Arctic Institute of North America 1945

CANADA BIOGENOME PROJECT

Marine Animal Genomics in Kuujjuaq (MAGIK) Workshop – Summary Report

NUNAVIK

ARCTIC GENOMICS

UNIVERSITY OF CALGARY

Athabasca University

Carleton University

Workshop organization:

The Marine Animal Genomics in Kuujjuaq (MAGIK) Workshop was a collaboration of the Canada BioGenome Project (CBP), the Arctic Institute of North America, and the Nunavik Tourism Association.

Financial support for workshop:

The Canada BioGenome Project

Recommended citation:

Crookes, S., Gordon, A., Angulalik, E., Mishra, S., Caudill, C., Marston, E., Schott, S., Bhatnagar, S., Pulsifer, P., and Murray, M. (2025). *Marine Animal Genomics in Kuujjuaq Workshop: Summary Report*. Arctic Institute of North America, Technical Report No. 2026-01. doi:10.33174/AINA2026tr01MAGIKreport

Table of Contents

Acknowledgements

We extend our heartfelt thanks to the community of Kuujjuaq, QC, including the Nunavik Tourist Board and the Makivvik Corporation, for hosting the meeting and for providing it with a sound cultural and geographical grounding. Special thanks to elder Eva Lapage who graced the meeting with a blessing ceremony and to Michael Kwan who presented an overview of the work conducted by the Nunavik Research Centre, both of whom generously gave of their time.

This work would not be possible without the financial support of Genome Alberta, Genome British Columbia and Genome Canada.

Executive Summary

Following the success of the MAGIC (Muskoxen and Genomics in the Community) workshop held in Cambridge Bay, January 2024, many of the attendees were determined to hold other genomics-IQ co-discovery workshops in Inuit Nunangat pertaining to food security in the Arctic region. To that end, an organizing committee was set up to prepare for a second meeting to be held in Kuujjuaq, Nunavik. This meeting – Marine Animal Genomics in Kuujjuaq (MAGIK) - occurred on March 17th - March 19th, 2025. The agenda loosely paralleled the original MAGIC meeting, although the focus was broader, encompassing the potential for the co-development of genomics and DNA-based tools for aquatic animal applications in the service of communities within Nunavik and beyond. Additionally, the meeting was contextualized by its location – Kuujjuaq – which bestrides the Arctic and Sub-Arctic border, a changing ecological buffer zone that is responding to the direct and indirect effects of climate change on terrestrial and aquatic geomorphology, water chemistry and biodiversity.

MAGIK was a hybrid in-person and virtual event. Among the attendees were representatives of two Inuit Nunangat regions– Nunavut and Nunavik, including our host Allen Gordon, bringing exceptional traditional ecological knowledge (TEK) and cultural expertise. Amongst others in attendance were biologists from academia (Universities of Calgary, Athabasca and Carleton University) and Canadian agencies (DFO, CFIA and ECCC), purveyors of the humanities (e.g., economists and anthropologists), conservationists (e.g., Canada Museum of Nature), and resident experts from the Nunavik Research Centre (NRC) in Kuujjuaq. The primary aims of the meeting were to share knowledge on the marine and aquatic ecosystems of Nunavik, how they provide for communities, how genomics – and DNA-based tools – might be codeveloped to serve communities, and to determine which species are of special interest (as candidates for whole genome sequencing).

Introduction

General Introduction

It is arguable that the marine realm will suffer the most from cataclysmic climate change. The warming Arctic Ocean and melting ice will change hydrological regimes, expose Arctic shorelines to violent tempests (Kavan et al. 2025), alter currents (Timmermans & Marshall, 2020), change water chemistry (e.g., acidity (Qi et al. 2022)), and perhaps most impactfully of all, radically alter the amount of sea ice (e.g., in Baffin Bay, Ballinger et al. 2022). This litany of liabilities will have profound impacts on the occupancy, abundance and distribution of many Arctic marine and aquatic animal species (Deb & Bailey, 2023), the consumption of which provide for Inuit communities.

Regions such as Nunavik that span the border between Arctic and Sub-Arctic biomes will perhaps experience the greatest flux in biological resources, as organisms respond to shifting baselines in temperature, snow/ice cover, and permafrost, with its concomitant cascading influences on water chemistry (e.g. release of methylmercury into ecosystems and food webs). Additionally, Boreal forests are moving northwards, tracking a warming climate, bringing with it boreal animal species. Similarly, hitherto southerly marine, aquatic and semi-aquatic species (e.g., beavers) will follow in the wake of the melting ice and warming shelves and waters. It is to be expected that Arctic ecosystems - marine and terrestrial - will be put under enormous, and potentially existential, pressure in the struggle for existence. These are worrisome times for people dependent upon a healthy, productive and functioning northern ecosystem. A warming Arctic will impact food security (factors that effect the safety, reliability and predictability of food organisms (country food)) and biological security (determined by the vulnerability of a region to novel biological agents (e.g., pathogens and invasive species) that may cause ecological and sociological damage).

New tools are often brought to bear in times of crisis. The science of conservation genetics (now more broadly called conservation genomics due to the burgeoning use of whole genomes in studies of natural systems) has been incorporated into many actionable conservation plans to determine the genetic vulnerabilities of extant populations of imperilled or important organisms; and to determine genetic methods to alleviate some of the external pressures (climatic, anthropogenic, and otherwise environmental) that may prove to be damaging to the future longevity of vulnerable or important species. Through the scanning the genomes of animals, and by using related conservation genetic tools (such as environmental DNA-based (eDNA) screening of the habitats in which they live), Western science may provide the potential for information-rich data workflows that can be performed and developed alongside, in partnership, or subservient to, traditional data gathered by Indigenous ways of knowing, and be driven by cultural and local priorities (Inuit Qaujimajatuqangit (IQ)). Indigenous knowledge as a distinct, ‘lived-in’ and valuable repository of information of local ecosystems, biotas, and emergent issues, is key to the deployment of any conservation or management initiative in the Arctic.

In the Canadian Arctic, we are embarking on a similar journey, the first steps of which involve direct dialoging with communities to identify the needs (resource management, harvesting, etc.) of the community that require addressing. The subsequent step involves the exchange of expertise, where both Indigenous and non-Indigenous parties share their conceptual bases of knowledge (e.g., IQ and Western science (genomics)), explicate examples of resource management using their own ways of knowing, and discussing if there is a role for Western science to play in mitigating the impacts of a changing Arctic on its harvestable biota under the direction of communities. Finally, how Western science may be incorporated into management schemes need to be codified in a way that ensures equanimity, or indeed primacy, of developmental input from local communities.

To facilitate the above conceptual workflow, we arranged for a genomics-in-the-community workshop (MAGIK: Marine Animal Genomics in Kuujjuaq) to take place in the community of Kuujjuaq, Nunavik - a region at the interface of a rapidly changing ecological bridging zone between the Arctic and Sub-Arctic - whereby the potential role of genomics and DNA-based tools were discussed in the context of marine biological resources and the communities of Nunavik that depend on them. What follows is a report that presents the sociocultural and environmental (climatic) context behind the meeting, knowledge-sharing by the attendees at MAGIK, and identification of potential avenues of investigation for future co-development, including specifying species or ecological priorities for genome sequencing efforts, followed by closing remarks.

Marine Biological Resources and the Nunavimmiut

The relationship between the Inuit of Nunavik and living off the land and sea is a deep-seated cultural axiom and central to Nunavimmiut beliefs and *IQ*. The security by which biological resources (in the form of ‘country foods’) provision Nunavimmiut is realised by having access to a reliable and predictable source of nutritious country food that meets the community dietary requirements for a healthy and active life (Inuit Tapiriit Kanatami, 2017; Little et al. 2020). Of particular importance to the cultural, psychological and physical wellbeing of the Nunavimmiut, is the bounty provided by both marine and aquatic animals and plants (Inuit Tapiriit Kanatami, 2017; Allaire et al. 2021).

Marine mammals and fishes are key sources of nutrition. Iconic country food animals such as beluga (Qilalugaq; *Delphinapterus leucas*) are critical sources of minerals such as selenium (Lemire et al. 2015) and iron (Allaire et al. 2021). A key component of traditional diets in Nunavik, anadromous Arctic char (Iqaluppik; *Salvelinus alpinus*) is the second most consumed food within the population (Allaire et al. 2021). It contains fats (e.g., omega-3 fatty acids) that are excellent sources of multiple vitamins, as well as antioxidant pigment proteins such as carotenoids (Hatlen et al. 1997; Bolduc et al. 2024). Carotenoids influence the colour and texture of char meat, which is a critical part of the sociocultural relationship Nunavimmiut have with this fish (Allaire et al. 2021; Borduc et al. 2024). It is also the main source of n-3 PUFAs (n-3 polyunsaturated fatty acids) in the region (Lemire et al. 2015), further bolstering its status of a primary element of Nunavik food security.

Nutrition represents only a single facet of the relationship between Inuit and the Arctic aquatic ecosystems. The process by which country foods (animal and plants) are hunted, herded, harvested and distributed amongst the community is pivotal to providing social cohesion and forms the common cultural basis for living with the land and sea (Freeman, 2000). Seal hunting, for example, is emblematic of the profound relationship that Inuit across the Arctic have with the hunting, processing, distribution and consumption of country food alongside members of the community (Wenzel, 1991; Nuttall, 1992). However, seal meat consumption has been declining since 1992 (Allaire et al. 2021) which may reflect the role that changing cultural or generational mores and/or environmental influences are having on marine biota, especially those at risk of climate change.

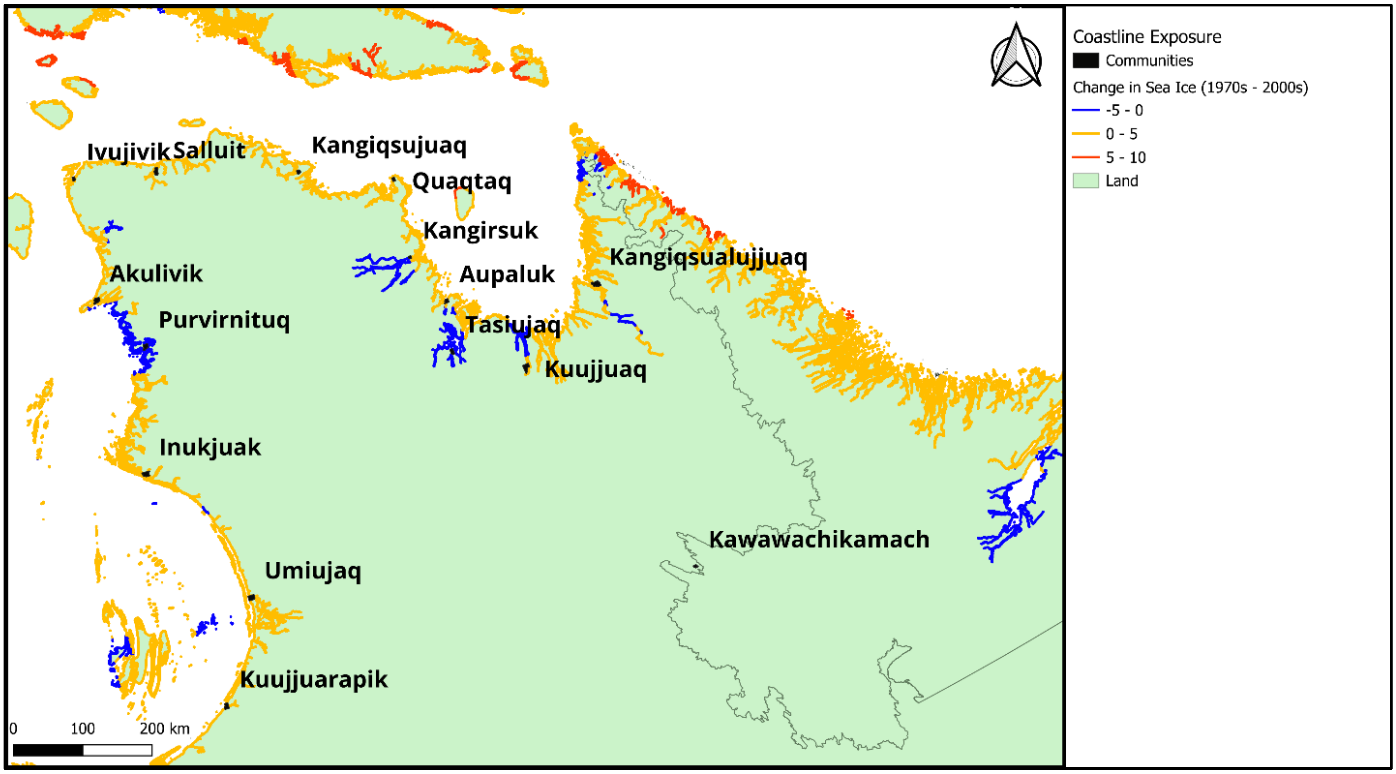
Although the rights to hunt and harvest from the land and waters are ringfenced in law (Nunavik Inuit Land Claims Agreement Act S.C. 2008, c. 2), the consumption of country food as a major component of diets in Nunavik has changed over time. Qanuilirpitaa? is a health survey (Nunavik Inuit Health Survey) conducted periodically to ascertain all aspects of community wellbeing, including nutritional and psychological wellbeing, that emerges from participation in harvesting activities, which historically was composed mostly of country food items. The most recent survey conducted in 2017, but published in 2021 (Allaire et al. 2021), documents the changes in dietary profiles over time since the last survey (Qanuilirpitaa? 2004, Blanchet & Rochette, 2008) which itself documented a decline in the consumption of certain country food items from an earlier 1992 survey (reporting a decline in consumption of most country food). In the 2017 survey, some of the decline in consumption of some marine foods has reversed (e.g., beluga, geese, dried fish). However, the consumption of seal meat has continued to trend downwards. One constant through the survey period(s) has been the consumption of Arctic char, which has remained high, underscoring how essential this particular item is to Nunavik Nunavimmiut health and culture.

What are the potential consequences of a diet reduced in country food? A reduction in iron-rich foods (such as beluga, walrus and seal meat) is likely to lead to increase in rates of anemia (Jamieson et al. 2012), which in Nunavimmiut women are ten-fold higher than the general Canadian population (Plante et al. 2011; Lavoie et al. 2024). Minimizing exposure to mineral-rich country foods may reduce nutritional resilience to toxicity caused by dietary mercury (Hu et al., 2017). Proust et al. (2013) found that younger individuals possessed less n-3 PUFAs and higher levels of trans fats in red blood cells compared to older community members, perhaps due in part to a ‘colonizing’ of the diet. Possibly most importantly, if the ties that bind community members are rooted in the shared experience of hunting, harvesting, distributing and consuming country food, there is a risk that there may be cultural erosion within Nunavik, and Arctic communities more broadly, which could be exacerbated if southern and market foods take their place – in effect, colonising the diets of Nunavimmiut.

Communities and Ecosystems in the Crosshairs of Climate Change

The coastline of Nunavik and surrounding areas has changed dramatically in the past forty years. The degree to which the cover of sea ice – a vital element of the Arctic that facilitates the harvesting of marine mammals - has altered within this time is illustrated in Figure 1. This map – derived from data gathered by the Canadian Ice Service – shows the summed percentage change in sea ice cover per week for which there was > 50% ice cover for each decade of the past forty years or so (1970s to 2000s). For most of the coastline, the number of weeks of sea ice cover has contracted (orange and red regions), whereas a few sheltered inlets have experienced an increase in cover (blue regions).

