Concepts and Synthesis

Climate-linked evolution and genetics in a warming Arctic

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Abstract

The extent to which species might be able to evolutionarily respond to rapid environmental change relies strongly on their genetic diversity. Accurate knowledge of both patterns of evolution and genetic variation across the species range is important for determining appropriate conservation and management strategies. The Arctic is the fastest-warming region on the planet, with the rest of the world expected to reach temperature increases currently experienced in the Arctic by the turn of the century. Here, we review and synthesize research on evolutionary processes in polar bears. Polar bears are perhaps the best-studied species living at the forefront of climate-mediated habitat change, so patterns of evolutionary change in this species should be instructive for understanding the consequences of warming that are expected to occur elsewhere in the near future. Global warming has led to significant sea ice loss that has altered patterns of gene flow across the Arctic and contributed to declines in genetic variation in some, but not all, polar bear populations. Natural selection due to warming may be driving the evolution of smaller body sizes in polar bears. However, evidence of adaptive change remains limited, despite considerable behavioural plasticity in the species in response to changing sea ice conditions. Following our review, we suggest ways that identifying the effects of warming on evolution and genetic variation in polar bears could improve strategies for locally supported conservation and management decisions. Our results point to variable responses to warming that we can expect to occur across different genetically distinct populations in the same species and the general complexity of predicting the consequences of warming for wide-ranging species.

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 species surpass their thermal thresholds, they must adapt to new conditions, respond plastically, disperse to more suitable habitats, or face local extinction (Berg et al. 2010, Morris 2014). 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 one genotype produces multiple phenotypes, can offer an opportunity to persist in sub-optimal habitats without requiring slow evolutionary responses. Ultimately, the ability of populations to cope with rapid environmental change will shape ecosystem structure and resiliency to further changes.

The evolutionary consequences of warming should be most advanced, and thus particularly apparent, in areas where the climate is changing rapidly. The Arctic is currently the fastest-warming region on Earth, warming nearly four times faster than the rest of the planet (Rantanen et al., 2022). Historically, much of the Arctic Ocean was covered by ice year-round, however some climate models predict that the Arctic Ocean could experience completely ice-free days within 10 years (Docquier and Koenigk 2021, Shen et al. 2023). The Arctic is at the frontline of climate change making studies on Arctic populations instructive for how populations in other regions may respond to warming in the coming decades.

Questions pertaining to evolutionary change are often best addressed with consistent long-term individual-based data collection across decades (Clutton-Brock and Sheldon 2010).

Sustaining such long-term research efforts is difficult even under the best of conditions, making such studies disproportionately rare relative to their value in terms of the knowledge gained about ecological and evolutionary processes. Long-term studies of northern 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 populations, and significant shorter-term complementary research and extensive Indigenous knowledge throughout their range (Biddlecombe et al. 2024a). Given the wealth of data available for polar bears, the species is ideal for exploring questions and generating predictions about how populations may respond to warming. Here, we compiled knowledge of evolutionary responses to warming in polar bears and proposed actions for conservation and management (Figure 1).

There are an estimated 23,315 (range: 15,972–31,212) polar bears distributed across the circumpolar Arctic (Hamilton and Derocher 2019). For management purposes, these have been grouped into 20 subpopulations primarily based on geographic, ecological, and genetic differences among regions (Figure 2; Obbard et al. 2010, Laidre et al. 2022b). 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. The consensus across oversight bodies is that the species could become endangered if factors contributing to its population decline are not stopped or reversed (Durner et al. 2018). Continued sea ice loss is predicted to lead to a ~30% decline in the global polar bear population by 2050 (Regehr et al. 2016), an estimate that may be conservative. 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 change, and may be missing genetic contributions to adaptation and evolutionary potential in the future. Given the central role that evolution and genetics play in shaping species' responses to environmental change, both should be considered when forecasting population viability (Allendorf 2017, Bernatchez et al. 2023).

