting that recommendations for sample processing are being adopted across Canada, which should allow for more robust assessment of trends in plastic ingestion in the future.

There are also other factors that may influence the occurrence of plastic pollution in these species, such as age or time of year. Indeed, the amount of plastic in northern fulmars may differ between juveniles and adults (Avery-Gomm et al., 2012), but not always (Avery-Gomm et al., 2018), and a recent study from the European Arctic suggested that chicks ingest higher levels than adults (Collard et al., 2022). While most studies included in this review focused on adults

(but see Avery-Gomm et al., 2018, 2012), future work assessing the difference in plastic ingestion between age classes is encouraged. Similarly, plastic ingestion can differ based on the time of year that the samples were collected. For example, Mallory (2008) showed that plastic ingestion by northern fulmars at Cape Vera differed throughout the breeding season. While the majority of studies in Canada assess plastic pollution in birds during the breeding season (but see Table 5.1), many of these birds remain in Canadian waters (e.g., the Labrador Sea) throughout the non-breeding season, thus future work could assess plastic ingestion by these species in the non-breeding period. However, it is important to note that seabirds are less accessible when away from their breeding colonies, particularly in winter when harsh conditions and limited observations may reduce sample collection opportunities.

Trends in plastic ingestion

The differences in methodology throughout the studies within Canada influences our ability to compare spatial trends across regions. For example, while both studies on fulmars from Cape Vera (Byers et al., 2010; Mallory, 2008) did not use a 1 mm sieve and examined both the gizzard and proventriculus, and can thus be analyzed for temporal trends (see below), these studies cannot be easily compared spatially to other regions where sieves and other processing methods were used (e.g., Hanifen et al., this issue). Moreover, beached fulmars collected from Sable Island (e.g., Bond et al., 2014) have to be carefully compared to fulmars sacrificed for research (e.g., Baak et al., 2020b; Poon et al., 2017) or collected through bycatch (Mallory et al., 2006) due to these differences in sample collection methods. However, despite differences in methodologies and limited sample sizes in some years (e.g., $n = 3$ on Sable Island in 2022;

Hanifen et al., this issue), there is a clear north-south gradient in the frequency of plastic ingestion by fulmars (Figure 5.2). For example, fulmars from more southern regions (e.g., mean frequency of occurrence across years on Sable Island, Nova Scotia, 93%; Vancouver Island, 97%), generally have higher rates of plastic ingestion than those in higher latitudes (e.g., mean frequency of occurrence from south to north: Qikiqtarjuaq, 71%; Pond Inlet, 42%; Prince Leopold Island, 89%; Cape Vera, 9%), similar to spatial trends in Europe (van Franeker et al., 2021). While northern fulmars breed sporadically across the coast of Atlantic Canada, with one colony in British Columbia on the Pacific coast, the majority of the Canadian population breeds at 11 colonies in the eastern Canadian Arctic (up to 137,500 breeding pairs; Mallory et al., 2020a, 2020b). Thus, plastic pollution monitoring in Canada to date covers a large portion of their range (Figure 5.2). While there are no data on plastic ingestion in Newfoundland and Labrador, these colonies are relatively small (>100 breeding pairs; Mallory et al., 2020b) and are not currently a part of existing, long-term monitoring programs, thus assessing plastic ingestion in birds at these colonies would be logistically and financially challenging. As such, we recommend continued research at the colonies that are a part of existing long-term monitoring programs, but also suggest that plastic ingestion is assessed at these smaller colonies if the opportunity arises through other research at these sites.

Temporally, some regions could not be assessed due to limited sample size (e.g., Sable Island), which emphasizes the need for targeted sampling efforts in these regions in the future to facilitate trend analyses. Additionally, while the results from others should be interpreted with caution based on differences in sample processing. For example, frequency of plastic ingestion by

fulmars in Pond Inlet increased over time, but the samples from 1978 to 1979 (M.S.W. Bradstreet unpub. in Day et al., 1985) were not processed using a 1 mm sieve or light microscope, whereas the samples from 2021 were (Hanifen et al., this issue), which may result in a difference between studies (Avery-Gomm et al., 2016). Besides these cases, rates of plastic ingestion were generally stable in the Labrador Sea, Prince Leopold Island and Qikiqtarjuaq, but increased at Cape Vera. At Cape Vera, both studies used similar methods (Byers et al., 2010; Mallory, 2008) with sample sizes greater than the recommended 40 individuals (van Franeker et al., 2011), suggesting that plastic ingestion by fulmars may have increased in the Canadian High Arctic between 1980 to 1984 and 2003 to 2004. However, plastic ingestion by fulmars was relatively low compared to the European Arctic (see Hanifen et al., this issue), where many studies reported a frequency of occurrence of $\geq 80\%$ (Ask, 2016; Camphuysen and van Franeker, 1997; Trevail et al., 2015) or even 90% (Trevail et al., 2014; van Franeker, 2012; van Franeker and the SNS Fulmar Study Group, 2013), and more southern regions in Europe, where average frequency of occurrence also averaged $\geq 80\%$ (van Franeker et al., 2021).

Frequency of plastic ingestion by kittiwakes appears to be stable in Qikiqtarjuaq, Pond Inlet, and Prince Leopold Island. However, samples from Pond Inlet in 1978 to 1979 (see Day et al., 1985) were not processed using a 1 mm sieve or light microscope as they were in 2021 (this study). Moreover, while samples from Prince Leopold Island in 2008 indicate a 20% frequency of occurrence (the highest reported in the Arctic to date; Baak et al., 2020a), sample sizes were much smaller ($n = 5$; one bird ingested plastic) than the recommended minimum of 40 individuals. Overall, plastic ingestion rates in these three regions were relatively low, similar to

other regions across the Nearctic (Day, 1980; Robards et al., 1995) and Palearctic (Gjertz et al., 1985; Lydersen et al., 1989; Mehlum and Gjertz, 1984; J. K. Jensen unpubl. data in O’Hanlon et al., 2017). However, plastic ingestion studies for kittiwakes across the Arctic generally have low sample sizes or are outdated (Baak et al., 2020a), and to our knowledge, there are no other regions where trends in plastic ingestion have been assessed over time. Given the concern over kittiwake population status in much of the Arctic (Johansen et al., 2020; Vihtakari et al., 2018) future studies on kittiwakes across their range is recommended. In Canada, kittiwakes breed across the Atlantic coast with some colonies in the Pacific, with high densities in the Canadian High Arctic, the Gulf of St. Lawrence and Newfoundland (Hatch et al., 2020). While kittiwakes have been assessed for plastic ingestion in the Canadian High Arctic (Figure 5.3), we lack information on plastic pollution in this species in the Gulf of St. Lawrence and Newfoundland. As plastic generally decreases with increasing latitude (seen in this study with the northern fulmar), we encourage future studies in these two regions as well as continued monitoring in the Canadian Arctic when possible to facilitate comparisons across both space and time.

For murre, samples from Pond Inlet in 1978 to 1979 (see Day et al., 1985) were also not processed using a 1 mm sieve or light microscope, whereas samples from 2021 were (Maddox et al. this issue), so the increase in plastic ingestion at this site must also be interpreted with caution. In other geographic areas, details on processing methods are not known (e.g., Provencher et al., 2014) or birds were sampled from multiple regions across the province (e.g., Newfoundland; Bond et al., 2013; Provencher et al., 2014), or during different times of the year (e.g., Newfoundland birds from 2005 and 2006 were collected during the breeding season while

the remainder were collected outside of the breeding season; Bond et al., 2013; Provencher et al., 2014). Despite this, plastic ingestion appears to be stable across most regions (except for Pond Inlet where plastic ingestion increased), and levels were similar to studies across the Nearctic (Day, 1980; Robards et al., 1995) and Palearctic (Falk and Durinck, 1993; Gjertz et al., 1985; Lydersen et al., 1989; Mehlum and Giertz, 1984). Thick-billed murres breed across Atlantic and Arctic Canada in high numbers (30,000-500,000 breeding pairs), with one small colony (Cape Parry, >1200 breeding pairs; Hogan and Sidler, 2023) in the western Arctic (Gaston and Hipfner, 2020). Besides Cape Parry, plastic ingestion by thick-billed murres has been assessed across their Canadian range (Figure 5.4), with low occurrences in each region and no clear spatial trends in ingestion.

While plastic ingestion by murres is low compared to surface-feeding species (fulmars and kittiwakes), this species may be particularly useful to monitor because it is harvested in several countries and carcasses often wash up from storms or oil spills (e.g., Wiese et al., 2004; Wiese and Robertson, 2004), so samples in many locations may be relatively easy to acquire. Thus, continued monitoring of this species in these regions, including sampling for plastic pieces < 1 mm in size and plastic-associated contaminants (Provencher et al., 2022a), is recommended as a means of monitoring plastic pollution in the Arctic environment. For example, Bourdages et al. (2021) found that 17% of murres with no plastic pieces (> 1 mm in size) in their gastrointestinal tract had microplastics in their guano, highlighting the importance of considering other methods of assessing the impacts of plastic ingestion on seabirds.

Black guillemots have been assessed for plastic ingestion at four sites in Arctic Canada, with no detections of plastic pollution >1 mm in size to date, similar to other regions in the European Arctic (Gjertz et al., 1985; Lydersen et al., 1989; Mehlum and Giertz, 1984; Weslawski et al., 1994). However, black guillemots have not been assessed for plastic pollution in the southern portion of their Canadian range (e.g., from the southwest coast of Nova Scotia to Newfoundland and Labrador), where the species is common (Natcher et al., 2012) and is likely exposed to more plastic debris (e.g., Mallory et al., 2021). Indeed, there is limited information for this species outside of the Arctic across its range. Thus, we encourage future research on plastic ingestion, including plastics <1 mm in size, in black guillemots in the southern portion of their range when possible (e.g., building onto existing monitoring programs).

Conclusions and future directions

Overall, despite differences in sample collection or processing over time, the plastic ingestion monitoring program in Canada suggests that, regardless of the methods used, plastic ingestion by seabirds in the Canadian Arctic is relatively low and stable, although plastic ingestion by fulmars appeared to increase in some sampling areas. This study demonstrates that long-term monitoring programs provide important trend data, even considering the differences in how studies were conducted, but that programs should continue to focus on standardized collection, analysis and reporting to allow more robust comparisons across regions and time (Baak et al., 2021; Kühn et al., 2022; Provencher et al., 2019, 2017).

Plastic ingestion monitoring in Canada is ongoing, and scientists across the country are working to increase sampling and collaboration, as well as examine other plastic pollution metrics. Indeed, research in the Canadian Arctic has expanded to microplastics (Provencher et al., 2018), plastic-related chemical contaminants (Sühring et al., 2022), physical effects of plastic ingestion (Fackelmann et al., 2023), cumulative effects (Rooney et al., 2023), as well as the sources and fate of plastic pollution and its associated chemical contaminants (Bourdages et al., 2021; Hamilton et al., 2022; Provencher et al., 2022b). Here, we show that fulmars continue to have higher levels of plastic ingestion than other Arctic-breeding seabirds, emphasizing their utility as the key monitoring tool for plastic pollution in the Canadian Arctic and across the North Atlantic. While black-legged kittiwakes, thick-billed murres and black guillemots are not as vulnerable to the ingestion and accumulation of plastics >1 mm in size, we show that monitoring in sympatric species using the same methods can add to our understanding of how plastic pollution affects ecosystems, and we encourage continued monitoring of these species as a part of existing, long-term monitoring programs. Predictions are that plastic pollution will continue to enter the Arctic marine environment, perhaps at an increasing rate due to increases in tourism, shipping and fisheries activities (all expanding due to global warming; Collard and Ask, 2021; Dawson et al., 2020), and thus monitoring plastic ingestion by these Arctic-breeding seabirds will be of increasing importance.

