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Review

Climate-linked evolution and genetics in a warming Arctic

L. Ruth Rivkin[1,2,3*], Kiersten C. K. King[1], Jon Aars[4], Kristin L. Laidre[5], Alexandra Langwieder[6], David McGeachy[7], Levi Newediuk[1,8], Stephen D. Petersen[9], Nicholas Pilfold[2], Aryn P. Wilder[2], Geoff York[3], Evan S. Richardson[10], and Colin J. Garroway[1]

Author Affiliations:

[1]Department of Biological Sciences, University of Manitoba, Winnipeg, Manitoba, Canada

[2] Conservation Science Wildlife Health San Diego Zoo Wildlife Alliance, Escondido, California, USA

[3]Polar Bears International, Bozeman, Montana, USA

[4]Norwegian Polar Institute, FRAM Centre, 9296 Tromsø, Norway

[5]Polar Science Center, Applied Physics Laboratory, University of Washington, Seattle, Washington, USA

[6]Centre for Indigenous Peoples' Nutrition and Environment, McGill University, Ste-Anne-de-Bellevue, Quebec, Canada

[7]Environment and Climate Change Canada, Edmonton, Alberta, Canada

[8]Current Address: Department of Biology, Mount Royal University, Calgary, Alberta, Canada

[9]Conservation and Research Department, Assiniboine Park Conservancy, Winnipeg, Manitoba, Canada

[10]Environment and Climate Change Canada, Winnipeg, Manitoba, Canada

* Corresponding author: Ruth Rivkin, ruth.rivkin@umanitoba.ca

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Abstract

Knowledge of evolutionary patterns and genetic variation across a species' range is important for determining conservation and management strategies. The Arctic is the fastest-warming ecosystem on Earth and has already reached temperature increases not expected in the rest of the world until the end of the century. Consequently, synthesizing patterns of evolutionary and genetic change in Arctic species will be instructive for understanding future change in other systems. Here, we present a literature review of peer-reviewed published research exploring evolutionary processes in polar bears, a sentinel species for climate action. The wealth of knowledge generated from the long-term monitoring of polar bears has provided data for exploring patterns of evolutionary change associated with climate change. Warming temperatures have led to significant reductions in sea ice coverage and availability, contributing to declines in genetic variation in some, but not all, polar bear subpopulations. Natural selection driven by warming and selective subsistence harvests may be contributing to the evolution of smaller body sizes in polar bears. However, evidence of adaptive change in polar bears remains limited, despite clear behavioural and phenological plasticity in the species in response to changing sea ice conditions. Following our review, we suggest pathways for identifying the effects of climate warming on the evolution and genetic variation in polar bears, which may improve strategies for locally supported conservation and management decisions. Our results highlight the general complexity of predicting the consequences of warming for wide-ranging, genetically structured, and adaptively specialized species such as polar bears, and underscore the importance of developing evolutionarily informed management and conservation priorities for species threatened by climate change.

1. Background

Climate change poses a significant threat to global biodiversity. By 2100, as many as 30% of species are predicted to be exposed to temperatures beyond those they have evolved to tolerate (Murali et al. 2023, Pigot et al. 2023). As environments surpass species' thermal tolerance thresholds, populations must adapt to new conditions, respond plastically, disperse to more suitable habitats, or face local extinction (Berg et al. 2010, Morris 2014). Associated changes in connectivity, dispersal, and population sizes affect the strength and direction of evolutionary responses to climate change by altering the amount and distribution of genetic variation in the population. In turn, genetic variation shapes adaptive evolutionary responses to environmental selection pressures. Phenotypic plasticity, where a single genotype produces multiple phenotypes, can enable individuals to persist in sub-optimal habitats without requiring population-level evolutionary responses (Whitman and Agrawal 2009). Given current warming trajectories, the ability of many populations to cope with rapid environmental change will depend on their capacity for evolutionary adaptation.

The evolutionary consequences of warming should be particularly apparent in areas where the climate is changing most rapidly, as well as in species with narrow thermal tolerances or restricted habitat ranges (Parmesan 2006, Hoffmann and Sgrò 2011). The Arctic is currently the fastest-warming region on Earth, experiencing a rate of warming nearly four times that of the rest of the planet (Rantanen et al., 2022). Warming temperatures have contributed to a 12% decline per decade in the extent of sea ice across the Arctic over the last 50 years (Meier and Stroeve 2022). The loss of this critical habitat presents a challenge for ice-adapted Arctic species. Given the degree of specialization required to thrive in the Arctic environment, species often have nowhere else to go if rising temperatures surpass their climatic niche. Because warming in the Arctic is progressing more rapidly than in the rest of the planet, knowledge gained from Arctic populations will be instructive for understanding how populations in other regions may respond to warming in the coming decades.

Questions pertaining to evolutionary change are, in general, best addressed with consistent, long-term, individual-based data collection spanning decades (Clutton-Brock and Sheldon 2010, Stroud and Ratcliff 2025). Sustaining long-term research efforts is challenging under the best of conditions, making such studies disproportionately rare relative to their significant value in terms of the knowledge gained about ecological and evolutionary processes. Long-term studies of Arctic species are rarer still, given the additional logistical difficulties of working in the region, but they remain critical for understanding how populations respond to environmental change (Clutton-Brock and Sheldon 2010).

Polar bears (*Ursus maritimus*) are one of the best-studied Arctic species, with over 50 years of long-term monitoring in some regions, and significant amounts of shorter-term complementary research and extensive Indigenous knowledge throughout their range (Biddlecombe et al., 2025, Miller et al., 2025). Given the wealth of data available for polar bears, the species is well-suited for exploring questions and generating predictions about how populations may be evolving in response to climate warming. Polar bears are a long-lived, ice-adapted species that exhibit considerable behavioural plasticity, which may buffer some of the negative effects of warming (Refsnider and Janzen 2012, Snell-Rood 2013). However, sea ice loss in the Arctic imposes strong selection pressure on polar bears to adapt to changing conditions or risk local extinction. Here, we evaluate evidence on how polar bears have begun to respond evolutionarily, genetically, and plastically to rapid warming, and offer ways for these processes to be integrated into conservation and management strategies (Figure 1). Polar bears are a flagship species that often represent a public face for climate change impacts on species survival. Understanding the effects of rapid habitat change in polar bears can drive climate action and promote public interest in preserving ecosystem resilience in the Arctic.

There are an estimated 26,000 (range: 22,000–31,000) polar bears distributed across the Arctic (Regehr et al. 2016). These have been grouped into 20 management units (i.e., subpopulations) primarily based on geographic, ecological, and genetic differences (Figure 2; IUCN/SSC Polar Bear Specialist Group 2024). Due to forecasted declines in the global population, polar bears are listed as Vulnerable under the International Union for the Conservation of Nature (IUCN) Red List (Wiig et al. 2015), although regional conservation designations vary. Several lines of scientific evidence suggest that this species could become endangered if factors contributing to its population decline are not stopped or reversed (e.g., Durner et al. 2018, Molnár et al. 2020; Rivkin et al. 2024; Stroeve et al. 2024; Newediuk et al. 2025). One circumpolar model predicts that continued sea ice loss could lead to a 30% or higher decline in the global polar bear population by 2050 (Regehr et al. 2016). Other models predict that local extirpation may occur as certain regions of the Arctic become unable to support polar bear survival (Stroeve et al. 2024).

However, these and other models focus primarily on habitat loss and may overlook genetic contributions to adaptation and evolutionary potential in the future. Evolutionary history plays a central role in shaping species' responses to environmental change by determining the amount of genetic diversity available for adaptation, the rate at which adaptations can occur, and the level of extinction risk faced by populations (Allendorf 2017, Bernatchez et al. 2023). Population viability models that incorporate genetic data have proved to be effective for recovery efforts of several large mammal species (e.g., Mexican wolves (*Canis lupus baileyi*; Harding et al. 2022) and pumas (*Puma concolor*; Gustafson et al., 2021)), allowing for the assessment of important demographic processes such as inbreeding depression and genetic drift under various management and recovery strategies.