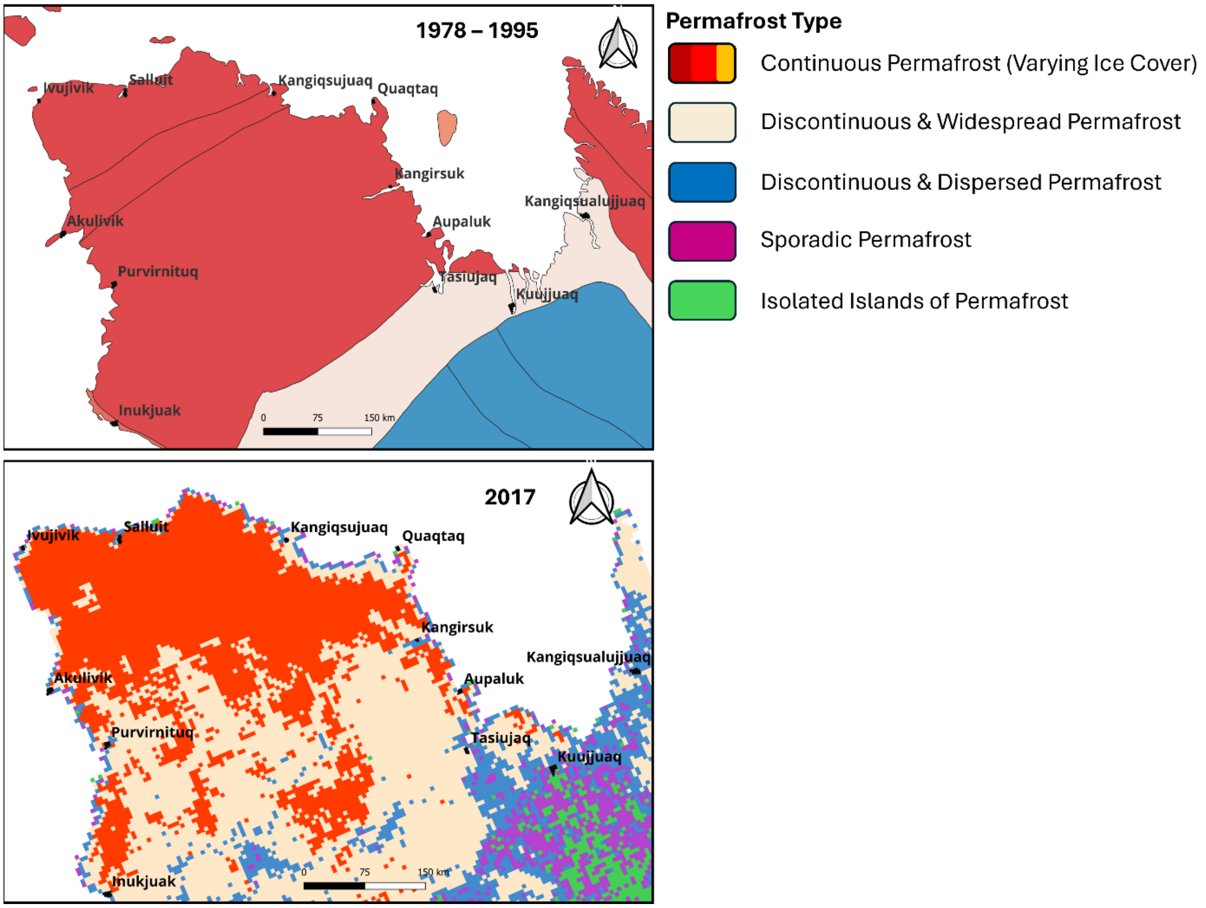
Figure 1. Map of Nunavik coastline showing the change of decadal sea ice cover (>50%) from the 1970s through to the 2000s. Positive values (orange and red) indicate a reduction of Sea Ice cover; negative values (blue) indicate an increase in sea ice cover. Values represent the change in the number of weeks with sea ice cover > 50%. Map generated using GIS data layers (Greenan and Grayson, 2022).



Restricted increases in sea ice or sustained levels of sea ice, such as within inlets, may have implications for localized ecosystems that are not well understood. For instance, in the eastern Antarctic there have been increases in sea ice cover which have altered benthic trophic (food web) relationships (Michel et al. 2019). Changes in food web structure may have negative impacts on species as such changes may be cascading and unpredictable, especially in complex food webs. Variation of microenvironments caused by sporadic sea ice (Arrigo, 2014) may produce localized and regionally distinct biotas which may influence the regional quality of food organisms like char (Bolduc et al. 2024). However, despite highly localized increases, the overall trend in the Arctic has been for a long-term decline of sea ice cover, which is expected to continue given the predicted increases in sea temperatures and concomitant rises in sea level, despite local anomalies (Hayden et al. 2020).

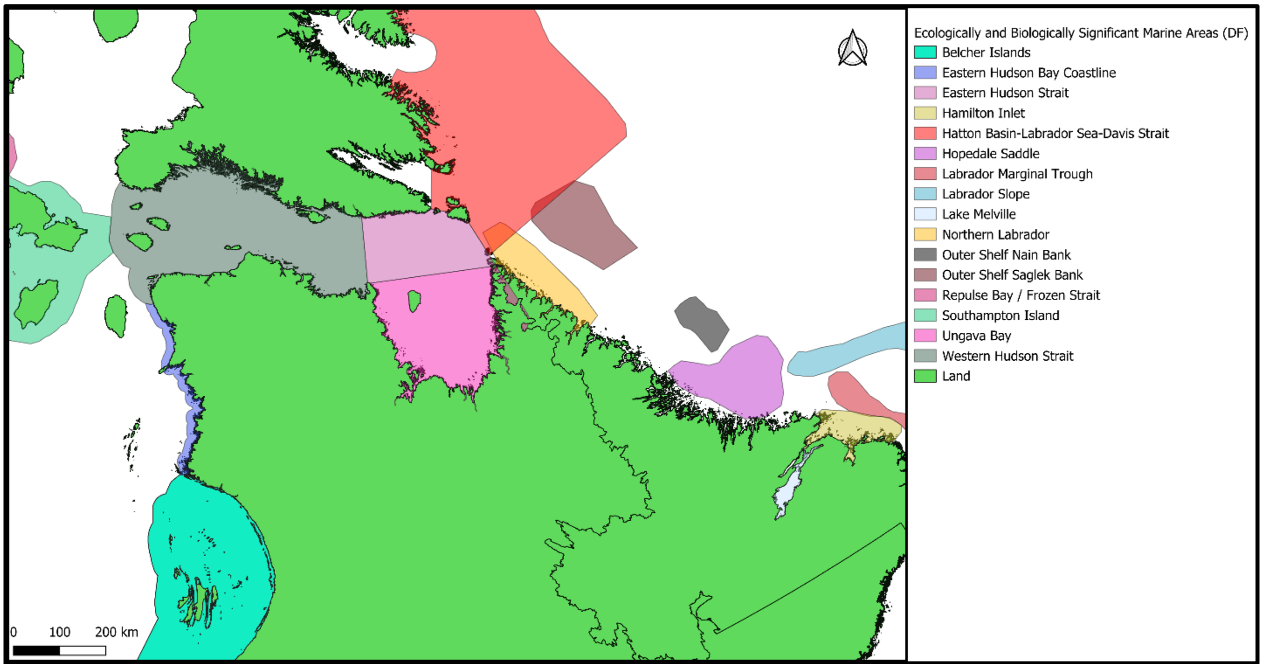
Figure 2 shows the changes in permafrost type as recorded over a period of 40 years (5th Permafrost Atlas of Canada; L'Hérault & Allard, 2017). Although the two maps differ in the granularity of the surveying effort, the large sheets of continuous permafrost and widespread discontinuous permafrost present in 1995 have contracted and fragmented significantly; in some cases becoming isolated islands of permafrost in a sea of seasonally impacted soil. A serious consequence of melting permafrost, apart from the issuing forth of greenhouse gases once stored away for millennia, is the release of harmful chemicals such as mercury (Smith et al. 2024). Transformed into a highly neurotoxic bioaccumulatory form (methylmercury) through bacterial metabolism (Schuster et al. 2011), mercury is released in large quantities in Arctic thermokarst wetlands and lentic and lotic habitats (Jonsson et al. 2022). Methylmercury can become entrained in Arctic food webs (Campbell et al. 2005) and be transported throughout the Arctic through conveyance by arterial networks of rivers (Schuster et al. 2011; Smith et al. 2025). Ultimately, humans, sitting atop the food chain, are at risk of mercury poisoning through consumption of country food that has accumulated enough mercury for it to have a toxic effect (de Moraes Pontual et al. 2021).

Figure 2. Contracting and fragmenting permafrost. Distribution maps of permafrost adapted from the 5th Permafrost Atlas of Canada (data collected from cores drilled in 1978 – 1995) and from the Centre d'études nordiques, Université Laval, Quebec (L'Hérault & Allard, 2017).



The evidence is compelling that the waters within and surrounding Nunavik will be impacted through climate change and its interaction with marine and terrestrial ecosystems, affecting several ecologically distinct regions (Figure 3). These regions are characterized according to their unique ecological, hydrological and taxonomic qualities. Nunavik is surrounding by the Hudson Bay Complex, which contains 13 EBSAs (ecologically and biologically significant areas). Each of these 13 regions represents important migratory corridors, nursing areas, haul-outs, or known areas of occupancy for various important food species such as polar bear, bowhead whale, Arctic char, walrus, seabirds and beluga (see Table 1, DFO, 2011). For example, the Ungava Bay EBSA contains the largest number of breeding thick-billed murres in Canada, is a site of importance for polar bear breeding, is populated by an endangered population of beluga, is critical for seabird (including sea duck) nesting and foraging, and contains a rich epibenthic community (DFO, 2011). These areas are vulnerable to the cascading impacts of climate change.

Figure 3. Map of ecologically and biologically significant areas (EBSAs) of northeastern Canada based on DFO guidelines (DFO, 2011).



Can genomics and DNA based tools play a role in the conservation of aquatic animals of import to local communities within Nunavik at risk of a warming climate? MAGIK was convened to discuss this issue in detail.

MAGIK Workshop

The MAGIK workshop took place between March 17th and 19th 2025, in Kuujjuaq, Nunavik, Quebec (see Appendix 5.1 for workshop flyer). In attendance were representatives of Inuit Nunangat (Kuujjuaq, Nunavik and Cambridge Bay, Nunavut, respectively), alongside academic, scientific and government stakeholder participants (see Appendix 5.2 for a list of in-person and remote attendees). As a hybrid event, discussions and presentations were conducted by both in-person attendees and remote participants. The meeting followed a flexible agenda which was amenable to change to accommodate as much participation as possible, and to follow interesting and useful tangents to their completion. The agenda as originally formulated can be found in Appendix 5.3. Proceedings began with a ceremonial blessing ceremony performed by a community elder, Eva Lapage. Presentations were given in person or via virtual link, and covered a broad range of topics, including introducing genomics and DNA-based tools, through to the need for the development of a cross-cultural glossary/lexicon to further knowledge exchange between the two pillars of philosophy: Indigenous and Western (Appendix 5.3).

To be expected, discussions were heavily influenced by site location, focussing on the needs and the priorities of Nunavik communities. Thus, much of the concern for the security provided by food organisms was rooted in species harvested by community (includes those listed under schedule 30.1 in the Inuit Nunavik Land Agreement – see Appendix 5.5). However, some species garnered more attention than others, in line with local community-level consumptions levels (Blanchet & Rochette, 2008; Allaire et al. 2021). Figures 4 and 5 provide an infographic on a sample of these species (or 'collectives' of species such as 'geese' and 'wild birds' eggs'), that exemplify their importance to the community through the acts of both harvesting and consumption. The figures also enumerate the existence of significant population units in the region, which may include aggregated (grouped) types of species (e.g., "seals" and "Arctic birds"), as well as traditional stocks or populations (e.g., four distinct beluga stocks in the "Hudson Bay complex"). For each animal, toxicological and biological agents (contaminants and disease organisms, respectively) are listed that have been published as occurring in Arctic populations, thus presenting ongoing potential threats to food security. Moreover, the figures identify which species possess published reference quality genome sequences (WGS), or are in the process of acquiring WGS, and those currently lacking.

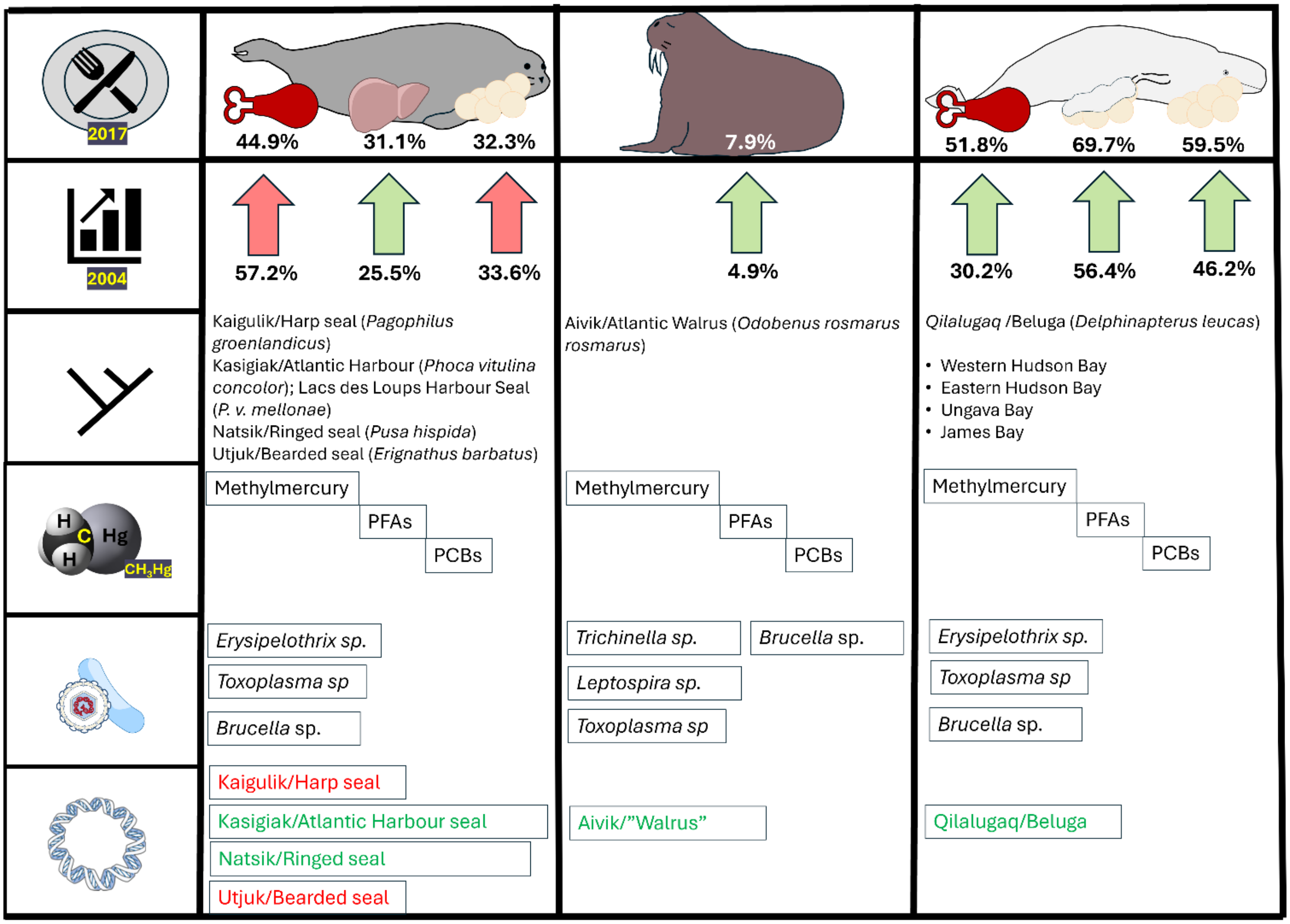
The aims of the workshop were broadly like those of the MAGIC (Muskox and Genomics in the Community) workshop held in Cambridge Bay, January 2024. The meeting was a consultation to link local knowledge (traditional ecological knowledge) with scientific studies of the region and its marine and aquatic animals, and to determine if scientific advances, represented by conservation genomics and DNA-based tools, have a place in management of local food fauna and the ecosystems in which they live. Additionally, both species-level and ecosystem-level priorities were identified to provide the basis for selecting taxa for potential WGS. Finally, ways of addressing the gaps that exist between knowledge systems, discussions on ethical co-development practices, and how best to communicate genomics tools that may benefit communities (e.g., linguistic/terminological/conceptual barriers) were addressed.