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LINKING STATEMENT

In Chapter 5, I presented new data and reviewed historical work on plastic ingestion by four seabird species across Canada. Plastic ingestion increased in northern fulmars, but was relatively stable in black-legged kittiwakes, thick-billed murre, and black guillemots. Northern fulmars had consistently higher levels of plastic pollution compared to the other three species and exhibited a clear north-south gradient in this occurrence, where northern fulmars from more southern regions tend to have higher levels of plastic ingestion than those from more northern regions. Overall, these differences among species, regions, and time underscore the importance of standardized, long-term monitoring to assess trends and inform conservation and management. However, as birds can acquire plastic pollution throughout their annual cycle, and plastics can remain in the gastrointestinal tract for months, levels of plastic ingestion in birds captured in the breeding season may reflect plastics acquired throughout migration. Thus, information on the source, transport, and fate of these contaminants is crucial. For example, for a contaminant to be listed on the Stockholm Convention for Persistent Organic Pollutants, there must be evidence that the contaminant is persistent, toxic to humans or wildlife, and that it can be transported long ranges. Migratory birds have been identified as a mechanism to identify long-range transport of contaminants, but there is little information on the methods to examine this. In Chapter 6, I review the current knowledge on using tracking devices to examine the relationship between avian movements and contaminant concentrations. With this information, I identify knowledge gaps and provide recommendations for future research to enhance our ability to identify the source, transport, and date of contaminants in avian species to inform policy and conservation decisions across the globe.

CHAPTER 6: SPATIAL ECOTOXICOLOGY: WHAT WE KNOW ABOUT THE RELATIONSHIP BETWEEN AVIAN MOVEMENTS AND CONTAMINANT LEVELS

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Abstract

Birds are widely used as indicators of environmental contamination because they integrate signals across space and time. However, this advantage also means that locating the source of pollution can be challenging, especially for species that migrate large distances. Historically, assignment of contaminant burden to particular life stages or locations has been made by sampling tissues of varying time signals and associating those signals with locations assigned from band recoveries or stable isotope analyses. Unfortunately, these assignments are geographically coarse. More recently, tracking devices have been increasingly used to determine more precisely where and when contamination likely occurred. Here, we review current knowledge on using tracking devices to examine the relationship between avian movements and contaminant loads. We found 42 published articles with samples collected from 1986 to 2021 that used tracking devices to examine the relationship between avian movement and contaminant loads, where studies were primarily concentrated in the northern hemisphere, notably in the North Atlantic. Tracking methodology varied widely across studies to date, but the use of radiotransmitters and satellite tags generally decreased as newer technologies, such as global positioning systems and geolocation sensors, were developed. Blood and feathers were the most commonly used tissues to assess contaminant concentrations, but sample sizes were often low (<40, the recommended sample size for some tracking or contaminant studies) and one quarter of studies did not statistically test the relationship between tracking data and contaminant concentrations. Moving forward, studies should: 1) consider statistical power; 2) consider tissue turnover rates, contaminant turnover rates, and tracking device resolution; 3) examine tissues that inform different time scales; 4) explore the impacts of contaminants on behaviour and

movement; and 5) increase collaboration, standardization, and information sharing across existing tracking or contaminant monitoring programs. Focusing on these aspects will enhance our ability to identify the source, transport, and fate of contaminants in avian species across the globe.

Keywords

Birds; distribution; pollutants; pollution; tracking; biological indicator

Introduction

Environmental contaminants, or chemicals that are either naturally, deliberately or accidentally released into the environment, have been found in environments across the globe, from deep seas (Storelli et al. 2009) to mountaintops (Guzzella et al. 2016), and from the Arctic (Macdonald et al. 2000) to the Antarctic (Bargagli 2008). These contaminants have a range of impacts on these environments and the biota that inhabit them. For example, dichlorodiphenyltrichloroethane (DDT), an insecticide once used for both agricultural and residential purposes in the early 1940s, was released into the rivers and lakes through agricultural runoff, where it biomagnified up the trophic food web to top predators such as bald eagles (*Haliaeetus leucocephalus*; Colborn 1991). The high concentrations of DDT in eagles interfered with their ability to metabolize calcium, leading to eggshell thinning that caused eggs to desiccate during incubation (Colborn 1991). This then reduced the overall reproductive success of bald eagles, which led to substantial population declines across North America (Grier 1982; Best et al. 2010). More recently, the use of

diclofenac, an anti-inflammatory drug used in livestock, caused renal failure and subsequent population declines of over 95% in various vulture species (*Gyps spp.*) across southeast Asia (Oaks et al. 2004; Shultz et al. 2004). Similar effects have been observed in a suite of top avian predators globally (Hellou et al. 2013), and by the 21st Century, a cocktail of contaminants have been uptaken by wildlife, even in remote locations (Bianchini et al. 2022). To mitigate impacts on both humans and wildlife, international agreements to restrict or regulate the use of toxic contaminants are imperative.

There are various international agreements to restrict or regulate the use of toxic contaminants, such as the Minamata Convention on mercury (<http://www.minamataconvention.org>), the Basel Convention on hazardous waste (<https://www.basel.int/default.aspx>), and the Stockholm Convention on Persistent Organic Pollutants (POPs; <http://www.pops.int>). For example, the Stockholm Convention is an international treaty aimed to regulate and restrict the use of selected POPs across the globe. To regulate or restrict a contaminant under the Stockholm Convention, there must be evidence that the chemical is persistent, can bioaccumulate, causes harm, and can be transported long-range. For example, the persistence (Turusov et al. 2002) and movement of DDT in the environment, combined with its toxicity to humans and wildlife (Colborn 1991), led this contaminant to be restricted under the Stockholm Convention upon its signing in 2001. Since then, we have seen a gradual decline, but continued persistence of this chemical in terrestrial and marine environments (Van Oostdam et al. 2005). As new chemicals are developed each year, there is an ongoing need to assess how these chemicals move through the environment.

To assess the efficacy of international treaties, migratory birds are widely used as bioindicators to monitor the transport and fate of contaminants in the environment (Egwumah et al. 2017). Early studies of the movement of contaminants by migratory birds were carried out by examining differences in contaminant loads between known breeding colonies, stopover sites and/or overwintering grounds based on mark-recapture techniques (e.g. from band recoveries; Elliott and Shutt 1993). For example, Elliott and Shutt (1993) sampled blood from sharp-shinned hawks (*Accipiter striatus*) caught during routine banding at various migration points in North America, and showed that many organochlorines, a group of chlorinated compounds often used as pesticides, were higher in birds that overwintered in more southern regions. Based on these early studies, the Stockholm Convention included migratory animals as one of the mechanisms to determine if contaminants can be transported long-range (The Stockholm Convention on Persistent Organic Pollutants 2001).

While our ability to detect diverse and low concentration contaminants has improved since the 1960s, advances in stable isotope analyses have simultaneously allowed researchers to more easily assess the spatial and temporal differences in contaminant concentrations. Indeed, sampling an individual once during breeding can now provide information on multiple points in time and space, rather than simply winter versus breeding contamination provided by migration points (Jarman et al. 1996). For example, feathers are metabolically inert, and thus analyses of feathers can provide information on contaminant loads during the time of feather growth, allowing for comparisons of contaminant concentrations between stopover sites or overwintering grounds (e.g., Morrissey et al. 2004; Kardynal et al. 2020). However, stable isotopes often only

provide very crude estimates of approximate locations, such as habitats (coastal/pelagic) or terrestrial locations with a few hundred kilometer accuracy, and isotopes can vary with changes in temperature, nutrient availability, or prey sources (Rubenstein and Hobson 2004). In many cases, more precise information is needed to provide spatial data relevant to management. Nonetheless, this method has been increasingly used to determine differences in contaminant levels between regions and time of year, and is widely used today in conjunction with tracking devices (e.g. Shoji et al. 2021).

The advancement of individual-based tracking technology provided new opportunities to examine how contaminants may be transported by migratory birds. Henny and Blus (1986) were the first to use a combination of band recoveries and radiotelemetry tracking devices to track black-crowned night herons (*Nycticorax nycticorax*) from different populations to their wintering grounds, and suggested that differences in wintering area may explain differences in contaminant concentrations. However, this method requires researchers to physically track the individuals, thus is both resource-intensive and biased towards individuals that occur where researchers think they will. Following this, the development of satellite tags that transmit signals remotely allowed researchers to track individuals more easily (e.g., Elliott et al. 2007), but the size of tracking units and the associated animal welfare concerns (Barron et al. 2010; Vandenabeele et al. 2011) inhibited our ability to track smaller species, such as passerines, for many years. With the development and miniaturization of archival or remote-downloading tracking devices in recent years, such as Global Positioning System (GPS) and geolocation sensors (GLS, Burger and Shaffer 2008), researchers are now able to obtain more detailed information on the spatial

movements of birds, including those that spend the majority of their annual cycle at-sea and/or in remote locations (Burger and Shaffer 2008).

Regardless of how migratory birds are tracked, studies combining tracking with contaminants are an important tool in studies focused on the fate and transport of contaminants. By combining detailed spatial information with individual contaminant loads, we can better delineate the sources, movement, and fate of contaminants in the environment. Such information can be used to inform both domestic and international policies on the regulation or restriction of these contaminants. However, studies that combine these approaches are relatively scarce. Here, we review studies that examine the relationship between avian movements and contaminant levels to: 1) assess the state of current knowledge on linking the fields of telemetry and avian contamination; 2) synthesize how studies are collecting, analyzing and presenting these data; and 3) provide recommendations for future research that aims to integrate data on exposure and location in migratory species.

Approach

We used the following search terms in Scopus (<https://www.scopus.com/>) to find literature on avian contamination and tracking up until February 2023: bird AND contamina* OR pollut* OR pcb OR mercury OR pop OR organochlorine AND tracking OR movement OR migrat* OR biologging OR "stable isotope". We included articles if the publication discussed a physical or chemical contaminant in an avian species in relation to avian movement. We defined

contaminants as a substance that falls into one of the following groups: organochlorines (OCs), organophosphate esters (OPEs), per- and polyfluoroalkyl substances (PFASs), phthalates, polybrominated diphenyl ethers (PBDEs), polychlorinated biphenyls (PCBs), polychlorinated dibenzo-p-dioxins and dibenzofurans (PCDD/Fs), polychlorinated naphthalenes (PCNs), substituted diphenylamine antioxidants (SDPAs), UV-stabilizers, trace elements and metals; or particulates (e.g. plastic pollution, carbon nanotubes, etc.). We defined avian movement as any bird movements that were tracked (during the breeding and/or non-breeding season) using a tracking device (i.e., radio transmitters, satellite tags, GLS and GPS devices). For each paper, we extracted data on the tracking method/device used, the contaminants analysed, other metrics used (e.g., stable isotope analyses, video analyses), and metadata for each project (study location, year, species, sample size). We did not limit this work to a particular group of birds, and therefore included all papers that reported on novel movement and/or contaminants in an avian group.

Findings and discussion

We found 42 peer-reviewed articles that used tracking devices to examine the relationship between avian movement and contaminant loads of 44 different bird species (see Table 6.1 for complete list), that were distributed across the globe, but primarily in the North Atlantic (Figure 6.1). These studies include samples collected from 1986 to 2021 (Figure 6.2).

