



Muskoxen and Genomics in the Community (MAGIC) Workshop

A Detailed Report



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Executive Summary

The muskox (*Ovibos moschatus*) or *Umingmak* (Inuktitut) is an iconic Arctic mammalian fauna. It is a keystone species in the Arctic terrestrial ecosystem, and plays a vital role in Inuit culture, economies and food security. However, some populations are experiencing demographic instability correlated with a warming Arctic and associated changes in the distribution of predators, disease vectors, food plants, parasites and pathogens. These pressures create uncertainty about the future of muskoxen. The continued viability of muskoxen is important for the long-term sustainability of Inuit subsistence and mixed economies and may also be critical to the sustainability of the ecosystem. Thus, muskoxen present an ideal use case for consideration of ways in which potential genomics tools based on genome sequencing technology (in addition to DNA-based tools predicated on the detection of fragments of genomes) may be applied and incorporated into Indigenous-led management plans, facilitating cross-cultural engagement and multi-directional flow of knowledge. The applicability and suitability of genomics tools for muskoxen management is informed by the priorities and needs of Inuit communities, identification of appropriate taxa with which muskoxen interact, whether such tools are impactful in supporting ecosystem health and food- and bio-security; and whether they are practical to deploy or are achievable in practice, especially given that recent conservation genetics research suggests low species-wide genetic diversity.

To achieve a consensus on the potential use of genomics- and DNA-based tools for muskoxen management, a community-based and ecosystem-level genomics workshop (MAGIC: Muskoxen and Genomics in the Community) was held at the Canadian High Arctic Research Station (CHARS), Cambridge Bay, NU, from January 9 -12, 2024. The workshop was organized as part of the *Canadian BioGenome Project* and the *Role of Genomics in Fostering and Supporting Arctic Biodiversity* project, both funded by Genome Canada, with additional support from Genome British Columbia (Genome BC) and Genome Alberta.

The hybrid (in person and online) workshop brought together Indigenous knowledge holders and decision makers, hunter and trapper organizations, wildlife biologists and managers, genomics experts, data experts and others from Canada, the USA and Denmark. Participants agreed in principle on adopting genomics tools into community-based monitoring and management

programs, with environmental DNA (eDNA) eliciting the most enthusiasm. A range of topics were addressed such as: 1) Priority species with a known or suspected relationship with muskoxen impacting food security were identified for whole genome sequencing (e.g., parasites, pathogens and their vectors); 2) Knowledge gaps were highlighted such as what are the complex relationships between pathogens and parasites of muskoxen and Arctic transmission (vector) and reservoir taxa, and can genomics assist in their elucidation?; 3) How does gut microbiota diversity impact muskoxen wellbeing?; 4) What does the low genome-wide diversity across muskox tell us – or predict - about the muskox’s ability to adapt via selection or phenotypic plasticity to rapid environmental change?; 5) Can the incorporation of ancient genomes (aDNA) contextualize this low genome variation in the wider-context of Arctic terrestrial mammal biodiversity and adaptability to global climate-change?; and 5) Future work was codified including authoring reports and manuscripts, constructing a roadmap to developing and deploying genomic tools, defining benefits to stakeholders and rightsholders, and assessing the need and interest for MAGIC 2.0.

Introduction

This report provides an overview and summary of the Muskoxen and Genomics in the Community (MAGIC) Workshop held in Cambridge Bay, Nunavut in January 2024. The workshop brought together Inuit Knowledge Holders, hunters, and decision makers, scientists from a variety of disciplines and international participants. Together the group considered Inuit knowledge of and priorities for muskoxen, scientific knowledge and gaps, and the potential for genomic and DNA-based tools to help secure a viable future for muskoxen in the face of multiple climate-related stressors. Indigenous Knowledge combined with application of novel scientific advances, such as whole genome sequencing (WGS) of target organisms and use of DNA-based molecular ecological tools (such as environmental DNA markers for species detection from the soup of DNA molecules found within environmental samples), and consideration of the broader ecosystem offers the opportunity to change the way in which healthy wildlife populations are sustained.

Background

Rapid climate change is profoundly impacting Arctic ecosystems (Opdam et al., 2009), influencing the health and population dynamics of numerous Arctic species which are essential to the structure and function of the marine and terrestrial ecosystems and many of which are key to the socio-cultural well-being of Arctic Indigenous People and serve as crucial sources of food and income. Through understanding the impacts of climate change and associated phenomena such as increasing pathogen diversity in the Arctic and investigating unusual mortalities associated with novel infections, action plans may be formulated to conserve biodiversity and help protect country foods and support biosecurity. Parallel knowledge systems that facilitate the exchange of Indigenous Knowledge and scientific knowledge provide a more comprehensive and inclusive perspective and pathway to determine appropriate, effective, and accepted courses of conservation and management actions to sustain and protect Arctic biodiversity. Community-driven and community-engaged training programs and workshops are a means to encourage participation in such parallel knowledge exchange processes. Facilitating dialogue across cultures, expertise, and knowledge systems can also enhance our ability to better predict future outcomes for species and ecosystems under ongoing conditions of change.

The muskox (*Ovibos moschatus*), or *Umingmak* (Inuktitut, translation: the Bearded One) is a key herbivore in the Arctic tundra ecosystem (Kutz et al., 2017) and the only living member of the *Ovibos* genus (Cuyler et al., 2020). Whether or not there are two subspecies needs to be updated since Tener (1965) did not find supporting evidence from morphological measurements and Groves (1997) did not find any genetic evidence for two distinct subspecies of muskox (Groves, 1997). The two potential sub-species are *O. m. moschatus*, which is endemic to mainland Northwest Territories (NT) and Nunavut (NU) and *O. m. wardii*, also known as white-faced muskox or ‘island’ muskox, that historically ranged across most Canadian islands and eastern Greenland (Tener, 1965).

The significance of muskoxen to Arctic Indigenous peoples cannot be understated. As noted by participants at the 2016 Muskox Health Ecology Symposium (Kutz et al., 2017), muskoxen hold economic, sociocultural, environmental, and nutritional value (Rowell et al., 2001; Tomaselli et al., 2018). For example, they provide income from sport hunting, serve as an alternative food source to caribou, and contribute to the maintenance of biodiversity in terrestrial ecosystems.

Muskoxen are among a few cold-adapted ice age survivors, alongside wolves, caribou, and several rodent species (Raghavan et al., 2014). Today, they are endemic to the Canadian Arctic Archipelago, mainland Northwest Territories, Yukon, Nunavut, and northeast Greenland and there are introduced or translocated populations in Alaska, northern Quebec, southwest Greenland, Russia, Sweden and Norway (Kutz et al., 2017). The endemic populations represent approximately 65% of the global population (Cuyler et al., 2020). However, natural populations once existed in Siberia and Alaska during the last glaciation before local extirpation and an eastward range shift at the end of the Pleistocene (Canteri et al., 2022).

Global abundance of muskoxen is slightly declining since 2019 and is about 148,300 in 2023 (Tomaselli et al., 2023). Regional trends vary although determining trends in muskox abundance can be challenging (see Cuyler et al. 2020 for a review of survey methods). However, the surveys that revealed sharp declines in muskox numbers across the large Canadian Arctic Islands over the last 20 years were systematic and regular aerial surveys (Gunn et al., 2024). Those aerial surveys revealed that muskoxen on Banks Island peaked at $68,585 \pm 6,972$ (95% Confidence Limits) in 2001 but rapidly declined to $10,980 \pm 1,148$ (95% Confidence Limits) by 2019. The

decline of populations in Canada significantly impacts Indigenous food security, economic opportunities and community well-being, raising concerns for both human and ecosystem health(Cuyler et al., 2020).