Genomics of Aquatic Animals in Nunavik

Figures 4 and 5 highlight some of the broad categories of animal biology and ecology which may benefit from the combination of traditional ecological knowledge (TEK) and genomics or DNA-based tools. Notably, genetic data derived from genomics sequences (whole or partial) or from genetic markers can inform on the presence and potential adaptive qualities of population structure (e.g., are some populations more robust to withstand infection or infestation?), if populations vary in levels of genetic variability (a useful proxy for the potential of a population to survive future – and often unknown and unpredictable - environmental threats), and can provide conservationists with useful metrics (e.g., effective population size (N_e), effective migration (geneflow), etc) that can tell us how well populations are connected. Knowing how populations are connected and whether such populations are sources of migrants – and by extension, genetic variation - or sinks (where genetic variation may be lost through zero or limited reproduction), may be informative to choosing which stocks to harvest each year. Genetic data can also allow us to peer into familial relationships to assess which males, for instance, sire most offspring. The same markers allow us to track individual animals and potentially even allow for specific individuals to be selected for harvest or otherwise excluded.

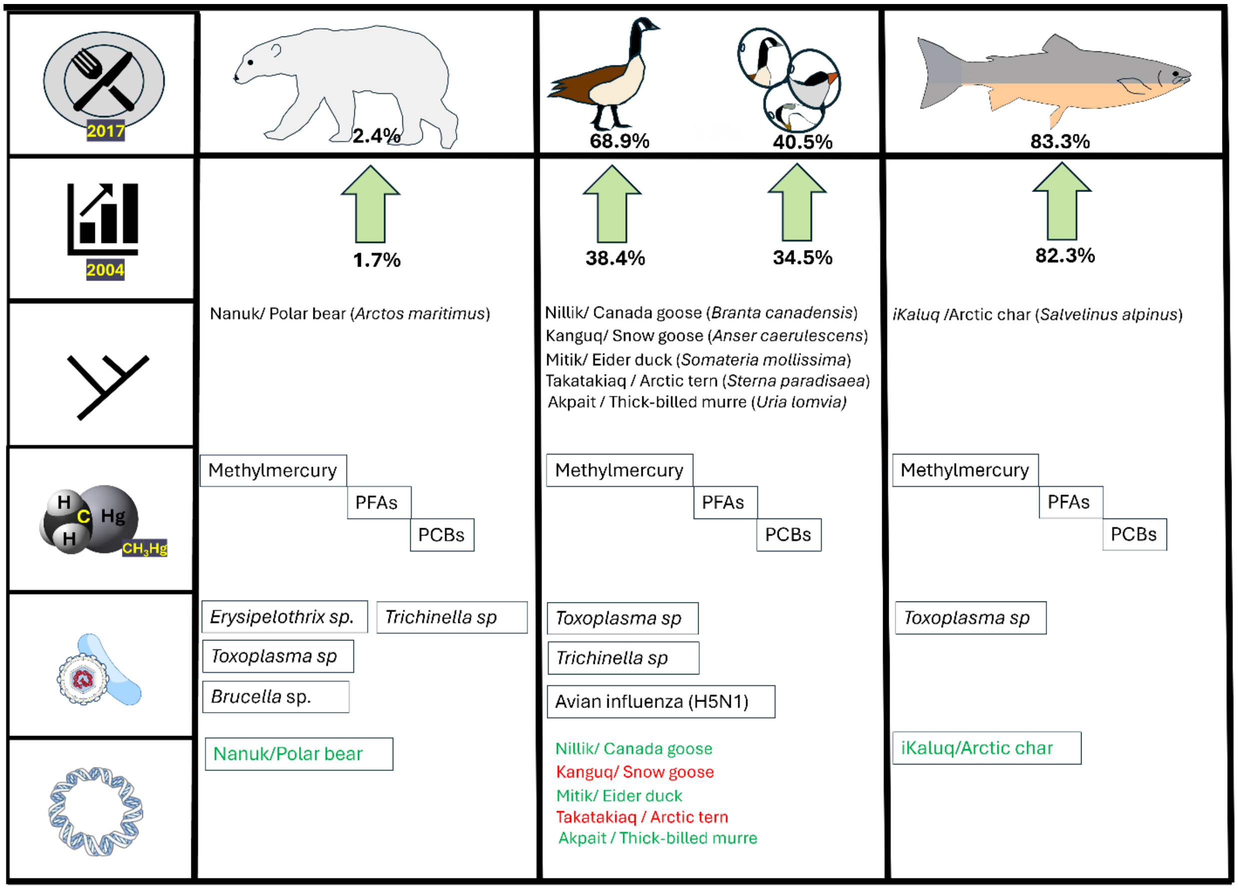
The determination of stocks (genetically and/or geographically distinct or demographically cohesive populations) is key to the successful management of biological resources. Because populations may be cryptic, the use of genetic data has been used for decades. However, the ascent of whole genome sequencing (WGS) gives custodians potentially much more data to make increasingly robust inferences of population structuring and stock assessments. For instance, the Hudson Bay Complex of Beluga consists of four distinct stocks, previously listed by COSEWIC (committee on the status of endangered wildlife in Canada) (Figure 6), but recently validated by WGS (Montana et al. 2024). An individual beluga can be assigned to each stock to avoid over-harvesting of particularly vulnerable populations (e.g., Ungava population, (N = 70; Sauvé et al. 2023)), especially through commercial whaling. Migration among genetic stocks was minimal, indicating that even when present in mixed stocks during the summer, Belugas tend to reproduce within their genomic designatable unit (DU) population. This suggests that natural repopulation of regions by migrating Beluga may be rare or would occur at a rate too low to allow natural repopulation.

Figure 4: Graphical and textual representation of information pertaining to the consumption, security and genome-sequencing status of some pivotal marine/aquatic animals in Nunavik (2nd column: “seals”, 3rd column: Atlantic walrus; 4th column: Beluga). The first row shows the percentage respondents to the 2017 Qanuilirpitaa? survey to confirm consumption of each country food animal. Where available, respondents identified tissues of the animals consumed (e.g., seal meat, liver or *misirak*; beluga dried meat (*nikku*), *mattaaq*, or *misirak*). The second row shows the percentage of respondents who confirmed consumption in the 2004 Qanuilirpitaa? survey and the direction of change (decrease or increase) that was observed in 2017. The third row delimits taxonomical units for each animal (species and/or significant populations). The fourth row determines which of three classes of toxic contaminant may be found in each animal (methylmercury, per- and polyfluoroalkyl substances (PFAs) and polychlorinated biphenyls (PCBs)). The fifth row identifies potential biological threats (zoonotic disease organisms) to the animals and human. The final row specifies whether reference genome sequences exist or progressing (green) or if lacking (red).



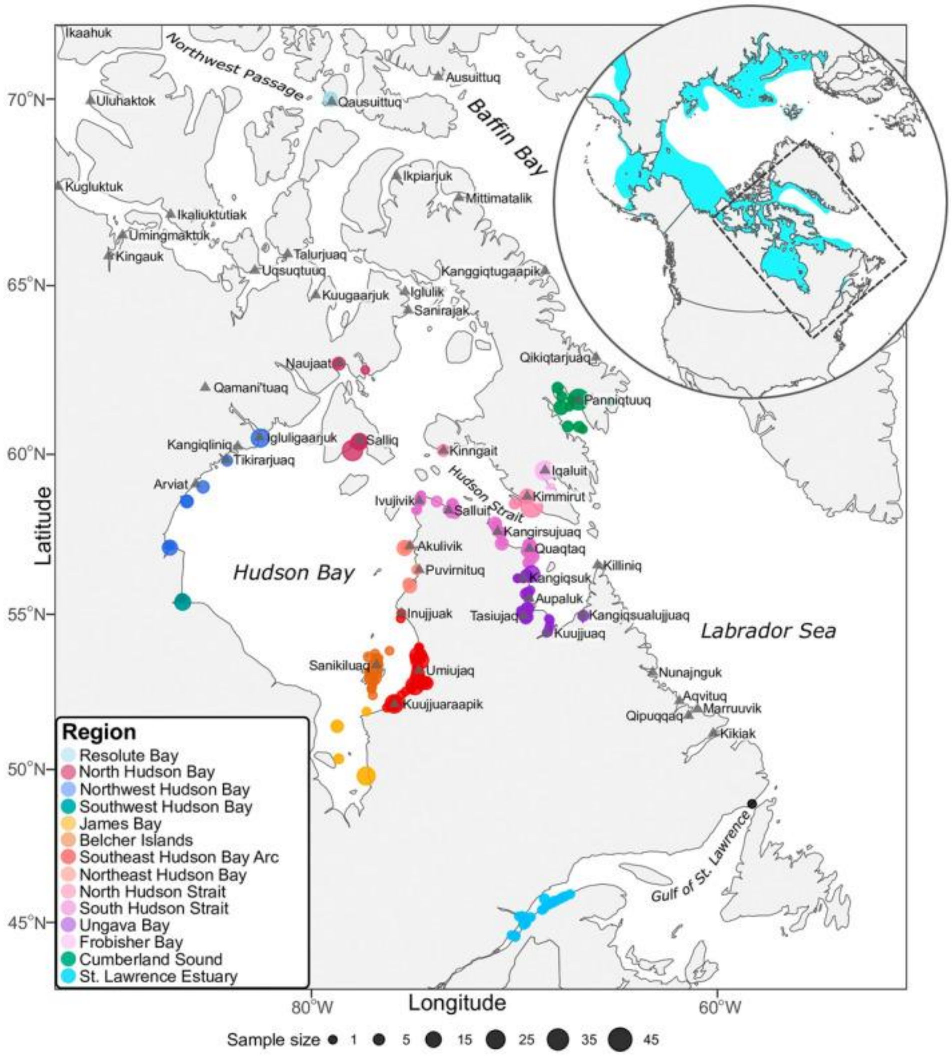
2017	44.9% 31.1% 32.3%	7.9%	51.8% 69.7% 59.5%
2004	57.2% 25.5% 33.6%	4.9%	30.2% 56.4% 46.2%
	Kaigulik/Harp seal (*Pagophilus groenlandicus*) Kasigiak/Atlantic Harbour (*Phoca vitulina concolor*); Lacs des Loups Harbour Seal (*P. v. mellonae*) Natsik/Ringed seal (*Pusa hispida*) Utjuk/Bearded seal (*Erignathus barbatus*)	Aivik/Atlantic Walrus (*Odobenus rosmarus rosmarus*)	*Qilalugaq* /Beluga (*Delphinapterus leucas*) • Western Hudson Bay • Eastern Hudson Bay • Ungava Bay • James Bay
H C Hg H CH_3Hg	Methylmercury PFAs PCBs	Methylmercury PFAs PCBs	Methylmercury PFAs PCBs
	Erysipelothrix sp. *Toxoplasma sp* *Brucella* sp.	*Trichinella sp.* *Brucella* sp. *Leptospira sp.* *Toxoplasma sp*	*Erysipelothrix sp.* *Toxoplasma sp* *Brucella* sp.
	Kaigulik/Harp seal Kasigiak/Atlantic Harbour seal Natsik/Ringed seal Utjuk/Bearded seal	Aivik/”Walrus”	Qilalugaq/Beluga

Figure 5. Graphical and textual representation of information pertaining to the consumption, security and genome-sequencing status of some pivotal marine/aquatic animals in Nunavik (2nd column: polar bear, 3rd column: “birds” (goose meat and wild bird eggs); 4th column: Arctic char). The first row shows the percentage respondents to the 2017 Qanuilirpitaa? survey to confirm consumption of each country food animal. The second row shows the percentage of respondents who confirmed consumption in the 2004 Qanuilirpitaa? survey and the direction of change (decrease or increase) that was observed in 2017. The third row delimits taxonomical units for each animal (species and/or significant populations). The fourth row determines which of three classes of toxic contaminant may be found in each animal (methylmercury, per- and polyfluoroalkyl substances (PFAs) and polychlorinated biphenyls (PCBs)). The fifth row identifies potential biological threats (zoonotic disease organisms) to the animals and human. The final row specifies whether reference genome sequences exist or progressing (green) or if lacking (red).



2017	2.4%	68.9% 40.5%	83.3%
2004	↑ 1.7%	↑ 38.4% ↑ 34.5%	↑ 82.3%
	Nanuk/ Polar bear (*Arctos maritimus*)	Nillik/ Canada goose (*Branta canadensis*) Kanguq/ Snow goose (*Anser caerulescens*) Mitik/ Eider duck (*Somateria mollissima*) Takatakiaq / Arctic tern (*Sterna paradisaea*) Akpait / Thick-billed murre (*Uria lomvia)*	*iKaluq* /Arctic char (*Salvelinus alpinus*)
CH_3Hg	Methylmercury PFAs PCBs	Methylmercury PFAs PCBs	Methylmercury PFAs PCBs
	Erysipelothrix sp. *Trichinella sp* *Toxoplasma sp* *Brucella* sp.	*Toxoplasma sp* *Trichinella sp* Avian influenza (H5N1)	*Toxoplasma sp*
	🟩 Nanuk/Polar bear	🟩 Nillik/ Canada goose 🟥 Kanguq/ Snow goose 🟩 Mitik/ Eider duck 🟥 Takatakiaq / Arctic tern 🟩 Akpait / Thick-billed murre	🟩 iKaluq/Arctic char

Figure 6. Identification of Beluga stocks (designatable units, DUs) based on WGS (lcWGS – low coverage WGS libraries) and partial (via ddRADSeq – double digest restriction-site associated DNA sequencing) genomic scans of individuals sampled throughout the eastern Canadian Arctic and Hudson Bay. Figure taken from Montana et al. 2024 (Figure 1, therein).



Genomic-based inferences of beluga genetic structuring corroborate with Inuit TEK, whereby communities reported low abundance of Belugas in areas where they used to summer ("Proceedings–Beluga Whale Workshop, Kuujjuaraapik", cited in Montana et al. 2024). Without the active, ground-level participation of Inuit Hunter and Trapper organisations (who also procure tissue samples for genomic analysis), and the communities they represent, our understanding of the dynamics of beluga population biology would be much diminished. The data co-generated between Inuit and Western scientists can be taken on board by the NMRWB to manage take allowances and any potential seasonality and geographical restrictions (e.g., Species and Area [H2])

Genomic data has been used in similar circumstances to determine the genetic distinctness of Polar bear populations (*Ursus maritimus*), where the two populations resident in Nunavik (Southern Hudson Bay and Foxe Basin) were found to belong to the same genetic cluster after analyzing over 3000 genetic markers (Jensen et al. 2020). This study corroborated an earlier paper using fewer markers finding shallow population structure in the Hudson Bay and Foxe Basin region (Viengkone et al. 2016). Low levels of genetic differentiation of Polar bears from a wide area may be explained by their large territories and highly migratory behaviour. The ephemeral nature of Polar bear residency and fleeting occupancy in each area possibly explains its consumption as part of country food being relatively low compared to other country food animals (Figures 4 and 5), although the hunt of the bears, in and of itself, represents a rite of passage for Nunavimmiut youth, underscoring the Polar bear's overall importance for the region (NMRWB, 2018).

Freshwater fishes especially tend to differentiate genetically as contemporary populations become isolated from ancestral ones as lakes and rivers form and themselves become isolated, limiting the amount of genetic material that can be exchanged through migration (gene flow). This may manifest in biological or ecological differences within species (e.g., anadromous (sea-run) or potamodromous (resident) populations of Arctic char), that can then manifest in observable differences in the behaviour and appearance of individuals from distinct populations. These observable differences (called 'phenotypes' by biologists) may include traits of vital importance to Inuit culture, such as taste, and can be made the focus of studies of direct importance to communities. Genetic studies using genomic sequences of fishes in Nunavik have, until recently, been few, but Dallaire et al. (2021) found evidence for structuring amongst populations of Arctic char around Ungava Bay, noting evidence for adaptation to sea surface and air temperature in both marine and freshwater populations.