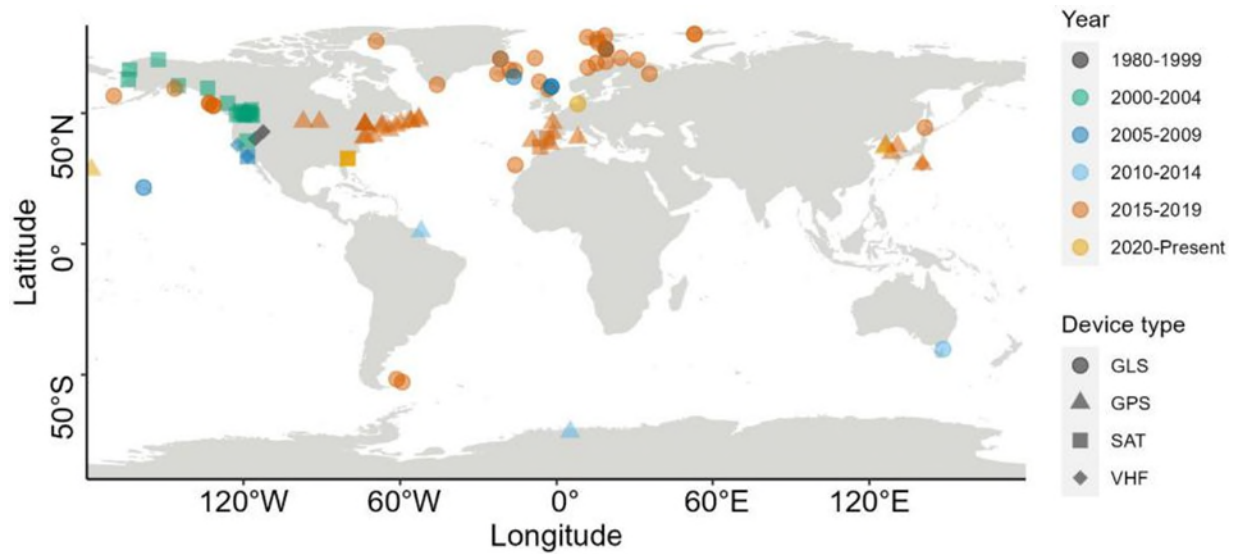


Figure 6.1: Distribution of sampling locations of studies that examine the relationship between avian movement and contaminant loads using tracking devices, by tracking device type and year of sampling. Studies that spanned across multiple year bins were placed in the bin corresponding to the last sampling year. Tracking methods include: global location sensors (GLS); global positioning systems (GPS); satellite telemetry (SAT, which includes GPS-PTT devices); and very high frequency transmitters (VHF).

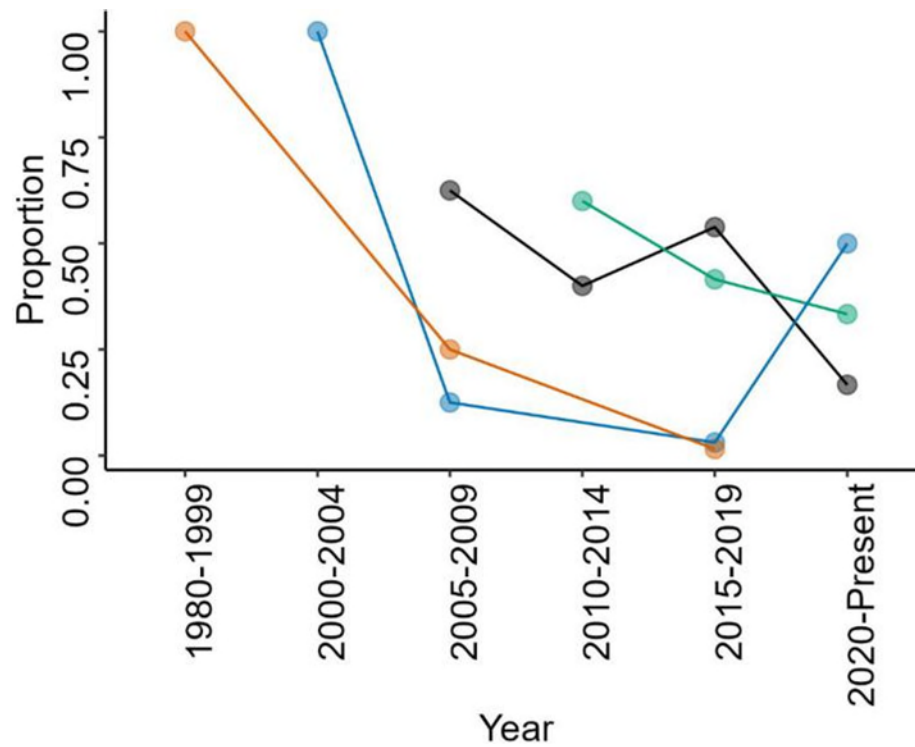


Figure 6.2: Proportion of tracking device types used over time in studies that examined the relationship between avian movement and contaminant loads. Studies that spanned across multiple year bins were placed in the bin corresponding to the last sampling year. Tracking methods include: global location sensors (GLS); global positioning systems (GPS); satellite telemetry (SAT, which includes GPS-PTT devices); and very high frequency transmitters (VHF).

Table 6.1. List of all peer-reviewed articles included in this review. Brackets indicate sample sizes. Tracking methods include: global location sensors (GLS); global positioning systems (GPS); satellite telemetry (SAT, which includes GPS-PTT devices); and very high frequency transmitters (VHF). We have also recorded band recovery (BR) and stable isotope analysis (SIA) when it was used to improve accuracy of tracking, and video logger (VL) when used to identify contaminants visually.

Source	Species	Location	Sample year	Tracking method	Sample type	Contaminants examined	Statistical methods
(Ackerman et al. 2007)	Black-necked stilt (<i>Himantopus mexicanus</i>)	USA	2005-2006	VHF (94)	Blood (157 adults)	Mercury	Relationship between contaminant data and tracking device data not specifically tested statistically
(Ackerman et al. 2007)	American avocet (<i>Recurvirostra americana</i>)	USA	2005-2006	VHF (115)	Blood (373 adults)	Mercury	-
(Albert et al. 2021)	Black-legged kittiwake (<i>Rissa tridactyla</i>)	Iceland, Norway (Mainland)	2014-2017	GLS (13)	Back feathers (13)	Mercury	Linear mixed models
(Albert et al. 2021)	Thick-billed murre/Brünnich's guillemot (<i>Uria lomvia</i>)	Iceland, Norway (Mainland and Svalbard)	2014-2017	GLS (65)	Head feathers (65)	Mercury	-
(Albert et al. 2021)	Common eider (<i>Somateria mollissima</i>)	Faroe Islands, Iceland, Norway (Mainland and Svalbard), Russia	2014-2017	GLS (22)	Head feathers (22)	Mercury	-
(Albert et al. 2021)	Common murre/Common guillemot (<i>Uria alga</i>)	Iceland, Norway (Mainland and Svalbard)	2014-2017	GLS (39)	Breast feathers (39)	Mercury	-
(Albert et al. 2021)	Dovekie/Little auk (<i>Alle alle</i>)	Norway (Svalbard), Russia	2014-2017	GLS (6)	Head feathers (6)	Mercury	-

(Albert et al. 2021)	Northern fulmar (Fulmarus glacialis)	Iceland, Norway (Svalbard), United Kingdom	2014-2017	GLS (38)	Breast feathers (38)	Mercury	-
(Albert et al. 2022)	Great skua (Stercorarius skua)	Norway (Svalbard)	2014-2017	GLS (40)	Breast or back feathers (40)	Mercury	Linear mixed models
(Arrondo et al. 2020)	Griffon vulture (Gyps fulvus)	Spain	2014-2018	GPS (58)	Blood (58 adults)	Lead	General linear models
(Bertram et al. 2022)	Common tern (Sterna hirundo)	Germany	2017-2021	GLS (80)	Back feathers (80)	Mercury	Linear mixed models
(Blanco et al. 2018)	Black kite (Milvus migrans)	Spain	2007-2016	SAT (6); BR (96)	Eggs (51)	PBDEs, Dechloranes	Generalized linear models
(Bourgeon et al. 2013)	Great skua (Stercorarius skua)	United Kingdom	2009	GLS (3); SIA (32)	Blood (33 adults, 40 chicks)	OCs	Generalized linear mixed effects models
(Bracey et al. 2020)	Common tern (Sterna hirundo)	USA	2016-2017	GPS (19)	Blood (12 adults); Breast feathers (65 chicks); Secondary feathers (22 adults)	Mercury	Generalized linear models
(Brown et al. 2019)	Ring-billed gull (Larus delawarensis)	Canada	2011, 2012, 2016	GPS (38)	Liver (87 adults)	Trace elements (As, Cd, Pb and Se) including 14 rare earth elements (Y, La, Ce, Pr, Nd, Sm, Eu, Gd, Tb, Dy, Ho, Er, Yb, and Lu)	Spearman correlation rank test
(Carravieri et al. 2018)	Antarctic petrel (Thalassoica antarctica)	Antarctica	2012-2014	GPS (91)	Blood (266 adults)	Mercury	Generalized linear models
(Carravieri et al. 2023)	Dovekie/Little auk (Alle alle)	Greenland	2018-2019	GLS (28)	Blood (79); Head feathers (28)	Mercury	Principal component analysis; Generalized linear models
(De Pascalis et al. 2022)	European storm-petrel (Hydrobates pelagicus)	Italy	2019	GPS (7)	Bolus (30)	Physical plastic pollution	Relationship between contaminant data and tracking device data not specifically

(Elliott et al. 2007)	Osprey (<i>Pandion haliaetus</i>)	Canada	1995-2003	SAT (16)	Eggs (16)	OCs	tested statistically ANOVA
(Fleishman et al. 2019)	Red-legged kittiwake (<i>Rissa brevirostris</i>)	USA	2010, 2013-2017	GLS (89); SIA (79)	Blood (89), Nape feathers (80)	Mercury	Global linear regression models
(Fort et al. 2014)	Dovekie/Little auk (<i>Alle alle</i>)	Greenland	2009-2011	GLS (82)	Blood (82), Head feathers (82), Breast or back feathers (82)	Mercury	Multiple linear regression models
(Furtado et al. 2020)	Black-browed albatross (<i>Thalassarche melanophris</i>)	Falkland Islands	2016, 2017	GLS (12)	Blood (38)	Mercury, Trace elements (As, Se, Sr, some individuals also included Cd, Co, Mn, V)	ANOVA
(Gatt et al. 2020)	Cory's shearwater (<i>Calonectris borealis</i>)	Portugal	2016-2017	GLS (182)	Secondary feathers (120)	Mercury	ANOVA; Linear regression models
(Gentes et al. 2015)	Ring-billed gull (<i>Larus delawarensis</i>)	Canada	2010-2012	GPS (76)	Blood (76)	PBDEs	Principal component analysis; Multiple linear regression models
(Henny and Blus 1986)	Black-crowned night-heron (<i>Nycticorax nycticorax</i>)	USA	1982-1983	VHF (12); BR (16)	Eggs (220)	DDE, PCBs	Relationship between contaminant data and tracking device data not specifically tested
(Jang et al. 2022)	Black-tailed gull (<i>Larus crassirostris</i>)	South Korea	2015-2019	GPS (11)	Eggs (620)	PCBs, HCHs, CHLs, HCB, PBDEs, HBCDs, PFAAs	statistically Relationship between contaminant data and tracking device data not specifically tested
(Jouanneau et al. 2022)	Herring gull (<i>Larus argentatus argenteus</i>)	France	2016-2019	GPS (18)	Blood (44)	Mercury	statistically Generalized least square models