Polar bears depend on sea ice for basic biological needs such as hunting, movement, mating, and in some areas maternal denning (Stirling and Archibald 1977). On the sea ice, polar bears primarily feed on ringed (*Pusa hispida*) and bearded (*Erignathus barbatus*) seals but often supplement their diets with various other marine mammals (Thiemann et al. 2008). Approximately 70% of the Arctic Ocean is covered by seasonal sea ice that melts during summer, resulting in an ice-free period lasting 4-6 months (Stroeve and Notz 2018). In seasonal sea ice ecoregions, polar bears fast onshore during open-water periods, relying on their fat stores until the sea ice reforms (Lunn and Stirling 1985, Pagano et al. 2024). Although polar bears will forage on land, the net energetic gain is negligible, and bears may lose approximately one kilogram of body mass per day while onshore (Derocher and Stirling 1995, Hobson et al. 2009, Pilfold et al. 2016, Pagano et al. 2024).

There is strong evidence that climate warming has already altered the ecology of polar bears (Box 1; Derocher et al. 2004, Wiig et al. 2008, Stirling and Derocher 2012). By 2100, the ice-free period is predicted to lengthen by at least one month in many parts of the Arctic (Crawford et al. 2021), which could force fasting periods to extend beyond the physiological limits of many polar bears (Molnár et al. 2020, Archer et al. 2025). Fasting periods that exceed 117 days increase the likelihood of starvation, particularly for cubs, young adults, and pregnant or lactating females, diminishing recruitment into the population (Boonstra et al. 2020, Molnár et al. 2020). Reductions in sea ice availability are correlated with declines in subpopulation sizes in several areas, and continued sea ice loss will likely exacerbate this problem (Regehr et al. 2007, Lunn et al. 2016, Bromaghin et al. 2021). However, some subpopulations appear to be stable or increasing in size despite occupying areas with declining sea ice availability (IUCN/SSC Polar Bear Specialist Group 2024). The newly recognized Southeast Greenland subpopulation (SE; Figure 2) persists with only an average of 100 days of sea ice per year due to access to glacial ice (Laidre et al. 2022b), suggesting the potential for behavioural responses to changing sea ice conditions. Similarly, regions with high prey productivity have been shown to offset the impacts of sea ice decline, enabling bears to maintain body size, body condition, and robust levels of population recruitment (Rode et al. 2014).

Shifts in polar bear ecology have raised questions about the species' evolutionary responses to warming. To date, patterns of evolution in polar bears have not been reviewed or synthesized, despite the central importance of evolutionary responses to changing environments for the persistence of polar bear populations. The rapid pace of habitat loss in the Arctic requires conservation and management practices that are flexible, integrative, and scientifically sound (Huxel and Hastings 1999, Sgrò et al. 2011). The most effective conservation strategies integrate genetic diversity and evolutionary processes to build sustainable management policies (Cook and Sgrò 2017, DeWoody et al. 2021). Management programs that collect genetic data enable the incorporation of information about evolutionary processes into decisions related to subpopulation designation, harvest sustainability, and conservation status assessments. Additionally, local observations provide a record of long-term change, offering essential and often unique information on the effects of warming on the Arctic ecosystem. Integrating western science practices with local Indigenous knowledge can expand existing knowledge bases, improving resource allocation to maximize the effectiveness of conservation efforts (Wong et al. 2017).

This paper emerged from an international meeting on polar bear evolution in Winnipeg, Canada, in 2023. We developed a series of questions that highlight the knowledge gaps in evolutionary responses to warming for polar bears in particular and Arctic species in general. We asked:

(1) Is there evidence that polar bears are undergoing neutral and adaptive evolution in response to warming?
(2) How can we best use knowledge of evolutionary processes to guide conservation and management decisions?
(3) How can we apply Indigenous and western knowledge about polar bear evolution to meet community and research priorities?

To address these questions, we first summarize research on the effects of climate warming on six key evolutionary processes that shape genetic diversity and evolutionary change: mutation, recombination, hybridization, genetic drift, gene flow, and natural selection. We then explore the role of phenotypic plasticity in facilitating adaptive and non-adaptive responses to warming. We discuss how a better understanding of these processes can inform conservation and management decisions and identify opportunities for bridging Indigenous and western science practices for community co-management and scientific research. Lastly, we emphasize the need for a genetic management plan for polar bears to be co-developed by Indigenous and western scientists to ensure that policies are supported by both local and scientific knowledge, providing ecosystem-level benefits across the Arctic.

2. Summary of trends across 40 years of genetic research on polar bears

Evolutionary processes shape how species respond to rapid environmental change. Genetic drift, gene flow, and mutation rates determine how much genetic variation is found within populations, and shape how that variation is distributed across the range. These processes can also dampen the efficiency of natural selection when population sizes are small and genetic drift is strong (Charlesworth 2009). In turn, rapid adaptive evolutionary responses to environmental selection pressure rely on genetic variation and, less frequently, *de novo* mutations (Barrett and Schluter 2008). In this section, we review research and identify unanswered questions about how warming has shaped neutral and adaptive evolutionary processes in polar bears.

We conducted a literature search to assess the number of peer-reviewed studies that examined recent and historical evolutionary trends in polar bears. Our goal was to summarize general trends in genetic research in polar bears over the last 40 years. We searched Google Scholar using the search string: “("Polar bear*" OR "Ursus maritimus") AND (("Microsat*" OR "SNP" OR "AFLP" OR "ISSR" OR "Genetic*" OR "Genom*" OR "Transcriptome" OR "Methylome*" OR "Epigenetic") AND ("Gene flow" OR "Genetic drift" OR "Natural selection" OR "Plasticity" OR "Adaptation" OR "Mutation"))”. We identified 11,000 results and searched through the first 30 pages of output until the remaining studies were no longer relevant to polar bears. We identified 53 studies published between 1983 and 2024 that estimated genetic or evolutionary trends in polar bears, with several examining multiple processes concurrently (Figure 3; Appendix S1). Publications increased through time and were primarily focused on gene flow (42%, N = 28). Of the remaining studies, 24% (N = 16) were focused on divergence from brown bears (*U. arctos*), 18% (N = 12) on natural selection, and 16% (N = 11) on genetic drift. We did not find any published studies that estimated contemporary mutation or recombination rates in polar bears. One-third of studies (N = 26) attempted to link, directly or indirectly, the genetic or evolutionary patterns they observed to the current climate change event.

2.1 Mutation, recombination, and hybridization

Mutations are the ultimate source of genetic variation, providing the raw material for evolutionary change. The background mutation rate of polar bears has not yet been quantified and would be informative for interpreting general patterns of evolution in the species. Given that mutations are slow to accumulate in populations and occur at random with respect to function, it is most likely that rapid evolutionary responses in polar bears are driven by standing genetic variation or structural genomic variation underlying phenotypic divergence (Lin et al. 2024). Even with slow mutation rates, recombination can offer an opportunity for generating novel genotypes. Recombination generates new allelic combinations and breaks down linked regions of the genome, accelerating the fixation of beneficial alleles and allowing more efficient selection against deleterious mutations (Dumont and Paysur 2008). As a result, species with higher rates of recombination may have a greater capacity to adapt to environmental change (Dumont and Paysur 2008). The recombination rate for polar bears is currently unknown.