Multiple factors appear to contribute to the decline of muskox populations. Among the challenges they face are low genetic variability across their range, shifting weather patterns, increasing stress during summers, and an increase in the spread of infectious diseases (Kutz et al., 2015). Muskoxen have experienced several bottlenecks and extinction events (Campos et al., 2010), leading to their low genetic diversity (Hansen et al., 2018) and potentially affecting their ability to respond to infectious diseases (Gordeeva et al., 2009; Thulin et al., 2011). Rising temperatures, particularly during fall and winter, increase the chances of extreme weather occurrences, such as higher-than-usual snow accumulation (Gunn et al., 1989; Reynolds, 1998), ice crust development (Forchhammer and Boertmann., 1993), and rain-on-snow events (Gunn et al., 1989; Putkonen et al., 2009). These factors can diminish forage accessibility, leading to higher mortality rates and reduced productivity (Gunn and Adamczewski 2003; Miller and Barry 2009).

Population declines in the Canadian Arctic are occurring alongside the emergence of novel diseases and altered disease dynamics (Kutz et al., 2015). For example, changing pathogen distribution and disease dynamics are observed with climate-driven range expansion of the lung nematode *Umingmakstrongylus pallikuukensis* in the Northwest Territories and Nunavut (Kafle et al., 2017; Kutz et al., 2013), the emergence of *Parapoxvirus*, and increasing observations of *Brucella*-like lesions in muskoxen on Victoria Island, Canada (Tomaselli et al., 2016). To better understand the epidemiology of the disease in muskoxen, more genomes of different pathogens and their wildlife hosts are needed to understand the dynamics of infection with life-history and phenology (seasonality) of both host and disease agent, the varying tolerance to parasites and pathogens of vectors and intermediate hosts, the underlying mechanism for breaching species barriers (zoonoses), and the adaptive basis of evolutionary arms races between infectious agents and host organisms.

Understanding the genomic basis of diseases and the vulnerability of afflicted organisms, such as muskoxen, to infection or infestation, as well as the genomic basis for opportunistic infections and parasitism in disease-causing organisms, may provide potential insights.

Although much of our understanding of mammalian genetics is derived from studies of human and mouse genomes, similar tools could, in principle, be applied to muskoxen if genomic data were to be generated at appropriate geographical scales and genomic resolutions.

To address these challenges, whole genome sequencing (WGS) can be used (Prewer et al., 2022), supplemented by nucleic acid (DNA and/or RNA) detection methods where appropriate. These include environmental DNA (eDNA), which is a tool that has been rapidly incorporated across all scales of biodiversity monitoring since the end of the 2000s. Environmental DNA detection uses nucleic acid proxies (usually DNA, but also RNA) in environmental samples as evidence of the occurrence of the species to which the DNA belongs, assuming the organism has shed the DNA directly into its surroundings. There are many benefits to eDNA workflows that use PCR assays to detect trace amounts of DNA, notably the non-invasive monitoring of animals, plants, and pathogens from a myriad of sample types (e.g., hair, feces, air, snow prints) allowing: a) monitoring of individual species/pathogen presence/absence in a given survey area (e.g., using qPCR, dPCR or CRISPR-Cas9 systems); b) determining community of DNA types in sample such as for microbiomes, of community of fish or vertebrates in a water body from fragments of DNA (metabarcoding); and c) sometimes for full genomic analyses of single species (genomics and genome-wide association studies - GWAS) and/or community of species (metagenomics). The non-invasive nature (collection of snow, feces, water, etc.) of eDNA detection allows for data acquisition while minimizing disturbances to the landscape and to the muskoxen. The non-dependency on physical sampling, also allows practitioners to broaden the scope of surveys to sample much broader areas with relative benefits to cost-effectiveness of biomonitoring surveys. With minimal training, anyone can collect samples for sequencing, thus giving agency back to grassroots and community guardians of biodiversity and biological resources.

Despite this, WGS and nucleic acid-based surveillance tools have yet to be widely applied in polar environments. These tools provide opportunities to explore how climate change and related environmental changes, including the distribution of other species, can influence the biology of

polar species (Kole et al., 2015). Genetic analyses based on sequencing can characterize genetic variation within species and potentially predict their adaptive potential to cope with significant environmental stress (Funk et al., 2012; Whittaker et al., 2017). Climate change is expected to alter the connectivity of northern populations through habitat fragmentation, putting populations with minimal genetic variation, such as muskoxen, under increased stress. Low levels of genomic variation are often linked with a reduced ability of a species to adapt to a rapidly changing – and often unpredictable – environment (Canteri et al., 2022). While we do not know how true this may be for muskoxen, they are currently facing the challenges of rapid environmental change.

Previous Conservation Genomics and Genetic Analyses of Muskoxen

Reference Genome Studies

Reference genome assemblies enhance our ecological and evolutionary understanding of species. Erin Prewer, Susan Kutz, Lisa-Marie Leclerc, and Christopher J. Kyle presented the first draft genome for muskoxen in 2022 (Prewer et al., 2022). The genome assembly and annotation were used to reconstruct a phylogenetic tree which estimated that muskoxen diverged from other ungulate species approximately 12 million years ago. Pečnerová et al. (2023) analyzed 108 whole genomes through genome resequencing using the reference genome as a scaffold, sampled from across its contemporaneous range (including both subspecies) and found muskoxen demographic history was profoundly shaped by past climate changes and post-glacial recolonization during the Pleistocene and Holocene glaciations and interglacials. The white-faced muskox has the lowest genome-wide heterozygosity (a measure of genetic diversity) recorded in an ungulate. Their study provided insights into how species with a history of population bottlenecks, small population sizes and low genetic diversity managed to survive against all the odds. Recent work by Pečnerová et al. suggests that the rate of loss of genetic diversity may have purged deleterious genes as contemporary genomes do not seem to possess the signals of significant inbreeding depression. Muskoxen experienced a series of founder events during the colonization of the Canadian Arctic and Greenland in the Holocene (Hansen et al., 2018). Founder events are generally associated with reduced levels of genome-wide diversity as low census sizes are prone to the loss or fixation of genetic diversity through stochastic effects of genetic drift.

Palaeogenomics or Ancient DNA Studies

Campos et al. (2010) utilized ancient DNA sequences to infer muskoxen population dynamics throughout the late Pleistocene and Holocene. Their results revealed that the genetic diversity of muskoxen was much higher during the Pleistocene than at present, having undergone several expansions and contractions over the past 60,000 years. Li et al.(2023) have provided an understanding of the molecular mechanisms involved in arctic adaptation and proposed that muskoxen and reindeer are the only ruminants that have evolved to survive in harsh polar environments. However, with expected levels of Arctic warming, which are likely to exceed those experienced by the species during the Pleistocene interglacial may provide a mismatch between their cold-adapted genomes and phenotypes. Ancient DNA samples from before and after each successive colonization event across the Canadian Arctic and Greenland may help contextualize finer-scale changes in diversity and the impact of founder events on muskoxen populations. Palaeogenomics, or ancient DNA studies are valuable tools to study evolutionary changes in a species and can also reveal information about the genetic traits of ancient inhabitants from various geographical regions. In addition, paleogenomics may also elucidate the genetic basis of both modern and prevalent diseases and the novel infections to which the species has not previously been exposed. This presents both opportunities and challenges for forensics, population genetics, evolutionary genetics, conservation biology and the study of ancient DNA samples.