(Jouanneau et al. 2022)	Lesser black-backed gull (<i>Larus fuscus graellsii</i>)	France	2016-2019	GPS (18)	Blood (54)	Mercury	-
(Jouanneau et al. 2022)	Great black-backed gull (<i>Larus marinus</i>)	France	2016-2019	GPS (7)	Blood (37)	Mercury	-
(Jouanneau et al. 2022)	Yellow-legged gull (<i>Larus michahellis</i>)	France	2016-2019	GPS (0)	Blood (5)	Mercury	-
(Kerric et al. 2021)	Ring-billed gull (<i>Larus delawarensis</i>)	Canada	2018	GPS (26)	Air (26)	OPEs, PBDEs	Wilcoxon rank-sum test; Kruskal-Wallis test
(Laranjeiro et al. 2021)	Cory's shearwater (<i>Calonectris borealis</i>)	Portugal	2017	GPS (26)	Blood (26); Secondary feathers (26)	Trace elements (As, Ca, Cd, Co, Cr, Cu, Fe, Hg, K, Mn, Na, Ni, P, Pb, S, Se, Sn, Sr, Ti, Zn) OCs, PBDEs	Pearson's correlations
(Leat et al. 2013)	Great skuas (<i>Stercorarius skua</i>)	Iceland, Norway (Svalbard), Scotland	2008-2009	GLS (19)	Blood (141)		Principal component analysis; Redundancy analysis; General linear models
(Miller et al. 2020)	Ancient murrelets (<i>Synthliboramphus antiquus</i>)	Canada	2014-2015	GLS (43); SIA (43)	Blood (43)	PBDEs, PFASs, OCs, PCBs, Mercury	Generalized linear models
(Nishizawa et al. 2021)	Black-footed albatross (<i>Phoebastria nigripes</i>)	Japan	2017	GPS (13); VHF (13); VL (13)	NA	Physical plastic pollution	Douglas-Peucker algorithm; Mann-Whitney U tests; Exponential regression analysis
(Nunes et al. 2022)	Brown booby (<i>Sula leucogaster</i>)	Brazil	2011-2020	GPS (35)	Blood (17); Contour feathers (17)	Trace elements (Cu, Cr, Fe, Mn, Zn, Cd, Pb, and As)	Mann-Whitney U tests
(Nunes et al. 2022)	Trindade petrel (<i>Pterodroma arminjoniana</i>)	Brazil	2006-2019	GLS (29)	Blood (19); Contour feathers (19)	Trace elements (Cu, Cr, Fe, Mn, Zn, Cd, Pb, and As)	-
(Nunes et al. 2022)	Red-billed tropicbird (<i>Phaethon aethereus</i>)	Brazil	2011-2020	GPS (25)	Blood (20); Contour feathers (20)	Trace elements (Cu, Cr, Fe, Mn, Zn, Cd, Pb, and As)	-

(Pagel et al. 2012)	Bald eagle (<i>Haliaeetus leucocephalus</i>)	USA	2002-2006	SAT (61)	Liver (2); Femur (7)	Lead, Mercury, Trace elements (As, Se, Al, B, Ba, Be, Cd, Cr, Cu, Fe, Mg, Mn, Mo, Ni, Sr, V, Zn)	Relationship between contaminant data and tracking device data not specifically tested statistically
(Pollet et al. 2023)	Leach's storm-petrel (<i>Hydrobates leucorhous</i>)	Canada	2014-2019	GPS (130)	Blood (742), Eggs (121)	Mercury	Linear mixed-effects models
(Renedo et al. 2020)	Dovekie (<i>Alle alle</i>)	Greenland, Norway (Svalbard), Russia	2015-2017	GLS (40)	Blood (50); Head feathers (50); Body feathers (50)	Mercury	Linear regression models; Spearman correlation rank tests
(Schmutz et al. 2009)	Red-throated loons (<i>Gavia stellata</i>)	USA	1999-2003	SAT (32)	Blood (55); Eggs (62)	PCBs	ANOVA
(Sebastiano et al. 2016)	Magnificent frigatebird (<i>Fregata magnificens</i>)	French Guiana	2011, 2013	GPS (7)	Blood (20 adults, 20 chicks)	OCs, PCBs, PBDEs, Mercury	Relationship between contaminant data and tracking device data not specifically tested statistically
(Shoji et al. 2021)	Rhinoceros auklets (<i>Cerorhinca monocerata</i>)	USA, Japan	2016-2018	GLS (25); SIA (25)	Blood (12), Feathers (25 body, 25 retrices)	Mercury	Linear regression models
(Sorais et al. 2020)	Ring-billed gulls (<i>Larus delawarensis</i>)	Canada	2015-2017	GPS (67)	Air (67)	PBDEs, other HFRs	Linear mixed-effect models
(Sorais et al. 2021)	Ring-billed gulls (<i>Larus delawarensis</i>)	Canada	2015-2017	GPS (58)	Liver (58)	PBDEs, other HFRs	Linear mixed-effect models
(Thorne et al. 2021)	Herring gulls (<i>Larus smithsonianus</i>)	USA	2016-2018	GPS (51)	Blood (51)	Mercury	Linear regression models
(Vorkamp et al. 2018)	Peregrine falcons (<i>Falco peregrinus</i>)	Greenland	1986-2003, 2004-2016	GLS (3)	Eggs (48)	PBDEs	ANOVA; Linear regression models
(Watanuki et al. 2015)	Short-tailed Shearwaters (<i>Puffinus tenuirostris</i>)	Australia	2009-2011	GLS (40)	Primary feathers (28)	Mercury	Generalized linear models
(Wilkinson et al. 2022)	Brown pelican (<i>Pelecanus</i>)	USA	2017-2020	SAT (68)	Eggs (36)	PFAS	Relationship between contaminant

	occidentalis carolinensis)						data and tracking device data not specifically tested statistically Relationship between contaminant data and tracking device data not specifically tested statistically Relationship between contaminant data and tracking device data not specifically tested statistically Relationship between contaminant data and tracking device data not specifically tested statistically Relationship between contaminant data and tracking device data not specifically tested statistically
(Yang et al. 2022)	Black-tailed gull (Larus crassirostris)	South Korea	2020	GPS (5)	Bolus (10)	Physical plastic pollution	
(Yates et al. 2009)	White-faced ibis (Plegadis chihi)	USA	2000- 2003	SAT (15)	Blood (20); Eggs (10)	DDE	
(Young et al. 2009)	Laysan albatross (Phoebastria immutabilis)	USA	2005- 2007	GLS (22)	Bolus (23, chicks)	Physical plastic pollution	

Tracking methods for location information

Tracking methods varied widely across studies. The first tracking devices used to assess the relationship between avian movements and contaminants were radio transmitters (starting from 1982), followed by satellite tags (starting from 1995), but the use of these techniques generally decreased over time as newer technologies, such as GLS (2005) and GPS (2010), were developed (Figure 2). Indeed, we found that GPS and GLS tracking devices were the most common devices used, with 44% and 35% of studies using these methods, respectively (Table 6.2). Importantly, 51% of studies used tracking devices in conjunction with other devices or

analyses, such as stable isotope analyses (21 studies), band recoveries (3) and video loggers (1). The choice of tracking device, and whether to combine it with another device or analysis, is an important consideration in all studies, particularly those that aim to relate movements to exposure to a particular threat. The decision on which to use involves a variety of factors, including cost, species biology and ecology (e.g., species size, short- versus long-distance migrants), the ability to recapture the species, and the question being answered (e.g., local or regional scale versus national or international scale). Indeed, the choice of tracking device is often limited by the species in question, where larger devices are primarily used on larger species (Bridge et al. 2011). Consequently, we are not recommending the use of a specific device, but instead want to highlight the importance of considering the benefits and costs of each device in relation to the question being asked (Table 6.3).

Radiotelemetry is a relatively inexpensive tracking method where the device emits a signal that can be tracked using ground-based or aircraft-based antenna systems (fixed or mobile). Therefore, this method can be labour intensive and has limited coverage (especially in the marine environment), depending on fixed antenna locations or the ability of the research team to follow an individual (Mech and Barber 2002), but high spatial resolution as the birds are tracked to an individual location. These devices can be lightweight (e.g., 0.3 g; Bridge et al. 2011), thus can be used on smaller birds (e.g., down to 30 g while respecting the 1-5% guideline) when other device types may not be an option. Thus, in the context of contaminants research, this method is better suited for birds that move shorter distances (e.g., breeding movements or short-distance

migrants), birds that have known wintering areas (e.g., fixed receivers at these locations), or for studies where species-specific information on behaviour and habitat is needed (e.g., monitoring birds visiting point-source locations of contaminants). For example, Ackerman et al. (2007) used radiotelemetry to track short-distance movements of and black-necked stilts (*Himantopus mexicanus*) and American avocets (*Recurvirostra americana*) in San Francisco Bay, then assessed how mercury concentrations in their blood differed among salt ponds in the bay.

Light geolocation systems, such as GLS devices, are another lightweight (as low as 0.3 g) and relatively inexpensive method to track birds. These devices record light levels at regular intervals to estimate locations (often two locations per day), which can lead to an error upwards of 400 km (Halpin et al. 2021). Moreover, positions cannot be accurately estimated around the spring and autumn equinoxes or polar night due to the lack of a differential in day lengths (Hill and Braune 2001), but there are some methods to reduce this error (e.g., Fauchald et al. 2019). Moreover, while these devices are lightweight and may last up to two years, the data are archived in the tag, and individuals must be recaptured to obtain data. Thus, for contaminants research, these devices would not be useful for tracking short-distance movements, visits to point-sources of contaminants, or species where there is a low probability of recapture (especially as tissue sampling often occurs at recapture as well). Moreover, for acutely toxic contaminants, those individuals that do not survive would provide no data because they could not be recovered (whereas carcasses from GPS studies can be tracked and recovered in some instances, e.g., Pagel et al. 2012). Instead, GLS devices are an ideal choice when cost and/or size is a limitation, and can be used to track long-distance movements to general foraging, stopover or wintering areas. When coupled with the analysis of tissues that represent different timepoints, these devices can

be used to identify general marine areas used at some point in the annual cycle that may be contaminant hotspots. For example, Renedo et al. (2020) were able to show that mercury isotopes varied east to west across the Atlantic Ocean.

GPS devices use signals from satellites to calculate positions in real-time, providing highly accurate positions (within a few metres) at many timepoints throughout the day, allowing for fine-scaled analysis on movements and timing. While some GPS devices are archival, others can transmit information remotely (provided that cellular coverage is available and/or there is a central base station to receive information when birds return to the area), which is advantageous for birds that are difficult to recapture and/or breed in remote locations. However, as these devices are currently not as lightweight as radiotelemetry or GLS devices, their use is limited to larger birds in most cases (e.g., the general rule that devices should weigh less than 1-5% of the individual's mass, as currently recommended by the Canadian Bird Banding Office; Bridge et al. 2011), but these devices have been deployed on smaller birds with the need to recapture (e.g., Leach's storm-petrels (*Hydrobates leucorhous*), Pollet et al. 2023). Thus, when coupled with contaminant analyses, these devices provide fine-scale information that can be used to determine potential point-sources of contaminants. An example of this is from Sorais et al. (2021), where the authors combined GPS data with a passive air sampler to examine how landfill use by ring-billed gulls (*Larus delawarensis*) influences their exposure to PBDEs and halogenated flame retardants (HFRs).

Satellite tags (or Platform Transmitter Terminals (PTTs)), such as the Argos system (<https://www.argos-system.org/>) and ICARUS (www.icarus.mpg.de/en), transmit signals to satellites that then relay information to ground stations to obtain the birds location. This allows researchers to follow bird movements over long distances and in remote regions. While these devices have a higher location accuracy than light geolocation systems, they are not as accurate as GPS systems (several kilometres versus several metres) and are also limited by the cost and somewhat larger size. Importantly, the increase in the proportion of satellite tags used in the past few years (Figure 2), was driven by one study that used GPS-PTTs (Wilkinson et al. 2022), which have the resolution of GPS, but the battery of a satellite tag. Thus, similar to GPS devices, satellite tags are ideal for larger birds, and can provide important information on timing and movements that can identify potential sources of contaminants in a general region. For example, Blanco et al. (2018) deployed satellite tags on black kites (*Milvus migrans*) from multiple colonies to assess how migratory movements influenced PBDE and Dechlorane concentrations in eggs. The authors found that individuals from separate breeding sites overlapped at their wintering areas, suggesting that the differences in contaminant concentrations were a result of accumulation at the breeding grounds.

Table 6.2: Number and percentage of tracking devices and tissue types used in the 42 articles examining contaminants in relation to avian movements. The total number of tracking methods ($n = 48$) and tissue types ($n = 51$) are higher than the number of papers examined ($n = 42$) because some studies report data from multiple device or tissue types.