Polar bears depend on sea ice for basic biological needs such as hunting, movement, mating, and some maternal denning sites (Stirling and Archibald 1977). On the sea ice, polar bears feed primarily on ringed (*Pusa hispida*) and bearded (*Erignathus barbatus*) seals but will 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, leading to 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). Polar bears have been observed to forage onshore; however, the energetic gain is significantly less than consuming lipid-rich prey on the sea ice and bears may lose up to 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 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 times to extend beyond the physiological limits of many polar bears (Molnár et al. 2020, Archer et al. 2025). Fasting times 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). In several areas, reductions in sea ice availability are correlated with declines in population sizes, 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 population size (IUCN/SSC Polar Bear Specialist Group 2024). The newly recognized Southeast Greenland subpopulation (SE; Figure 2) persists with only 100 days of sea ice per year due to access to glacial ice (Laidre et al. 2022b), suggesting the potential for behavioural adaptation to changing sea ice conditions. Similarly, regions with high prey productivity have been shown to offset the impacts of sea ice decline, allowing bears to maintain body size, body condition, and high levels of recruitment (Rode et al. 2014).

Shifts in polar bear ecology have raised questions about the evolutionary responses of the species to warming. To date, patterns of evolution in polar bears have not been synthesized, despite the central importance of evolutionary responses to species survival. The rapid pace of habitat loss in the Arctic requires management and conservation 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 and effective management policies (Cook and Sgrò 2017, DeWoody et al. 2021). Subpopulation monitoring programs that collect genetic data allow for evolutionary mechanisms to be incorporated into management decisions on subpopulation designation, harvest sustainability, and conservation status assessments. Additionally, local observations provide a record of long-term change, essential and often unique information on the effects of climate change. Weaving Western science practices with local Indigenous knowledge together can expand existing knowledge bases, improving resource allocation to maximize the effectiveness of conservation efforts (Wong et al. 2017).

This synthesis paper emerged from the first international meeting on polar bear genetics in Winnipeg, Canada, in 2023. We developed a series of questions highlighting the knowledge gaps on evolutionary responses of polar bears to warming. 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 review the evidence for the effects of global warming on four key evolutionary processes that shape genetic diversity in polar bears: mutation and hybridization rates, 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 for polar bears and identify opportunities for weaving Indigenous and Western science for community co-management and scientific research. Lastly, we describe 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. Patterns of recent evolutionary processes in 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, for example when population sizes are small and genetic drift is strong. In turn, adaptive evolutionary responses to environmental selection pressures rely on genetic variation and, less frequently, *de novo* mutations. In this section, we review research on and identify unanswered questions about how warming has shaped neutral and adaptive evolutionary processes in polar bears.

We conducted a literature search to estimate the number of studies that examined recent and historical evolutionary trends in polar bears. Rather than a comprehensive review of the literature, our goal was to summarize general trends in publishing 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 published studies that estimated genetic or evolutionary trends in polar bears, with several examining multiple processes at a time (Figure 3; Table 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 rates in polar bears. A 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 and hybridization

Mutations are the ultimate source of genetic variation in all species and thus provide the raw material for evolutionary change. 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 through structural genomic variation underlying phenotypic divergence (Lin et al. 2024).

However, hybridization presents an alternative scenario where the species could gain novel neutral and adaptive variants (Barton 2001, Bashir et al. 2014). New alleles introduced by hybridization may be exposed to selection in different environments and are thus potentially valuable for local adaption to changing environments (Seehausen 2004, Mallet 2007). Since 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 beyond the eight already identified, suggesting that the frequency of contemporary hybridization is limited by reduced hybrid survival (Miller et al. 2024). As warming temperatures allow for brown bears to expand their range northward (Rockwell et al. 2008, Rode et al. 2021b), there may be more opportunities for gene flow of new, fitness-relevant alleles into the polar bear population. With climate-facilitated hybridization expected to be a major force in both adaptations and extinctions in the future, using genetic markers to identify and monitor hybrid zones will be an important consideration for genetic management of species (Chunco et al. 2014)