Introgression following hybridization events may offer one avenue for adaptation to changing environments (Barton 2001, Bashir et al. 2014). Following the divergence of polar bears from brown bears approximately 500,000 years ago, there has been extensive historical gene flow between the species, but only eight cases of contemporary hybridization (Cahill et al. 2013, 2015; Pongracz et al. 2017). A genetic survey of 819 polar bears and brown bears sampled between 1975 and 2016 did not identify any new hybrids, suggesting that the frequency of contemporary hybridization is limited by reduced hybrid survival (Miller et al. 2024). However, there may be more opportunities for gene flow of new, fitness-relevant alleles into the polar bear population if warming temperatures allow for brown bears to expand their range northward (Clark et al. 2022). Given that climate-facilitated range shifts are expected to increase hybridization rates between many species (Chunco et al. 2014), the use of genetic markers to identify and monitor hybrid zones between bear species can serve as a helpful model for genetic monitoring of other remote or long-lived species.

2.2. Genetic Drift

Standing genetic variation is shaped by genetic drift, the strength of which is measured by effective population size (N_e). N_e is the size of an idealized population (i.e., a randomly mating population of constant size with no gene flow or natural selection) that has the same level of genetic drift and inbreeding as the observed population (Wright 1931). N_e and census population size (N_c) are frequently very different, although both are critically important for conservation (Frankham et al. 2019). Whereas ecological processes within populations are governed by N_c, N_e shapes many important evolutionary processes (Waples 2022). Populations lose genetic diversity at higher rates as N_e declines. This is of conservation concern because genetic diversity contributes to a population's capacity to adapt to environmental change (Kardos et al. 2021). Additionally, the efficiency with which natural selection can act is inversely proportional to the strength of genetic drift (Lande 1976). As N_e decreases, the random process of genetic drift can overpower the deterministic process of selection, allowing deleterious alleles to accumulate and adaptive alleles to be lost to chance, limiting adaptive responses to environmental change.

In polar bears, genetic diversity has been strongly influenced by multiple population bottlenecks, population size fluctuations, and periods of introgression, beginning with their divergence from brown bears (Miller et al. 2012; Liu et al. 2014; Lan et al. 2022). Genome-wide genetic diversity is lower in polar bears than in other bear species (Clendenin et al. 2025). Slightly lower levels of genetic diversity in modern polar bear genomes relative to the genome of an ancient polar bear (110,000–130,000 years old) suggest that genetic diversity in polar bear genomes has continued to erode since their divergence from brown bears (Lan et al. 2022). The estimated long-term N_e for polar bears is 5,500 (Wilder et al. 2023), significantly lower than the global N_c of 26,000 (Regehr et al. 2016). Subpopulation estimates of N_e vary widely, ranging from the 100's to 1000's (Cronin et al. 2009, Peacock et al. 2015). Historical reductions in sea ice were correlated with declines in N_e in Greenland, likely contributing to evolved genetic and morphological differences in polar bears on the west and east coasts of the country (Westbury et al. 2023). However, recent fluctuations in N_e associated with climate warming have not yet been investigated.

Most polar bear subpopulations are connected by gene flow, which can bolster their genetic diversity. However, small subpopulations may lose genetic diversity if they are isolated. Limited dispersal opportunities have isolated the Southeast Greenland subpopulation for at least 200 years, and the subpopulation now has some of the lowest genetic variation and highest inbreeding rates of all subpopulations (Laidre et al. 2022b). Reductions in genetic diversity have also been documented in polar bears on the Svalbard Archipelago (Maduna et al. 2021) and in Norwegian Bay (Paetkau et al. 1999, Rivkin et al. 2024).

Across taxa, strong genetic drift has been linked to organismal fitness costs and extinction risk (Kardos et al. 2021, Wilder et al. 2023). Increased levels of genetic drift from low historic N_e have likely contributed to the greater proportion of harmful genetic variants estimated in polar bear genomes relative to other bear species (Clendenin et al. 2025), which may become expressed if inbreeding rates increase as connectivity declines with sea ice coverage. Genetic diversity at functional loci is also critical for resilience (Wilder et al. 2023). Polar bears have low levels of diversity at major histocompatibility complex (MHC) genes, a group of genes involved in immune function (Weber et al. 2013), which may increase their susceptibility to disease as warming increases their exposure to novel pathogens. However, genetic diversity still needs to be quantified at other functional loci to fully investigate the extinction risk of polar bears.

2.3 Gene flow

Gene flow among genetically distinct populations increases standing genetic variation by introducing novel alleles into connected populations. High dispersal capacity and few geographic barriers in the Arctic have allowed for extensive long-distance gene flow among polar bears. Genetic structure is weak over large distances in regions where bears can travel unhindered on the sea ice, such as between northeast Greenland and the Norwegian and Russian Arctic seas, and eastward to the Beaufort Sea (Paetkau et al. 1999, Cronin et al. 2006, Peacock et al. 2015, Sorokin et al. 2023). In contrast, areas with geographical land barriers, such as the Canadian Arctic Archipelago, show more population structure (Paetkau et al. 1999, Campagna et al. 2013, Peacock et al. 2015, Jensen et al. 2020, Rivkin et al. 2024). Other regions of the Arctic, such as James Bay in the southern Hudson Bay and the Norwegian Bay subpopulation are genetically structured, suggesting restricted gene flow in these areas (Crompton et al. 2008, Malenfant et al. 2016b, Rivkin et al. 2024).

Local genetic structure may partially be due to behavioural differences among polar bears (Viengkone et al. 2018). Female polar bears within the Svalbard archipelago exhibit limited dispersal and strong philopatry to denning locations, resulting in local scale genetic structuring and a unique behavioural ecotype where ~300 bears stay near shore year-round (Zeyl et al. 2009, 2010, Aars et al. 2017). A second “pelagic” ecotype migrates between Svalbard and the western Russian Arctic, exhibiting behavioural differences that have been maintained despite gene flow between the ecotypes (Paetkau et al. 1999, Mauritzen et al. 2002). Similarly, dispersal was restricted to glacial ice in several fjord systems in the Southeast Greenland subpopulation, resulting in genetic isolation from other bears in the region due to this habitat choice (Laidre et al 2022b).

Several studies have detected recent shifts in gene flow through time. Directional gene flow northward into the Canadian high Arctic and Alaska was reported over recent generations (Peacock et al. 2015), although this observation was disputed by Malenfant et al. (2016b) based on the same dataset. Genetic structure increased and genetic diversity declined over a period of two decades as sea ice availability decreased in Svalbard (Maduna et al. 2021). As sea ice loss continues to restrict opportunities for dispersal, gene flow and genetic variability are predicted to also decline, reducing the adaptive capacity of more isolated subpopulations (Maduna et al. 2021, Rivkin et al. 2024).

2.4 Natural Selection

Differential survival and reproduction drive evolution by natural selection, assuming traits and genes are sufficiently heritable across generations (Linnen and Hoekstra 2009). As a species, polar bears rapidly adapted to extreme cold during their divergence from brown bears, with evidence for selection on genes associated with coat colour, cardiac function, and lipid metabolism (Welch et al. 2014, Samaniego Castruita et al. 2020, Sun et al. 2024). However, we know little about the role of natural selection in more recent adaptation in polar bears, despite strong selection pressure exerted by warming temperatures on survival and reproduction (Box 1). Increased exposure to environmental pollutants associated with climate change in Svalbard has altered gene regulation in metabolic pathways in mothers and cubs, possibly leading to downstream energetic costs in highly exposed bears (Herst et al. 2020). Polar bears across the Canadian Arctic are adapted to their local sea ice habitats, providing a foundation for continued adaptation to changing sea ice (Rivkin et al. 2024). However, polar bears in the Western Hudson

Bay subpopulation lack additive genetic variation for lifetime reproductive success—a direct estimate of adaptive potential—suggesting a limited capacity for adaptation to the changing environment (Newediuk et al. 2025).