Although not as culturally pivotal as Arctic char, Atlantic salmon may provide a type of food security insurance, at least where fish protein is concerned. The Atlantic salmon fishery in the Koksoak River has become a vital subsistence fishery in southern Nunavik, consisting of two populations identified by TEK. These two populations represent different ecotypes: a resident estuarine population, and a typical anadromous (sea-run) population. However, a recent comparison of the genomes of Atlantic salmon from both ecotypes suggests there is enough similarity between their respective genomes that they do not represent distinct genetic units based on a holistic analysis (Carbonneau et al. 2024). However, specific regions within the genome were identified with either an anadromous life history or with an estuarine residential life history. It may be that these two ecotypes are only recently diverged from a common ancestral population which has yet to make its mark across the respective genomes of the two types. Taken together, the evidence of both TEK (habitat preferences, morphology and behavioural observations) and genomics (distribution of genetic variants and functional genes specific to the ecotypes) suggests that the two ecotypes *are* worth considering as distinct entities from a management perspective.

The Arctic is becoming a repository for numerous pollutants, industrial particles, contaminants, and even pathogens. In addition to passive transportation by prevailing winds, humans can actively transport pollutants through transportation and industrial activity; and migratory organisms (notably birds such as geese, cranes and gulls) may transport pathogens to polar latitudes from southerly regions. These actions put enormous pressure on the health of Arctic ecosystems and thus potentially of the people who live there. The transportation into the Arctic and subsequent bioaccumulation in country food animals of persistent organic pollutants (POPs) such as polychlorinated biphenyls (PCBs) has been long-established (Noyes et al. 2025). Pollutants enter the food chain and make their way up the trophic ladder to accumulate in predators and upper-level trophic consumers (e.g., Per- and polyfluoroalkyl substances (PFAs) in ringed seals and polar bears) and ultimately consumed by Inuit with potentially serious consequences (Sonne et al. 2025). Few genomic studies (and other 'omics studies such as transcriptomics) have looked at the impact of such pollutants in important Arctic food taxa. However, one study found that PCBs have altered the pattern of the activity of some genes in beluga, such that those genes are now either more or less active than the same genes in uncontaminated individuals (Noël et al. 2014). Screening genomic variation in populations of Arctic char can determine which populations have been exposed to persistent organic pollutants so successfully that only a few genetic markers (numbering from 4 – 32) may be needed to determine which stocks are safe to consume (Walker et al. 2020). The relative lack of such studies compared to other regions of the world means that much work needs to be conducted in Arctic taxa.

The prevention and mitigation of disease in Arctic foodstuffs is a pivotal component of food security, especially zoonotic diseases that can make humans ill if infected meat is consumed. Although some infections are both well-established and accounted for, including routine testing (see Figure 8), with melting permafrost, ice floes, glaciers, and expansion northwards of diseases-carrying organisms (vectors) that stay in the Arctic for longer, there exists the potential for both novel biological threats and the establishment of known infectious agents. Scientists at the CFIA in Winnipeg perform genomics sequencing of all new infected samples that are sent to them – this often involves the complete sequencing of the genomes of bacteria, viral and unicellular eukaryotes (e.g., amoebas) associated with human or animal morbidity or mortality. Genomics allows scientists to survey more samples (animal tissue, for example) and more quickly than before for signs of infections.

The more we look, the more we find, so not all new pathogen organisms we identify necessarily pose a threat. Yet, vigilance through genomics allows us to identify potential problematic patterns or new centres of infection. To give a few examples: genomics sequencing on Canada and Snow goose samples derived from a large die-off near Cambridge Bay in 2017 identified a new species of coronavirus – CB17 (Papineau et al. 2019). Similar efforts on samples derived from a beached harbor porpoise and an identically stranded beluga in Alaska uncovered a new species of senecavirus (Cetacean picornavirus 1), which is of particular interest as this virus has shifted its host ecosystem from a terrestrial (pig) to a marine (whale) host system (Vernygora et al. 2024). WGS of avian influenza viruses (such as the highly pathogenic H5N1 strains) are identifying new host organisms including those that may be found in the Arctic, such as harbour seals (Lair et al. 2024). Other DNA-based tools might be brought to bear on scanning the Arctic for pathogens. It is conceivable that eDNA surveillance may be used to canvass a wide area, sampling water for example, for miniscule traces of novel or previously unrecorded infectious biological agents within Arctic waters. Although such work has yet to be carried out in the Arctic, as far as we are aware at the time of publication, the processing of water for DNA belonging to pathological agents is maturing (e.g., Sieber et al. 2020; 2024).

The last act of conservation in extreme circumstances is to preserve the genomes of species at acute risk of extinction, so that in a more convivial future, species may be resurrected (see the increasingly popular, although controversial, science of deextinction); or more realistically, frozen samples of genetic variation may be used to replenish the gene pools of highly at risk wild or captive populations and used as 'genetic restitution'. It is with the aim of keeping a sample of the genetic diversity of – currently – still extant organisms, that the Canadian Museum of Nature set up the National Biodiversity Cryobank of Canada (https://nature.ca/en/our-science/collections/national-biodiversity-cryobank-canada/). Not only is this facility the last line of defense against extinction, but this repository could also be used to sample hitherto overlooked taxa or unique genetic lineages for WGS, without the need to disturb hunts or vulnerable habitat when sourcing new samples for genomic analysis.

MAGIK Perspectives

Discussions began with an introduction to genomics, DNA and tools derived from genome sequencing and DNA sequences (genetic markers). The application of such tools to some important taxa, addressing some critical issues, have been discussed in the previous section. Potential applications to Nunavik taxa will be discussed subsequently. What follows in this section is the lived-in experience of communities and scientists, telling tales of their experiences in and around western science – but especially conservation genomics - and determining priorities for engagement between two pillars of human knowledge in Canada: TEK (via IQ in Kuujjuaq)) and Western scientific methods.

TEK from within Nunavik represents a vast horde of expertise on locally important aquatic animals (e.g., ringed seals (*Pusa hispina*) (Furgal et al. 2002), beluga (Breton-Honeyman et al. 2016), Arctic terns (*Sterna paradisaea*) (Henri et al. 2020), and Arctic char (Dubos et al. 2023)), that can direct potential genomic studies, drive research priorities to maximise animal health and longevity, target community priorities pertaining to biological resource management (individually or through the Nunavik Marine Region Wildlife Board (NWRBB)), and provide an interpretative framework from which to make sense of genetic data and genomic patterns within species and ecological relationships of interest. The fundamental importance of Indigenous ecological data as a foundational tenet of any incorporation of genomics tool into Inuit life was stressed by Inuit participants.

In Nunavik, biological trends have been observed and reported by Nunavimmiut which have been utilised to direct studies of import to their own community priorities (e.g., work done by the Nunavik Research Centre) or in partnership with the Department of Fisheries and Oceans (DFO) or with southern academic institutions. The observations of HTOs, harvesters and communities inform entities like the NWRBB to determine take/harvest allowances, offer guidance to subsistence harvesters, and to inform commercial policies within the region. That such data would be informative to southern scientists is an emergent property and those given access to this data hold a privileged position. In using such data, a covenant should be brokered that any scientific or technological advance that may so derive (in this case: monitoring tools based on genomics data and/or DNA-sequence surveys) must be in the service of communities. Research must have the potential for the development of direct benefits to the community (in terms of management of wild or established populations (e.g., Arctic char)) and should yield tools and/or data that can be readily accessed, interpreted and utilised by individuals within communities (e.g., Schott et al. 2020; Walker et al. 2020).

Nunavimmiut prioritise Arctic char as a key food source (Bolduc et al. 2024; Allaire at al. 2021). Using their own initiative, residents of Nunavik have used lived-in experiences to found new fisheries through provisioning of juveniles that are grown in a purpose-built hatchery prior to release in newly established, and hitherto virgin, territory. Participants at MAGIK were privileged to be able to tour an Arctic char hatchery – established from scratch and used to create a *de novo* fishery in a local previously char-free stream - and experience the palpable benefits that having such a facility within a community such as Kuujjuaq brings (Figure 7). The hatchery rears young char (alevins and parr) from eggs collected from known spawning sights from around Nunavik, to ensure a mixture of genetic variation within the hatchery to minimize any possible ill effects of inbreeding in the area to be stocked. The hatchery fish are released into rivers that have been prepared (by having fishways constructed to allow upstream migration) such as the Nepihjee River. The establishment of this hatchery in 2002 can not be understated as a practical and pragmatic solution to pre-empt a possible food security issue, but also as a symbolic testament to the autonomy and self-determination of the Kuujjuaq community in managing their food security. Any addition of genomics or DNA based tools must be *additive*, otherwise they may be distractive at best, and even potentially be harmful if such tools results in any erasure of Inuit cultural hegemony.

With climate change, it is expected that further northerly expansion into Nunavik's lotic and estuarine systems will occur (Master et al. 2025). The impact of such immigration into Nunavik on endogenous stocks of Arctic char, however, are not well understood, but there may well be advantages (e.g., new commercial fishery) as well as potential negative consequences (competition with Arctic char) to a reorganizing of Arctic fishery assemblages in the wake of climate change. Climate change is also likely to increase the preponderance of invasive species taking hold. TEK has identified various points of invasion within Nunavik of the Pacific pink salmon (*Oncorhynchus gorbushka*), consistent with its northwards and easterly advance in the wake of a warming Arctic (Farly Jr. et al. 2020). TEK within Nunavik has only recently identified a new occurrence of Pink salmon in the George River. eDNA methods, performed within and by the community, may be a value-added tool for use in Nunavik as has been the case in the example of community and DNA-based surveillance of the Kapisillit River, Greenland (Nielsen et al. 2024). eDNA can detect minute traces of the pink salmon's DNA allowing detection of very early invasion events. The earlier in time that nonnative species are detected, the easier it is to manage a potential invasion. Once identified as being pink salmon positive, a river or stream may be targeted for mitigation or even eradication, if so desired, depending on the desires of the community.

Figure 7: The Napukkaaliurvik Kuujjuaq Fish Hatchery in Kuujjuaq, Nunavik (19th March 2025). Insert: tray containing char alevins, fed and oxygenated on a timer to maintain regular and predictable rates of growth.

TEK also reports the increasing abundance – and northerly progression – of various terrestrial taxa that may have an impact on aquatic or semi-aquatic food organisms. With the northward expansion of the boral treeline have come various taxa emblematic of a high latitude forest biome, including American robins, moose, and some predatory birds such as golden eagles and ospreys. Lynx is also moving north, potentially bringing with it a replenishing source of the *Toxoplasma gondii* parasite which has made its way into the aquatic food chain (see next section). Arguably, the most impactful potential relative newcomer is the North American beaver. The beaver can radically alter aquatic habitats in months, impacting fish habitats in various ways. Beavers are ecosystem engineers and whilst their economic value is potentially high (for trappers and tanners), their impact on local wetlands and fisheries can be significant or injurious (Sigourney et al. 2006; Weber et al. 2017; Needham et al. 2021). Interestingly, a number of these pioneer beavers are coloured white (albinos or otherwise), which could provide them with a selective advantage, through escape from predation in increasingly snowy terrains when they're logging trees on *terra firma*. Future TEK observations will be telling.

Another animal having an influence is the black bear (*Ursus americanus*). This generalist consumer has drastically altered the breeding behaviour of some harvestable aquatic birds, such as Canada goose. Canada goose is heavily consumed in springtime by the communities. The eastern flyway geese that used local islands in southern Ungava Bay (e.g., at the mouth of the Whale River) have all but disappeared, or have been displaced, due to predation pressure by the bear. At one time, the Whale Island geese represented the single biggest nesting colony of the eastern flyway population. Geese have probably relocated north as far as Baffin Island. The Kuujjuaq spring goose hunt, therefore, has suffered as a result. In concert, populations of Arctic tern in southern Ungava Bay have crashed. The tern, as well as being harvested itself, would once be used by locals to find populations of ringed seal for hunting, but both the tern and the seal have begun to disappear from the area. There are questions to be asked of the drivers affecting both tern and seal populations in this region, and whether genomics tools might be used to address them (e.g., newly emergent or particularly heavy pathogen loads?). The thinning of the coastal ice is almost certainly a factor in the reduced numbers of both ringed and bearded seals, although harp seals have yet to suffer population reductions. As previously noted, the Ungava Bay population of beluga is verging on extirpation and is afforded "endangered" status by COSEWIC. Thus, southern Ungava Bay represents a hotspot for imperiled country food organisms.

Living close to the sea and rivers, fishes (and shellfish) can comprise a significant portion of a country food diet. Apart from those discussed, various freshwater fishes such as brook trout (*Salvelinus fontinalis*), lake trout (*Salvelinus namaycush*), lake whitefish (*Coregonus clupeaformis*), sculpin such as the shorthorn sculpin (*Myoxocephalus scorpius*), and various species of mussel and other bivalve molluscs, make up the bulk of this diet. However, some of these aquatic species are adept at accumulating contaminants, with methylmercury a particular concern. Personnel at the Nunavik Research Centre conduct routine testing of bioaccumulated methylmercury in various fishes, but especially lake trout which has a greater propensity than other fishes for building up toxic amounts of mercury within their flesh, which, depending upon the physiological condition of the human (e.g., pregnancy or age), can be dangerous to consume. The removal of mercury through bioremediation means (which may involve genomic manipulation of microorganisms present in the aqueous environment) might have applicability here.

For Inuit, vale-added elements of Western science must be incorporated alongside, or integrated within, IQ in a process of *co-development* (e.g., Chapman & Schott, 2020). In Inuktitut, Inuit Qaujimajatuqangit means “that which has been known by Inuit”, so any Western perspective necessarily builds on generations of expertise and must add to, and not subtract or detract from, this foundation. Previous sections have discussed how genomics data may be deployed in an Arctic context, focussing on important elements of the subsistence fauna in the Arctic. The next section will discuss some real-world examples of tool deployment and areas in which genomics or DNA-based tools may provide tangible and additive benefits to the animals and by extension communities. However, communicating Western scientific terms to non-experts is a problem in Western science if ideas are to be effectively communicated. Conveying this knowledge is even more challenging when communicating between systems of knowledge that are based on very different linguistic models and philosophical bases. In Canada, Western science is communicated in either English or French, both Indo-European languages with grammatical rules quite at odds with the dialects of Inuktitut, which is a language that is more descriptive and uses multiple elements of grammar in naming objects and activities. It is essential that if genomics tools are to be used, that there must be a means of effectively communicating the tools, the underlying science/knowledge, and how to interpret data into meaningful actions for communities. Such work has begun in Nunavut (Kitikmeot Heritage Society), whereby scientific terms are being translated into terms which describe the scientific undertaking or scientific aim in a way that is accessible in plain language, in this case Inuinnaqtun. This work is part of a broader project to revitalize the use of the language in communities such as Cambridge Bay. By decolonizing English or French scientific terms into native languages, not only will scientific engagement increase, but the appetite to learn and maintain indigenous languages be incentivized. Table 1 provides some examples by which scientific terms have been successfully translated into Inuinnaqtun. There is no reason why the same effort could not be expended to all dialects in Inuit Nunangat.

Table 1. A selection of English scientific terms and their newly constructed or historical counterparts in Inuinnaqtun.* OED = Oxford English Dictionary.

Western Term	OED Definition.	Inuinnaqtun	Inuinnaqtun -> English
Disease	Sickness (in a person, animal, or plant); disturbance or impairment of the function (and often also the structure) of the body, a part of the body, or the mind. In later use frequently with modifying word, indicating the site, nature, cause, etc., of sickness.	Aanniarut	One that causes hurt or discomfort

Infection	The transmission, communication, or acquisition of (a) disease; spec. transmission of a disease or its causative agent by indirect means, as by contaminated water, food, etc., rather than by close contact with an infected individual.	Aanniarutit	Spread of hurt and/or discomfort
Genomics	The branch of molecular biology concerned with the structure, function, evolution, and mapping of genomes	Aallanngurninga uumajuvaluit ihumaaluktut qanurinninganik, aulavallianinganik, nunaujiurnirmilu naunairutikhangit	Changes in wildlife are concerned about the status, progress, and mapping information
Parasite	A foreign entity that lives at the expense of a host.	Qupilruit	Worms

Genomics and IQ – Bridging the Parallel Paths of Natural Philosophy to Co-Develop Tools

In Nunavik, Arctic char remains the most consumed species of fish (Allaire et al. 2021; Dubos et al. 2023). Global expertise in the ecology and biology of Arctic char of the Ungava Bay region resides within Nunavik itself (Dubos et al. 2023), where the TEK of harvesters and community members is built upon generations of accumulated knowledge. This knowledge is reflected in specific terminologies for different ecological castes of char. For example, anadromous char is called Iqaluppik, landlock char is called Nutillik, and significant source populations (i.e., significant reproducers) have been identified and given the epithet Aupalujaak (or Aupalujaalik) (Dubos et al. 2023). This knowledge of char ecology is paralleled by observations of the changing Arctic and Sub-Arctic environment, and by knowledge of changing approaches to fishing, all of which will impact the abundance of fish stocks. To any geneticist interested in the study of Arctic char generally, but within populations in Nunavik specifically, the knowledge reported by residents will prove invaluable to providing context and explanations for patterns of genetic variation. Such information includes direction and timing of migration, reports of declining abundances, behavioural differences amongst cohorts (e.g., size-related behavioural differences), and so on (Dubos et al. 2023). In return, genetic surveys may indicate which populations or stocks are most resilient to warming associated with climate change or other environmental or biological variables (e.g., contamination and infection) and could be used to make predictions on stock resilience or vulnerability. Yet, a recent survey of genomic variation of Nunavik Arctic char did not place the findings in the context of indigenous knowledge (Dallaire et al. 2021), although they did note that the genomic data might be used to inform stocking practices, including the setting up of *de novo* populations.