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 (e.g., randomly mating with no gene flow or natural selection) that has the same level of genetic drift 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. As N_e decreases, the random process of genetic drift can overpower the deterministic process of selection, deleterious alleles can accumulate, and adaptive alleles can 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 (i.e., hybridization), beginning with their divergence from brown bears (Miller et al. 2012; Liu et al. 2014; Lan et al. 2022). 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 eroded since their divergence from brown bears (Lan et al. 2022). The long-term N_e for polar bears is 5,500 (Wilder et al. 2023), significantly lower than the global N_c of 26,000 (Wiig et al. 2015). Within-population 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 global 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. For instance, the southeast Greenland subpopulation has been isolated for more than 200 years and has some of the lowest genetic variation and highest inbreeding 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, levels of genetic diversity have been linked to organismal fitness and extinction risk (Kardos et al. 2021, Wilder et al. 2023). Genetic diversity at functional loci may be especially critical for resilience. Polar bears have low levels of diversity at major histocompatibility complex (MHC) genes, a group of genes critically involved in immune function, which may make polar bears more susceptible to disease, putting them at risk as warming increases their exposure to novel pathogens (Weber et al. 2013). Low MHC diversity is linked to susceptibility to emerging pathogens across species and may be a conservation priority when developing genetic management plans for some species (Acevedo-Whitehouse and Cunningham 2006, Siddle et al. 2007). However, genetic diversity still needs to be quantified at other functional loci fully investigate the adaptive potential and extinction risk of polar bears.

2.3 Gene flow

Gene flow among genetically distinct populations increases standing genetic variation by introducing novel alleles. High dispersal capacity and relatively 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 eastward through the Norwegian and Russian Arctic Seas, and further east to the Beaufort Sea (Paetkau et al. 1999, Cronin et al. 2006, Peacock et al. 2015, Sorokin et al. 2023). In contrast, areas with geographic 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). Additionally, smaller regions of the Arctic, such as James Bay in the southern Hudson Bay and the Norwegian Bay subpopulation are genetically unique, suggesting restricted gene flow in these areas (Crompton et al. 2008, Malenfant et al. 2016b, Rivkin et al. 2024).

Even with long-distance gene flow, significant genetic structuring exists at a local scale, likely due to behavioural differences among bears. Female polar bears within the Svalbard archipelago exhibited limited dispersal and strong philopatry to denning location, resulting in local scale genetic structuring and a unique behavioural ecotype where ~300 bears stayed 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). Lastly, the Southeast Greenland subpopulation consists of a few hundred bears living on glacial ice in several fjord systems that are genetically isolated from other bears in the region due to this habitat choice.

Several studies have detected recent shifts in gene flow through time. Directional gene flow northward into the high Canadian Arctic and American Arctic was reported over the 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 continue to decline in the area in future decades, potentially reducing the capacity of more isolated subpopulations to adapt (Maduna et al. 2021, Rivkin et al. 2024).

2.4 Natural Selection

Differential survival and reproduction drive evolution by natural selection, but for species to evolve, there must be heritable variation underlying traits and genes (Linnen and Hoekstra 2009). Warming temperatures place considerable selection pressure on polar bear survival and reproduction rates (Box 1), however, we know little about the role of natural selection on recent adaptations in polar bears. The divergence from brown bears was marked by rapid adaptation of genes involved in coat colour, cardiac function, and lipid metabolism (Welch et al. 2014, Samaniego Castruita et al. 2020, Sun et al. 2024). In a more contemporary timeframe, increased exposure to environmental contaminants 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 were adapted to their local sea ice ecoregion (multiyear versus seasonal sea ice; Amstrup et al. 2007), providing a foundation for continued adaptation to changing sea ice (Rivkin et al. 2024). However, polar bears in Western Hudson Bay lack additive genetic variation for lifetime reproductive success—a direct estimate of adaptive potential—suggesting a limited capacity for adaptation to the changing environment in this subpopulation (Newediuk et al. 2025).

There are other 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 high Canadian 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 potential targets 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 to allow for greater fasting periods. Unlike other bear species that hibernate, polar bears gradually reduce their metabolic rate throughout the summer to cope with the summer fasting period (Whiteman et al. 2015). However, denning 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 (Atkinson and Ramsay 1995, Molnár et al. 2020). Hypothetically, polar bears that can reduce their metabolic rate can survive longer periods of fasting. The lengthening fasting season may select for genes that enable bears to fast for extended periods by lowering metabolic processes or promoting energy conservation, as has been observed in other systems (reviewed in McGaughran et al. 2021). These genes could already be under strong selection in southern subpopulations that are already experiencing >4-month fasting seasons. Comparative whole genome sequencing across a spatial gradient in the ice-free season or through time would help establish if metabolic rates are indeed under selection from sea ice loss.