Muskox Health and Disease Dynamics

The health of the ecosystem, along with the flora and fauna that coexist within it, is interconnected with human health. Indigenous peoples have long understood this connection and have maintained a strong bond with nature. Indigenous Knowledge holders have vast experience in predicting change in animal health (Ostertag et al., 2018) and while the scientific community identified the need for monitoring disease in muskoxen nearly 85 years ago (Jennov, 1941), the actual focus on doing so is relatively recent, with early literature containing only sporadic reports of parasitic infections and infectious disorders (Mathiesen et al., 1985; Tener, 1965). Recent reports have highlighted population declines in areas where novel diseases and altered disease dynamics have been observed. For example, acute and extensive infectious disease-associated summer mortalities in Alaska and Canada have led to significant population declines (Forde et al., 2016; Kutz et al., 2015).

Erysipelothrix rhusiopathiae (ER)

Erysipelothrix rhusiopathiae, a facultative, anaerobic, gram-positive bacillus found in both terrestrial and marine environments (Wang et al., 2010) has been associated with multiple unusual mortality events in *Ovibos moschatus wardi* on two islands (Bank and Victoria) in the Canadian Arctic Archipelago (Kutz et al., 2015). The identification of ER as a significant cause of mortality in muskoxen has potential implications for wildlife conservation, food safety, and food security. Mavrot et al. (2020) provide new information on the serodiagnosis and epidemiology of ER indicating the widespread exposure of ER in muskoxen in western Canada and Alaska. Work by Tomaselli et al. (2022) suggests that contagious ecthyma dermatitis may serve as a point of entry for ER in the muskoxen of the Canadian Arctic.

The importance of comprehending the diversity of pathogens, the adaptability of their hosts, and the intricate host-pathogen interactions in the changing Arctic is highlighted by the discovery of ER as a significant pathogen in muskoxen and the investigation of other unusual mortality events of multiple etiologies in this species. Understanding the causes for the increased occurrence of ER and its association with large-scale mortality events for muskoxen is critical to evaluating the implications for wildlife and wildlife-dependent human populations in the Arctic.

Lung Nematode

Changing pathogen distribution and disease dynamics have also been observed with the climate-driven range expansion of the lung nematode *Umingmakstrongylus pallikuukensis* in the Northwest Territories and Nunavut (Kafle et al., 2017; Kutz et al., 2013). Kutz et al. (2001) discovered an unusual new genus of *protostrongylid* lung nematode in muskoxen from the central Canadian Arctic and described the intricacies of the parasite's relationship with its definitive hosts, its gastropod intermediate hosts, and the wider Arctic environment (Fig.1).

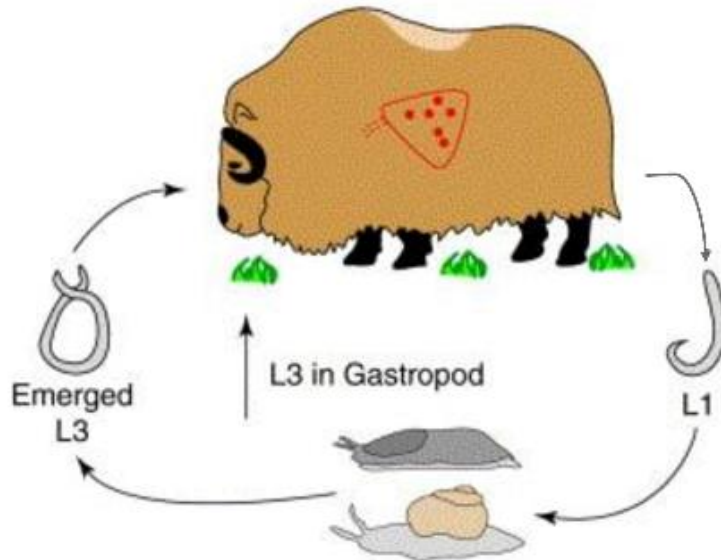


Figure 1: Lifecycle of a lungworm, *Umingmakstrongylus pallikuukensis*, highlighting the stages from egg laying in the lungs to the development of larvae in gastropod intermediate hosts. The figure shows the progression from first-stage larvae (L1) to the infective third-stage larvae (L3), emphasizing the critical role of gastropods in the transmission. This life cycle highlights the complex interactions between the lungworm, its hosts, and the environment. Adapted from Kutz et al. (2001).

Other Infections

Outbreaks of *Pasteurella* spp., *Mycoplasma* spp., and *Parapoxvirus* in muskoxen in the Dovrefjell, Norway, have been identified in declining populations (Handeland et al., 2014; Ytrehus et al., 2008, 2015). Tomaselli et al. (2016) highlight the emergence of the *Parapoxvirus* and increasing observations of Brucella-like lesions in wildlife on Victoria Island, Canada, raising concerns about the health of local ecosystems and the potential impacts on both wildlife populations and human health. Genomics tools may help to further interpret the transmission of brucellosis between caribou and muskoxen (Kamath et al., 2016). Concerning the frequency of zoonotic pathogens, Berg et al. (2021) identified the initial molecular presence of *Giardia duodenalis*, *Cryptosporium parvum*, and *Erysipelothrix rhusiopathiae* in West Greenland. Past outbreaks of yersiniosis (caused by *Yersinia pseudotuberculosis*) have been detected on Banks Island, NWT, by Blake, McLean, and Gunn (Blake et al., 1991). These findings highlight the potential risks of zoonotic transmission, emphasizing the importance of monitoring these pathogens in wildlife populations and their environments. Understanding the interplay between these diseases and the environment of muskoxen is crucial for conservation efforts.

Vision and Goals of the MAGIC Workshop

The workshop aimed to facilitate dialogue, identify Inuit concerns about muskoxen and their future in a rapidly changing Arctic, and brainstorm pathways for addressing problem areas through the lens of genomics and DNA-based tools. The specific goals were to:

1. Enable community-led identification of concerns, priorities, and needs regarding muskoxen conservation and the long-term viability of populations.
2. Increase awareness and understanding of genomics and DNA-based tools and how they can be used for monitoring, research, and conservation.
3. Advocate for bilateral and reciprocal training, education, and capacity building to enhance knowledge transfer between science approaches and Inuit Knowledge Systems.
4. Demonstrate ways to easily access data and support information sharing through open cyberinfrastructure platforms and identify ways such platforms can be used to support co-development and co-implementation of research on muskoxen and their ecosystems.
5. Generate a best practices framework on the use and applicability of genomics and DNA-based tools for supporting muskoxen conservation and other species as prioritized by the Inuit.
6. Co-create a conceptual framework for documenting species wellness and species and ecosystem monitoring using genomics and DNA-based tools with muskoxen as a template or pilot use case.

Workshop Sessions

The workshop began with a *qulliq* lighting by Elder Mabel Etegik, who discussed the meaning and significance of the *qulliq*. This was followed by an introduction to the purpose and goals of the workshop. Information sheets on foundational genetic and genomic concepts were provided to facilitate discussions about genomics. (Appendix III). Members of the Kitikmeot Heritage Society provided live translations between Inuinnaqtun and English. Throughout the workshop, discussions occurred during breakout sessions, community meals, and in unstructured settings. All the speakers highlighted various aspects related to safeguarding muskoxen populations and the potential role of genomics in fostering sustainable muskox populations. Hands-on sessions demonstrated the use of muskox tissue sampling kits, sample processing methods, lungworm

microscopy, and DNA extraction. The workshop was divided into four sessions, with plenary talk(s) and breakout opportunities in each session.