Method used	N (%)
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<i>Tracking device</i>	
GPS	21 (44)
GLS	17 (35)
SAT	6 (13)
Radio transmitters	4 (8)
<i>Tissue type</i>	
Blood	23 (45)
Feathers	15 (29)
Eggs	9 (18)
Liver	3 (6)
Femur	1 (2)

Table 6.3: A brief overview of the advantages and disadvantages of different tracking methods.

For more detailed information, see: Bridge et al. 2011 and Lahoz-Monfort and Magrath 2021.

Tracking type	Example	Cost (\$CAD)	Minimum weight (g)	Retrieval necessary?	Accuracy (km)
Radiotelemetry	- VHF - UHF	150	0.2	No (but need receiver(s))	0.005 (tracked)
Light geolocation	- GLS	200	0.5	Yes	50-400

Global navigation satellite system	- GPS	40-1000	1	Yes	30
Satellite tracking	- Argos System - ICARUS	5000	5	No	0.001

Contaminant groups and sampling matrices

The contaminants examined in relation to avian movement varied among studies, where the majority of studies (40%) examined mercury, followed by PDBEs (13%) and other trace elements (pooled together; 8%). This was expected, as the relationship between sampling matrices (see below) is well known for mercury (e.g., (Bearhop et al. 2000; Bottini et al. 2021; Shoji et al. 2021) and there have been various recommendations developed for examining mercury in these sampling matrices (e.g., Peterson et al. 2019; Albert et al. 2019), which has expanded to other trace elements (e.g., Agusa et al. 2005; Vizuite et al. 2019; Rodriguez-Álvarez et al. 2022). Whereas the relationship between tissues for various POPs, such as PBDEs, is relatively new (compared to mercury) and somewhat less clear (e.g., Jaspers et al. 2007; Svendsen et al. 2018). This warrants future research on the relationship of contaminants between tissues, particularly novel or emerging contaminants.

The sampling matrix also varied among studies, where blood was the most common sample type used (45%), followed by feathers (29%) and eggs (18%; Table 6.2). Using a combination of tissue types was less common, where 25% of studies used multiple tissue groups (e.g., blood and

feather analyses). Importantly, some studies did not examine a specific tissue, but rather the pollutant in the environment where the birds were found as a proxy for exposure. For example, Nishizawa et al. (2021) used a combination of GPS, radio transmitters and video loggers to examine how black-footed albatrosses (*Phoebastria nigripes*) interact with physical plastic pollution in the water column, while Kerric et al. (2021) combined GPS and passive air samples to examine how exposure to HFRs and OPEs is influenced by landfill use. Another way that information on contaminant exposure has been inferred is from excreted contaminants. For example, Young et al. (2009) examined plastic pollution in the boluses of in GPS-tracked Laysan albatrosses (*Phoebastria immutabilis*).

There are various factors to consider when choosing a tissue to sample for contaminant analyses, such as knowledge of the timing of deposition into the tissue (e.g., capital or income breeders), the cellular turnover rate of that tissue and properties of the contaminant in question. For example, red blood cells in domestic chickens, pigeons and ducks have relatively short turnover before they are replenished, with an average between 35 to 45 days (Rodnan et al. 1957). In contrast, feathers are metabolically inert, meaning that contaminant deposition into feather tissue depends on the time that the feather was grown (e.g., the previous fall or winter season). Shoji et al. (2021) combined GLS data and stable isotope analyses to examine the year-round differences in mercury in rhinoceros auklets (*Cerorhinca monocerata*). To do this, the authors collected samples that represented mercury concentrations throughout the annual cycle: blood (current breeding season, “spring”), breast feathers (“winter”) and rectrices (tail feathers; previous breeding season to early winter, “autumn”). They then compared mercury concentrations to GLS

data (to determine location) and stable isotope values (to account for diet) and showed that rhinoceros auklets acquire mercury from multiple sources throughout the annual cycle. While there are issues with comparing different tissue types (see below), combining tracking, diet (stable isotopes) and contaminants is an excellent approach to assess contaminant uptake of a migratory species throughout the annual cycle because of the ability to obtain information on physical location (from tracking data), as well as foraging location (trophic position and habitat from stable isotope data). This allows researchers to further pinpoint potential sources of contaminants to these birds, as well as provide insights on the spatial distribution of the contaminant in the environment. However, the concentration of a contaminant in a tissue at a given time will not only depend on the turnover rate of the tissue, but also the turnover rate of the contaminant.

Knowledge on the turnover rates of contaminants in tissues is another important factor in understanding contaminant loads, both when comparing different contaminants and also when comparing contaminant levels among regions. If the turnover rate of a contaminant is shorter than that of the tissue (e.g., it is metabolised), results may differ depending on the time of deposition in the tissue. For example, the turnover rate of Dichlorodiphenyldichloroethylene (DDE) in bird eggs can be multiple years (Pearce et al. 1989), so DDE found in eggs could be acquired on the breeding grounds, stopover sites, and/or wintering areas during the non-breeding period (Elliott et al. 2007). In these cases, if birds have high migratory connectivity, contaminant levels cannot be attributed to a particular geographic location that the bird inhabited during its annual cycle without more information on contaminant levels in the food web or large sample

sizes from each life cycle stage (e.g., feathers grown at different times of the year instead of liver samples that can accumulate contaminants across these periods). In cases of low connectivity, this relationship is more difficult to discern and also depends on the resolution of the tracking device (see above). Thus, tissue turnover rate, contaminant turnover rate and tracking device resolution are important factors to consider together when comparing contaminant levels between tissue types.

Finally, we recognize that not all contaminant groups can be analyzed in each tissue type. It is difficult to use feathers to examine microplastics and plastic-related additives because there is a high risk of contaminating the sample in the field, and feathers may have both internal (feather matrix) and external contamination (from water or air; Dehnhard et al. 2019). Some contaminants may be lipophilic (e.g., PCBs), so fatty tissues such as egg, fat or liver may be needed to detect concentrations in an individual. In the case of trace elements, some are physiologically restricted in their movement to certain tissues (e.g., follicle walls acting as a barrier of cadmium to egg yolk ; Sato et al. 1997). Moreover, while there are advantages to using multiple tissues (Shoji et al. 2021), the cost and availability (amount that can be sampled at one time; e.g. blood) of samples can also limit our ability to examine certain relationships. For instance, a minimum of 2 mL of blood is recommended for detecting plastic-related additives in blood, and higher volumes are required to analyze more additives (Dehnhard et al. 2019), but 2 mL may be above the amount of blood that can be withdrawn from small birds without negative impacts.

Sample collection and statistical analyses

Sample collection methods varied between studies. Both lethal and non-lethal sampling methods were used, where 93% of studies used non-lethal (blood, feathers, boluses, opportunistic carcass collection) or less invasive (eggs) sampling methods. The remainder (6%) used lethal sampling methods to examine tissues that cannot be assessed otherwise (e.g. liver; Brown et al. 2019; Sorais et al. 2021), or a combination of both lethal and non-lethal sampling (e.g., collecting blood samples from live individuals as well as sacrificing individuals; Ackerman et al. 2007). All lethal sampling was from studies within North America, perhaps reflecting different opinions and abilities towards lethal sampling in Europe relative to North America, or perhaps the species euthanized were considered abundant in North America at the time of sample collection. Studies that examine contaminant concentrations in both lethal (e.g., liver) and non-lethal (e.g., blood) tissues should also assess the relationship between lethal and non-lethal samples. This would allow us to assess whether non-lethal samples can be used as a proxy for understanding contaminant concentrations in tissues that can only be obtained through lethal sampling, which may not be possible for certain species and/or regions. While opportunistic carcass collection (e.g., beached birds) is another way to obtain information on internal organs that cannot be otherwise sampled without lethal methods, the state of decay must be considered (Pagel et al. 2012). Taking non-lethal samples also provides a unique opportunity to assess temporal changes in contaminants (such as upon deployment and recapture; Carravieri et al. 2018). However, to detect temporal changes, sufficient sample sizes are needed.

Sample size varied widely among studies but also between the number of birds tracked and the number of birds analyzed for contaminants. Indeed, the sample size for tracking devices ranged from three devices to 182 (median: 27), whereas sample size of tissues analyzed for contaminants ranged from two to 373 (median: 40; Table 6.1), depending on the tissue type. While tracking only a subset of individuals is common due to cost limitations, adequate sample sizes are needed to accurately estimate migration patterns (Soanes et al. 2013). Specifically, low sample sizes may not capture individual differences in foraging patterns or migration routes, especially for species or colonies that are known to have high individual variation (Soanes et al. 2013). Indeed, birds from the same colony that overwinter or stopover in different areas will be exposed to contaminants differently, and low sample sizes may not catch this difference. For example, Bourgeon et al. (2013) analyzed OCs in 72 blood samples of great skua (*Stercorarius skua*) adults and chicks Shetland, United Kingdom, to estimate the influence of maternal wintering area on OC concentrations in chicks. However, only three adults from the colony had known wintering areas determined by tracking devices. As great skuas exhibit high individual variation in behaviours (Magnusdottir et al. 2012), identifying a relationship between contaminant loads and wintering grounds would be difficult without additional information on their movements. To compensate for this, Bourgeon et al. (2013) also analyzed stable isotopes of 32 individuals to infer the distribution of non-tracked birds. This again highlights the utility of combining multiple tracking methods when assessing how contaminant loads are influenced by avian movements.

Importantly, 24% of studies did not directly analyze the relationship between movements and contaminant loads. For example, Schmutz et al. (2009) examined PCBs in blood and egg samples of red-throated loons (*Gavia stellata*) from Alaska, USA, and found that PCB concentrations differed between sampling regions, likely as a result of wintering areas. However, wintering areas were known based on unpublished satellite telemetry data, and the relationship between satellite telemetry locations and PCB concentrations was not specifically statistically tested in this study. It is also unknown whether the satellite telemetry data were from the same individuals sampled for contaminants. Similarly, Sebastiano et al. (2016) analyzed a suite of contaminants (PCBs, PBDEs and OCs) in magnificent frigatebirds (*Fregata magnificens*) breeding in the south Atlantic. The authors compared contaminant loads of these individuals to GPS tracks from different individuals sampled within the same colony but in different years, thus both inter-individual and inter-year variation were not considered. Similar to Bourgeon et al. (2013), the authors analyzed stable isotopes of the GPS-tracked birds to compensate for this issue. As trophic position did not differ between adults and nestlings, but contaminant profiles did, the authors suggested that foraging area likely influenced contaminant load. Again, because individual variation in migration is common in birds (Åkesson and Helm 2020), it may result in differences in contaminant loads among individuals breeding at the same site. Given that we now know there may be high variation among individuals in both movement and contaminant burdens. Thus future studies should, when feasible, examine contaminant loads and movements in the same individuals (e.g., Miller et al. 2020; Shoji et al. 2021; Albert et al. 2021) to better understand how individual movement impacts contaminant loads in avian species.

Exposure pathways

An important factor when studying contaminant loads in relation to avian movements is assessing both the source and fate of contaminants in the environment. While spatial information is key in identifying the environment in which the species acquired the contaminant, it is beneficial to then assess the specific exposure pathways, such as diet. A few studies examined contaminant concentrations in bird species as well as their prey, and then related this to movement. For example, Yates et al. (2009) examined DDEs in white-faced ibis (*Plegadis chihi*) and the earthworms they consumed, and found that earthworms on the wintering grounds were a significant source of DDE. Elliott et al. (2007) used satellite telemetry data to spatially target the sampling of osprey (*Pandion haliaetus*) prey and found that DDE concentrations differed between prey types and wintering sites. However, breeding site had a stronger effect on DDE concentrations in osprey eggs than wintering site, suggesting that DDE was primarily acquired during the breeding season (Elliott et al. 2007). Importantly, most birds of prey are likely to obtain contaminants from more sources than their breeding, wintering and stopover sites because they may also feed on other migratory birds (e.g. passerines; Vorkamp et al. 2018). This highlights the value of examining contaminants in prey to further understand the source of contaminants in avian species in the context of movement ecology.