Body size is another trait that appears to have sufficient heritable variation in polar bears and may be an important factor in adapting to a changing environment (Malenfant et al. 2018). Some evidence suggests that natural selection against large body sizes may be leading to the evolution of smaller polar bears. In general, bigger bears can survive longer fasting periods, and bigger females may be accompanied by cubs and yearlings with larger masses and higher survival weights (Ramsay and Stirling 1988, Rode et al., 2020). However, persistent declines in body size were observed between 1958 and 1989 in female polar bears in western Hudson Bay (Derocher and Stirling 1995, Atkinson et al. 1996) and between 1982 and 2006 in polar bears in the southern Beaufort Sea (Rode et al. 2010). Smaller skull sizes were also documented in Svalbard and Greenland after 1960 (Bechshøft et al. 2008, Pertoldi et al. 2009). Larger body sizes may be selected against due to greater energy requirements in poor ice years and the preferential harvest of larger bears. The decline in body size may also reflect phenotypic plasticity as environmental conditions become poorer or may be a signal of inbreeding depression associated with declining population sizes (Pertoldi et al. 2009), suggesting that the effects of natural selection act in concert with other evolutionary processes to affect trait evolution. There is little evidence for adaptive body size reductions in response to warming in other systems (Teplitsky and Millien 2013); thus, identifying whether size changes in polar bears are adaptive can be of broader use for establishing general trends of climate change on species evolution.

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 physiological or behavioral traits (Whitman and Agrawal 2009). In contrast to evolutionary change, plasticity provides an avenue for acclimation to changing environments within the lifetime of an organism (Boutin and Lane 2014). Behavioural and reproductive plasticity is 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 Beaufort and Chukchi Seas 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 serves as a bet-hedging strategy to allow females to survive lean periods when caring for too many cubs would reduce their body condition below critical levels (Burggren and Mendez-Sanchez 2023). However, while polar bears in Western Hudson Bay can modify their foraging strategies and energy expenditure onshore (Pagano et al. 2024), they do not demonstrate physiological mechanisms to cope with starvation (Whiteman et al. 2018). These studies suggest that while polar bears exhibit considerable behavioural plasticity when faced with poor conditions, physiological plasticity may be limited.

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. The increasing availability of genetic data for polar bears should facilitate the inclusion of evolutionary processes into conservation and management policies. Below, we outline how this data can be incorporated into management strategies to guide emerging priorities in polar bear conservation and management. We also identify opportunities for weaving Indigenous and Western science to build an integrated understanding to facilitate locally supported research and management. Bridging these fields in polar bears can serve as a case study for other species experiencing environmental changes caused by continued warming.

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 taken (e.g. skin, blood, hair, fat, claw; Laidre et al. 2022a). Several long-term capture-handling programs exist for polar bears in the Western Hudson Bay, Southern Beaufort Sea, and Barents Sea subpopulations. The monitoring program in the Western Hudson Bay has generated a robust pedigree with tissue samples collected each year dating back to 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), aspects of the polar bear mating system that are likely to influence selection and gene flow (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.

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 identify individuals to assess survival and movement, estimate population sex ratios and abundance, and quantify contaminant exposure (McKinney et al. 2017, Laidre et al. 2018, Bromaghin et al. 2021, Dunham et al. 2024). Epigenetic aging from biopsy samples has emerged as a potential tool for estimating age structure and collecting health data on populations with minimal animal handling. A recently developed polar bear epigenetic clock uses the DNA methylation patterns from known-age tissue samples to estimate age in unknown-age samples within ±2 years of the chronological age (Newediuk et al. 2025). When used to estimate age in other known-age samples, the epigenetic clock can also detect epigenetic age acceleration, the presence of DNA methylation patterns typical of older bears. Epigenetic age acceleration can be influenced by factors such as stress and diet (Oblak et al. 2021), individual health, body condition, or contaminants (Beissinger and Westphal 1998, Larison et al. 2021), and is associated with all-cause mortality (Marioni et al. 2015). The development of these epigenetic markers for polar will assist with population age structure estimations, improve population growth models for harvest sustainability, and strengthen estimates of population viability under continued habitat loss.

Collaboration with local communities opens additional opportunities to fill data gaps. Specimen samples are regularly collected from hunter-harvest or polar bears killed in defence of life or property across many jurisdictions and have been used in many existing genetic studies (e.g., Paetkau et al. 1999; Malenfant et al. 2018; Rivkin et al. 2024, and many others). These samples provide high-quality DNA from bears over continuous time periods, particularly in remote areas where research may be conducted infrequently 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 population abundance and inbreeding rates from community collaborations.