Session I: Relationship to Muskoxen

This session began with insights from Indigenous Elders, representatives of Hunters and Trappers Organizations/Committees, and other community members, both in person and online. They shared Traditional Knowledge (TK), observations, and experiences related to muskoxen. This was followed by the presentation of scientific information on muskox health and an open discussion about concerns regarding population viability, adaptability, and the muskox's relationships with its environment. The discussions were largely open forums, allowing participants to share their expertise with the group in line with the concept of “two-eyed seeing” (Kutz & Tomaselli, 2019). Integrating Traditional Knowledge with Scientific Knowledge is essential for making well-informed, timely, and effective decisions regarding wildlife health and conservation.

Outcome: A comprehensive discussion among the participants produced a schematic that highlights the muskox's relationships with various animals, plants, other taxa and environmental interactors (Fig 2).

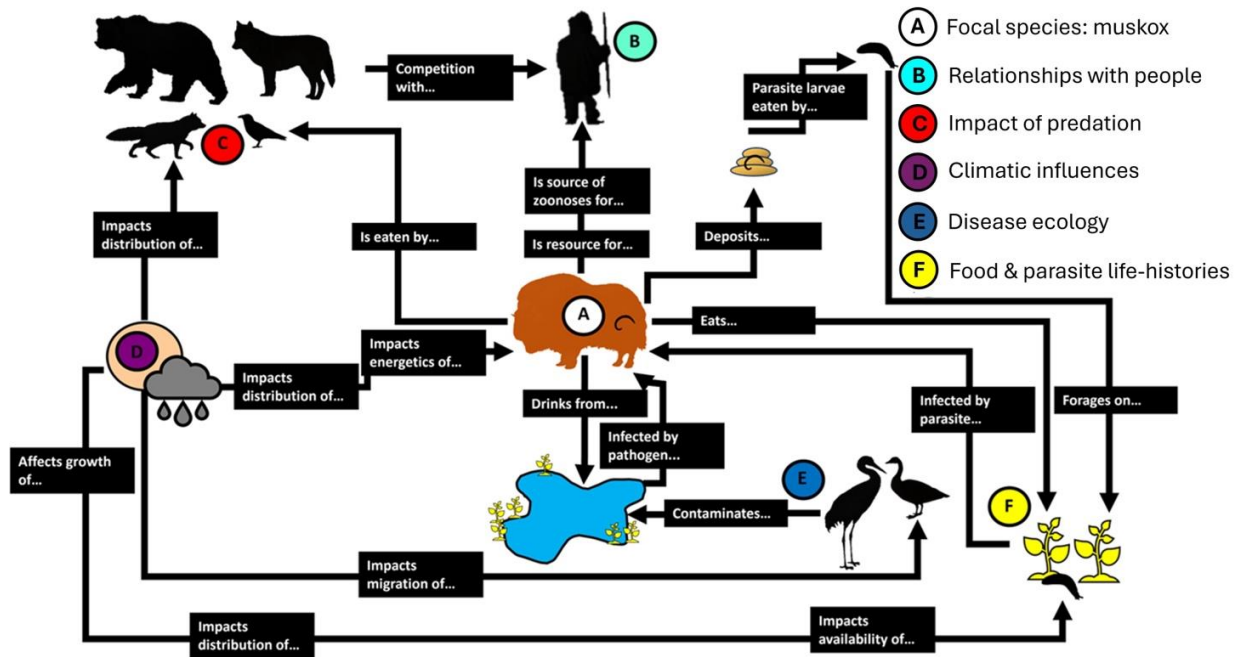


Figure 2. Schematic view of the muskox’s interactions with other taxa embedding the muskox in the wider context of Arctic life, to identify other species of interest for genomic investigation.

Session II: Concerns for the Muskox’s future

In this session, ongoing scientific research related to muskoxen was presented, followed by breakout sessions to prioritize concerns identified in Session I. These were then shared with the entire group. The potential of genomics for co-management of species in the Arctic was highlighted in the discussion titled “Muskoxen and Genomics Use Cases.” Examples of ways genomic tools could be applied were also presented, emphasizing the necessity of having a high-quality genome and its significance for various evolutionary questions and conservation efforts.

Discussion addressed muskox diseases and genomics, and specifically the prevalence of *Erysipelothrix rhusiopathiae* (ER – and see above), a bacterium commonly associated with domestic swine and poultry. Recently, it has been linked to multiple mortality events in white-faced muskoxen (*Ovibos moschatus wardi*) on Banks and Victoria Islands in the Canadian Arctic Archipelago. Understanding the factors contributing to this zoonotic pathogen’s seemingly elevated prevalence and its correlation with extensive muskoxen mortality is crucial for assessing the long-term implications for muskoxen and other wildlife and the human communities that depend on them.

Outcome: All the participants shared their views and experiences regarding the changes in climate and the impact on muskoxen and people living in close association with them. Elders and members of the Hunters and Trappers Organizations/Committees (HTO/HTC) identified their concerns as follows: diseases in muskoxen, changes in muskox range, shifts in vegetation patterns, invasive species, and the impacts of these factors on their lives (Fig 3). There was consensus on the importance of collaborating to leverage new technologies like genomics and DNA-based tools to address these concerns, grounded in a shared interest in land and animal health.

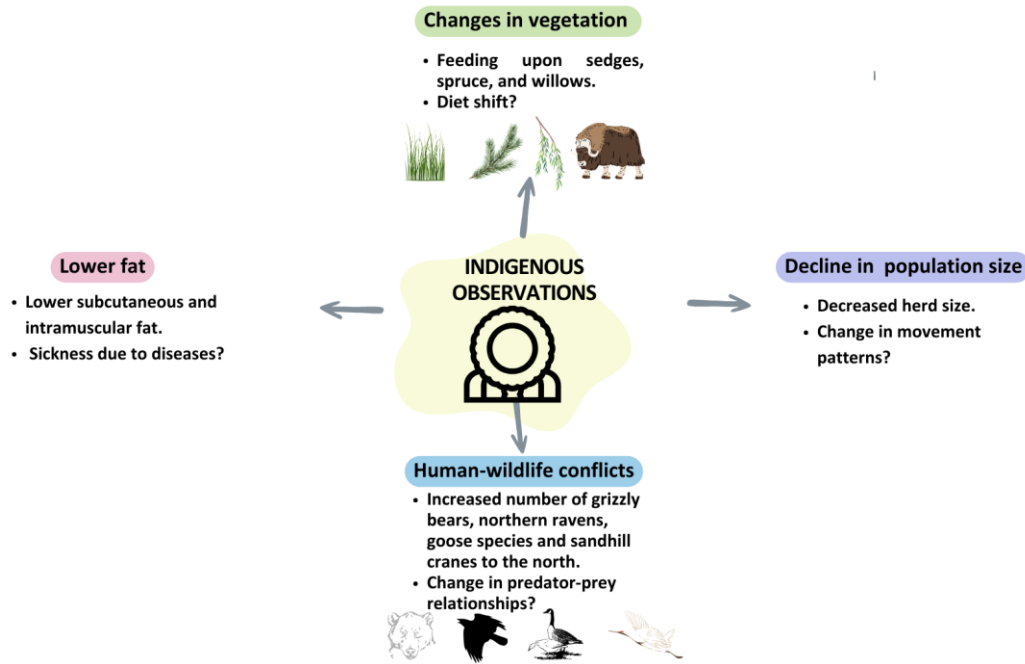


Figure 3. Observations shared by Indigenous Participants as well as concerns about changes in the ecosystem, including the changes in vegetation types, changes in species behaviour and the increasing presence of ravens, cranes, and other southern species.