Recently published genomics tools (e.g., Genotyping-in-Thousands by sequencing (GTSeq) tool) may make stock identification in Arctic char more robust and may even identify sexes to assist in the genesis and maintenance of sustainable fisheries, which could be used as an value-positive additive measure by communities when managing or establishing char fisheries (Li et al. 2023). However, there does exist a will to contextualize Arctic char genomics within the context of Inuit culture in the wider Canadian Arctic where agency over the use of genomics tools can be set by community priorities, with ongoing projects involving some of the participants of this meeting. Examples include providing support in the management of sustainable fisheries (e.g., Schott et al. 2020)) and using tools to identify biosecure stocks (i.e., those less associated with contaminants (Walker et al. 2020)).

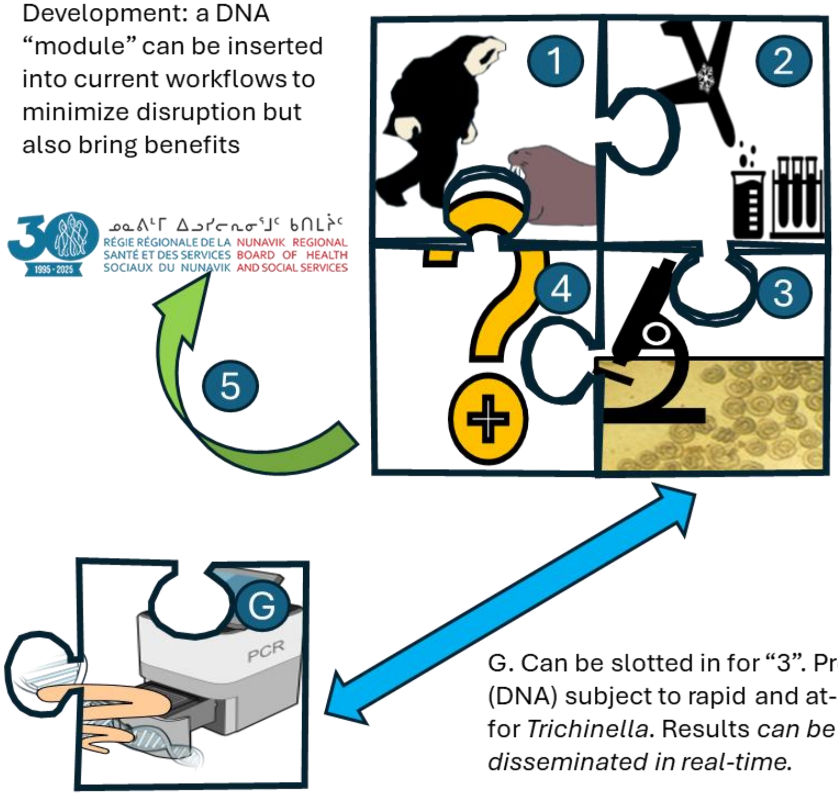
The presence of the coccidian parasite, *Toxoplasma gondii*, most closely associated with the tropics, in high Arctic fauna has proven mysterious, as the most prevalent primary host – cats (Felidae) - are only present by virtue of the Canadian lynx (*Lynx candensis*), a species that does not exist north of the boreal treeline. However, the presence of this parasite, which causes toxoplasmosis, is increasingly problematic in Arctic communities (Reiling & Dixon 2019). Determining its route into the Arctic could provide investigators with opportunities to manage intermediary hosts or target specific transmission pathways. Jenkins et al. (2025) summarise the current state of knowledge regarding *T. gondii* transportation to the Arctic. They postulate that the parasite is carried northwards from lynx and domestic cat territory via avian vectors – nominally geese – who carry oocyte cysts from land to sea to land, whereby they infect a wide range of marine species (Oskanen et al. 2022), including the polar bear which is experiencing an increase in exposure to the parasite. As the boreal treeline extends northwards, border areas such as southern Nunavik will likely face an increase in exposure to *T. gondii* (via lynx, wolverine, beaver and black bear) and potentially other parasites. Thus, identifying genomic means to control or mitigate exposure may be an appropriate use of genomics or DNA-based tools (e.g., genomic surveillance of *T. gondii*, Sundararaman et al. 2024; or eDNA-based detection of *T. gondii* in air samples).

Some parasites are already endemic within the region and protocols based on prior established scientific methods are in place to relay to communities if any harvested meat might be contaminated. The walrus hunt is a significant part of Inuit culture and has been for centuries (Desjardins & Gotfredsen, 2021), however there is a small, yet significant, risk that walrus (and Polar bear) meat might contain the parasitic nematode worm *Trichinella nativa* which may cause debilitating Trichinosis in humans if consumed. Figure 8 shows the current protocol in place as used by the researchers at the Nunavik Research Centre, Kuujjuaq. Hunters can send samples of walrus tongue to the lab where the tissue is processed so that the parasite may be observed under the microscope. Numerous sub-samples are checked for the occurrence of the parasite. If there is a positive identification this information is sent to the Nunavik Regional Board of Health and Social Services (NRBHSS). The NRBHSS assess the evidence of contamination before making the decision to inform the harvester and/or community. This process is necessarily delicate, balancing the rights to harvest, the central role walrus harvesting plays in the community, and the politics and optics of making snap-judgements. This process is also time-consuming (meat may begin to spoil) and relies on limited personnel working around the clock during harvest.

In a hypothetical example of a value-added DNA-based proposition, one could apply a much more sensitive genetic test for the presence of *Trichinella nativa* within the tissues of harvested animals, using in-house equipment. The laboratory in which the traditional testing is undertaken, contains a genetics station, which – as of March 2025 – was unused due to the scientist who procured the genetics equipment (including a QuantStudio qPCR thermocycler and an Ion Torrent parallel DNA sequencer) having left the centre some weeks previously. A qPCR (quantitative real-time PCR) genetic test could be designed to detect miniscule fragments of the *T. nativa* genome, with the ability to detect just a few single individual DNA fragments in any given test. This hypersensitivity would allow even early infections of walrus to be detected, increasingly the confidence in the community to consume the meat. DNA extraction and running the test can be done in a typical 8 hour working day. If working 24 hours, the lab can send the results to the NRBHSS in batch-form or in real-time. Another benefit of qPCR is it can allow the quantification of the worm's DNA in any given sample or individual, allowing the screening of walrus populations to determine latent infestation levels or rates of increase or decrease, and thus providing information to harvesters on which populations to avoid in the short-term. Training personnel to perform qPCR tests is not complicated, following sufficient mentorship. Such a test, however, is not a panacea, and there are important quality controls that must be conducted. The walrus tissue needs to be kept cold - as before - and TEK applied to circumvent the harvesting of obviously ill animals or suspected unhealthy animals. qPCR is extremely sensitive to contamination, and the PCR should be performed in a room separate from any in which walrus tissue is processed, for example. One must also perform 'DNA extraction' controls, 'negative' PCR and 'PCR inhibition' controls to determine the risks of both false positive and false negative detection. However, there are standard protocols to use in such a workflow, both methodological and statistical. Currently, there is no specific *T. nativa* qPCR assay that has been developed (at least published), but there is a lot of expertise in Canada to do so, and qPCR test development is not a lengthy process if appropriate developmental samples and materials are procured.

Figure 8: Two alternate pathways to detect *Trichienlla nativa* in harvested meat (e.g., walrus and polar bear). Both the standard method, currently in use, and a potentially alternative, DNA-based detection, pathway is shown. Swapping a DNA-based detection "module" for the current microscopy-based "module" would minimize disruption to established workflows whilst potentially reaping the benefits of expedited discovery time and data dissemination of molecular and digital technology. Using a DNA-based pathway, incorporating a quantitative PCR (qPCR) workstation already in situ in the Nunavik Research Centre, using bespoke genetic assay known to detect *Trichinella nativa* DNA only, could potentially reduce determination time of *Trichinella* infection in hours (< 8 hours from DNA extraction to test results and dissemination to the NRBHSS).

A modular model of Genomic/DNA-Based Co-Development: a DNA "module" can be inserted into current workflows to minimize disruption but also bring benefits



1. Walrus hunted and sample attained

2. Sample shipped and meat processed

3. Processed sample subject to visual ID of Trichinella through microscopy

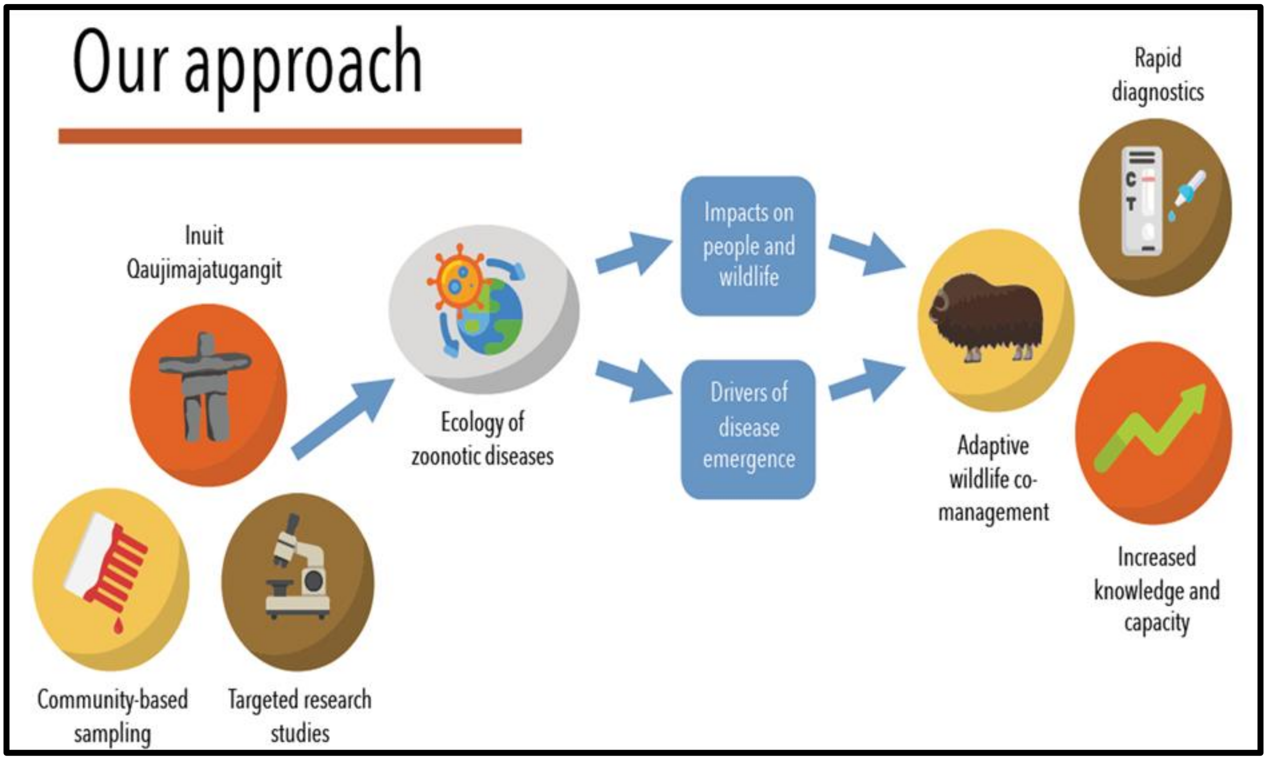
4. Presence of Trichinella confirmed or otherwise

5. Data used by NRBHSS to determine public message on walrus hunt

G. Can be slotted in for "3". Processed meat (DNA) subject to rapid and at-scale qPCR testing for *Trichinella*. Results *can be generated and disseminated in real-time.*

An illustration of a cross-cultural operational and cooperative model through which Indigenous ways of knowing and western scientific knowledge-building can work together is presented in a conceptual diagram by the Canada – Inuit Nunangat – United Kingdom Research Program (CINUK) (Figure 9, Arctic Emerging Infectious Diseases - CINUK). This example illustrates the individual elements developed in partnership with communities, uniting IQ and western scientific methods, to fill in knowledge gaps pertaining to the ecology of zoonotic diseases in the Arctic. Genomic methods would slot into 'targeted research studies' and may result in similarly deliverable rapid diagnostic tools (e.g., qPCR tests for *Trichinella*)). For other issues of food security in the Arctic, for example establishing new fisheries, or identifying cryptic stocks, one need only substitute these topics for 'Ecology of zoonotic diseases' in this conceptual model.

Figure 9: Conceptual overview of CINUK's approach to combatting emergent zoonotic diseases within the Arctic, including concrete deliverables for communities to use (e.g., app-based diagnostics) and add to the knowledge base.



Conclusion

Until recently, global consensus sought to mitigate or dampen the impacts of climate change and the production of pollutants (such as POPs). A volte-face on such efforts to tackle these issues by some of the most powerful and influential nations on earth in the past

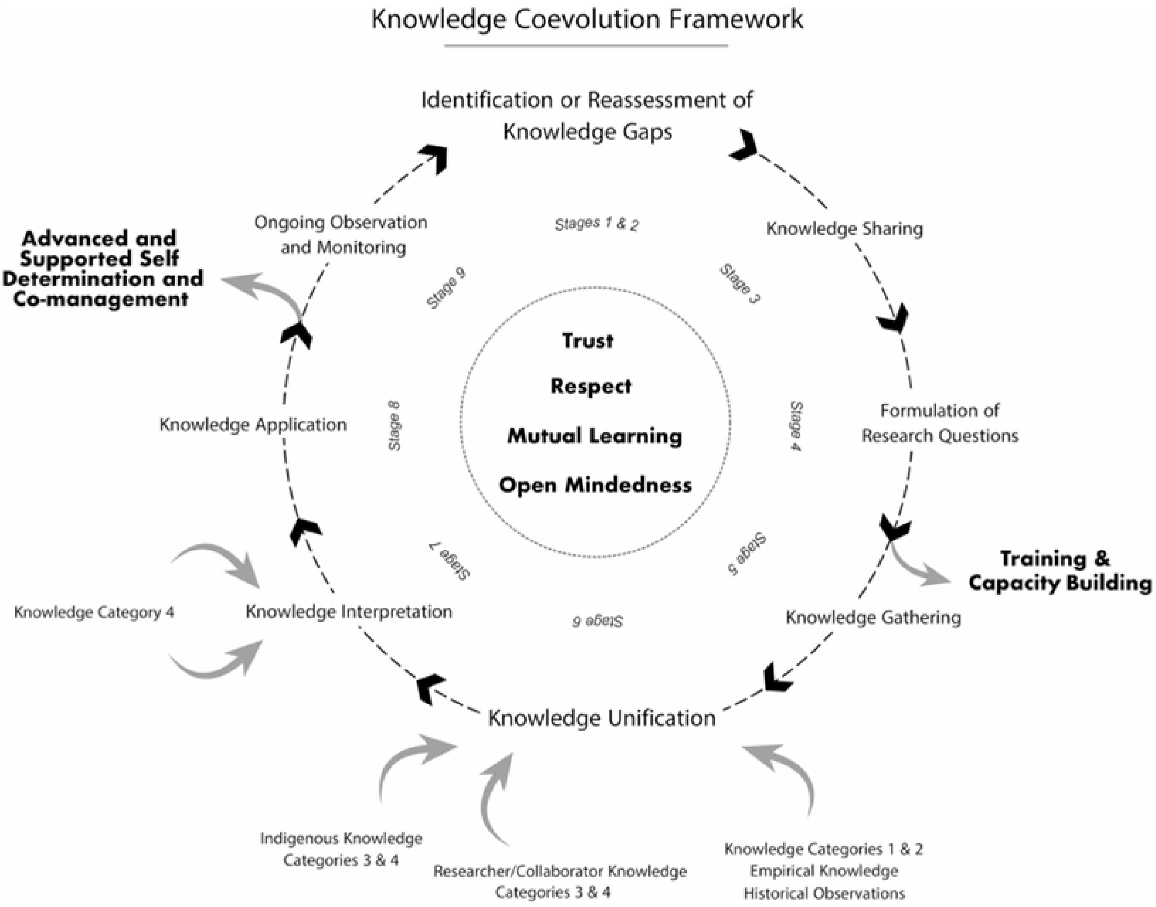
12 months has returned the Arctic to a state of extreme peril. Where once it was thought POPs may be eventually phased out of the food chain from global disuse, their continuing production now is probably assured (Noyes et al. 2025). The continuing melting of the permafrost will continue to release concerning amounts of methylmercury into aquatic Arctic environs. The physical changes to marine, coastal and ice-shelf habitats will have a profound effect on how, when and where Inuit go to hunt traditional country food, resulting is the potential loss of some country food from the cultural diet. A possible negative corollary of this is a continuing trajectory of a 'colonized diet', which is anathema to the cultural tenets held dear by Nunavimmiut and to the food security of the Arctic as a whole.