Genetic data may also be obtained non-invasively, for example from hair snags (Langwieder et al. 2023), tracks left in the snow (Hellström et al. 2023), or fecal samples

(Hayward et al. 2022). Despite recent technological advances, the quality of DNA obtained from these methods may 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 remote locations. Thus, careful consideration of the potential biases and return on capital invested is required to assess the efficacy of these approaches.

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 many subpopulations are admixed, others are genetically isolated and contain unique genetic variants (Malenfant et al. 2020, Rivkin et al. 2024). Changing sea ice conditions may require that subpopulation boundaries be reevaluated if certain habitats become unsuitable for polar bear occupation or if movement across current subpopulation boundaries increases. If range contractions due to sea ice loss become more common (Laidre et al. 2018), polar bears will disperse across subpopulation boundaries or become isolated. Additionally, unique genetic variation may be found outside of traditional subpopulation boundaries, thus the management unit assessments would benefit from range-wide genome scans to ensure that boundaries accurately capture genetic variation among polar bears.

3.3 Harvest sustainability

Polar bears experienced a period of prolonged overharvesting in the early-mid 1900s. In 1973, the Agreement on the Conservation of Polar Bears banned commercial hunting, limiting hunting primarily to subsistence-based harvests based on traditional rights (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). Many jurisdictions require that hunters document their harvests, which is a valuable source of genetic data and can provide an early indication of immigration and emigration that inform harvest management interpretations of trends in abundance and shifts in distribution. Harvest management groups frequently involve Indigenous co-management (i.e., cooperative management by the regional and local governments, wildlife boards, and Indigenous authorities), and quotas differ between jurisdictions depending on the number of bears found in each region (Polar Bear Range States 2015).

Maintaining sustainable harvest relies on accurate estimates of subpopulation abundance and distribution. To promote stable population growth, 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 population trajectories in each region, ensuring harvests continue to operate at sustainable levels.

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. The conservation designation of polar bears differs across regions, although most agree that polar bears are threatened by habitat loss and anthropogenic development. The global census population size of polar bears is uncertain due to their wide distribution and challenging field conditions that make it difficult to accurately estimate population trends (Wiig et al. 2015). Combined with comprehensive population sampling, genomic data can provide accurate estimates of recent population trajectories and bolster inferences from census population estimates. Contemporary N_e estimators may capture very recent population fluctuations well before changes in genetic variation are detected and can provide critical information when census estimates are unavailable. Additionally, genomics-informed simulations of population trajectories under future climate change scenarios can help predict the potential impacts of changes in gene flow and inbreeding in declining populations (Rivkin et al. 2024). Lastly, continued monitoring of more well-studied subpopulations will provide insights into the effects of inbreeding on population viability if population declines continue in response to degrading environmental conditions.

3.5 Weaving Indigenous and Western knowledge for co-management

Sharing and respecting the priorities, knowledge, and interpretations from Indigenous and Western science perspectives should be considered throughout the research and management processes. Polar bears hold significant cultural and economic value for Indigenous communities across the Arctic. Polar bears are spiritually and symbolically important to many northern communities and are fundamentally 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). Through generations of sharing the land, depending on polar bears as a food source, and encountering and observing bears throughout the year, northern Indigenous communities have cultivated a deep knowledge about polar bears and the Arctic environment (Born 2011, Voorhees et al. 2014, Wong and Murphy 2016, Rode et al. 2021b).

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 data. 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. 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.

As part of co-management efforts, it is important to recognize that Indigenous and Western science findings may differ, for example, in subpopulation management approaches, appropriate research methods, and the resiliency of polar bears to warming (Dowsley and Wenzel 2008, Dowsley 2009, York et al. 2016, Wong et al. 2017, Tomaselli et al. 2022). Topics where perspectives differ can serve as valuable indicators to 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. 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 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 species 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, 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 policies, 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 measure the vulnerability of subpopulations to continued warming

(Figure 1). Regardless of which criteria are included, preserving the genetic integrity of polar bears will help achieve management and conservation goals across the Arctic.