Session III: Genomics and DNA-Based Tools to Address Concerns Around Muskoxen

During this session, the science underlying genomics and DNA-based tools were discussed to provide pertinent information about these technologies to all participants. Using plain language the foundational concepts of genomics were explained, including the definitions of genes and genomes, the underpinnings of WGS with examples of analyses based on SNP data generated from WGS, and the importance of DNA-based monitoring of species. Of particular emphasis was discussion of how eDNA can aid in predicting the ecological responses of species to climate change and forecast the future distributions of invasive and pathogenic species that may impact food security. A graphical overview of the kinds of tools that can be generated from WGS and DNA-based detection chemistry, was presented with visual animations and pictures while minimizing technical jargon. This was followed by an example using eDNA as a tool for predicting the ecological responses of species to climate change. Environmental DNA because of its scalability and extreme sensitivity is becoming increasingly incorporated into biomonitoring for early detection, mitigation, or eradication of non-native species. Non-native species include *ex-situ* pathogens transported into the Arctic from the south.

Entire ecosystems can be monitored by DNA fragments shed by a species (e.g., waterborne or bird-spread pathogens in Arctic thermokarst lakes). Environmental DNA analysis can even be used to identify individual animals from scats or snow prints (Von Duyke et al., 2023). Very little work of this type has been done in the Arctic to an appropriate degree – representing a significant knowledge gap.

The genomics team shared studies demonstrating the potential use of eDNA tools to analyse samples of muskox feces to identify zoonotic pathogens, changes in diet, and monitor muskox gut health via microbiome metabarcoding (Prewer et al., 2023). Similar studies of polar bear feces indicate low levels of predation on muskoxen, with seals being much more prevalent prey in samples. Another example of the potential for DNA-based assessments of muskox health is infection by *Erysipelothrix rhusiopathiae* - a bacterial disease with a high muskox mortality (Kutz et al., 2015). DNA tests may both quantify infection levels and identify significant vectors and reservoir organisms that harbor this potent pathogen. The discussion also addressed caribou which is an exemplar of the application of WGS analyses for an Arctic species. Caribou has benefitted from a high-resolution survey of its genomes across Canada to identify population structure, incidences of inbreeding depression, and estimates of gene flow from which information can be used to inform effective co-management programs (Solmundson et al., 2023)

Outcome: Potential Genomics and DNA-based solutions were discussed (Table 1). Candidate species for whole genome sequencing were identified, and priorities were assessed for Inuit communities. All species and ecological relationships within taxonomic groups (e.g., parasites and their vectors) associated with muskoxen were identified in consultation with Inuit participants at MAGIC (Appendix III).

Table 1. Potential Genomics and DNA-Based Solutions for the Muskox

| Solutions | Description |
|----------------------------|--|
| Species Monitoring | <ul style="list-style-type: none"> • Environmental DNA (eDNA) analysis • Metabarcoding using DNA barcodes • Species-specific assays • Non-invasive, scalable and cost-effective tool |
| Microbiome Analyses | <ul style="list-style-type: none"> • Diet composition and changes • Fecal sampling • Gut health using metabarcoding |

| | |
|--|---|
| Whole Genome Sequencing | <ul style="list-style-type: none"> • Comprehensive analysis of entire genome • Holistic analysis of genomic variation within species, identify favourable regions (e.g., high MHC variation) • Develop suite of genomic markers (SNPs-Single Nucleotide polymorphisms) from which parameters of importance for conservation can be elucidated (e.g., effective population size, inbreeding coefficients, geneflow etc.) at scale and lower costs |
| Ancient DNA Analyses | <ul style="list-style-type: none"> • Historical genetic change in populations • Phylogenetic information and identify unique lineages • Source and spread of diseases |
| Non-Native Species Surveillance | <ul style="list-style-type: none"> • Detection and distributional mapping of nonnatives (e.g., identify rate and routes of northerly ingress of novel disease vectors and diseases, predators, parasites, putative food organisms, and competitors). |

Session IV: Practical Aspects of Genomics for Improved Understanding of Muskoxen

This session focused on the current potential and limitations of genomics for filling knowledge gaps about muskoxen and their adaptability going forward. The importance of community engagement, involvement, and relationship building across expertise was emphasized as necessary for the effective and appropriate use of genomic tools in any management or conservation efforts. Discussion also focused on data sovereignty and participants considered frameworks for combining different knowledge systems in easily accessible and useable data management and access systems. The important applications for enhancing data accessibility for various stakeholders and rightsholders were demonstrated, with a focus on Indigenous data sovereignty.

Outcome: A roundtable discussion focused on ways to collaborate and harmonize data to address the Inuit community's concerns about food security, wildlife, and ongoing and future monitoring efforts. As a result of these discussions, a Miro board was created to illustrate changes in the muskoxen ecosystem (Fig. 4).

Knowledge Gaps/ Recommendations

The presence of zoonotic pathogens like *Brucella* and *Erysipelothrix rhusiopathiae* in Arctic regions emphasizes the need for public health education and communication to ensure the safe collection and processing of food species, thereby avoiding human exposure.

Integrating Inuit Knowledge with community-based monitoring is vital to monitoring health and disease and expanding the scope and effectiveness of emerging technologies (Kutz et al., 2017).

Knowledge gaps were identified in several areas related to muskoxen, including their health and disease, predator-prey relationships, physical traits, microbial genomics, and paleogenomic studies. (Table 2).

Table 2. Key Knowledge Gaps Identified from The Workshop

| Category | Key Focus Areas |
|--------------------------------------|--|
| Monitoring Health and Disease | <ul style="list-style-type: none"> • Epidemiology of diseases • Zoonotic pathogens especially <i>E. rhusiopathiae</i>. • Brucellosis in muskox • Lungworms in muskox • Identifying significant Arctic reservoirs for pathogens of muskox |
| Predator-Prey Relationships | <ul style="list-style-type: none"> • Trophic guild in the High Arctic • Analyse distributional shifts of muskox predators, food, and pathogens • Use fecal metabarcoding to identify dietary shifts within and among populations of muskox |
| Muskox Traits | <ul style="list-style-type: none"> • Morphological, phenological, behavioural – are there genomic regions with sufficient heritability to adapt to a warming Arctic • Can genome scans identify MHC loci within and among populations to triage susceptible muskoxen |
| Microbial Genomics | <ul style="list-style-type: none"> • Contamination of muskox meat via trophic pathways • Rumen microbiology • The relation of diet composition with the microbiome, gut health, and food security |
| Paleogenomic Studies | <ul style="list-style-type: none"> • Ancient genome samples – test recent hypotheses related to low genetic variation, lack of inbreeding depression |

Proposed Next Steps

This workshop aimed to identify community priorities, address concerns regarding muskox health, and introduce genomic tools and recent research on muskoxen. Additionally, we strived to determine the key taxa relevant to the sustainability of muskoxen from the Inuit communities’

perspectives. A curated list of species identified as candidates for WGS is provided in Appendix V. The next step is to organize a follow-up workshop, MAGIC 2.0, where we will further discuss species selection. We will also formulate a roadmap or action plan for specific genomics tools to be deployed in the to support ecosystem-scale monitoring and management ensuring that this knowledge is accessible for dissemination among northern communities.

Concluding Remarks

Throughout the workshop, participants were encouraged to engage in dialogue and conversation using breakout discussions, community meals, unstructured conversation, and hands-on demonstrations, which included DNA extraction, muskox sample processing methods, and an explanation of lungworm lifecycle and its infections in muskoxen.

A better understanding of muskox genomics will be instrumental in steering future management and conservation efforts. With continued surveillance integrating emerging technologies with Inuit Knowledge and community-based monitoring and further genomic studies in muskoxen and cohabiting animals, we can enhance our understanding of the pathogen-host dynamics and their impacts in the far north.