There has been recent advancement of studies that combine bird movements and modelling to estimate where birds may be most at risk to contaminant exposure, without measuring contaminants directly (Ludwigs et al. 2022; Blanco et al. 2022). Indeed, some studies in this review did not analyze contaminants in the birds themselves, and instead examined the contaminant in the environment. For example, Kerric et al. (2021) equipped ring-billed gulls

from Quebec, Canada, with passive air samplers and GPS tags to examine how movements impact exposure to halogenated flame retardants (HFRs). The authors found that gulls that visited landfills were exposed to higher HFR concentrations than those that did not. These types of exposure studies are important, as these studies can give us baseline information about the external environment and can be used for estimating potential threats to avian species. However, exposure studies paired with data on contaminant loads in the species examined can provide more information on how these contaminants move through the environment and food web. For example, Sorais et al. (2021) also used a combination of passive air samplers and GPS tags to examine ring-billed gull exposure to HFRs, but upon recapture, gulls were euthanized to examine contaminant loads in the liver. Interestingly, the authors found no relationship between HFR concentrations in the liver and individual gull exposure to HFRs, but concentrations increased with the probability that a gull visited a landfill. This emphasizes the importance of examining multiple exposure pathways (indirect exposure through the environment and direct exposure through diet) to better understand how these pathways play a role in contaminant loads of mobile species.

Another important factor to examine is the length of time that tracking devices are deployed. For example, Thorne et al. (2021) examined mercury in blood from herring gulls (*Larus smithsonianus*) tracked with GPS tags over the course of two months. While the authors found a strong relationship between mercury levels and foraging location, they suggested that foraging location before GPS tagging also impacted the birds, suggesting that longer tracking periods

would provide more information on how habitat use impacts mercury levels over time (Thorne et al. 2021).

Importantly, as these “legacy” contaminants are restricted or banned under international conventions, they are often replaced by contaminants with similar properties that may pose similar threats (i.e., “emerging” contaminants), which may also cause adverse impacts on the environment. For example, PBDEs, chemicals added to consumer products to reduce flammability, were shown to be persistent, bioaccumulative, and toxic, leading to their restriction under the Stockholm Convention in 2009 and a subsequent decline in their use in most countries (Greaves and Letcher 2017; Blum et al. 2019). However, this decline was coupled with a subsequent increase in the use of OPEs, another group of flame retardants that are also used as plasticizers (Schreder et al. 2016; Greaves and Letcher 2017). While OPEs were originally expected to be less persistent than PBDEs, the concentration of OPEs in the environment is now higher than PBDEs were at their peak use (Blum et al. 2019), and these chemicals have shown a variety of negative impacts on wildlife (e.g., reduced reproductive success and survival; Greaves and Letcher 2017). As more contaminants are considered for restriction under international conventions, understanding long-range transport and where birds may be exposed is of increasing importance.

Recommendations for future research

Our review demonstrates that studies on the relationship between avian movements and contaminant loads are expanding, but many knowledge gaps remain on how movement plays a

role in the transport and fate of contaminants. Below we provide some recommendations for future research on this relationship.

1. Consider statistical power

To enable a reliable, statistical assessment on whether movements influence contaminant concentrations, it is important to sample the same individuals for both movement and contaminant analyses. Studies that compare contaminant loads in one individual to tracking data from another individual (e.g., Sebastiano et al. 2016) cannot accurately assess this relationship because contaminant concentrations can differ between individuals due to a variety of factors, including age (Bassi et al. 2021), sex (Provencher et al. 2016), breeding status (Mallory et al. 2006), as well as movement-related factors, such as foraging area (Peterson et al. 2017) and wintering area (Bertram et al. 2022). Moreover, differences in wintering area can result in differences in contaminant concentrations among years (Albert et al. 2021). To alleviate the issue of inter-individual and/or inter-year variation and increase the ability to draw conclusions on potential sources of contaminants, researchers should sample the same individual, in the same timeframe, for both movements and contaminants when possible.

Power analyses have been conducted for certain contaminant groups (e.g., Provencher et al. 2015) and movement analyses (e.g., Soane et al. 2013). For example, Provencher et al. (2015) showed that between a few dozen to hundreds or thousands of individuals are needed to detect changes in plastic pollution levels over time, but this number varied depending on the percent change detected, as well as the species and region (due to differences in the prevalence of plastic

ingestion between species and regions). Similarly, Soanes et al. (2013) showed that the number of individuals required to predict the home range of a colony differs between species, but this varied depending on the number of foraging trips included in the sample. As the minimum sample size needed may vary between contaminants, species, and regions, researchers should conduct power analyses for their specific question. However, power analyses require knowledge of an effect size (the relationship between contaminant and movement), which is exactly what is unknown. When adequate data are not available to calculate statistical power, we suggest following recommendations from power analyses conducted in similar studies, if available. Using the two studies above as an example, the minimum sample size for both contaminant and movement analyses is approximately 40 individuals. Based on this, only 50% and 37% of studies in this review had an adequate sample size for contaminants or movement analyses, respectively, and only 33% had a sample size ≥ 40 for both. While the minimum sample size needed for each of the studies in this review may differ from this example, these results nonetheless highlight the need to determine the minimum sample sizes needed to detect differences between regions and determine potential sources of contaminants.

Another way to improve statistical power when assessing the relationship between avian movements and contaminants is to advance the statistical tools used. Here, studies used various statistical techniques to analyze this relationship, from simple *t*- or *u*-tests to more complex mixed effects models (see Table 6.1). However, 24% of studies did not specifically test the relationship between contaminant data and tracking device data. While some of these studies may have been limited by sample size (e.g., Yang et al. 2022), or by the inability to track the

same birds as those analyzed for contaminants (e.g., Sebastiano et al. 2016), studies that are not limited by these factors should aim to test this relationship statistically when possible. However, the choice of methodology largely depends on what is possible with the data in hand (e.g., do the data meet the assumptions of the test?). For this reason, instead of a blanket recommendation for a single statistical approach, we want to reinforce the importance of considering the statistical approach and potential effect size when planning, collecting and/or analyzing data. For example, general linear models are useful to assess the relationship between contaminants and movement because other factors that may influence contaminants, such as species, sex or age, can be considered in the model.

Finally, to understand the full picture of the relationship between avian movements and contaminant loads, we need to advance the statistical tools to predict and map the likely distribution of contaminants. For example, integrating isoscapes (that depict spatial variations in isotopes) and chemoscapes (that depict spatial variations in contaminants) into a joint statistical framework can help pinpoint contaminant sources or hotspots, while also providing information on potential pathways of transport through the food web. Indeed, studies are already combining tracking technology with stable isotope analyses to develop isoscapes (St. John Glew et al. 2019; Atkins et al. 2023), and chemoscapes geo-referenced by tracking data (Sorais et al. 2021). For example, Atkins et al. (2023) used GLS devices to track northern gannets (*Morus bassanus*) to their wintering grounds, then analyzed stable isotopes in feathers moulted at that time to develop an isoscape for that region. While this technique may introduce uncertainty in areas with few location points, and timing on moult must be known to use this method, this approach could be

applied to contaminants to develop chemoscapes for large-scale regions. On a smaller scale, Sorais et al. (2021) combined GPS data on ring-billed gulls with the concentration of HFRs in their liver to develop a chemoscape that demonstrates the influence of landfills on exposure to HFRs. This combined approach would not only help us better understand the relationship between avian movements and contaminants, but also the spatial distribution of contaminants in the environment, which can inform conservation strategies for the birds or the environments in which they inhabit. However, some contaminants, such as mercury, are deposited into feathers over different time periods than stable isotopes (Bond 2010), thus it is important to consider the relationship between the deposition of contaminants and stable isotopes prior to analysis.

2. Consider turnover rates and tracking device resolution

Both tissue and contaminant turnover rates influence the contaminant load in the tissue at the time of sampling or time of tissue growth. By better understanding both tissue and contaminant turnover rates, we can better interpret the relationship between bird movements and contaminant loads. For example, if a bird is exposed to high concentrations of a particular contaminant in a contaminant hotspot, but then moves to an area with relatively low concentrations of this contaminant, the tissue concentration of said contaminant may decrease over time (e.g., Mallory et al. 2019), and the time that this takes depends on both the tissue turnover rate and the contaminant turnover rate. In general, tissues with short turnover rates, such as blood, can provide important information about recent contaminant exposure, which is valuable for monitoring short-term changes in contaminant exposure. On the other hand, tissues with longer turnover rates can provide important information on historical contaminant exposure and/or the

persistence of contaminants in an individual. However, tissue turnover rates can be influenced by various factors, including species, age, metabolism, and environmental conditions, and thus should be studied in the context of the specific study system. As turnover rates are not well known for many species or tissues, we stress the importance of more laboratory work to better understand how contaminants are metabolized in specific body systems.

Importantly, the relationship between avian movements and contaminant loads can only be assessed if the resolution of the tracking device is relevant to the turnover rate of the tissue and/or contaminant, and the movement scale of the species. For example, if birds have low migratory connectivity, you can estimate where in the annual cycle the individual acquired the contaminant, but only at the scale of the tracking device. With fine scale, high resolution devices such as GPS, you may be able to determine that birds spending more time in a hotspot (e.g., landfill) have higher contaminants levels than those that do not. However, if you have GLS devices with an error upwards of 400 km (Halpin et al. 2021), then you can only determine if birds wintering in one general area have higher or lower concentrations than those in another (e.g., a gradient of east to west). On the other hand, if birds have high migratory connectivity, it will be difficult to disentangle where in the annual cycle the individuals acquire a contaminant unless you have tissues with different time scales.

Indeed, most statistical analyses to date have worked best where birds move between discrete locations. For example, it is straightforward to compare birds wintering in sites A, B and C. However, if birds are moving in different proportions between these different sites, then it would

be necessary to calculate the time in each location and consider the half-life of the contaminant in the particular tissue. Given the inherent uncertainty, we recommend that this technique is best employed where birds winter or forage in particular discrete patches with no (or limited) movement among them. Overall, studies should consider both tissue and contaminant turnover rates, along with the resolution of the tracking device, to better estimate the relationship between avian movements and contaminant loads.

3. Examine tissues that inform different time scales

In addition to understanding turnover rates and device resolution, increasing studies that sample non-lethal tissues at different times of the year and/or in different years is crucial to better understand how both contaminant concentrations and exposure to contaminants can change over time. However, studies that assess multiple time points have been limited to date (e.g., Shoji et al. 2021). For example, obtaining feathers, a blood sample upon arrival at the colony, a blood sample before egg-laying, and a blood sample during incubation, would allow us to strengthen inferences about where contaminants were obtained. If the contaminant declined, then we could infer that it was obtained (more) on wintering grounds than breeding grounds. If it increased, then we could infer it was obtained (more) on breeding grounds. The rate of change among wintering or breeding sites would allow us to infer which wintering or breeding sites have higher levels, especially when coupled with locations of where the birds went in the winter. Similarly, collecting blood or feathers from the same individuals across multiple years, and combining this with tracking information, can help us understand how exposure may change over time and how this may impact these individuals. However, it is important to note that different tissues may

result in differences in contaminant concentrations, and this must be considered when assessing temporal changes in contaminants. For example, preen oil has a high lipid content, and thus may have higher concentrations of hydrophobic contaminants, such as many POPs, compared to plasma and feathers (Solheim et al. 2016; Briels et al. 2019). Moreover, feathers can contain contaminants deposited at the time of tissue growth, as well as contaminants obtained from preen oil or other external sources (e.g. air) making it challenging to confidently assess differences over time (e.g., Dehnhard et al. 2019; Briels et al. 2019). This again highlights the importance of understanding tissue turnover rates, but also understanding individual contaminant properties and using proper quality assurance and quality control procedures when collecting and processing contaminant samples (Jaspers et al. 2019).