There are several outstanding questions in the field that, if addressed, will aid in the implementation of a genetic management plan for polar bears. These include, but are not limited to:

(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) How well does individual-level genetic variation predict population-level health and fitness?
(5) Can genomics-informed population viability models be integrated with habitat distribution and energetics models to build holistic predictions of subpopulation viabilities?
(6) 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 of many subpopulations have set the stage for the development of a comprehensive conservation genetics program 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 (Figure 1).

5. Broader implications

The Arctic is a sentinel ecosystem for climate change. By the end of the century, most of the planet will have warmed to the same degree that the Arctic has already warmed (i.e., a 2-4 °C increase above the historical average; Fan et al. 2020, Rantanen et al. 2022). Advancing 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. As expected, given their large range and ecological variability, evolutionary responses to warming varied, and the likely consequences of climate change will clearly be complex. Some populations appear threatened with respect to their capacity to evolve, whereas others seem to be doing well. However, while genetic diversity varies significantly among populations there is currently little evidence for adaptive change in response to warming. The hope of the Kunming–Montreal GBF is that by conserving genetic diversity, we can maintain the capacity for populations to adapt to future environmental change. Our synthesis calls for more work exploring adaptive change to warming, but currently available data points to the possibility that adaptive responses to warming are difficult. 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 global warming on polar bear ecology

Polar bears depend on the sea ice to meet many of their basic 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. 2024a) 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, decreasing 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 regions of the Arctic Ocean that are covered by persistent, multiyear sea ice, have exhibited increased population sizes 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 endure (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. 2022a). 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. 2024b). 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 the magnitude of 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

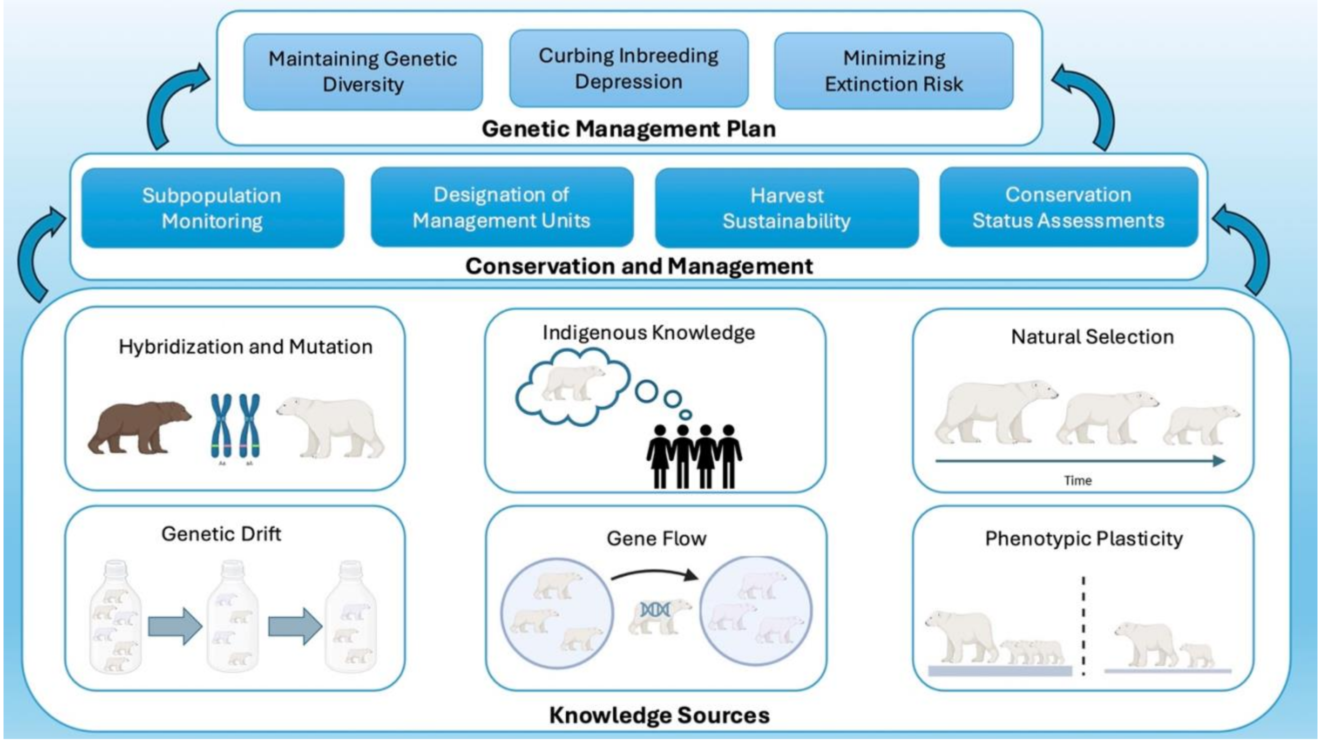

Figure 1/Graphical Abstract: Pathway toward integrating evolutionary genetics research into polar bear conservation and management. Bridging knowledge sources by assessing patterns of recent evolution in polar bears and weaving Indigenous and Western knowledge can inform conservation and management decisions 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.