More information about this and other Arctic Genomics workshops can be found at <https://arcticgenomics.org/workshops/>. Anyone interested in sharing their views about muskoxen, genomics and DNA-based tools for monitoring and conservation is welcome to contact workshop organizers at muskoxengenomics@gmail.com and/or ainagenomics@gmail.com.

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APPENDIX-I

Abbreviations, Acronyms, Genomic Terms, and Definitions

- **Admixture:** Interbreeding of genetic lineages that were previously isolated from one another.
- **Allele:** Different variants of a gene or DNA sequence.
- **Chromosomes:** The thread-like structures located inside the nucleus of animal and plant cells. Each chromosome is made of protein and a single molecule of deoxyribonucleic acid (DNA). Passed from parent to offspring, DNA contains the specific instructions that make each type of living creature unique. In mammals, like muskox, individuals inherit one set of chromosomes from each parent. Each set contains a single nuclear genome. After conception, the fertilized eggs contain a full set of complementary genomes (diploid), necessary for development.
- **Demography:** the study of life history statistics such as births, deaths, or the incidence of disease, which illustrate the changing structure of populations.
- **DNA barcodes:** Standardized short sequences of DNA that are used to identify species.
- **DNA sequencing:** Determining the exact nucleotide sequence of a DNA molecule.
- **DNA:** DNA or deoxyribonucleic acid is the hereditary material that constitutes genomes in humans and almost all other organisms.
- **eDNA:** Environmental DNA is DNA that is collected from a variety of environmental samples such as soil, water, snow, or air, rather than directly and invasively sampled from an individual organism. As various organisms interact with the environment, DNA is expelled and accumulates in their surroundings from various sources.
- **ER:** *Erysipelothrix rhusiopathiae*
- **EHTO:** Ekaluktutiak Hunters and Trappers Organization
- **Fitness:** It is the quantitative representation of the individual reproductive success of a given genotype in a particular environment. It is also equal to the average contribution to the gene pool of the next generation, made by the same individuals of the specified genotype or phenotype.
- **Founder effect:** The decrease in genomic variability that happens when a small group of individuals becomes isolated from a larger population leads to the formation of new subpopulations. These subpopulations may exhibit different genotypes and physical traits

(phenotypes) compared to the original larger population.

- **Genes:** The basic physical and functional unit of heredity. Genes are made up of DNA.
- **Genetic drift:** Random fluctuations in the frequency of an existing gene variant in a population, leading to the loss or fixation of genetic variants (alleles), whether they are beneficial or deleterious to an organism, in small, decreasing, or fragmented populations.
- **Genetic load:** The presence of unfavorable genetic variation (alleles) in the genomes of a population.
- **Genetic variation:** A term used to describe the variation in the nucleotide sequence in individual genes or across entire genomes between individuals, populations or species.
- **Genetics:** The scientific study of genes and heredity—how certain qualities or traits are passed from parents to offspring because of changes in DNA sequence and/or changes in gene (allele) frequencies or influences on the expression of their translated forms (mRNA) or products (e.g., proteins or other RNAs).
- **Genome:** The complete set of DNA (genetic material) in an organism.
- **Genomics:** The branch of molecular biology concerned with the structure, function, evolution, and mapping of genomes.
- **Heterozygosity:** The condition of having inherited different versions (alleles) of a genomic marker from each biological parent. Homozygosity is the converse, whereby the same variant is inherited from both parents.
- **HTC:** Hunters & Trappers Committee
- **Inbreeding depression:** The reduced survival and fertility of offspring of related individuals.
- **Inbreeding:** The production of offspring from the mating or breeding of individuals or organisms that are closely related genetically or inherit the same genetic material by chance in small populations.
- **KHS:** Kitikmeot Heritage Society
- **MHC:** Major Histocompatibility Complex
- **Mutation:** The process of generating change in the structure of a gene, resulting in a variant form (allele) that may be transmitted to subsequent generations, caused by the alteration (swap, insertion, or deletion) of a single base unit in DNA; or the deletion, insertion, translocation or rearrangement of larger sections of genes or chromosomes. Even whole chromosomes or genomes may be duplicated or deleted.

- **Non-native species (also called ‘exotic’, ‘alien’ or ‘invasive’):** Species that originated somewhere other than their present Indigenous location and which have been introduced to an area where they now live. *Invasive* species always have negative consequences for the naïve ecosystem and economies in which they have newly arrived.
- **Nucleotide:** Building block of DNA or RNA consisting of a nucleoside linked to a phosphate group. Adenine (A), cytosine (C), guanine (G), thymine (T; in DNA only), and uracil (U; in RNA only) are nucleotides. Specific combinations of nucleotides encode the genes.
- **Nucleic acid-based surveillance tools:** Using DNA and/or RNA to assess species diversity, population sizes, detection of invasive species, etc.
- **NUMT:** Nuclear Mitochondrial DNA segments also called pseudogenes are the mitochondrial DNA (mtDNA) fragments that have been inserted into the nuclear genome.
- **Paleogenomics:** The branch of molecular biology concerned with reconstructing and analyzing the genomes of organisms that are not alive in the present day.
- **Phylogenetics:** The study of the evolutionary history and relationships among or within groups of organisms.
- **Reference genome:** An established representative genetic sequence for a particular organism with which other sequenced genomes can be compared.
- **SNP (Single Nucleotide Polymorphism):** A DNA sequence variation that occurs when a single nucleotide (Adenine, Thymine, Cytosine, or Guanine) in the genome sequence is altered, and the alteration is present in at least 1% of the population.
- **TEK:** Traditional Ecological Knowledge
- **TIK:** Traditional Inuit Knowledge or Traditional Knowledge (TK) Inuit or *Qaujimajatuqangit* (IQ) or Inuit way of knowing is the knowledge based on historical and/or current observations by Inuit which have been passed on from several generations.
- **WGS (Whole Genome Sequencing):** DNA sequencing of the entire genome, including all chromosomes and intracellular organelles.
- **Zoonotic disease:** Infectious diseases transmission from humans to animals and animals to humans.

APPENDIX-II

Workshop Agenda

9 January 2024 (Tuesday)

| | |
|------------------|--|
| 10:30 – 10:45 am | Ceremony and Prayer |
| 10:45 – 12:00 pm | Lab Demo: MuskoX Sample Processing |
| 12:00 – 1:00 pm | Lunch |
| 1:00 – 3:00 pm | Participant Introductions |
| 3:00 – 3:50 pm | <u>Presentations</u> <ul style="list-style-type: none">• Introduction to Project and Workshop Goals <i>Srijak Bhatnagar, Athabasca University</i>• Environmental DNA <i>Caren Helbing, University of Victoria</i> |
| 3:50 – 4:00 pm | Refreshment Break |
| 4:00 – 5:00 pm | <u>Open Discussion</u> – Relationality to MuskoX <i>Moderated by Susan Kutz</i> |
| 5:15 pm | Dinner |

10 January 2024 (Wednesday)

| | |
|------------------|--|
| 09:00 – 10:30 am | <u>Breakout Session</u> – Concerns for MuskoX’s Future <i>Moderated by Susan Kutz and Srijak Bhatnagar</i> |
| 10:30 – 10:45 am | Refreshment Break |
| 10:45 – 12:00 pm | <u>Presentations</u> <ul style="list-style-type: none">• Genomics and Genomics-Based Tools <i>Steve Crookes, Arctic Institute of North America</i>• MuskoX Genomics in Literature <i>Shivangi Mishra, Arctic Institute of North America</i>• MuskoX and Genomics Use Cases |