There are several possible targets for selection and opportunities for adaptation in polar bears. For instance, there is the potential for pathogen resistance or tolerance to evolve as warmer temperatures facilitate the rapid transmission of disease in the Arctic (Bradley et al. 2005). Zoonotic pathogens have been detected at higher frequencies than historical levels in the Canadian high Arctic, driven primarily by the lengthening summer season (Pilfold et al. 2021, Tschritter et al. 2024). Polar bears in the southern Beaufort Sea who summer on land, and thus have greater pathogen exposure risk, exhibit heightened immune function relative to bears who summer on sea ice (Whiteman et al. 2019). Bears in this region also exhibit transcription differences in genes involved in immune function (Bowen et al. 2015b, 2015a), offering a potential target for selection. Further investigation into patterns of genomic and transcriptomic upregulation of immunity genes across generations is necessary to determine if and how immune function may be evolving in polar bears.

Lengthening fasting seasons could also contribute to the evolution of metabolic rates in polar bears, increasing tolerance for longer fasting periods. Unlike other bear species that hibernate, polar bears gradually reduce their metabolic rate throughout the summer to cope with the fasting period (Whiteman et al. 2015). However, denning pregnant females will fast for almost double the length of the typical fasting period of males and non-denning females, demonstrating considerable plasticity in fasting duration and endurance (Atkinson and Ramsay 1995, Molnár et al. 2020). The lengthening fasting season may select for genes that enable bears to fast for extended periods of time by lowering metabolic processes or promoting energy conservation, as has been observed in other species (reviewed in McGaughran et al. 2021). These genes may already be under strong selection in southern subpopulations that experience fasting seasons lasting > 4 months. Transcriptomic assessments of gene expression levels across a spatial gradient in the ice-free season would help establish if metabolic rates are indeed under selection from sea ice loss.

Selection against large body sizes may be driving the evolution of smaller sizes in polar bears. Malenfant et al. (2018) demonstrated that body size is heritable in polar bears, with a narrow sense heritability (h^2) of skeletal size traits between 0.34–0.48. Persistent declines in body size were observed between 1958 and 1989 in female polar bears in the Western Hudson Bay subpopulation (Derocher and Stirling 1995, Atkinson et al. 1996) and between 1982 and 2006 in polar bears in the Southern Beaufort Sea subpopulations (Rode et al. 2010). Smaller skull sizes were also documented in Svalbard and Greenland after 1960 (Bechshøft et al. 2008, Pertoldi et al. 2009). However, there is little evidence to suggest that smaller body sizes convey a fitness advantage for polar bears, because bigger bears can survive longer fasting periods, and bigger females are typically accompanied by cubs and yearlings with larger masses and higher survival weights (Ramsay and Stirling 1988, Rode et al., 2020).

At present, the decline in body size appears to be a maladaptive response in polar bears. Body size varies with latitude, where species with larger body sizes are more likely to be found in colder climates (i.e., Bergmann's Rule; Bergman 1847). Although climate warming is hypothesized to lead to adaptive reductions in body size, there is currently little evidence for this trend across taxa (Teplitsky and Millien 2013; Radchuk et al. 2019). In line with other species, the decline in polar bear body size is unlikely to be an adaptive change. Instead, smaller sizes may reflect phenotypic plasticity as environmental conditions deteriorate or could be the result of preferential harvest of larger bears or inbreeding depression associated with declining abundances (Pertoldi et al. 2009).

2.5 Plasticity

Phenotypic plasticity, where multiple phenotypes can be produced by one genotype, is a mechanism that allows individuals to respond to very rapid environmental change by altering their behavioural, phenological, or physiological traits (Whitman and Agrawal 2009). In contrast to evolutionary change, plasticity provides an avenue for acclimation to changing environments within the lifetime of an individual (Boutin and Lane 2014). Behavioural and reproductive plasticity are common in polar bears. The Southeast Greenland subpopulation has circumvented reduced sea ice coverage by switching to hunting seals on glacial ice (Laidre et al. 2022b), and females in the Barents Sea subpopulation exhibit annual differences in den site fidelity depending on their ability to access preferred denning areas on sea ice (Zeyl et al. 2010). Similarly, in years with longer ice-free periods, females in Baffin Bay in poorer body condition produced smaller litters (Laidre et al. 2020b). Plasticity in litter sizes may serve as a bet-hedging strategy, allowing females to survive lean periods when caring for too many cubs would reduce their body condition below critical levels (Burggren and Mendez-Sanchez 2023). Females also demonstrate phenological plasticity in the timing of den emergence, fasting longer and emerging later when in better body condition (Rode et al. 2018).

However, although polar bears in the Western Hudson Bay subpopulation can modify their foraging strategies and energy expenditure onshore (Pagano et al. 2024), they do not demonstrate physiological mechanisms to cope with starvation, suggesting a limited capacity for physiological plasticity (Whiteman et al. 2018). These studies suggest that for polar bears, behavioural or phenological plasticity, and not physiological plasticity, are the most common responses to warming. The lack of physiological plasticity to warming is perhaps unsurprising in a mammal that has evolved to thrive in extreme cold. Mammals that have demonstrated physiological responses to increased temperatures (e.g., adaptive heterothermy), have primarily evolved in warm climates (Fuller et al. 2016). The behavioral and phenological responses to warming that have been observed in polar bears are likely a typical response for other Arctic mammals.

3. Applying evolutionary and genetic data to polar bear conservation and management

Identifying the effects of environmental change on contemporary evolutionary processes and genetic variation can improve the effectiveness of conservation and management strategies and policies. Below, we outline how the increasing availability of genetic data for polar bears can facilitate the inclusion of evolutionary processes into management decisions to guide emerging priorities in polar bear conservation and management. We also identify opportunities for combining Indigenous and western knowledge to facilitate locally supported research and management. Bridging these fields for polar bears is instructive for other species experiencing environmental changes caused by continued climate change.

3.1 Subpopulation monitoring

Capture-handling programs provide some of the best data for estimating evolution in the field. During capture-handling programs, free-ranging polar bears are chemically immobilized and tagged, and standardized morphometric measurements and biological samples are collected (e.g. skin, blood, hair, fat, claw shavings; Laidre et al. 2022a, Biddlecombe et al. 2025)). Several long-term capture-handling programs exist for polar bears in the Western Hudson Bay, Southern Beaufort Sea, East Greenland, and Barents Sea subpopulations. The monitoring program in the Western Hudson Bay subpopulation has generated a robust pedigree with tissue samples collected annually since the 1980s (Malenfant et al. 2016a). This level of data collection makes it possible to estimate phenotypic and genetic change between generations, providing a unique opportunity to measure the effects of climate warming in real-time. For instance, this pedigree was leveraged to assess the heritability of size-related morphological traits (Malenfant et al. 2018), document the lifetime reproductive success of males (Richardson et al. 2020), and quantify the adaptive potential of the subpopulation (Newediuk et al. 2025). Continuation of long-term monitoring programs can directly address outstanding questions and assess the evolutionary potential of the species, providing significant benefit to conservation programs aimed at preserving polar bears in the warming Arctic.

Genetic surveying through remote biopsy darting is becoming increasingly common as a tool for monitoring subpopulations. Remote biopsy darting collects a small amount of skin, hair and adipose tissue from the bear (Pagano et al. 2014), which can then be used to genotype individuals to assess survival and movement, estimate subpopulation sex ratios and abundance, and quantify contaminant exposure (McKinney et al. 2017, Laidre et al. 2018a, Bromaghin et al. 2021, Dunham et al. 2024). Epigenetic aging from biopsy samples can be used to estimate age structure and collect health data on populations with minimal animal handling. A well-validated polar bear epigenetic clock successfully aged independent samples to within ±2 years of an individual's chronological age (Newediuk et al. 2025). When used with known-age samples, the epigenetic clock can detect epigenetic age acceleration associated with stress from sea ice loss (Newediuk et al. 2025). Estimating unknown ages of individuals using tissue samples will also improve subpopulation growth models for harvest sustainability and strengthen estimates of subpopulation viability under continued habitat loss. Genetic data collected from biopsy darting can also enable the quantification of genetic variation across the population, providing insights into variation at functional loci that may be useful when assessing extinction risk in isolated subpopulations.