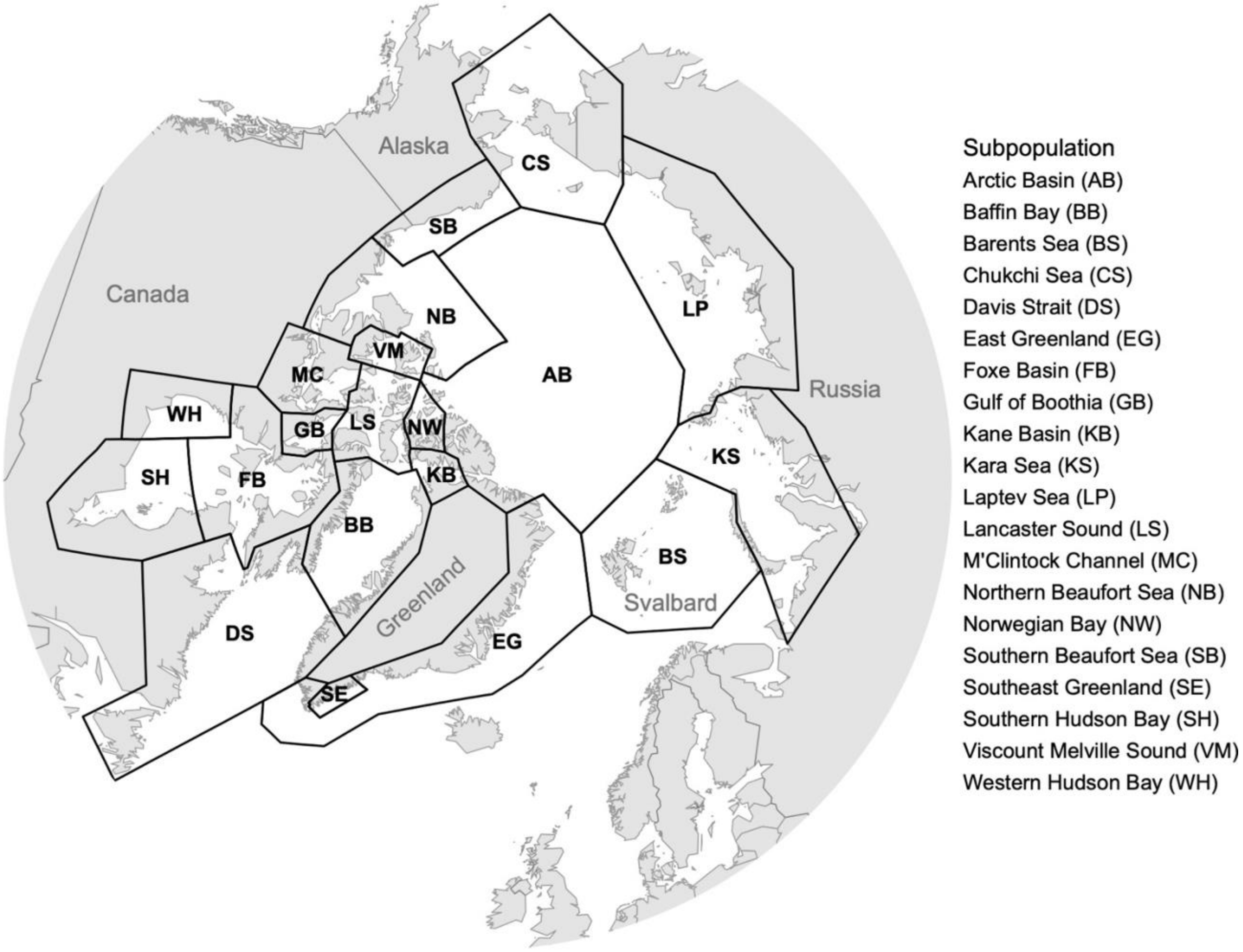

Figure 2. 2024 subpopulation boundaries for polar bears designated by the IUCN Species Survival Commission Polar Bear Specialist Group (https://www.iucn-pbsg.org/population-status/).