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| | <i>Chris Kyle, Trent University</i> |
| 12:00 – 1:00 pm | Lunch |
| 1:00 – 3:30 pm | <u>Presentations</u> <ul style="list-style-type: none"> • Genomics Informed Co-Management <i>Rebecca Taylor and Micheline Manseau, Environment and Climate Change Canada</i> • Co-Management of Caribou in Northern Ontario <i>Sam Hunter, Weenusk First Nation</i> • Muskox Diseases and Genomics <i>McCaide Wooten, University of Calgary</i> |
| 3:30 – 3:45 pm | Refreshment Break |
| 3:45 – 5:00 pm | <u>Breakout Session</u> – Genomics Tools to Address Concerns <i>Moderated by Steve Crookes</i> |
| 5:15 pm | Dinner |

11 January 2024 (Thursday)

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|------------------|---|
| 09:00 – 09:10 am | Recap |
| 09:10 – 10:30 am | <u>Presentations</u> <ul style="list-style-type: none"> • Dialogues between Knowledge Systems and Data <i>Christy Caudill, Carlton University</i> • Demonstration of Accessible Data <i>Christy Caudill, Carlton University</i> |
| 10:30 – 10:45 am | Refreshment Break |
| 10:45 – 12:00 pm | <u>Open Discussion:</u> Practical Aspects of Genomics for Muskox <i>Moderated by Christy Caudill</i> <ul style="list-style-type: none"> • Advancements and current limitations • Knowledge gaps • Community engagement and relationships • Draft report and attendee recommendations |

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| 12:00 – 1:00 pm | Lunch |
| 1:00 – 3:30 pm | <u>Demos and Hands-On:</u> Participants free to attend one or more sessions <ul style="list-style-type: none"> • Musk Ox Sample Processing • DNA Extraction • Microscopy |
| 3:30 – 4:00 pm | Refreshment Break |
| 4:00 – 5:00 pm | Free time |
| 5:00 pm | Dinner |

APPENDIX-III

List of Participants

| <i>Organizers and Facilitators</i> | |
|------------------------------------|---|
| Name | Organization |
| Maribeth Murray | Arctic Institute of North America, University of Calgary, AB, Canada |
| Srijak Bhatnagar | Arctic Institute of North America & Faculty of Science and Technology, Athabasca University, AB, Canada |
| Peter Pulsifer | Geomatics and Cartographic Research Centre (GCRC), Carleton University, ON, Canada |
| Christy Caudill | Geomatics and Cartographic Research Centre (GCRC), Carleton University, ON, Canada |
| Steve Crookes | Arctic Institute of North America, University of Calgary, AB, Canada |
| Susan Kutz | Faculty of Veterinary Medicine, University of Calgary, AB, Canada |
| Emily Marston | Arctic Institute of North America, University of Calgary, AB, Canada |
| Shivangi Mishra | Arctic Institute of North America, University of Calgary, AB, Canada |
| Christopher Kyle | Forensic Science Department, Trent University, Peterborough, ON, Canada |
| <i>In-Person Participants</i> | |
| Emily A. Angulalik | Kitikmeot Heritage Society, Cambridge Bay, NU, Canada |
| Bessie Omilgoetok | Kitikmeot Heritage Society, Cambridge Bay, NU, Canada |
| Annie Atighioyak | Kitikmeot Heritage Society, Cambridge Bay, NU, Canada |
| Mabel Etegik | Kitikmeot Heritage Society, Cambridge Bay, NU, Canada |
| Mary Kaotalok | Kitikmeot Heritage Society, Cambridge Bay, NU, Canada |
| Helen Blewett | Kitikmeot Heritage Society, Cambridge Bay, NU, Canada |
| Dennis Kaomayok | Ekaluktutiak Hunters and Trappers Organization, Cambridge Bay, NU, Canada |
| Clarence Kaiybgana | Ekaluktutiak Hunters and Trappers Organization, Cambridge Bay, NU, Canada |
| Allen Gordon | Municipal Council, Kuujjuaq, Nunavik region of Quebec & Nunavik Tourism Association, QC, Canada |

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|----------------|---|
| Kyle Wolki | Sachs Harbour Hunters & Trappers Committee, Inuvik region, NT, Canada |
| Shelby Lucas | Sachs Harbour Hunters & Trappers Committee, Inuvik region, NT, Canada |
| Mathieu Dumond | Umingmak Productions Inc., Kugluktuk, NU, Canada |
| McCaide Wooten | University of Calgary, AB, Canada |
| William Justus | University of Calgary, AB, Canada |

| <i>Virtual Participants</i> | |
|-----------------------------|--|
| Anne Gunn | Circum-Arctic Rangifer Monitoring and Assessment (CARMA) Network, Salt Spring Island, BC, Canada |
| Tracy Davison | Government of Northwest Territories (GNWT), Yellowknife, NT, Canada |
| Frances Stewart | Wilfrid Laurier University, ON, Canada |
| Nick Luymes | Wilfrid Laurier University, ON, Canada |
| Steeve Côté | Université Laval, QC, Canada |
| Brynn Parr | Alaska Department of Fish and Game, AK, USA |
| Andy Dobson | Princeton University, NJ, USA |
| Caren Helbing | University of Victoria, BC, Canada |
| Jan Adamczewski | Northwest Territories Environment and Climate Change, Yellowknife, NT, Canada |
| Pam Groves | University of Alaska Fairbanks, USA |
| Kate Curtis | University of Victoria, BC, Canada |
| Alexandra Kanters | University of Calgary, AB, Canada |
| Oliver Lung | Canadian Food Inspection Agency (CFIA), ON, Canada |
| Fabien Mavrot | University of Calgary, AB, Canada |
| Rebecca Taylor | Environment and Climate Change Canada |
| Eleanor Dickinson | University of Calgary, AB, Canada |
| Rachel Guindon | Makivik Corporation, QC, Canada |

| | |
|------------------------|---|
| Niels Martin Schmidt | Aarhus University, Denmark |
| Christian Fohringer | Aarhus University, Denmark |
| Treeva Hakim | University of Calgary, AB, Canada |
| Fernando Alvarez | Qiviuk (Jacques Cartier Clothier, Inc.), AB, Canada |
| Francois Rossouw | Government of Northwest Territories (GNWT), Yellowknife, NT, Canada |
| Nathan Kogiak | Government of Northwest Territories (GNWT), NT, Canada |
| Hesther Yueh | Genome Sciences Centre, BC, Canada |
| Mark Austin | Musk Ox Development Corporation (MODC), Alaska, USA |
| Sreejith Radhakrishnan | University of Glasgow, UK |
| Lisa-Marie Leclerc | Government of Nunavut, NU, Canada |
| Shawna Karpovich | Alaska Department of Fish and Game, USA |

APPENDIX-IV

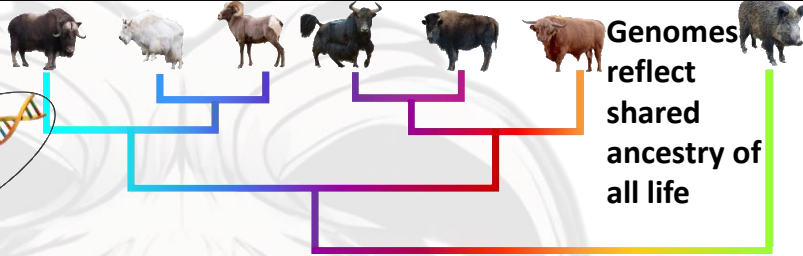
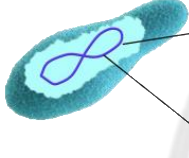
Information Sheets on Foundational Genetic and Genomic Concepts



Genomics

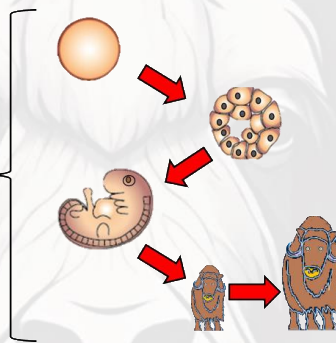


Genomes (DNA) found in all organisms



Genomes reflect shared ancestry of all life

Genomes instruct cells to make organisms from conception to maturity



In mammals, genomes represent two volume 'recipe books', with a volume coming from each parent

Specific instructions (**genes**) are written in a genomic language (a genetic or DNA 'code') made of a 4-letter alphabet (**nucleotides**)

FOUR LETTER ALPHABET (NUCLEOTIDES)

AGTCACAGTCA

INSTRUCTIONS (GENES)

ATG AAT AAT TGT CCG ATG ...