Collaboration with local communities opens additional opportunities to fill data gaps. Specimen samples are regularly submitted across jurisdictions from hunter-harvest or from polar bears killed in defence of life or property, and these have been used in many genetic studies (e.g., Paetkau et al. 1999; Malenfant et al. 2018; Rivkin et al. 2024). These samples provide high-quality DNA from bears over continuous time periods and from remote areas where research may be conducted less frequently or not at all. Communities that harvest from traditional hunting territories can also generate data for closely related bears, providing a potential genomic approach to monitoring subpopulation abundance and inbreeding rates.

Genetic data may also be obtained non-invasively from hair snags (Langwieder et al. 2023), tracks left in the snow (Hellström et al. 2023), or fecal samples (Hayward et al. 2022). These more community-inclusive methods can expand sampling coverage across much of the Arctic where capture or aerial-based methods are locally unsupported. Despite recent technological advances, the quality of DNA obtained from these methods may still be too low to allow for more in-depth sequencing efforts (Andrews et al. 2021), making it challenging to implement genomic or transcriptomic approaches to samples collected from these methods. While non-invasive sequencing methods will likely become more sensitive in the future, careful consideration of these approaches is currently needed to mitigate the potential biases and return on capital invested in DNA collection methodology.

Regardless of collection method, it will be important for standardization among datasets to be considered. Most genetic studies on polar bears rely on microsatellites or a small number of single nucleotides polymorphisms (Appendix S1). These marker types are inexpensive to generate and can be powerful tools to detect signals of population structure and local adaptation when candidate loci are known (Allendorf et al. 2010). However, a recent shift toward sequencing polar bear whole genomes (e.g., Laidre et al. 2022b) opens the possibility of detecting more nuanced signals of recent evolutionary change, such as demographic declines, genomic erosion, or genome-wide signatures adaptation. Ensuring that these sequences are available in public repositories will facilitate cross-compatibility and collaboration among researchers.

3.2 Designation of management units

Management unit designations for polar bears are determined using ecological, political, and genetic information. In 2005, low genetic differentiation across large geographic areas prompted the IUCN Species Survival Commission Polar Bear Specialist Group to adopt the term "population" to encompass all polar bears in the Arctic and the term "subpopulation" to identify management units (Aars et al. 2006, Laidre et al. 2022a). Although subpopulation boundaries are rarely updated, changing sea ice conditions may require that boundaries be reevaluated more regularly if certain habitats become unsuitable for polar bear occupation or if movement across subpopulation boundaries increases. Genetic differentiation between subpopulations can be regularly assessed using data collected from biopsy darting, offering a less costly alternative for tracking dispersal than aerial surveys. As dispersal patterns change, updating demographic models to include genetic data would ensure that subpopulation delineations align with expected changes in genetic divergence (Palsbøll et al. 2006). Lastly, range-wide genome scans could ensure that boundaries accurately capture genetic variation among subpopulations, creating a foundation for conservation strategies to be designed that maximize adaptive potential in the entire population (Kardos et al. 2021).

3.3 Harvest sustainability

Polar bears experienced a period of prolonged overharvesting in the early-mid 1900s, primarily due to unregulated sport hunting. In 1973, the Agreement on the Conservation of Polar Bears banned commercial hunting, limiting hunting primarily to subsistence-based harvests based on traditional rights (Dowsley, 2009, Vongraven et al. 2022). Since the signing of the Agreement, an annual average of 800 bears are harvested globally, accounting for ~4.6% of bears from each subpopulation (Vongraven et al. 2022). This level is considered sustainable for a male-biased harvest. In most jurisdictions, co-management frameworks (i.e., cooperative management by the regional and local governments, wildlife boards, and Indigenous authorities) are in place to determine harvest levels and allocate that harvest to communities (Polar Bear Range States 2015). Many jurisdictions require that hunters document their harvests and submit biological samples. This is a valuable source of genetic data and can provide an early indication of immigration and emigration trends in abundance and shifts in distribution that can inform harvest management.

Maintaining sustainable harvest relies on accurate estimates of subpopulation abundance and distribution. To maintain stable subpopulations, breeding females and cubs have historically been protected from harvesting, while a larger proportion of males are harvested (Lee and Taylor 1994, Derocher et al. 1997). A sex-selective harvest may have downstream evolutionary consequences for the evolution of polar bears (e.g., body size evolution) and population viability. A recent shift to a 1:1 male-female harvest system in Nunavut, whose jurisdiction overlaps with 12 subpopulations (Government of Nunavut 2019), will also have implications for population dynamics. Incorporating genetics-based assessments of current N_e and temporal changes in inbreeding coefficients across jurisdictions into harvest measurements would provide robust estimates of growth trajectories in each region, ensuring harvests continue at sustainable levels. While specific thresholds will need to be set in consultation with managers and communities, subpopulations where N_e is vastly different from N_c (e.g., $N_e/N_c < 0.1$; Frankham et al. 2014) or those at high risk of inbreeding depression (e.g., large proportions of the genome in long runs of homozygosity (RoH); Kyriazis et al. 2025) may be more vulnerable to harvesting, requiring additional considerations before quotas are set in place.

3.4 Conservation status assessments

Management strategies that promote large, well-connected populations provide the best chance for species persistence in a changing environment (Frankham et al. 2019). Accurate estimations of population sizes and trends are foundational for monitoring and developing appropriate conservation interventions if necessary. The conservation designation of polar bears differs across regions, although most agree that polar bears are threatened by habitat loss and anthropogenic activities. The global census population size of polar bears is uncertain due to their wide distribution and the challenging field conditions that make it difficult to accurately estimate population trends (Wiig et al. 2015).

Combined with comprehensive subpopulation sampling, genomic data can provide more accurate estimates of recent changes in population dynamics and bolster inferences from census subpopulation estimates. Contemporary N_e estimators may capture very recent population fluctuations well before declines in genetic variation are detected and can provide critical information when census estimates are unavailable (Santiago et al. 2025). Subpopulations that fall below the recommended levels of N_e necessary to preserve long-term adaptive potential ($N_e < 1000$) and those with elevated inbreeding risk ($N_e < 100$) may require increased conservation efforts (Frankham et al. 2014). Given their long lifespan and slow generation time, the precise relationship between N_e and N_c for polar bears will need to be better quantified to establish reasonable guidelines for the inclusion of N_e into conservation decisions. This verification would be possible for the WH subpopulation where abundance is tracked annually. Continued monitoring of this and other well-studied subpopulations will also provide insights into the effects of inbreeding on population viability. Genomics-informed simulations of subpopulation growth trajectories under future climate change scenarios can also help predict the potential impacts of changes in gene flow and inbreeding in declining populations (Rivkin et al. 2024).

3.5 Integrating Indigenous and western knowledge for co-management

The focus of this review has been from the perspective of using western science and technology to synthesize knowledge and gaps in this field. However, we recognize that northern communities and Indigenous peoples have cultivated a deep knowledge about polar bears and the Arctic environment. Polar bears are spiritually and symbolically significant to many northern communities and deeply tied to Inuit identity and well-being (Voorhees et al. 2014, Miller et al. 2025). Harvests support local economies and traditional practices by providing food, tools, clothes, and art (Dowsley 2010). Centuries of sharing the land, depending on polar bears as a food source, and encountering and observing bears throughout the year have created layers of generational knowledge about polar bears (Born 2011, Voorhees et al. 2014, Wong and Murphy 2016, Rode et al. 2021b). The genomic and evolution-based methods we discuss have the potential to add knowledge to the co-management framework but should not supersede or replace it. Sharing and respecting the priorities, knowledge, and interpretations from Indigenous and western science perspectives should be considered throughout the research and management processes.