We have described only some of the ways genomics and DNA-based tools may be applied to various marine and aquatic taxa in Arctic freshwater, estuarine and marine habitats. We hope we have also stressed the importance that any such tool be used only in the context of Nunavimmiut cultural and societal hegemony of the lands and waters of Nunavik (extending to all Inuit Nunangat). The ecological expertise of the Indigenous population often foreshadows the findings of more cryptic genomic data reported by Western scientists. Thus, TEK knowledge of Nunavimmiut should drive the incorporation, utilisation or integration of genomics tools when it is deemed necessary. Chapman and Schott (2020) provide a useful conceptual model maximizing engagement across cultures to drive knowledge coevolution – the knowledge coevolution framework (the model is reproduced here as Figure 10).

If a technology can be used that does not interfere with, or denigrate, tradition, so much the better. Non-invasive biodiversity surveys using eDNA detection chemistry to monitor species' DNA from environmental samples collected without injurious harm to any animal may fall into that category. Such an approach would work well for emergent and novel pathogens; and for tracking populations of important food species such as char and salmon (e.g., Jacobsen et al. (2023) found eDNA to be a more cost-effective means to monitor these fish than electrofishing in a Greenland river), as well as the expansion of invasive competitor species such as pink salmon. eDNA is a tool that is being adopted by Indigenous rightsholders and communities globally as part of wildlife monitoring toolkits. Working in partnership with HTOs to collect physical samples for genomic analysis, is also additive and not limiting to the actions of the hunters and harvesters themselves. In terms of selecting species for WGS, Inuit perspectives are the primary driver (see Table 2).

The meeting was bookended by introducing the science of conservation genetics, genomics and DNA-based tools at one end using English terms (as jargon-free as possible), and by the need for a novel set of Inuktitut terms to decipher some of the technical terms at the other. For genomic and DNA data to be used, understood and shared amongst Inuit, it needs to be in a form that is communicably efficient and follows the linguistic rules of the various Inuit dialects. Only when we can freely exchange knowledge without misinterpretation and free from the shackles of colonization, can this be achieved.

Figure 10. Knowledge coevolution framework that may be used as a template to guide the development of genomics and DNA-based tools in Nunavik and the broader Inuit Nunangat. See text in Chapman and Schott for details on elements within the model and the stages enumerated within the framework.



Avatittinnik Kamatsiarniq (the respect and care for the land, animals, and the environment), a fundamental principle of IQ, is what also drives biologists trained in classical Western scientific methods. This shared, deeply held appreciation and respect of animal life and the land and sea upon which it can thrive gives us all common ground upon which to build consensus. These conversations are perhaps late in coming, but given the grave peril that faces the Arctic, there is no better time than today to begin those dialogues and bring parallel ways of knowing that little bit closer in service of saving Arctic marine and aquatic fauna for future generations in Nunavik and across Inuit Nunangat.

Table 2: Putative species for WGS which currently not have WGS representation in Nunavik populations

Common Name	**Inuktuk name**	**Scientific Name**	**Justification**
Arctic char	Iqaluppik (anadromous) Nutillik (landlocked) Aupalujaak (source pop)	*Salvelinus alpinus*	Primary country food item. Wild and de novo (stocked) populations.
Canada Goose	Nillik	*Branta canadensis*	Local population (eastern flyway) impacted by predation. Country food.
Lesser Snow Goose	Kanguq	*Chen caerulescens*	Candidate vectors of pathogens and/or parasites. Country food.
Ross's Goose	ᖅᑳᕌᖅᓱᒃ	*Chen rossii*	Candidate vectors of pathogens and/or parasites. Country food.
Pink Salmon		*Oncorhynchus gorbuscha*	Invasive competitor with native salmonids
Atlantic Salmon	Sama	*Salmo salar*	Country food. Different ecotypes resident in region.
Shorthorn sculpin	Kanajuq	*Myoxocephalus scorpius*	Country food
Lake trout	Isiuralittaak	*Salvelinus namaycush*	Country food. Impacted by Hg contamination.
Brook trout	Aanak	*Salvelinus fontinalis.*	Second order country food.
Lake whitefish		*Coregonus clupeaformis*	Second order country food.
Black Bear	Atlak	*Ursus americanus*	Competitive consumer of geese, fish.
North American beaver	Kigiaq	*Castor canadensis*	Invasive species – aquatic ecosystem engineer
Arctic tern	ImmeKutaijak	*Sterna paradisaea*	Locally depleted populations. Food item.
None	Unknown	*Trichinella nativa*	Potential infectious agent in meat. Can cause trichinosis

References

Allaire, J., Johnson-Down, L., Little, M., Ayotte, P. (2021). Country and Market Food Consumption and Nutritional Status. Nunavik Inuit Health Survey 2017 Qanuilirpitaa? How are we now?. Quebec: Nunavik Regional Board of Health and Social Services (NRBHSS) & Institut national de santé publique du Québec (INSPQ).

Arrigo, K.R. (2014). Sea ice ecosystems. Ann Rev Mar Sci 6: 13.1–13.29. doi: https://doi.org/10.1146/annurev-marine-010213-135103

Baldwin, K., Allen, L., Basquill, S., Chapman, K., Downing, D., Flynn, N., MacKenzie, W., Major, M., Meades, W., Meidinger, D., Morneau, C., Saucier, J-P., Thorpe, J., Uhlig, P. (2019). Vegetation Zones of Canada: a Biogeoclimatic Perspective. [Map] Scale 1:5,000,000. Natural Resources Canada, Canadian Forest Service. Great Lake Forestry Center, Sault Ste. Marie, ON, Canada.

Ballinger, T. J, Moore, G. W. K., Garcia-Quintana, Y., Myers, P. G., Imrit, A. A., Topál, D., & Meier, W. N. (2022). Abrupt northern Baffin Bay autumn warming and sea-ice loss since the turn of the 21st century. Geophysical Research Letters, 49 (21). https://doi.org/10.1029/2022GL101472

Blanchet, C., & Rochette, L. (2008). Qanuippitaa? 2004 Nunavik Inuit Health Survey: Nutrition and food consumption among the Inuit of Nunavik. Nunavik Regional Board of Health and Social Services & Institut national de santé publique du Québec. http://nrbhss.ca/en/health-surveys

Bolduc, S., Lemire, M., Tremblay, J-E., Falardeau, M., Dallaire, X., Brochu M., Legros, J., & Moore, J-S. (2024). Assessment of inter-regional dietary differences in anadromous Arctic char (*Salvelinus alpinus*) in Nunavik, Canada, and links with flesh quality indicators. Arctic Science. 10(2): 372-385. https://doi.org/10.1139/as-2023-0018

Breton-Honeyman, K., Hammill, M. O., Furgal, C. M., & Hickie, B. (2016). Inuit Knowledge of beluga whale (*Delphinapterus leucas*) foraging ecology in Nunavik (Arctic Quebec), Canada. Canadian Journal of Zoology. 94(10): 713-726. https://doi.org/10.1139/cjz-2015-0259

Campbell, L. M., Norstrom, R. J., Hobson, K. A., Muir, D. C. G., Backus, S., & Fisk, A. T. (2005) Mercury and other trace elements in a pelagic Arctic marine food web (North water Polynya, Baffin Bay) Sci. Total Environ. 351–352 247–63

Carbonneau, A., April, J., Normandeau, E., Ferchaud, A-L., Nadeau, V., & Bernatchez, L. (2024). Population genomics, life-history tactics, and mixed-stock subsistence fisheries in the northernmost American Atlantic salmon populations. Evolutionary Applications, 17(2), e13654. https://doi.org/10.1111/eva.13654

Chang, L. W. (1977). Neurotoxic effects of mercury—a review Environ. Restor. 14 329–73

Chapman, J. M., & Schott, S. (2020. Knowledge coevolution: generating new understanding through bridging and strengthening distinct knowledge systems and empowering local knowledge holders. Sustainability Science, 15, 931-943. https://doi.org/10.1007/s11625-020-00781-2

Dallaire, X., Normandeau, É., Mainguy, J., Tremblay, J. É., Bernatchez, L., Moore, J. S. (2021) Genomic data support management of anadromous Arctic Char fisheries in Nunavik by highlighting neutral and putatively adaptive genetic variation. Evol Appl.,14(7):1880-1897. doi: 10.1111/eva.13248. PMID: 34295370; PMCID: PMC8287999.

Deb, J. C., &. Bailey, S. A. (2023). Arctic marine ecosystems face increasing climate stress. Environmental Reviews. 31(3): 403-451. https://doi.org/10.1139/er-2022-0101
DFO. (2011). Identification of Ecologically and Biologically Significant Areas (EBSA) in the Canadian Arctic. DFO Can. Sci. Advis. Sec. Sci. Advis. Rep. 2011/055. https://waves-vagues.dfo-mpo.gc.ca/Library/344747.pdf

Desjardins, S., & Gotfredsen, A. B. (2021). Chapter 6 - Subsistence walrus hunting in Inuit Nunangat (Arctic Canada) and Kalaallit Nunaat (Greenland) from the 13th century CE to present, in: The Atlantic Walrus (Eds): Keighley, X., Olsen, M. T., Jordan, P., & Desjardins, S. Academic Press, Pages 121-146. https://doi.org/10.1016/B978-0-12-817430-2.00004-2.

Dubos, V., May, P., Carole-Anne, G., St-Hilaire, A., & Bergeron, N. (2023). Nunavik anadromous Arctic char life histories, behaviour, and habitat use informed by both Inuit knowledge and western science: a year in Ungava Bay. Arctic Science. 9(3): 526-544. https://doi.org/10.1139/as-2022-0019

Furgal, C. M., Innes S., & Kovacs K. M. (2002). Inuit spring hunting techniques and local knowledge of the ringed seal in Arctic Bay (Ikpiarjuk), Nunavut. Polar Research, 21(1), 1-16. https://doi.org/10.3402/polar.v21i1.6470

Greenan, B. & Greyson, P. (2022). Coastal Environmental Exposure Layer. Ocean Ecosystem Science Division, Fisheries and Oceans Canada, Dartmouth, N.S.

Hatlen B., Arnesen A.M., Jobling M., Siikavuopio S., & Bjerkeng B. (1997). Carotenoid pigmentation in relation to feed intake, growth and social interactions in Arctic Charr, Salvelinus alpinus (L.), from two anadromous strains. Aquaculture Nutrition, 3(3): 189–199.

Hayden, A-M., Wilmes, S-B., Gomez, N., Green, J. A. M., Pan, L., Han, H., & Golledge, N. R. (2020). Multi-century impacts of ice sheet retreat on sea level and ocean tides in Hudson Bay. Journal of Geophysical Letters, 125(11), e2019JC015104. https://doi.org/10.1029/2019JC015104

Henri, D. A., Martinez-Levasseur, L. M., Weetaltuk, S., Mallory, M. L., Gilchrist, H. G., Jean-Gagnon, F. (2020) Inuit knowledge of Arctic Terns (*Sterna paradisaea*) and perspectives on declining abundance in southeastern Hudson Bay, Canada. PLoS ONE 15(11): e0242193. https://doi.org/10.1371/journal.pone.0242193

Hu, X. F., Eccles, K. M., & Chan, H. M. (2017). High selenium exposure lowers the odds ratios for hypertension, stroke, and myocardial infarction associated with mercury exposure among Inuit in Canada. Environ Int, 102, 200-206. https://doi.org/10.1016/j.envint.2017.03.002

Inuit Tapiriit Kanatami. (2017). An Inuit-Specific Approach for the Canadian Food Policy. https://www.itk.ca/wp-content/uploads/2019/01/ITK_Food-Policy-Report.pdf

Jacobsen, M. W., Nygaard, R., Hansen, B. K., Broberg, M., Hansen, M. M., Hedeholm, R., & Nielsen, E. E. (2023). Observing the Arctic: A comparison of environmental DNA (eDNA) and electrofishing for monitoring Arctic char and Atlantic salmon. Environmental DNA, 5(4), 782-795. https://doi.org/10.1002/edn3.442

Jamieson, J. A., Weiler, H. A., Kuhnlein, H. V., Egeland, G. M. (2012). Traditional food intake is correlated with iron stores in Canadian Inuit men. J Nutr. 2012 Apr;142(4):764-70. doi: 10.3945/jn.111.140475. Epub 2012 Feb 29. PMID: 22378332.

Jenkins, E., Bouchard, É., & Hernández-Ortiz, A. (2025). *Toxoplasma gondii*: a parasite pollutant in the Arctic. Trends Parasitol. S 4:S1471-4922(25)00128-X.
doi: 10.1016/j.pt.2025.05.003. Epub ahead of print. PMID: 40473482.

Jensen, E. L., Tschritter, C., de Groot, P. V. C., Hayward, K. M., Branigan, M., Dyck, M., Clemente-Carvalho, R. B. G., Lougheed, S. C. (2020) Canadian polar bear population structure using genome-wide markers. Ecol Evol., 10(8), 3706-3714. doi: 10.1002/ece3.6159. PMID: 32313629; PMCID: PMC7160183.

Jonsson, S., Mastromonaco, M. N., Wang, F., Bravo, A. G., Cairns, W. R. L., Chételat, J., Douglas, T. A., Lescord, G., Ukonmaanaho, L., & Heimbürger-Boavida, L-E. (2022). Arctic methylmercury cycling. Science of The Total Environment, 850,157445, ISSN 0048-9697, https://doi.org/10.1016/j.scitotenv.2022.157445

Kavan, J., Szczypińska, M., Kochtitzky, W. et al. (2025). New coasts emerging from the retreat of Northern Hemisphere marine-terminating glaciers in the twenty-first century. Nat. Clim. Chang. 15, 528–537. https://doi.org/10.1038/s41558-025-02282-5

Lair, S., Quesnel, L., Signore, A. V., Delnatte, P., Embury-Hyatt, C., Nadeau, M. S., Lung, O., Ferrell, S. T., Michaud, R., & Berhane, Y. (2024). Outbreak of Highly Pathogenic Avian Influenza A(H5N1) Virus in Seals, St. Lawrence Estuary, Quebec, Canada[1]. Emerg Infect Dis., 30(6):1133-1143. doi: 10.3201/eid3006.231033. PMID: 38781927; PMCID: PMC11138997.

