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Coming Together to Talk about Genomics and DNA-based Tools for *Umingmak* (Muskox, *Ovibos moschatus*) Conservation: Muskox and Genomics in the Community (MAGIC) Workshop

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INTRODUCTION

Rapid climate change is dramatically impacting Arctic ecosystems (Opdam et al., 2009) and affecting the health and population dynamics of many Arctic species. These species are vital parts of the ecosystem and important sources of food and income for Arctic Indigenous People. One such species is the muskox (*Ovibos moschatus*) or Umingmak (translation: the Bearded One), 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). There are two recognized subspecies: *Ovibos moschatus moschatus*, which is endemic to mainland Northwest Territories and Nunavut and *Ovibos moschatus wardii*, also known as white-faced muskox or island muskox, that historically ranged across most Canadian Arctic islands and eastern Greenland (Campos et al., 2010). Muskoxen are among a few cold-adapted ice age survivors, including 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), although natural populations once existed in Siberia and Alaska during the last glaciation before local extirpation and an eastwards range shift at the end of the Pleistocene.

The significance of muskoxen to Arctic Indigenous People cannot be underestimated. As described by participants at the 2016 Muskox Health Ecology Symposium (Kutz et al., 2017), muskoxen have economic, socio-cultural, environmental, and nutritional value (Rowell et al., 2001; Tomaselli et al., 2018). For example, they are a source of income derived from sport hunters, they replace caribou as an alternative food source, and help to maintain terrestrial ecosystem biodiversity.

Cuyler et al. (2020), in a recent review of the 55 global muskox populations, note that six are in decline, including one that was once the largest population in the world. These six populations are found at Cape Thompson, Alaska (n = 1), in Nunavut (n = 2) and Northwest Territories (n = 1), Canada, Greenland (n = 1), and Russia (n = 1). Population sizes range from as few as four animals to as many as approximately 20,000. Trends are difficult to determine (see Cuyler et al., 2020 for a review of survey methods), but the decline of populations in Canada has a significant negative impact on Indigenous food security, economic opportunities, and community well-being, which is increasingly concerning for both human and ecosystem health (Ruscio et al., 2015). Hence, ensuring a healthy future for the muskox is vital.

There appear to be multiple drivers of muskox population decline. Among the challenges they face are low genetic variability (the difference in the DNA of different individuals and populations) 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) that potentially affects 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 smaller calf sizes (Gunn and Adamczewski 2003; Miller and Barry 2009).

Population declines in the Canadian Arctic are co-occurring with the appearance of novel diseases and changing 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 Parapox virus, and increasing observations of Brucella-like lesions in muskoxen on Victoria Island, Canada (Tomaselli et al., 2016). To better understand the epidemiology of disease in muskoxen, more genomes of different pathogens and their hosts are needed to understand the dynamics of infection of Muskox 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 the afflicted organisms to infection or infestation (i.e., muskox) on the one hand, and the genomic basis for opportunistic infection and parasitism of disease-causing organisms on the other, may shed light on potential medical interventions to lower infection rates, ameliorate transmission between individuals, populations, and species, and increase individual survivorship. Although most of our understanding of mammalian genetics comes from studies of human genomes, similar tools could be applied, in principle, to muskoxen if genomic data were to be generated at appropriate geographical scales and genomic resolution.

To address these challenges, whole genome sequencing (WGS) approaches can be used (Prewer et al., 2022), supplemented by partial genomics methods where appropriate (whereby fragments of genomes are sequenced or form the basis of genetic tools), such as environmental DNA (eDNA). The non-invasive and no-contact nature (for example, the collection of snow, feces, or water) of eDNA especially, allows data gathering whilst also minimizing disturbances to the landscape and muskox. With minimal training, anyone can collect samples for sequencing. Despite this, WGS and other DNA-based tools have yet to be widely applied to the study of polar environments. These tools provide opportunities to explore how climate change and ancillary changes to environments (including the distribution of other species) can influence the biology of polar species (Kole, C. et al., 2015). Genetic analyses based on sequencing can characterize species' genetic variation and possibly predict 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 species populations through habitat fragmentation and put those populations with minimal genetic variation, such as muskoxen, under duress. Low levels of genomic variation are often associated with a reduced ability of a species to adapt to a rapidly changing and often unpredictable environment (Canteri et al., 2022). We do not know to what extent this may apply to the muskox, a species situated in a rapid changing environment.