4. Explore the impacts of contaminants on behaviour and movement

High contaminant loads may impact the behaviour of wildlife species, such as invertebrates, amphibians, fish and birds (Saaristo et al. 2018). Therefore, when conducting a study on avian movements and contamination to better understand potential sources of contaminants, it is important to consider that the contaminant load itself may be impacting the movement of the individual. Moreover, contaminants may have cumulative effects on individuals, either from multiple contaminants acting on the bird at once (e.g., Goutte et al. 2014), or multiple stressors in addition to contaminants (e.g., food shortage, disease; Sebastiano et al. 2022; Esparza et al. 2022). For example, climate change is altering animal movements (e.g., Hazen et al. 2013), which may result in more or less exposure to certain contaminants (e.g., McKinney et al. 2013), while the contaminants themselves may make the birds more or less resilient to other impacts of

climate change. As a result, exploring the impact of contaminant loads and how multiple contaminants or stressors may have additive effects on individual behavior and movement is an important avenue for future research.

5. Increase collaboration, standardization, and information sharing

Pooling resources, sharing data, and developing standardized methods of sampling, analysis and reporting will not only increase sample sizes and reduce overall research costs, but also help identify and compare trends across species, regions, or time. A great example of this type of collaboration is from Albert et al. (2021), where the authors worked with partners from SEATRACK (<https://seapop.no/en/seatrack/>), SEAPOPOP (<https://seapop.no/en/>), and ARCTOX (<https://arctox.cnrs.fr/en/home/>) to assess how variation in winter distribution impacts individual mercury contamination across multiple regions and time periods. These types of collaborations can increase the spatial and temporal scale of the project, but also provide additional resources to analyse more contaminants and/or more tissues (particularly if birds were sacrificed for research), which then allows for the analysis of cumulative effects. By increasing collaboration, we can collectively advance our understanding of the link between movements and contamination.

A common thread from the papers in this review was that synchronizing the measure of exposure/bioaccumulation and movement data is key to enhancing our understanding of the relationship between local, seasonal, and annual movements of birds and the relationship to their contaminant levels in various tissues. While we have a relatively good understanding of uptake

and turnover rates in many tissues (e.g., Renedo et al. 2021), and vastly improved knowledge of local and long-range movements of birds over the past two decades with the miniaturization of tracking technology (Bridge et al. 2011), our ability to link contaminant exposure and uptake through the year will only be possible when we design projects around an understanding of collecting and linking movement and contamination data temporally. The technology to do this is now available, and we are beginning to see studies that embrace this approach (Shoji et al. 2021), thus future studies that consider the temporal relationship between the movements of birds and their contaminant levels in various tissues are encouraged.

Conclusion

Overall, there are many ways to assess the relationship between avian movements and contaminants, and the choice of method depends on the question being asked. It was only four decades ago that researchers relied on recaptures of banded birds in wintering areas to link contamination and movement (e.g., Nygård 1999), but with the rapid technological development of tracking technologies in the decades since, we can now link foraging movements to short-term contaminant exposure (Sorais et al. 2021). The objective of this review was not to choose one method that is best, but instead provide an overview of the current knowledge, discuss the benefits and costs of certain methods, and highlight the important factors to consider when examining the relationship between avian movements and contaminants. Importantly, while this review is focused on birds, these recommendations can generally be applied to other marine fauna (e.g., Peterson et al. 2017). Currently, we need to consider statistical power, turnover rates, tracking methods and migratory connectivity in the study design to ensure that these

relationships can be examined in a meaningful way. Moving forward, studies should explore using tissues that inform different time scales, assess the impacts of contaminants on behaviour and movement, and develop new statistical tools to better understand the spatiotemporal relationship between migratory birds and the contaminants within them. Overall, we show that while there are various methods to answer the questions surrounding avian movement and contamination, collaboration, standardization, and information sharing will be key to collectively advance our understanding of the role that migratory birds play in the movement and fate of contaminants on a global scale.

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GENERAL DISCUSSION

There is no feeling more invigorating than the rush you experience as you raise your arms, open your palms, and gently toss a gull into the air, freshly equipped with a geolocator that you attached minutes before. As it flies away into the everlasting Arctic sunset, joining hundreds of others from the colony, you silently ask that it returns next year. The many failures in this type of research, including geolocators lost at sea and birds that return to the colony but are impossible to recapture, are not often mentioned in scientific publications, yet are an important part of the story. It is these experiences that offer a greater appreciation for the successes – the birds that are recaptured. A device the size of your fingernail, containing information from over a year of trans-Atlantic movements, ready to download and uncover the secrets of an individual's life. Modern technological advancements, such as the miniaturization of tracking devices like these, provide a unique opportunity to answer a diverse set of ecological questions, pushing wildlife ecology and conservation to new heights. Indeed, these devices have the potential to uncover patterns and relationships that extend beyond individuals, offering insights on the broader health of the marine environment.

Colonial-breeding seabirds serve as ideal models to address a multitude of diverse ecological questions about the marine environment. Their high trophic position, strong nest site fidelity, and relative accessibility at breeding colonies makes them important sentinels of the marine environment, revealing insights about these environments that may otherwise remain unknown (Cairns 1988; Parsons et al. 2008). This is particularly the case for at-sea or remote locations, such as the Arctic, where it is often financially and logistically challenging to conduct research

(Mallory et al. 2018). As such, Arctic seabirds have been used as indicators of the marine environment for decades (Mallory et al. 2006a, 2010b), uncovering key relationships and information on these ecosystems. However, the characteristics that make seabirds effective ecological indicators may also influence our ability to draw conclusions about the relationships that we observe. For example, seabirds may have large foraging ranges (e.g., several hundred kilometres for northern fulmars; Mallory et al. 2008) or migrate long distances (e.g., up to 60,000 km annually for Arctic terns; Alerstam et al. 2019), integrating signals from multiple environments as they travel throughout the year. As such, studying a characteristic in a seabird at its breeding colony may provide insights into the breeding period as well as other portions of the annual cycle. It is therefore important to consider how seabird movements may influence the answers to other ecological questions.

How movement plays a role in seabird ecology is a recurring theme throughout this thesis. As seabirds move, they are exposed to diverse, dynamic environments throughout their annual cycle. As climate change continues to alter these environments across the globe, particularly in the Arctic (AMAP 2021a), these changes may be reflected in Arctic-breeding seabirds. However, the impact of such changes may differ between individuals or populations, depending on their migration strategy (see Figure 1.2). In this thesis, I present evidence of both inter- and intra-individual variation in multiple Arctic-breeding gull species (Chapter 2, Chapter 3). In Chapter 2, I demonstrated that herring gulls exhibit individual variation in both southbound and northbound migration, where gulls took different routes to and from wintering areas, but largely overwintered in the same region in the Gulf of Mexico. In Chapter 3, I presented the first

evidence of diverging migration strategies in glaucous gulls, where one gull migrated to the Sea of Okhotsk in Russia and the remainder overwintered in the North Atlantic. While glaucous gull migration strategies were relatively consistent between years, I found that gulls wintering in the North Atlantic shifted their distribution between years, likely in response to changes in sea ice concentrations in that region.

As climate change continues to alter environments throughout the ranges of these gulls, this raises the question: Do these migration strategies make these populations vulnerable to environmental change? While these changes may have a variety of impacts at the individual level (e.g., reduced body condition; Amélineau et al. 2019), both of these populations have high inter- and intra-individual variation in migration strategies, which may make these populations less susceptible to climatic changes and anthropogenic stressors throughout their range compared to species that specialize on a certain region or prey (see Figure 1.2). For herring gulls, migration routes were remarkably different among and within individuals (Chapter 2), suggesting that an environmental change at a stopover site may not cause significant impacts on the overall population. However, while one individual overwintered in the Great Lakes, the remainder spent the winter in the Gulf of Mexico. This suggests that this population may be more vulnerable to environmental changes in their main wintering area in the Gulf of Mexico, although tracking more individuals from this colony would help us better understand the importance of the Great Lakes to this population, as well as the use of stopover sites that may be more susceptible to climate change, such as the Grand Banks and the Gulf of Maine. In Chapter 3, I provided evidence to support individual variation in the migration strategies of glaucous gulls. Gulls took

multiple routes to wintering grounds, overwintering in three distinct wintering areas: the Labrador Sea, the Gulf of St. Lawrence, and the Sea of Okhotsk (Chapter 3). Like herring gulls, these diverse migration strategies may make this glaucous gull population less susceptible to changes that occur in a portion of their range.

Notably, as generalists, gulls are also relatively flexible in their foraging and migration strategies (González-Solís et al. 2011; Frederiksen et al. 2012; Klaassen et al. 2012; Anderson et al. 2020; Gutowsky et al. 2021), which may also benefit these populations in a changing climate. For example, in Chapter 3, I showed that glaucous gulls wintering in the Labrador Sea shifted their wintering area between years, likely in response to changes in sea ice concentrations in this region. This suggest that, to some degree, these birds can be flexible in their migration strategies to accommodate changes in the environment, similar to great-black backed gulls (*Larus marinus*) in Newfoundland (Maynard and Davoren 2018) and black-legged kittiwakes and glaucous-winged gulls (*Larus glaucescens*) in the Bering Sea (Hunt et al. 2018). However, further tracking is required to better understand this relationship. Importantly, these populations may not always be able to respond in time with the changes in their environment. For example, while sea ice breakup advanced more than a month over a 30-year period in the Canadian Arctic, breeding thick-billed murres on Coats Island only shifted their lay date by one week (Whelan et al. 2022). However, as highly flexible generalists, gulls may not need to be as responsive to changes in sea ice compared to other Arctic-breeding seabirds (Gutowsky et al. 2022).

It is important to note that while the movement ecology of most gull species in the Canadian Arctic is either not well understood or has only recently begun to be uncovered (e.g., Gutowsky et al. 2020, 2021; Baak et al. 2021d), gull migration in the European Arctic is relatively well-documented for many species (Kilpi 1984; Kilpi and Saurola 1984; Schwemmer and Garthe 2006; Helberg et al. 2009). For example, black-legged kittiwake movements have been studied in both the European Arctic (e.g., González-Solís et al. 2011; Frederiksen et al. 2012; Ezhov et al. 2021) and North Pacific (e.g., Paredes et al. 2014; Orben et al. 2015b), where there has been tremendous progress in assessing risks to these populations, including identifying hotspots (Frederiksen et al. 2012; Orben et al. 2015a; Léandri-Breton et al. 2021) and examining the relationships between movement and reproductive success (Bogdanova et al. 2011), diet (Whelan et al. 2020), or contaminants (Léandri-Breton et al. 2024). However, the movements of black-legged kittiwakes, and many other Arctic-breeding seabirds, are not as well understood in the Canadian Arctic, likely as a result of the additional logistical and financial challenges of monitoring seabirds in these remote areas (Mallory et al. 2018). As climate change drives rapid and transformational shifts in Arctic environments, seabirds will exhibit varied responses to these changes among regions. Long-term monitoring of seabird movements will therefore be crucial to understand the impacts of these changes on Arctic-breeding seabird populations across the north, as well as to inform the development and management of conservation areas (e.g., Hughes et al. 2017; Augé et al. 2018; Arroyo et al. 2020; Davies et al. 2021a).