Lavoie, A., Lemire, M., Lévesque, B. et al. (2024). Determinants of iron deficiency and anemia among Nunavimmiut: results from the Qanuilirpitaa? 2017 Nunavik Health Survey. Can J Public Health 115 (Suppl 1), 152–167. https://doi.org/10.17269/s41997-023-00775-4

Li, P., de Groot, P. v. C., Sun, Z., & Lougheed, S. C. (2023). A new genomics tool for monitoring Arctic char (Salvelinus alpinus) populations in the Lower Northwest Passage, Nunavut, Fisheries Research, 258, 106523, https://doi.org/10.1016/j.fishres.2022.106523.

Little , M., Hagar, H., Zivot, C., Dodd, W., Skinner, K., Kenny, T., Caughey, A., Gaupholm, J., & Lemire, M. (2020). Drivers and health implications of the dietary transition among Inuit in the Canadian Arctic: a scoping review. Public Health Nutrition, 1-19.

Michel, L.N., Danis, B., Dubois, P. et al. (2019). Increased sea ice cover alters food web structure in East Antarctica. Sci Rep 9, 8062. https://doi.org/10.1038/s41598-019-44605-5

Montana, L., Bringloe, T. T., Bourret., A, Sauvé, C., Mosnier, A., Ferguson, S. H., Postma, L., Lesage, V., Watt, C. A., Hammill, M. O., Parent, G. J. (2024). Reduced Representation and Whole-Genome Sequencing Approaches Highlight Beluga Whale Populations Associated to Eastern Canada Summer Aggregations. Evol Appl., 17(12), e70058. doi: 10.1111/eva.70058.

Needham, R. J., Gaywood, M., Tree, A., Sotherton, N., Roberts, D., Bean, C. W., & Kemp, P. S. (2021). The response of a brown trout (Salmo trutta) population to reintroduced Eurasian beaver (Castor fiber) habitat modification. Canadian Journal of Fisheries and Aquatic Sciences. 78(11): 1650-1660. https://doi.org/10.1139/cjfas-2021-0023

Noël, M., Loseto, L. L., Helbing, C. C., Veldhoen, N., Dangerfield, N. J., & Ross, P. S. (2014). PCBs are associated with altered gene transcript profiles in arctic Beluga Whales (Delphinapterus leucas). Environ Sci Technol. 2014;48(5):2942-51. doi: 10.1021/es403217r. Epub 2014 Feb 19. PMID: 24490950.

Noyes, P.D., Miranda, D., Oliveira de Carvalho, G. et al. (2025). Climate change drives persistent organic pollutant dynamics in marine environments. Commun Earth Environ 6, 363. https://doi.org/10.1038/s43247-025-02348-4

Nunavik Marine Regional Wildlife Board (NMRWB). (2018). Nunavik Inuit Knowledge and Observations of Polar Bears: Polar bears of the Southern Hudson Bay sub-population. Project conducted and report prepared for the NMRWB by Basterfield, M., Breton

Honeyman, K., Furgal, C., Rae, J. and M. O'Connor. xiv + 73 pp

Papineau, A., Berhane, Y., Wylie, T.N. et al. (2019). Genome Organization of Canada Goose Coronavirus, A Novel Species Identified in a Mass Die-off of Canada Geese. Sci Rep 9, 5954 https://doi.org/10.1038/s41598-019-42355-y

Plante, C., Blanchet, C., Rochette, L., & O'Brien, H. T. (2011). Prevalence of anemia among Inuit women in Nunavik, Canada. International Journal of Circumpolar Health, 70(2), 154–165. https://doi.org/10.3402/ijch.v70i2.17811

Proust, F., Lucas, M., & Dewailly, E. (2014). Fatty acid profiles among the Inuit of Nunavik: current status and temporal change. Prostaglandins Leukot Essent Fatty Acids, 90(5), 159-167. https://doi.org/10.1016/j.plefa.2014.02.001

Qi, D., Ouyang, Z., Chen, L., Wu, Y., Lei, R., Chen, B., Feely, R. A., Anderson, L. G., Zhong, W., Lin, H., Polukhin, A., Zhang, Y., Zhang, Y., Bi, H., Lin, X., Luo, Y., Zhuang, Y., He, J., Chen, J., & Cai, W. J. (2022). Climate change drives rapid decadal acidification in the Arctic Ocean from 1994 to 2020. Science. 2022 Sep 30;377(6614):1544-1550. doi: 10.1126/science.abo0383

Reiling, S. J., & Dixon, B. R. (2019). Toxoplasma gondii: How an Amazonian parasite became an Inuit health issue. Can Commun Dis Rep, 45, 183–90. https://doi.org/10.4745/ccdr.v45i78a03

Sauvé, C., St-Pierre A. P., Hammill M. O., & Gosselin J.-F. (2023). "Abundance Estimate for Beluga (Delphinapterus leucas) in the Ungava Bay Area in Summer 2022." DFO Canadian Science Advisory Secretariat Research Document, 2023/055, Iv + 26 p

Schott, S., Qitsualik, J., Van Coeverden de Groot, P., Okpakok, S., Chapman, J. M., Lougheed, S., & Walker, V. K. (2020). Operationalizing knowledge coevolution: towards a sustainable fishery for Nunavummiut. Arctic Science. 6(3): 208-228. https://doi.org/10.1139/as-2019-0011

Schuster, P. F., Striegl, R. G., Aiken, G. R., Krabbenhoft, D. P., Dewild, J. F., Butler, K., Kamark, B., & Dornblaser, M. (2011) Mercury export from the Yukon River Basin and potential response to a changing climate Environ. Sci. Technol. 45 9262–7

Sieber, N., Hartikainen, H., & Vorburger, C. (2020). Validation of an eDNA-based method for the detection of wildlife pathogens in water. Dis Aquat Organ,141,171-184. doi: 10.3354/dao03524. PMID: 33089822.

Sigourney, D. B., Letcher, B. H., & Cunjak, R. A. (2006). Influence of beaver activity on summer growth and condition of age-2 atlantic salmon parr. Transactions of the American Fisheries Society, 135(4), 1068–1075. https://doi.org/10.1577/T05-159.1

Smith, M. I., Ke, Y., Geyman, E. C., Reahl, J. N., Douglas, M. M., Seelan, E. A., Magyar, J. S., Dunne K. B. J., Mutter, E. A., Fischer, W. W., Lamb, M. P., & West A. J. (2024). Mercury stocks in discontinuous permafrost and their mobilization by river migration in the Yukon River Basin. Environ. Res. Lett. 19 084041. https://doi.org/10.1088/1748-9326/ad536e

Sundararaman, B., Shapiro, K., Packham, A., Camp, L. E., Meyer, R. S., Shapiro, B., & Green, R. E. (2024). Whole genome enrichment approach for genomic surveillance of Toxoplasma gondii. Food Microbiology, 118,104403, ISSN 0740-0020, \
https://doi.org/10.1016/j.fm.2023.104403.

Timmermans, M.-L., & Marshall, J. (2020). Understanding Arctic Ocean circulation: A review of ocean dynamics in a changing climate. Journal of Geophysical Research: Oceans, 125, e2018JC014378. https://doi.org/10.1029/2018JC014378

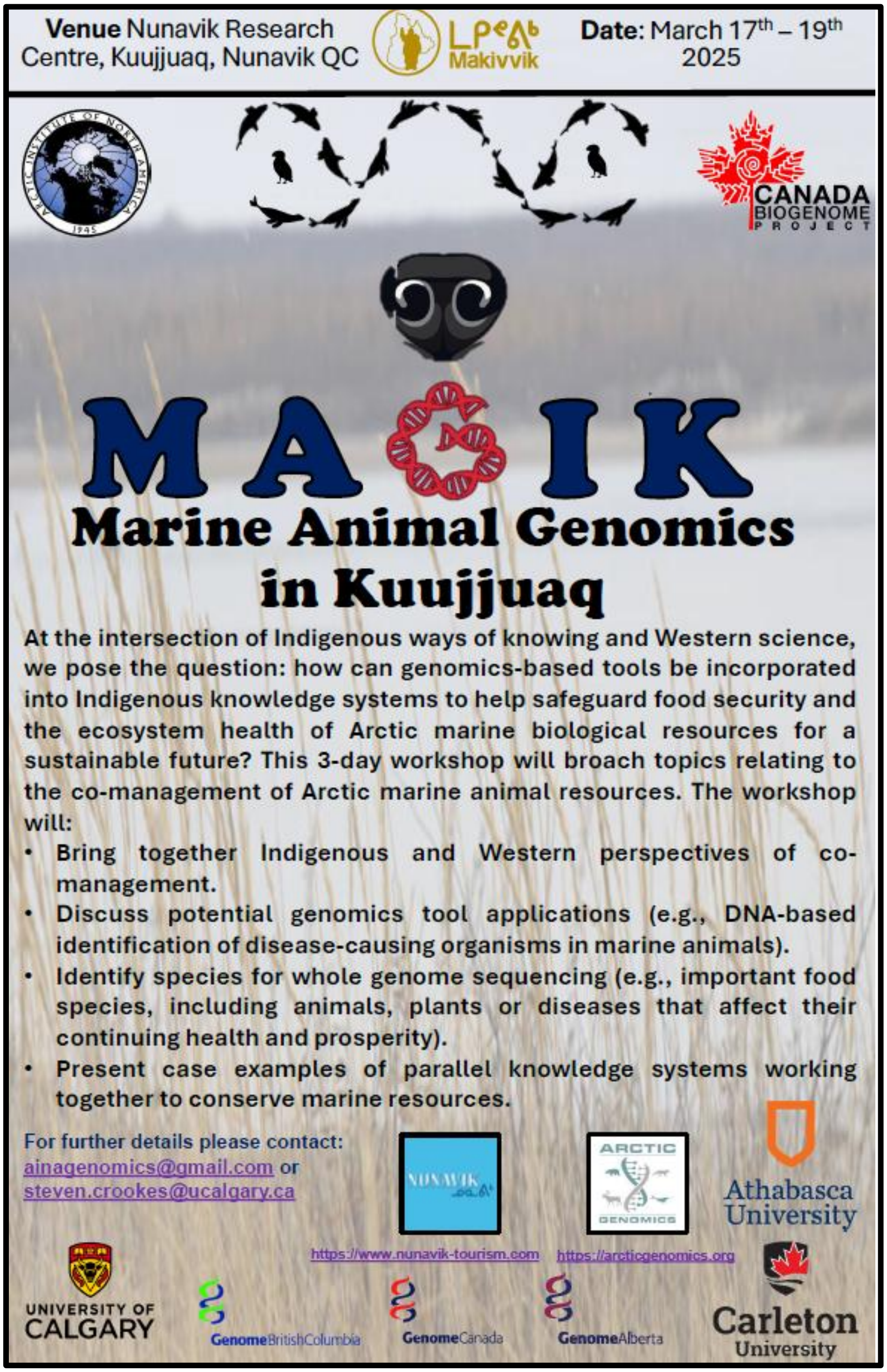
Vernygora, O., Sullivan, D., Nielsen, O., Huntington, K. B., Rouse, N., Popov, V. L., & Lung, O. (2024). *Senecavirus cetus* a novel picornavirus isolated from cetaceans represents a major host switching to the marine environment. Npj Viruses, 2(1):33. doi: 10.1038/s44298-024-00040-6. PMID: 40295809; PMCID: PMC11721122.

Viengkone, M., Derocher, A. E., Richardson, E. S., Malenfant, R. M., Miller, J. M., Obbard, M. E., Dyck, M. G., Lunn, N. J., Sahanatien, V., & Davis, C. S. (2016). Assessing polar bear (Ursus maritimus) population structure in the Hudson Bay region using SNPs. Ecol Evol., 6(23), 8474-8484. doi: 10.1002/ece3.2563. PMID: 28031799; PMCID: PMC5167041.

Walker, V. K., Das, P., Li, P., Lougheed, S. C., Moniz, K., Schott, S., Qitsualik, J., Koch, I. (2020). Identification of Arctic Food Fish Species for Anthropogenic Contaminant Testing Using Geography and Genetics. Foods, 9(12):1824. doi: 10.3390/foods9121824. PMID: 33302601; PMCID: PMC7764770.

Appendices

5.1. Workshop flyer



Venue Nunavik Research Centre, Kuujjuaq, Nunavik QC

Date: March 17th – 19th 2025

MAGIK

Marine Animal Genomics in Kuujjuaq

At the intersection of Indigenous ways of knowing and Western science, we pose the question: how can genomics-based tools be incorporated into Indigenous knowledge systems to help safeguard food security and the ecosystem health of Arctic marine biological resources for a sustainable future? This 3-day workshop will broach topics relating to the co-management of Arctic marine animal resources. The workshop will:

- Bring together Indigenous and Western perspectives of co-management.
- Discuss potential genomics tool applications (e.g., DNA-based identification of disease-causing organisms in marine animals).
- Identify species for whole genome sequencing (e.g., important food species, including animals, plants or diseases that affect their continuing health and prosperity).
- Present case examples of parallel knowledge systems working together to conserve marine resources.

For further details please contact:
ainagenomics@gmail.com or
steven.crookes@ucalgary.ca

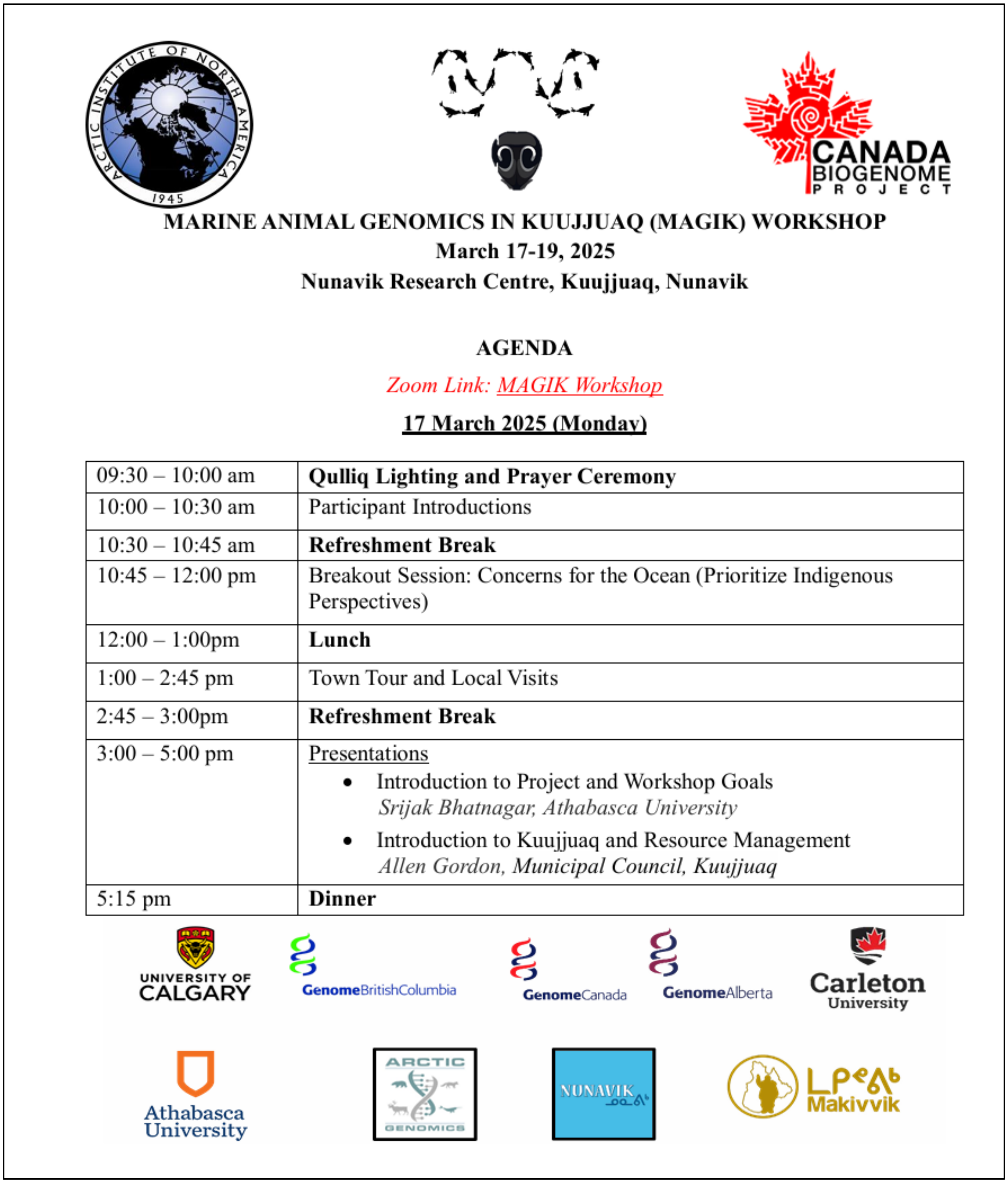
https://www.nunavik-tourism.com https://arcticgenomics.org