Community observations provide important records of behavioral plasticity, such as polar bears switching prey sources or maternity denning locations, and document long-term changes in polar bear health and habitat use. Such long-term monitoring data is essential for placing observed evolutionary responses into the context of ecological and environmental change. Co-development of research projects, collecting tissues through harvest sampling (Peacock et al. 2012), and community-based field projects (De Groot et al. 2013, Langwieder et al. 2023) are potential avenues for sharing knowledge. Joint research projects have been used to assess polar bear subpopulation abundances (York et al. 2016), impacts of climate change on polar bears and the land (Laidre et al. 2018b, Rode et al. 2021b), and polar bear demographics and body condition (Braund et al. 2022). Interpreting genetic patterns within the context of community knowledge of historical and current patterns of polar bear biology, as well as environmental change in the Arctic, can facilitate the development of regionally appropriate management plans that are locally supported within communities. The effectiveness of conservation efforts for flagship species such as polar bears can be maximized using genetic data generated from co-designed and co-led research projects (Buschmann 2022).

As part of co-management efforts, it is important to acknowledge that Indigenous and western science opinions may differ, for example, in subpopulation management goals, suitable research methods, and the resiliency of polar bears to warming (Wong et al. 2017, Tomaselli et al. 2022, Miller et al. 2025). Across the Arctic, northern communities have documented reductions in sea ice coverage in recent decades (Dowsley and Wenzel 2008, Voorhees et al 2014, Laidre et al. 2018b). However, communities have also observed stable or increasing polar bear abundances over time, often in contrast to observations from mark-recapture studies (York et al. 2016). Topics where perspectives differ can serve as valuable indicators of parts of the system where change is occurring or where additional investigation is needed (Frid et al. 2023), as well as identify important distinctions in ways of knowing and worldview. Historical and relational impediments should be acknowledged and addressed to advance a mutually beneficial understanding of polar bear ecology and evolution.

4. Development of a genetic management plan for polar bears

We recommend developing a genetic management plan for polar bears as a crucial component of future conservation and management decisions. Although genetic diversity is beginning to be incorporated into some management plans (e.g., 2025 proposed Management Plan for the Polar Bear (*Ursus maritimus*) in Canada; https://www.canada.ca/en/environment-climate-change/services/species-risk-public-registry/management-plans/polar-bear-proposed-2025.html), there does not yet exist a dedicated plan to maintain the genetic integrity of polar bears globally. Genetic management plans incorporate explicit goals for maintaining viable levels of genetic diversity and limiting inbreeding depression to minimize the extinction risk of vulnerable populations (Frankham et al. 2019). Implementing a genetic management plan for polar bears would align the field with the United Nations Convention on Biological Diversity Kunming–Montreal Global Biodiversity Framework (GBF). This framework commits signing parties to protect genetic diversity and adaptive potential of vulnerable species using three key indicators: the proportion of meta-populations with $N_e > 500$; the proportion of genetically unique populations; and the number of populations that are being monitored using DNA-based methods (CBD/COP/DEC/15/4 2022).

Genetic management plans exist for a small number of northern mammal species, including wood Bison (*Bison bison athabascae*; McFarlane et al. 2005) and Boreal Caribou (*Rangifer tarandus caribou*; Environment Canada 2012). While each plan prioritizes conserving genetic diversity across populations to maximize adaptive potential, the specific goals included in each plan differ. A genetic management plan for polar bears could focus on several core criteria, including the 1) establishment of guidelines for incorporating genetic markers and monitoring tools into existing conservation and management frameworks, 2) protection of existing global genetic variation and adaptive potential by promoting connectivity and preventing overharvest of genetically unique subpopulations, and 3) integration of evolutionary, ecological, and climate data into population viability projections to assess the vulnerability of subpopulations to continued warming (Figure 1). The specific population genetic metrics and thresholds selected to monitor genetic integrity and subpopulation health will depend on input from multiple groups and should be realistically supported within communities. This plan could serve as a template for genetic management plans to be developed for other Arctic species.

Several outstanding questions in the field remain that, if addressed, would aid in the implementation of a genetic management plan for polar bears. These include:

(1) How are current levels of standing genetic variation, inbreeding, and gene flow between subpopulations predicted to change with continued sea ice loss?

(2) Are there traits and genes under selection from warming that may facilitate adaptations to a warmer Arctic?

(3) What is the contribution of evolutionary change versus plasticity to polar bear survival?

(4) What are the relative contributions of harvest pressure and natural selection on trait evolution?

(5) How well does individual-level genetic variation predict subpopulation-level health and fitness?

(6) Can genomics-informed population viability models be integrated with habitat distribution and energetics models to build holistic predictions of subpopulation viabilities?

(7) Do genetic estimates of demographic history align with community observations of historical and contemporary demographic patterns?

Addressing these outstanding questions will reveal avenues for conservation and management policies that facilitate adaptation and promote survival in the changing Arctic environment. The long-term monitoring programs and extensive local ecological knowledge for many subpopulations have set the stage for the development of a comprehensive conservation genetics plan for polar bears. Bridging these fields with genetic data will allow conservation and management programs to be guided by leading-edge scientific and community knowledge, advancing polar bear conservation to provide ecosystem-level benefits throughout the Arctic.

5. Broader implications

We have reviewed evidence for evolutionary, genetic, and plastic responses to warming in polar bears. As expected, given their large range, long lifespan, and ecological variability, evolutionary responses to warming varied, and the consequences of climate change will clearly be complex. Some subpopulations appear threatened with respect to their capacity to evolve, whereas others seem to be doing well. However, while genetic diversity varies significantly among subpopulations, currently available data indicate that adaptive responses to warming may be limited. Conservation plans that do not rely on adaptive responses are likely to be the most effective for polar bears. As shipping traffic increases through the Arctic (Dawson et al. 2018), conservation plans that maintain connectivity among genetically diverse subpopulations may be most effective for buffering N_e against the effects of warming. Polar bears are apex predators that shape community structure by providing substantial amounts of carrion for Arctic scavengers (Gamblin et al. 2026). Thus, the benefits of evolutionarily informed conservation strategies that promote polar bear persistence extend to other Arctic species.

Our results are also instructive for other ecosystems. Much of the world is expected to warm to the same degree as the Arctic by the end of the century, with a projected increase of 2-4°C above the historical average (Fan et al. 2020, Rantanen et al. 2022). Identifying general trends in evolutionary knowledge about polar bears can provide an early warning system to predict how other species may respond to future warming. Polar bears, and other Arctic species, will be among the first to face the ‘adapt or die’ paradigm, where extreme habitat loss threatens the persistence of the entire species unless they can behaviourally or genetically adapt in time to survive. Polar bears are highly mobile, long-lived mammals with long generation times and low N_e which require carefully designed conservation strategies to maximize their resilience to habitat change and anthropogenic influences. We have provided a roadmap for how such strategies can incorporate evolutionary information to inform decision-making, which could serve as a model for other species with similar life histories. By conserving genetic diversity within vulnerable subpopulations, we aim to maintain the potential for polar bears to persist under future environmental change. Protections put in place for polar bears will benefit other Arctic species that also occupy this vulnerable ecosystem and will help generate public awareness for climate action. Ultimately, the most effective conservation strategies must include reducing carbon emissions to mitigate the level of warming experienced by the planet.

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Author Contributions

LRR conceived the study, led the road-mapping discussions, and wrote and revised the original draft. APW, LN, KK, JA, and AL wrote the original draft, and all authors contributed to revisions.

Conflict of Interest

The authors declare no conflict of interest.