AGTCACAGTCTCTGAAGTCACAGTCTCTGA

PARENT



MUTATION

ACTCACAGTCTCTGAAGTCACAGTCTCTTA

OFFSPRING



Variation exists in genes due to **mutation** producing nucleotide changes (**SNPs**). This may result in variable traits which we can see to preserve, harvest and manage.

VARIATION!

Scanning species for large numbers of nucleotide variants (**SNPs**) from **whole genome sequencing** technology forms the basis for multiple **genomics-based tool** applications

Whole Genome Sequencing Process: 1) Sequence a high-quality **reference genome** for species ; 2) Sequence multiple genomes from different populations using **reference genome** as guide; 3) Identify varying genomic areas (e.g., **SNPs**) as markers for tools.



Selected Applications



| | | |
|---|--|---|
| <p>Genomic basis of traits</p> <p>Populations may vary in genomic diversity underpinning desirable traits (e.g., pelt color/quality, immunity)</p> | | <p>E.g. Linking SNPs with traits may identify useful genes which could be introduced into vulnerable populations</p> |
| <p>Population structure</p> <p>Outwardly indistinct populations with limited interbreeding may reflect multiple independent or semi-independent populations</p> | | <p>E.g. Thousands to millions of SNPs can identify hidden populations and identify inbreeding</p> |
| <p>Metagenomics</p> <p>Analysis of DNA barcodes (species-specific DNA tags) may identify multiple species at once and place them in a broader ecosystem context</p> | | <p>E.g. Change in food eaten by Muskoxen may be monitored in response to climate-induced shifts in vegetation</p> |
| <p>Environmental DNA</p> <p>Non-invasive sampling may democratize, scale-up and empower community biodiversity surveys</p> | | <p>E.g. Informative predictions of future northerly movements by southern species (e.g., invasive species).</p> |

Funding

GenomeCanada GenomeAlberta GenomeBritishColumbia

Polar Knowledge Canada Savoir polaire Canada



Organizers

UNIVERSITY OF CALGARY Carleton University Athabasca University

APPENDIX-V

Candidate Animal species for Whole Genome Sequencing (WGS)

Species that already have a reference quality whole genome sequence have been omitted.

Note: Multiple species of plants have also been identified as being of interest for WGS (food species) and represent a parallel list for discussion at MAGIC 2.0. Plants, however, are difficult to identify in the field, especially in remote Arctic locations, and there is a diminishing level of taxonomic expertise to assist with this.

| Candidate Species (Common Name) | Candidate Species (Scientific Name) | Candidate Species (Indigenous Name) | Relation to Muskox |
|---------------------------------------|--|--|--|
| Common Raven (northern subspecies) | <i>Corvus corax principalis</i> | <i>Tuluqaq, Tulugaq; Killugak</i> | Seasonal migrant and putative disease vector and scavenger (potential disease reservoir) |
| Snow Goose | <i>Anser caerulescens</i> | <i>Kanguit; Kanguq; Kangoq</i> | Seasonal migrant and putative disease vector |
| Greater White- Fronted Goose | <i>Anser albifrons</i> | <i>Nirlivik; Niglik; Nerleq</i> | Seasonal migrant and putative disease vector |
| Ross's Goose | <i>Anser Rossii</i> | <i>Kaaraq</i> | Seasonal migrant and putative disease vector |
| Brant Goose | <i>Branta bernicla</i> | <i>Nerlernaq</i> | Seasonal migrant and putative disease vector |
| Sandhill Crane | <i>Antigone canadensis (syn Grus canadensis)</i> | <i>Tatigak</i> | Seasonal migrant and putative disease vector |

| | | | |
|------------------------------|----------------------------------|---|---|
| Willow Ptarmigan | <i>Lagopus lagopus</i> | <i>Aqiligiq uvvalu; Aqilgvik</i> | Co-distributed with muskoxen. May play some role in parasite/pathogen transmission. |
| Hooded Seal | <i>Cystophora cristata</i> | <i>Natsivak</i> | Arctic pathogen reservoir potential |
| Harp Seal | <i>Pagophilus groenlandicus</i> | <i>Qairulik</i> | Arctic pathogen reservoir potential |
| Ungava Collared Lemming | <i>Dicrostonyx hudsonius</i> | Unknown | <ul style="list-style-type: none"> Keystone species, commonly associated with muskoxen and may play a role in disease/parasite transmission. Major suspect to be a reservoir for <i>Erysipelothrix rhusiopathiae</i> |
| Collared Lemming | <i>Dicrostonyx greenlandicus</i> | <i>Qutulimik avin'ngak; Avin'ngaq; Aupajaaqtuq avinnqaq</i> | <ul style="list-style-type: none"> Keystone species, commonly associated with muskoxen and may play a role in disease/parasite transmission. Major suspect to be a reservoir for <i>Erysipelothrix rhusiopathiae</i> |
| North American Brown Lemming | <i>Lemmus trimucronatus</i> | <i>Kayuqtumik avin'ngak; Avin'ngaq; Avinnqaq</i> | <ul style="list-style-type: none"> Keystone species, commonly associated with muskoxen and may play a role in disease/parasite transmission. Major suspect to be a |

| | | | |
|------------------------------------|--|---|--|
| | | | reservoir for <i>Erysipelothrix rhusiopathiae</i> |
| Long-Tailed Vole | <i>Microtus longicaudus</i> | Unknown/None | May play similar ecological roles to other vole-like rodents such as lemmings and thus worthy of investigation |
| Arctic Char | <i>Salvelinus alpinus</i> | <i>Iqaluk; Tariungmiutaq; Iqaluppik</i> | Alternate food item, also vulnerable |
| Muskox Lungworm | <i>Umingmakstrongylus pallikuukensis</i> | Unknown/None | Muskox parasites and pathogens |
| None (terrestrial slug) | <i>Deroceras laeve</i> | Unknown/None | Intermediate host for the muskox lungworm |
| None (terrestrial snail) | <i>Euconulus fulvus</i> | Unknown/None | Intermediate host for the muskox lungworm |
| None (terrestrial snail) | <i>Columella columella alticola</i> | Unknown/None | Intermediate host for the muskox lungworm |
| Moss Bladder Snail (aquatic snail) | <i>Aplexa hypnorum</i> | Unknown/None | Intermediate host for the muskox lungworm |
| Arctic Mosquitoes | <i>Aedes nigripes</i> | Unknown/None | Potential vectors for muskox diseases |
| Arctic Mosquitoes | <i>Aedes impiger</i> | Unknown/None | Potential vectors for muskox parasites and pathogens |