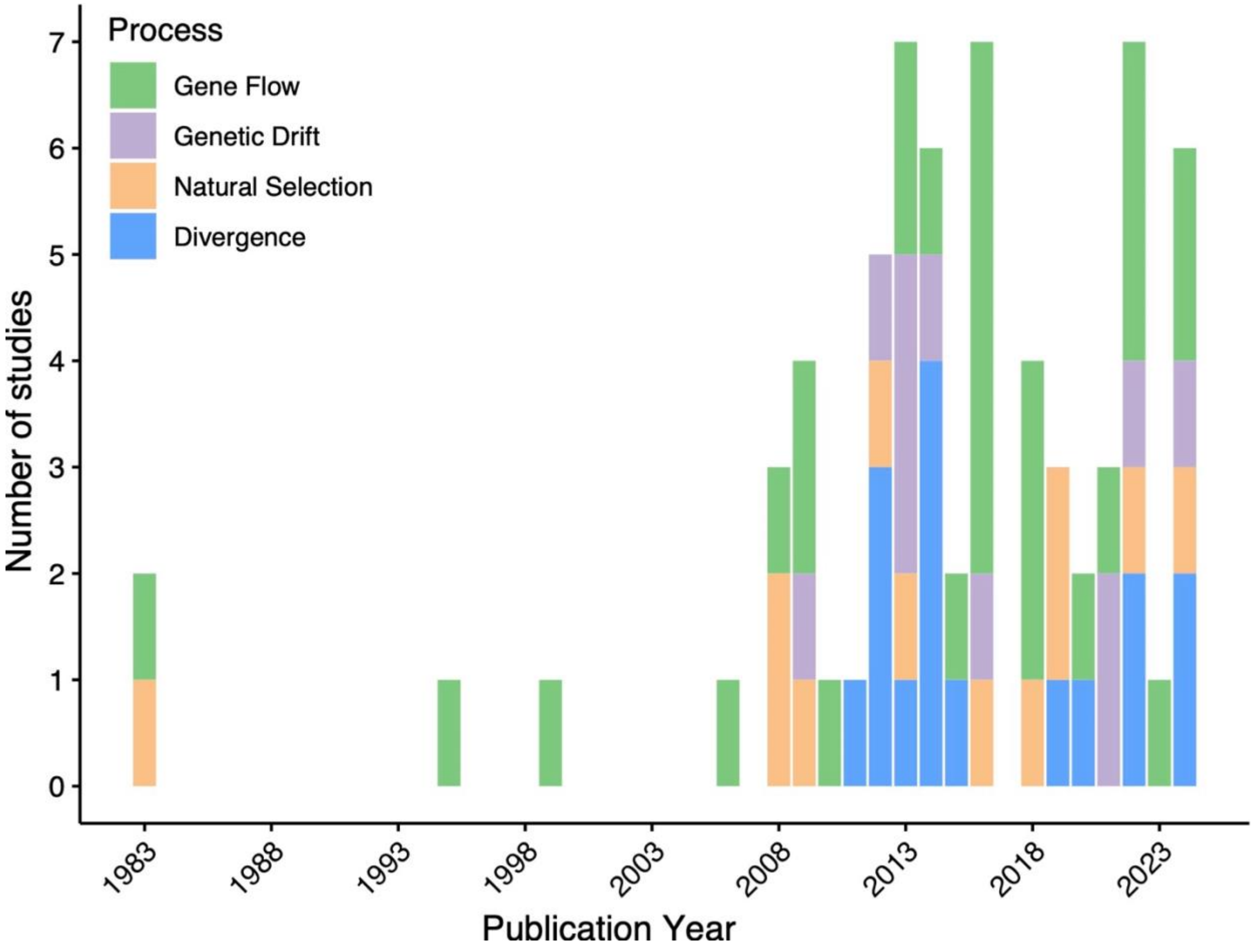

Figure 3. Summary of evolutionary genetics research studies published for polar bears. Bars have been color coded based on the type of process they represent.

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