Boxes

Box 1. The effects of climate warming on polar bear ecology

Polar bears depend on the sea ice to meet many of their biological needs (Stirling and Archibald 1977). Fifty years of monitoring in the Western Hudson Bay subpopulation by Environment and Climate Change Canada has identified clear effects of sea ice availability on survival (Regehr et al. 2007, McGeachy et al. 2024, Biddlecombe et al. 2025) that has led to declines in abundance in the subpopulation (Lunn et al. 2016). Reductions in body condition, increased stress responses, and altered reproductive timing have also been associated with sea ice loss in the subpopulation (Sciullo et al. 2016, Mislan et al. 2016, Newediuk et al. 2025). In other regions of the Arctic, sea ice availability has been correlated with reduced cub recruitment, decreased body condition, and smaller body sizes (Rode et al. 2010, Obbard et al. 2016, Tartu et al. 2017, Florko et al. 2021). However, these trends are not universal. The Kane Basin and Chukchi Sea subpopulations, whose ranges overlap the regions of the Arctic Ocean that are covered by persistent, multiyear sea ice, have exhibited increased abundances and stable or improving body condition (Laidre et al. 2020a, Rode et al. 2021a). These trends may be temporary as multiyear sea ice is rapidly being converted into seasonal sea ice, and further sea ice declines are expected in the region (Stroeve and Notz 2018, Kwok 2018).

Diminishing sea ice has also altered patterns of movement, habitat use, and health of polar bears. Satellite telemetry data demonstrate that the frequency of long- and short-distance swims has increased due to longer open-water periods (Pagano et al. 2012, 2021, Pilfold et al. 2017, Lone et al. 2018). Because swimming has a higher energetic cost than walking for polar bears, increased swimming frequency may shorten the maximum fasting time that bears can tolerate (Griffen 2018). Unstable ice conditions have led females to den on land more frequently than on ice, which could reduce reproductive success and cub survival (Laidre et al. 2020a). Sea ice loss also contributes to disease and contaminant exposure in polar bears (Atwood et al. 2017, Routti et al. 2019). Range expansions of host species have increased the prevalence and transmission rates of infectious diseases and parasites in the Arctic (Fagre et al. 2015, Pilfold et al. 2021, Biddlecombe et al. 2024). Increased pathogen exposure has led to heightened immune function in polar bears (Whiteman et al. 2019), which is energetically costly and may inhibit the fasting ability of smaller or sickly bears. Lastly, the frequency of polar bear-human conflicts is escalating with warming (Towns et al. 2009, Heemskerk et al. 2020). Attacks on humans are more likely to occur when bears are nutritionally stressed from extended periods on land (Wilder et al. 2017). These encounters pose threats to both bears and humans, and harm public perception of polar bears, resulting in reduced support for conservation programs in the North (Schmidt and Clark 2018, Schmidt et al. 2022).

Figures

Figure 1. Pathway toward integrating evolutionary genetics research into polar bear conservation and management decisions. Bridging knowledge sources by assessing patterns of recent evolution in polar bears and combining Indigenous and western knowledge can inform decisions on subpopulation monitoring, management unit designations, harvest sustainability, and conservation assessments. These decisions would benefit from the development of a genetic management plan to bridge these fields and bring polar bear conservation into line with global biodiversity frameworks. Such a framework can be extended beyond polar bears to preserve ecosystem-level biodiversity in the Arctic. Icons were created with BioRender.com (King 2026).

Figure 2. 2024 subpopulation boundaries for polar bears designated by the International Union for Conservation of Nature Species Survival Commission Polar Bear Specialist Group (https://www.iucn-pbsg.org/population-status/).

Figure 3. Summary of evolutionary genetics research studies published for polar bears. Bars have been color coded based on the type of process they represent.

Figure 1/Graphical Abstract.

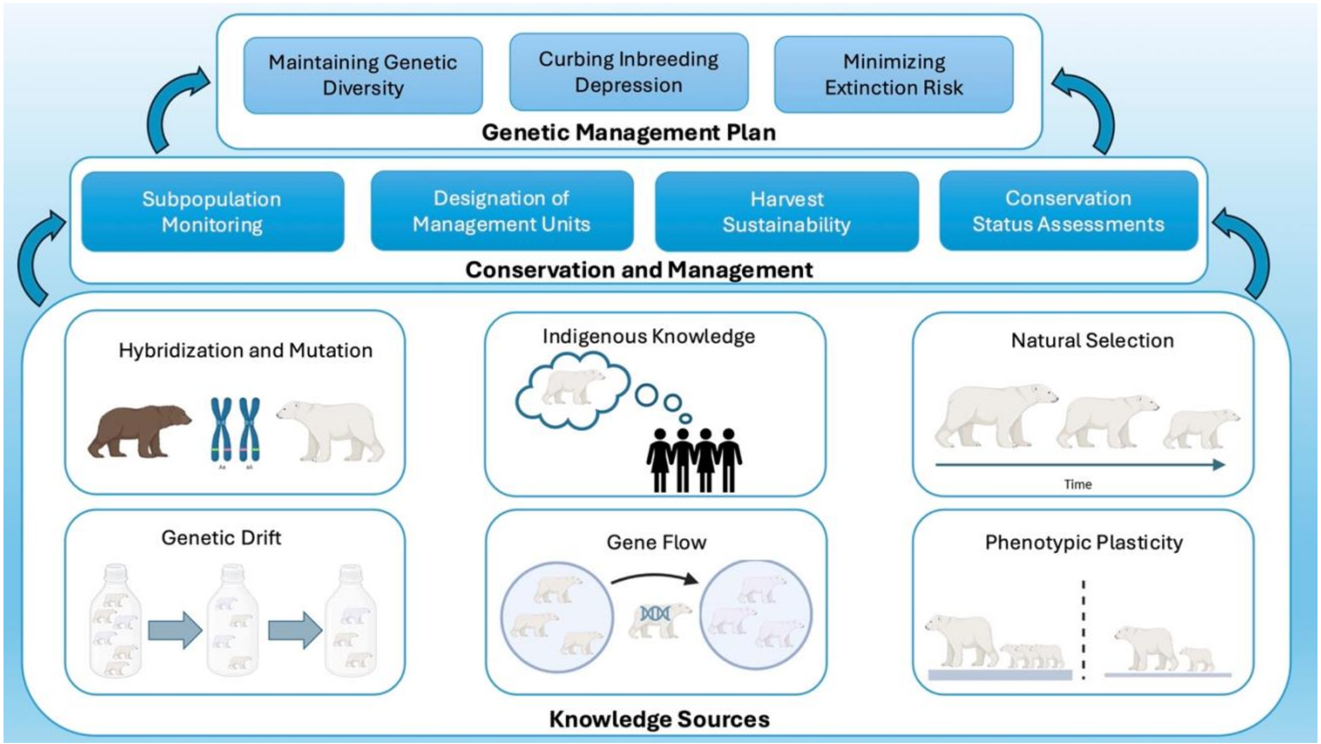


Figure 2.