5.2. Workshop participation

In person attendee (blue); Virtual attendee (green); Organizer (yellow)

Name	Affiliation
Emily Angulalik	Cambridge Bay Heritage Society, Cambridge Bay, NU
Stephan Schott	School of Public Policy & Administration, Carleton University
Michael Kwan	Nunavik Research Centre, Kuujjuaq
Roger Bull	Canadian Museum of Nature, Ottawa
Bronwyn Harkness	Environment and Climate Change, Canada, Ottawa
Natalia Ivanova	Laboratory Services, University of Guelph
Oliver Lung	Canadian Food Inspection Agency (CFIA), Winnipeg
J Rudar	
Yasemin Bodur	The Arctic University of Norway
Harri Pettitt-Wade	Department of Fisheries and Oceans (DFO), Halifax
Allen Gordon	Nunavik Tourism Board, Kuujjuaq
Srijak Bhatnagar	Athabasca University
Christy Caudill	Carleton University
Steve Crookes	Arctic Institute of North America, University of Calgary
Emily Marsten	Arctic Institute of North America, University of Calgary
Shivangi Mishra	Arctic Institute of North America, University of Calgary
Maribeth Murray	Arctic Institute of North America, University of Calgary
Peter Pulsifer	Carleton University

5.3. Workshop agenda (3 days)



MARINE ANIMAL GENOMICS IN KUUJJUAQ (MAGIK) WORKSHOP
March 17-19, 2025
Nunavik Research Centre, Kuujjuaq, Nunavik

AGENDA

Zoom Link: MAGIK Workshop

17 March 2025 (Monday)

09:30 – 10:00 am	**Qulliq Lighting and Prayer Ceremony**
10:00 – 10:30 am	Participant Introductions
10:30 – 10:45 am	**Refreshment Break**
10:45 – 12:00 pm	Breakout Session: Concerns for the Ocean (Prioritize Indigenous Perspectives)
12:00 – 1:00pm	**Lunch**
1:00 – 2:45 pm	Town Tour and Local Visits
2:45 – 3:00pm	**Refreshment Break**
3:00 – 5:00 pm	Presentations • Introduction to Project and Workshop Goals *Srijak Bhatnagar, Athabasca University* • Introduction to Kuujjuaq and Resource Management *Allen Gordon, Municipal Council, Kuujjuaq*
5:15 pm	**Dinner**

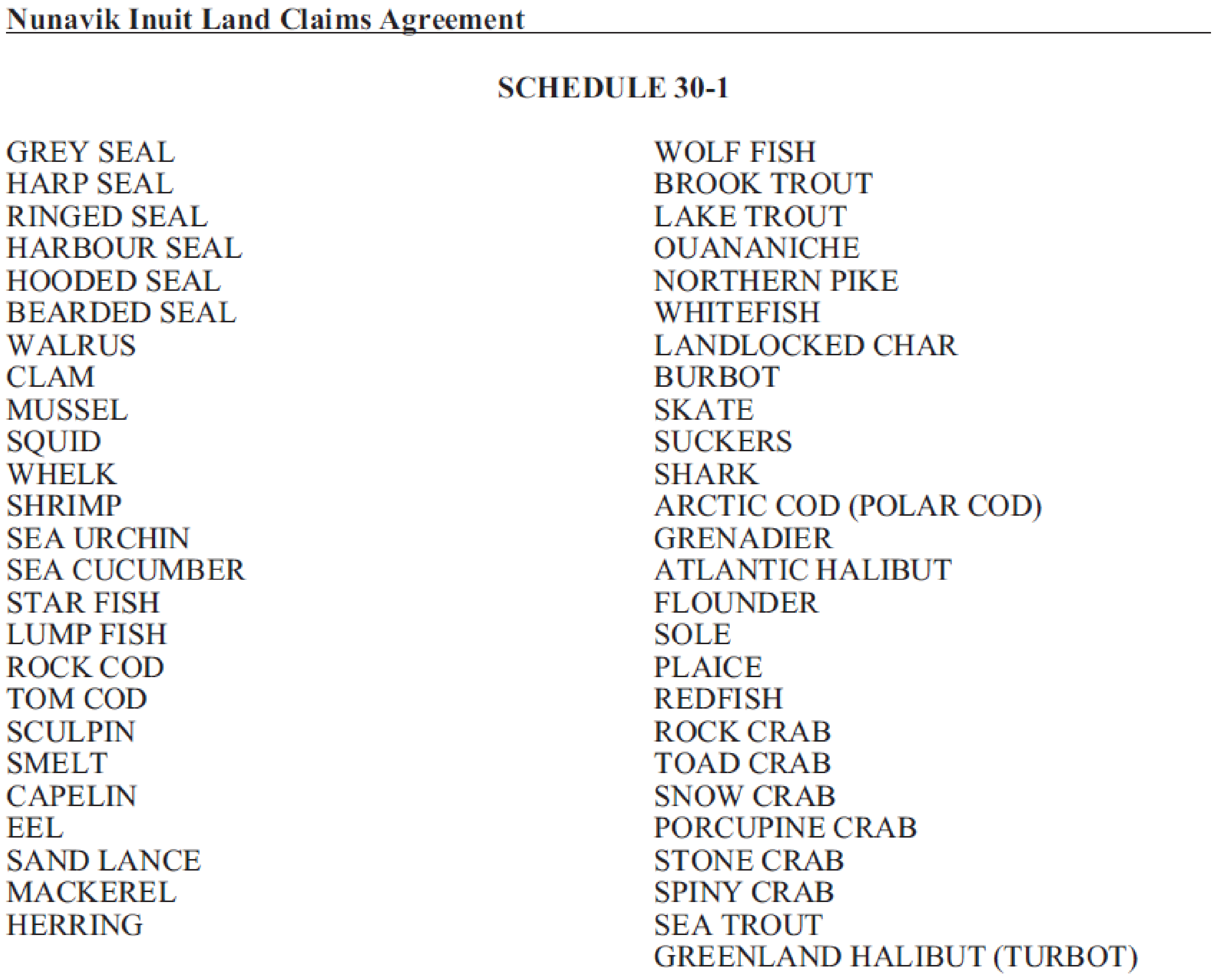
18 March 2025 (Tuesday)

09:00 – 10:30 am	Presentations - Genomics and Genomics-Based Tools – "Intro to" *Steve Crookes, Arctic Institute of North America* - Marine Animal Genomics in the Literature *Shivangi Mishra, Arctic Institute of North America* - Frozen Genomes: Biobanking at the Canadian Museum of Nature *Roger Bull, Canadian Museum of Nature, Ottawa* - Arctic Char Habitat Creation in Nunavik *Allen Gordon, Municipal Council, Kuujjuaq*
10:30 – 10:45 am	**Refreshment Break**
10:45 – 12:00 pm	Breakout Session: Genomics Tools to Address Concerns
12:00 – 1:00 pm	**Lunch**
1:00 – 2:45 pm	Presentations - Genomic Applications & Indigenous Knowledge for Arctic Fishery Stewardship & Co-management *Stephan Schott, Carleton University* - Detection of Pathogens Infecting Marine Mammals *Oliver Lung, Canadian Food Inspection Agency, Ottawa* - Applications of environmental DNA, Population Genomics, and Acoustic Telemetry to Inform Coastal Fisheries Management and Conservation *Harri Pettitt-Wade, Fisheries and Oceans Canada*
2:45 – 3:00 pm	**Refreshment Break**
3:00 – 5:00 pm	Tour of Arctic Char Cannery
5:15 pm	**Dinner**

19 March (Wednesday)

09:00 – 10:30 am	Presentations • Dialogues between Knowledge Systems and Data; Demonstration of Accessible Data *Christy Caudill, Carleton University* • Inuinnaqtun and Science Translation *Emily Angulalik, Kitikmeot Heritage Society, Cambridge Bay* • A Discussion on Guidelines for Wildlife Genomic Research in Inuit Nunangat
10:30 – 10:45 am	**Refreshment Break**
10:45 – 12:00 pm	Open Discussion: Call to Action *Moderated by Christy Caudill*
12:00 – 1:00 pm	Closing Remarks and Thanks, followed by Lunch

5.4 Schedule 30-1 species (taxon) list for management by the Nunavik Marine Region Wildlife Board (NMRWB) as manifested in the Nunavik Inuit Land Claims Agreement (2006).

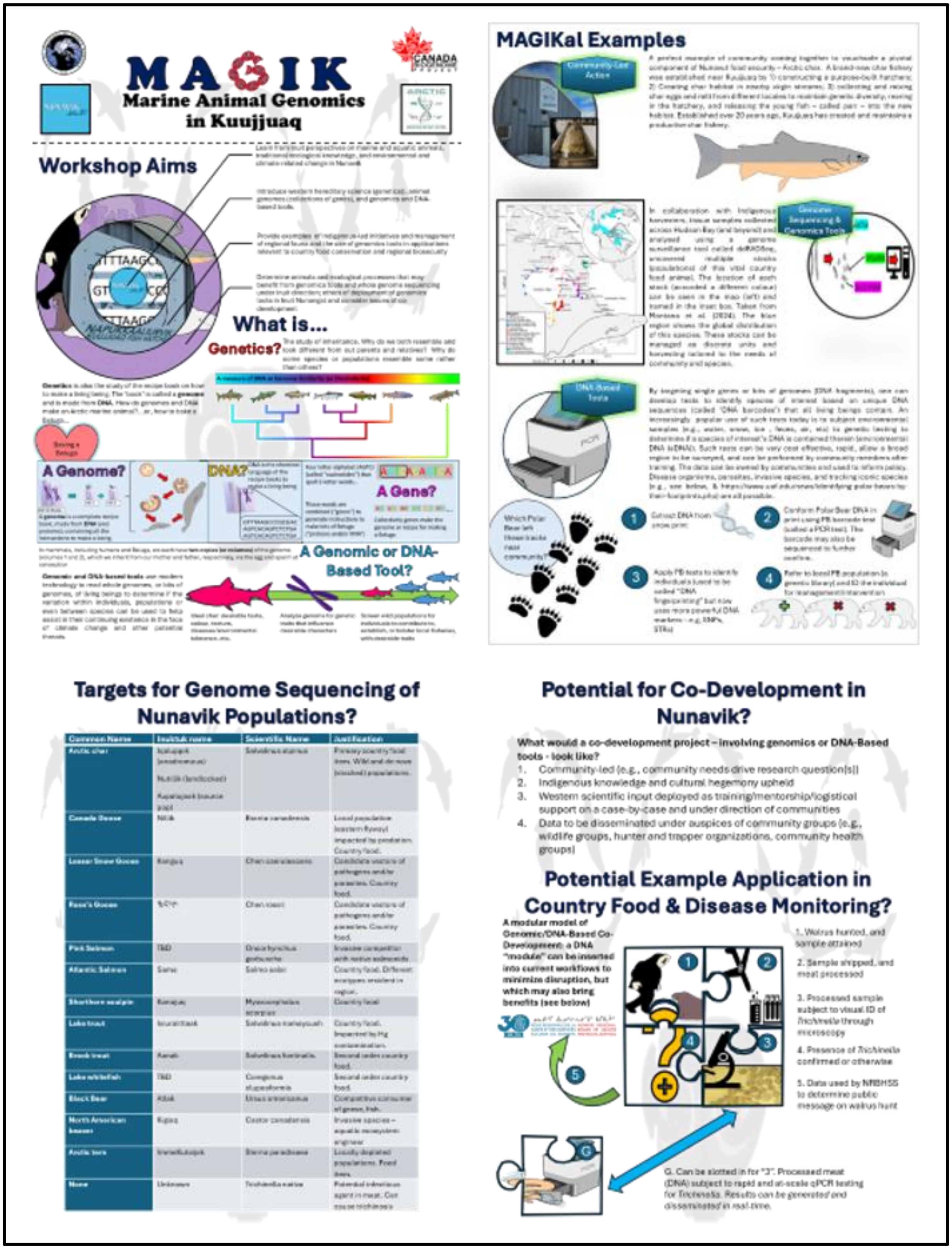


Nunavik Inuit Land Claims Agreement

SCHEDULE 30-1

GREY SEAL
HARP SEAL
RINGED SEAL
HARBOUR SEAL
HOODED SEAL
BEARDED SEAL
WALRUS
CLAM
MUSSEL
SQUID
WHELK
SHRIMP
SEA URCHIN
SEA CUCUMBER
STAR FISH
LUMP FISH
ROCK COD
TOM COD
SCULPIN
SMELT
CAPELIN
EEL
SAND LANCE
MACKEREL
HERRING
WOLF FISH
BROOK TROUT
LAKE TROUT
OUANANICHE
NORTHERN PIKE
WHITEFISH
LANDLOCKED CHAR
BURBOT
SKATE
SUCKERS
SHARK
ARCTIC COD (POLAR COD)
GRENADIER
ATLANTIC HALIBUT
FLOUNDER
SOLE
PLAICE
REDFISH
ROCK CRAB
TOAD CRAB
SNOW CRAB
PORCUPINE CRAB
STONE CRAB
SPINY CRAB
SEA TROUT
GREENLAND HALIBUT (TURBOT)

5.5 Summary Infographic



Workshop Aims

What is...

Genetics?

A Genome?

DNA?

A Gene?

A Genomic or DNA-Based Tool?

MAGIKal Examples

Targets for Genome Sequencing of Nunavik Populations?

Common Name	Inuktitut name	Scientific Name	Justification
Arctic char	[illegible]	[illegible]	Primary country food item. Wild and de novo (stocked) populations.
Canada Goose	[illegible]	[illegible]	Local population (eastern flyway) impacted by predation. Country food.
Lesser Snow Goose	[illegible]	[illegible]	Candidate vectors of pathogens and/or parasites. Country food.
Ross's Goose	[illegible]	[illegible]	Candidate vectors of pathogens and/or parasites. Country food.
Pink Salmon	TBD	[illegible]	Invasive competitor with native salmonids
Atlantic Salmon	[illegible]	Salmo salar	Country food. Different ecotypes resident in region.
Shorthorn sculpin	[illegible]	[illegible]	Country food
Lake trout	[illegible]	Salvelinus namaycush	Country food. Impacted by Hg contamination.
Brook trout	[illegible]	Salvelinus fontinalis	Second order country food.
Lake whitefish	TBD	Coregonus clupeaformis	Second order country food.
Black Bear	[illegible]	Ursus americanus	Competitive consumer of geese, fish.
North American beaver	[illegible]	Castor canadensis	Invasive species – aquatic ecosystem engineer
Arctic tern	[illegible]	Sterna paradisaea	Locally depleted populations. Food item.
None	Unknown	Trichinella nativa	Potential infectious agent in meat. Can cause trichinosis

Potential for Co-Development in Nunavik?

What would a co-development project – involving genomics or DNA-Based tools - look like?

1. Community-led (e.g., community needs drive research question[s])
2. Indigenous knowledge and cultural hegemony upheld
3. Western scientific input deployed as training/mentorship/logistical support on a case-by-case and under direction of communities
4. Data to be disseminated under auspices of community groups (e.g., wildlife groups, hunter and trapper organizations, community health groups)

Potential Example Application in Country Food & Disease Monitoring?

A modular model of Genomic/DNA-Based Co-Development: a DNA "module" can be inserted into current workflows to minimize disruption, but which may also bring benefits (see below)

1. Walrus hunted, and sample attained
2. Sample shipped, and meat processed
3. Processed sample subject to visual ID of *Trichinella* through microscopy
4. Presence of *Trichinella* confirmed or otherwise
5. Data used by NRBHSS to determine public message on walrus hunt

G. Can be slotted in for "3". Processed meat (DNA) subject to rapid and at-scale qPCR testing for *Trichinella*. Results can be generated and disseminated in real-time.