Muskoxen and Genomics in the Community (MAGIC) Workshop

From 9 to 12 January 2024, a diverse group of participants convened at the Canadian High Arctic Research Station (CHARS) in Cambridge Bay, Nunavut, for the Muskoxen and Genomics in the Community (MAGIC) Workshop. The hybrid in-person/online workshop brought together 30 individuals, including:

1. Elders from Kitikmeot Heritage Society (KHS), Cambridge Bay, Nunavut.
2. Representatives from the Hunters and Trappers Organization (HTOs) and Hunters and Trappers Committee (HTC) from Cambridge Bay and Sachs Harbour, respectively.
3. Academic and government scientists from Canada, USA, and Europe, including genomic experts, microbiologists, wildlife biologists, wildlife veterinarians, and social scientists.
4. Representatives from government scientists, academicians and other members of the Muskox Expert Network (MOXNET).
5. Representatives from the Nunavik Tourism Association, Makivik Corporation, and other Indigenous partners.
6. Other stakeholders such as outfitters and producers of Qiviut products.

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

1. Enable community-led identification of concerns, priorities, and needs with respect to muskox 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 Western 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 opened with a qulliq lighting led by Elder Mabel Etegik, who talked about the meaning of qulliq and its importance. The qulliq lighting was followed by an introduction to the purpose and goals of the workshop. Information sheets about foundational genetic and genomic concepts were provided to facilitate conversations about genomics. Members of the Kitikmeot Heritage Society provided live translations between Inuinnaqtun and English. Throughout the workshop, discussions occurred during breakout sessions, at community meals, and in unstructured settings. 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: Relationality to Muskoxen

This session opened with insights from the Indigenous Elders, representatives of the Hunters and Trappers Organizations/Committees, and other community members in person and online. They shared Traditional Knowledge, observations, and experiences of muskoxen. This was followed by scientific information sharing on muskox health, an open discussion of concerns about population viability and adaptability, and the muskox's relationships to its environment. The discussions were largely open forums, and the participants shared their expertise with the group following the concept of 'two-eyed seeing'(Kutz and Tomaselli, 2019). Integrating Traditional Knowledge with Western knowledge is key to making well-informed, timely, and effective decisions on wildlife health and conservation.

Session II: Concerns for Muskox's Future

In this session, the ongoing scientific work regarding muskoxen was shared, followed by breakout sessions to create prioritized lists of concerns identified in session I, which were then shared with the whole group. Elders and HTO/HTC members identified their concerns as follows: diseases in muskoxen, changes in muskox range, changes in vegetation patterns, invasive species, and the impacts of all these things on their own lives. There was consensus around the importance of working together to use new technologies like genomics and DNA-based tools to address some of these concerns, with that consensus grounded in a shared interest in land and animal health.

Session III: Genomics Tools to Address Concerns around Muskoxen

During this session, the basics of DNA and genomics tools were discussed to provide pertinent information about these technologies to all participants. This was followed by an example using eDNA as a tool for predicting the ecological responses of species to climate change. eDNA, 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). eDNA analysis can even be used to identify individual animals from scat or snow prints (Von Duyke et al., 2023). Such work is yet to be done in the Arctic—representing a significant knowledge gap.

Generally, genomics experts shared information about the potential use of DNA-based research, such as eDNA tools to monitor samples of muskox feces to identify zoonotic pathogens, changes in diet, and monitor muskox gut health via microbiome metabarcoding. In muskox, DNA from feces has been analyzed to determine diet and the gut microbial community (Prewer et al., 2023). Similar studies of polar bear feces have found low levels of predation of muskox DNA. Another example use of genomics for muskox health was the study of Erysipelothrix rhusiopathiae, a bacterial disease that causes high muskox mortality (Kutz et al. 2015). The discussion also addressed caribou and Arctic char and the application of DNA-based tools for managing those species. 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.

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.