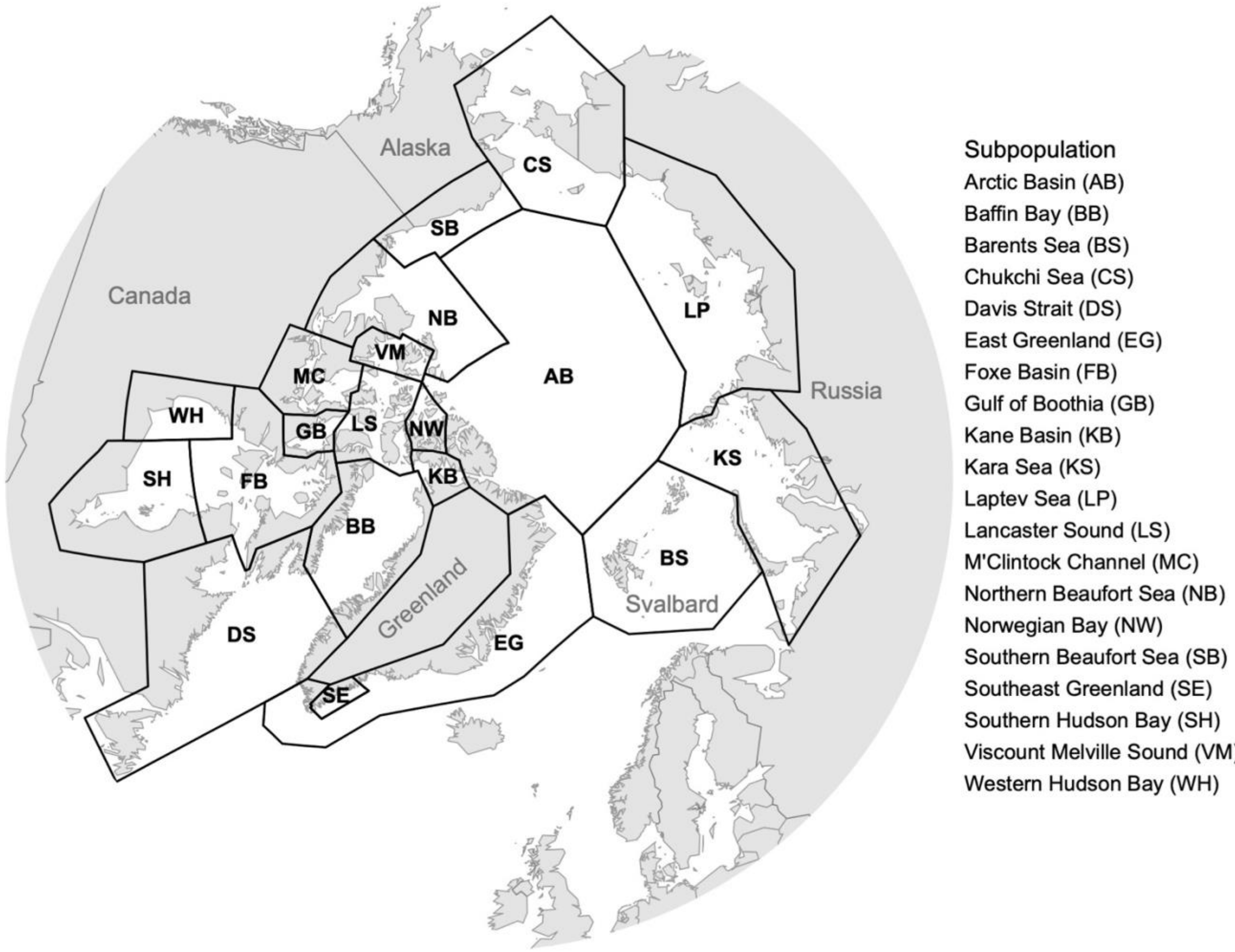
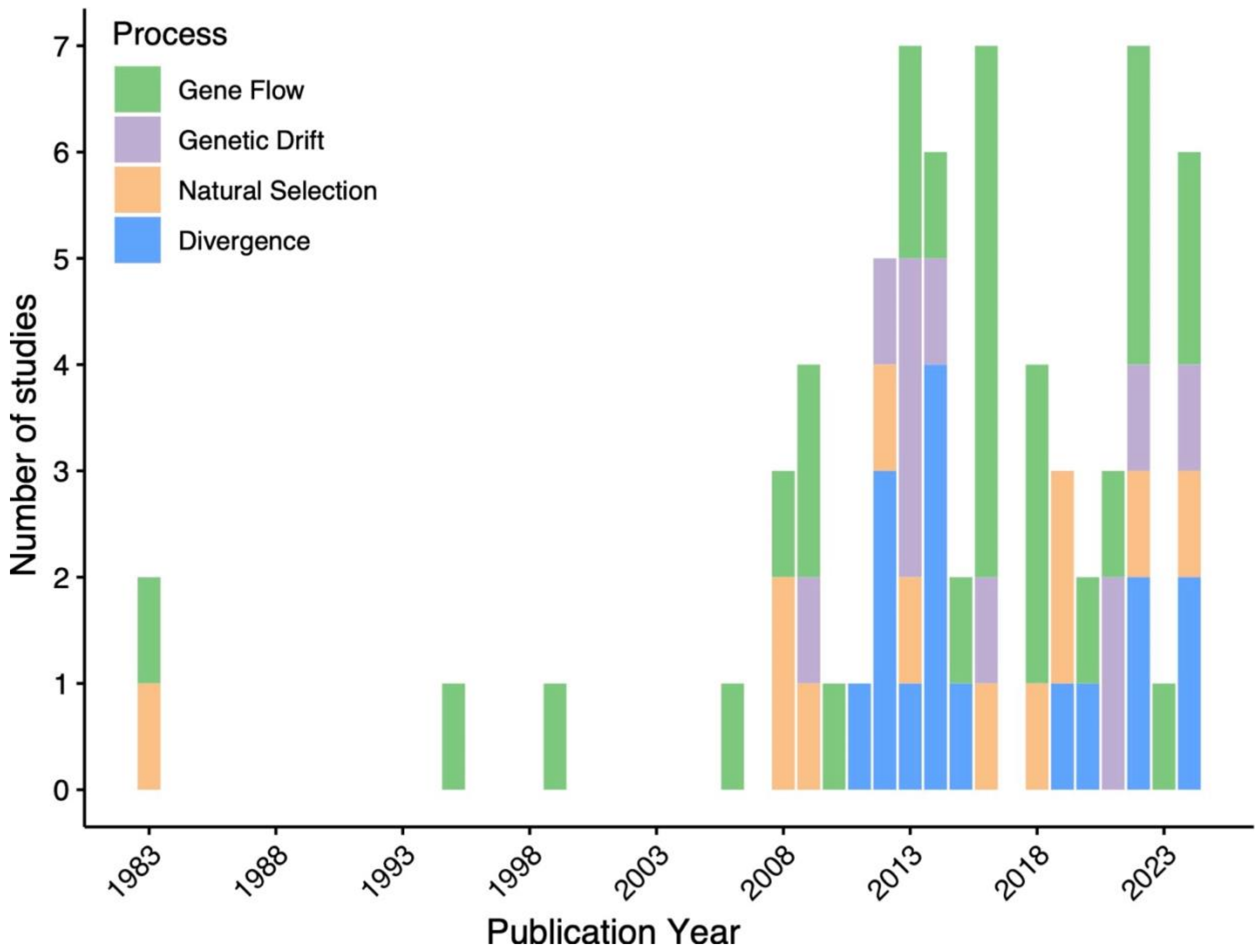

Alaska
Canada
Russia
Greenland
Svalbard
CS
SB
NB
VM
MC
WH
GB
LS
NW
KB
SH
FB
BB
AB
LP
KS
BS
DS
EG
SE
Subpopulation
Arctic Basin (AB)
Baffin Bay (BB)
Barents Sea (BS)
Chukchi Sea (CS)
Davis Strait (DS)
East Greenland (EG)
Foxe Basin (FB)
Gulf of Boothia (GB)
Kane Basin (KB)
Kara Sea (KS)
Laptev Sea (LP)
Lancaster Sound (LS)
M'Clintock Channel (MC)
Northern Beaufort Sea (NB)
Norwegian Bay (NW)
Southern Beaufort Sea (SB)
Southeast Greenland (SE)
Southern Hudson Bay (SH)
Viscount Melville Sound (VM)
Western Hudson Bay (WH)

Figure 3.


Process
Gene Flow
Genetic Drift
Natural Selection
Divergence
Number of studies
0
1
2
3
4
5
6
7
1983
1988
1993
1998
2003
2008
2013
2018
2023
Publication Year

Literature cited

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