One of the main drivers of seabird movements is access to prey resources (Somveille et al. 2015). Thus, evaluating seabird diet and trophic ecology is also important to understand how a

population will respond to, and be impacted by, environmental change. In Chapter 4, I used multiple approaches to quantify the diet of black-legged kittiwakes for the first time in Qikiqtarjuaq and Pond Inlet, Nunavut, and for the first time since the late 1990s in the Canadian Arctic. I found that kittiwakes in the Canadian Arctic heavily rely on Arctic cod, but that traditional stomach content analyses likely underestimate the contribution of soft-bodied organisms, such as invertebrates. I showed that these diet items may be identifiable through other techniques, such as stable isotope analyses, but that factors influencing these analyses (e.g., time, location) must be considered to make informed conclusions. Had we been able to incorporate predator and prey samples from the same location, in the same portion of the water column, and in the same year, we may have been able to better understand how invertebrates and other prey items play a role in the diet of black-legged kittiwakes. Nonetheless, this chapter demonstrates the utility of using multiple approaches to obtain a better understanding of seabird diet, which can be used to monitor dietary changes in these populations over time.

Black-legged kittiwake populations are in decline throughout most of their circumpolar range (Johansen et al. 2020). While intermittent population estimates suggest that kittiwakes may be increasing in some parts of the Canadian Arctic (Mallory et al. 2009; Gutowsky et al. 2022), forecasted impacts of climate change in these regions, such changes in sea ice (Cooley et al. 2020) and ice-associated fish (Geoffroy et al. 2023), may have negative implications for these populations in the future. Indeed, while kittiwakes are opportunistic piscivores that can consume a variety of prey species (Hatch et al. 2020), they may nonetheless exhibit sensitivities to changes in key prey species that they rely on (e.g., reduced breeding success with a shift from

ice-associated to open water-associated prey; Vihtakari et al. 2018). Importantly, black-legged kittiwakes are not the only species that rely on Arctic cod in this region; both northern fulmars (Mallory et al. 2010a) and thick-billed murres (Provencher et al. 2012) in the Canadian Arctic also consume relatively high proportions of Arctic cod. As these species often breed sympatrically in these regions (Mallory et al. 2019), a shift in the distribution or abundance of Arctic cod may have broader implications for this trophic community as a whole. This reinforces the importance of using information on diet to better understand trends in seabird ecology, which can provide important information on both the status of the population, as well as the surrounding ecosystem (e.g., Searle et al. 2023).

Changes in diet may also cause changes in the exposure to, acquirement of, and retention of contaminants in seabirds. In Chapter 5, I combined new and historical data on plastic pollution of four seabird species in the Canadian Arctic to assess spatial, temporal, and methodological trends in plastic ingestion. I demonstrated that northern fulmars consistently ingest more plastic pollution than black-legged kittiwakes, thick-billed murres, and black guillemots, likely due to a combination of their diet, surface-feeding foraging strategies, and inability to regurgitate hard, indigestible prey items. I also showed that plastic ingestion by northern fulmars generally followed a north-south gradient, where plastic ingestion was lower in more northern latitudes, but increased in two High Arctic regions. As plastic pollution continues to increase in the Arctic and across the globe (Borrelle et al. 2020), these results emphasize the utility of northern fulmars as a long-term monitoring tool for plastic pollution in Canada and across the Arctic (OSPAR 2015; Provencher et al. 2019; Baak et al. 2021b; van Franeker et al. 2021).

If northern fulmars consistently ingest more plastic pollution than other species, this provokes the question: Should we continue monitoring other Arctic-breeding seabird species for plastic pollution ingestion? The answer to this question is complex, and highly dependent on the answer to the follow-up question: Why are we monitoring plastic pollution ingestion in Arctic seabirds? If we are monitoring plastic ingestion to assess the effects of plastic pollution on individuals or populations, it would make sense to monitor plastic ingestion in a species that ingests high levels of this pollutant. If we are monitoring plastic ingestion to understand the occurrence and trends in plastic pollution across the environment, it may be valuable to monitor multiple species that differ in diet, foraging ecology, or morphology, to gain a better understanding of how plastic pollution is distributed throughout the food web. For example, as surface-feeders, northern fulmars can provide important information on plastic pollution at the surface, while thick-billed murres or black guillemots, as diving species, can provide information on plastic pollution in the middle of the water column. Overall, the decision on which species to monitor involves multiple considerations.

The decision on which species to monitor also depends on the type of plastic pollution that is of interest. For example, if the focus of study is macroplastics, or plastic pieces greater than 1 mm in size, monitoring species that do not generally ingest high levels of plastics in this size range, such as thick-billed murres or black guillemots, may not be valuable. However, when examining microplastics, or plastics less than 1 mm in size, these species may provide a unique opportunity to quantify the occurrence and potential sources of microplastic pollution in this portion of the

water column, while also enabling us to assess the fate of these plastics in the environment. For example, Bourdages et al. (2021) found that while thick-billed murres in the Canadian Arctic did not have macroplastics in their stomach, 17% contained microplastics in their faecal precursor (i.e., guano). These results, combined with information on population and behavior, allowed Bourdages et al. (2021) to estimate that thick-billed murres deposit around 45.5 million particles into the environment at one colony in one year. Ultimately, monitoring plastic pollution in Arctic seabirds is complex, but with prior consideration to the question being asked, these monitoring programs can yield valuable insights on both Arctic seabirds and the environments in which they use. The data from such programs can then be used to both inform and monitor the efficacy of national and international policies. For example, monitoring the occurrence, movement and fate of a contaminant can support the regulation or restriction of said contaminant under the international Stockholm Convention (The Stockholm Convention on Persistent Organic Pollutants 2001), and once regulated or restricted, continued monitoring can provide insights onto the efficacy of such policies (e.g., Braune et al. 2015).

As plastic ingestion by seabirds continues to increase across the globe, it is important to consider the methodology used to monitor plastic pollution, and how differences in these methods may impact our ability to compare information across species, regions, and time. In Chapter 5, I reviewed the methodologies used to examine plastic pollution in four seabird species across Canada. I found that sample collection and processing methods differed across Canada. For example, most samples in the Arctic were collected by sacrificing birds, whereas samples from southern Canada were from beached birds. The choice of sample collection method is often

limited by other factors (e.g., vast, uninhabited areas in the Canadian Arctic make it difficult to collect beached birds), but as long as these methods are reported, we can take this into consideration when assessing spatial and temporal trends. Moreover, I found that while only half of samples were processed using recommended methods (e.g., van Franeker et al. 2011; Provencher et al. 2017), the use of these methods has increased over time, indicating a promising future for more robust analyses of trends in plastic ingestion over time. Indeed, the need for consistent or standardized methods for plastic pollution studies has been thoroughly discussed (Avery-Gomm et al. 2016; Provencher et al. 2017, 2019), with both national (Provencher et al. 2015) and international (Baak et al. 2021b; Kühn et al. 2022) efforts to standardize methods to facilitate spatial and temporal assessments of this increasing environmental pollutant.

Importantly, plastic pollution is not the only contaminant of concern to Arctic wildlife and the habitats they use. Indeed, other contaminants, such persistent organic pollutants (e.g., PCBs), pesticides (e.g., DDT, organochlorines), heavy metals (e.g., mercury), flame retardants (e.g., PBDEs) and more, are increasing or remaining persistent in environments across the globe, where new compounds are added to this chemical cocktail each year. It is therefore important to identify the source, transport, and fate of these contaminants in the environment to inform regulation of these potentially harmful substances. Traditionally, banding recoveries and stable isotope analyses were used to determine potential sources of contaminants, but these estimates are geographically coarse. In Chapter 6, I reviewed 42 studies that used tracking devices to assess the relationship between avian movements and contaminants, and used this information to provide recommendations for future research in this field. I demonstrated that while the body of

literature examining this relationship is growing, methods varied widely. For example, many studies did not consider sample size, statistical power, and/or the temporal resolution of the tissue, contaminant, or tracking device in question. As more chemicals are reviewed for regulation under local, national, or international legislation, considering these matters in study design will be important to ensure that this research can indeed inform these decisions.

It is also important to consider that contaminants do not follow jurisdictional boundaries. Many contaminants can be transported long ranges through a variety of processes, including biotransport by birds (e.g., Bourdages et al. 2021), and the regulation of these contaminants often occurs at national or international scales (e.g., The Stockholm Convention on Persistent Organic Pollutants 2001). This stresses the importance of increasing collaboration, standardization, and information sharing across monitoring programs to facilitate large-scale, long-term monitoring of these environmental contaminants. In this review, I highlight how a standardized approach would facilitate comparisons across species, regions, and time, allowing for a more comprehensive understanding of the potential sources, effects, transport, and fate of these contaminants in the environment, which can be used to identify contaminant hotspots or areas of concern for these populations (e.g., Bertram et al. 2022). While this chapter focuses on birds, these recommendations can generally be applied to other marine fauna, such as polar bears or seals that are also experiencing changes in their environments and thus changes in the contaminants that they are exposed to (McKinney et al. 2009, 2013). Overall, this review emphasizes that both collaborative research and standardized methods are necessary to explore the complex interactions between movement, diet, and contaminants in a changing Arctic.

The need for standardized monitoring is another reoccurring theme throughout this thesis. To effectively use seabirds as indicators of the environment, the methods used to monitor these birds should not impede our ability to make meaningful comparisons across species, regions, or time. Throughout this thesis, I highlight how differences in methodology may influence our ability to assess trends over time. For example, in Chapter 1 and 4, I showed that the choice of method to examine seabird diet may result in an over- or underestimation of certain prey items (e.g., stomach content analyses may result in an underestimation of soft-bodied organisms that may be present, but unidentifiable, in this type of sample). In Chapter 5, I highlighted that differences in sample collection and processing may result in differences in plastic ingestion levels in seabirds (e.g., plastic particles in a seabirds gastrointestinal tract may be missed if not examined over a 1 mm sieve, resulting in differences in plastic ingestion compared to samples processed using these methods; Avery-Gomm et al. 2016). In both cases, the use of different methods may impede our ability to accurately detect changes in diet or contaminant levels over time. By employing standardized methods to monitor seabird movement, diet, or contaminants, researchers can generate more robust datasets that not only contribute to our understanding of seabird ecology, but also enhance our ability to confidently detect changes, thereby informing future conservation and management efforts for these species.

CONCLUSIONS

Climate change is altering Arctic ecosystems at unprecedented rates, with future projections indicating further increases in sea ice loss (Cooley et al. 2020), severe weather events (McCrystall et al. 2021), shipping and fishing activities (Ng et al. 2018), and pollution (Wit et al. 2022). Seabirds, as top predators that integrate signals across space and time, provide a unique opportunity to monitor both the changes in the marine environment as well as the impacts of these changes on the seabirds themselves. In this thesis, I used a multi-faceted approach to fill critical knowledge gaps on the ecology of multiple Arctic-breeding seabird species, while also establishing benchmarks for monitoring future change in these systems. First, I examined the migratory movements of two Arctic-breeding gull species, herring and glaucous gulls, demonstrating high inter- and intra-individual variation in migration. This may result in a resilience of these populations, at least in the short-term, to changes in climate in parts of their range. Next, I examined the diet of another Arctic-breeding gull, the black-legged kittiwake, and show that these birds heavily rely on ice-associated Arctic cod, indicating a vulnerability in the face of a warming climate. Then, I examined trends in plastic ingestion by four seabird species in the Canadian Arctic, and showed that plastic ingestion differed between species, regions, and time. Finally, I integrated these approaches by reviewing how avian movements play a role in contaminant research, highlighting the importance of considering key factors in study design (e.g., sample size, statistical power, and turnover rates) to better inform conservation and management decisions.

Overall, this thesis demonstrates that there are complex interactions among migration, diet, and contaminants, and that studying these topics in conjunction with each other can provide a more holistic understanding of seabird ecology as well as the ecosystems they inhabit. Offering new perspectives on the ecology of multiple Arctic-breeding seabird species and the multifaceted stressors they face, along with actionable recommendations for future monitoring of seabird populations in the Arctic and worldwide, this thesis lays the groundwork for understanding how seabirds will be impacted by, and respond to, environmental change. With this knowledge, we can better inform conservation, management, and policy decisions in a rapidly changing Arctic.

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