More information about this and other Arctic Genomics workshops can be found at https://arcticgenomics.org/. A full report on the MAGIC workshop is available at https://pubs.aina.ucalgary.ca/aina/AINA-TR-2025-01.pdf Anyone interested in sharing their views about muskoxen and genomics and DNA-based tools for monitoring and conservation is welcome to contact workshop organizers at muskoxengenomics@gmail.com.

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Community-partnered Research on Harvesting Practices and Wildlife Zoonoses in Arctic Canada

by Alexandra Kanters

INTRODUCTION

Warming nearly four times faster than the rest of the world, the Arctic is currently experiencing rapid socioecological change (Bush and Lemmen, 2019; Rantanen et al., 2022). Climate change poses potential health threats to both wildlife and people in the Arctic (Harper et al., 2021; Keatts et al., 2021) and is estimated to be a main driver behind the emergence of many infectious diseases in the region (Waits et al., 2018; Kafle et al., 2020; Finlayson-Trick et al., 2021; Aleuy et al., 2022; Reynolds et al., 2022; Grigorieva, 2024). The relationship between land, animals, and people has been known and embodied by Indigenous communities for millennia, as has recognition that the health of one impacts the health of others (Hillier et al., 2021; Riley et al., 2021; Reynolds et al., 2022; Mubareka et al., 2023; Sudlovenick et al., 2024). This is particularly true among Inuit in the northernmost regions of Canada, where the health of people is inextricably linked to both the land and cohabitating wildlife (Karetak et al., 2017; Harper et al., 2021; Reynolds et al., 2022). Many northern Inuit communities are traditionally subsistence-based societies where the harvesting, use, sharing, and consumption of wildlife is closely linked to health and wellbeing (Tomaselli et al., 2018; Keatts et al., 2021). Given the cultural, nutritional, social, economic, and spiritual importance of wildlife for Inuit (Tomaselli et al., 2018; Martinez-Levasseur et al., 2020; Snook et al., 2020; Di Francesco et al., 2021), emerging infectious diseases in wildlife significantly impact Inuit communities who rely on it for livelihood and food. Comprehensive, holistic strategies for addressing this challenge are urgently needed.

Increasingly, Western science has begun to recognize the value of holistic approaches through increasing adoption of the "One Health" paradigm – an approach that recognizes the interconnectedness and interdependence of human, animal, and environmental health. One Health now appears prominently in Arctic research (Dudley et al., 2015; Ruscio et al., 2015; Sonne et al., 2017; Jenkins and Leighton, 2019; Tryland, 2022) and is increasingly used as a framework for health programs, strategies, and policies in Arctic settings (Polar Knowledge Canada, 2024; University of Alaska Fairbanks, n.d.).

In 2024, I was honoured to be selected as the recipient of the Arctic Institute of North America's Lorraine Allison Memorial Scholarship and The H.M. Ali Family Education Award. I am a third-year doctoral student in Community Health Sciences at the University of Calgary's Cumming School of Medicine, working closely with colleagues and mentors in veterinary medicine. My research is part of an international, interdisciplinary project that looks at the emergence and spread of two pathogens in caribou and muskoxen in Arctic Canada. These pathogens are zoonotic, meaning that they can be transmitted from animals to people, mainly through butchering, handling, and consumption of infected harvested animals in this context (Tomaselli et al., 2018; Keatts et al., 2021). The project is part of the Canada-Inuit Nunangat-United Kingdom (CINUK) Arctic Research Programme, where members of each partnered community are co-investigators in the research.

My work specifically looks at how knowledge about these zoonotic pathogens is generated, circulated, and ultimately used for health protection by people who rely on the harvesting of wildlife for food and subsistence. It advances One Health questions to examine how multiple sectors (e.g., academia, government, co-management partners, and private industry) come together to tackle complex problems. Key to the work is recognition that Inuit communities have been protecting themselves against wildlife diseases since time immemorial. This approach emphasizes that a wealth of Inuit *Qaujimajatuqangit* (knowledge) already exists—independently of Western science—about how to live safely in harmony with both the land and its other inhabitants.

It is my great privilege to learn directly from Inuit harvesters in three communities in the Kitikmeot and Inuvialuit Settlement Regions of Inuit Nunangat—the