

INVITED REVIEW OPEN ACCESS

Advancing Marine Mammal Conservation Through Omics Tools and Integration of Indigenous Ecological Knowledge

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Received: 19 January 2026 | **Revised:** 10 September 2026 | **Accepted:** 17 September 2026

Keywords: cetaceans | eDNA | evolutionary genomics | indigenous peoples | pinnipeds | science communication

ABSTRACT

Conservation of biodiversity is a global priority as human-driven pressures continue to intensify and alter ecosystems worldwide. Marine mammals are vulnerable species, facing numerous escalating anthropogenic threats. Here, we evaluate how, as omics technologies become more accessible and affordable, established and emerging tools are advancing effective marine mammal research and conservation management. Assessments of genetic diversity, adaptive capacity, demographic history and local adaptation provide vital insights into how marine mammal populations respond to environmental change across contemporary and evolutionary timescales. Whole-genome sequencing, functional genomics, epigenetics and multi-omic integration enable deeper insights into the molecular basis of complex fitness-related traits. Approaches like epigenetics, ancient DNA and environmental DNA offer new opportunities to study cryptic, rare, or historical populations and evolutionary processes. Yet, effective marine mammal conservation management cannot rely exclusively on increased availability of omics tools and data. We emphasize the need and obligation for genuine collaboration and integration of Indigenous perspectives with marine mammal genomics approaches to foster ethical, inclusive and effective conservation, and suggest best practices for this. Additionally, we highlight that translating omics data into practical conservation outcomes remains challenging, requiring clear communication, collaboration and integration into management. Using marine mammal genomics to address conservation challenges in a changing world requires innovation, partnership and the integration of diverse knowledge systems, such as Indigenous Ecological Knowledge.

1 | The Positionality Statement

The authors primarily originate from the Global North, with most having undertaken academic training in colonized nations

within high-income countries, and only a few identifying as Indigenous. We recognize that collaboration with Indigenous custodians is both culturally and morally essential and critical for effective conservation outcomes. This paper highlights the

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value of integrating Indigenous Ecological Knowledge (IEK) into marine mammal genomics, showing how such partnerships strengthen cultural heritage and biodiversity protection. We present a practical workflow to guide researchers in building respectful, equitable collaborations. The research community must commit to the active involvement of Indigenous Peoples at all stages, to move beyond tokenism and dismantle Western science only perspectives. We must work toward mutually respectful research grounded in shared stewardship. The coauthors represent the LGBTQIA+ community and span early-career students to senior researchers.

2 | Introduction

The conservation of biodiversity is critical as intensifying anthropogenic pressures drive ecosystem change worldwide. Species across terrestrial, freshwater and marine ecosystems are experiencing declines, with varying susceptibility to demographic collapse and genetic erosion (von der Heyden et al. 2025). In recent decades, molecular tools have emerged as fundamental resources for conservation biology, offering novel insights into the evolutionary history, population dynamics and adaptive potential of taxa (Frankham et al. 2004; Allendorf et al. 2010). Among these, omics technologies encompassing genomics, transcriptomics, metagenomics, proteomics and metabolomics have significantly advanced the capacity to inform and refine conservation strategies for wildlife, particularly for cryptic species, delineating population boundaries, tracing illegal wildlife trade, and for elusive species where conventional ecological monitoring is challenging (Barceló et al. 2021; Smart et al. 2021; Carroll et al. 2021; Reeves et al. 2022; Kardos et al. 2023; von der Heyden et al. 2025).

Marine mammals represent diverse taxa that occupy critical ecological niches and serve as sentinels of ecosystem change through their roles as predators, grazers, nutrient cyclers and ecosystem engineers (Hazen et al. 2019). Across the diverse coastlines, land- and seascapes they inhabit, many marine mammal species also hold profound cultural, spiritual and social significance for Indigenous communities who have long engaged with marine mammals in multiple ways, including through mutualistic hunting relationships, subsistence use as food and recognition as totemic or ancestral species (Reeves et al. 2023; Breton-Honeyman et al. 2021; Bayliss and Hutton 2017). As a result, marine mammals, alongside other species and facets of the environment, often hold profound cultural, spiritual and social significance. Indigenous Peoples' long-standing, place-based relationships with marine mammals have generated detailed observational knowledge of these species (Salomon et al. 2015; Marsh et al. 2022; Reeves et al. 2023), and Indigenous Ecological Knowledge (IEK) is particularly well-suited to reveal differing cultures among marine mammal species. However, many marine mammal species are experiencing severe population declines due to anthropogenic pressures, including climate change, habitat degradation, pollution and overexploitation (Plön et al. 2024). As IEK uses knowledge of the past to inform the present and the future, the application and interpretation of knowledge accumulated before the shifting baselines of the last few centuries. Over the past two decades, there has been a growing recognition of the value of omics tools in marine mammal

conservation, which can also be of benefit to Indigenous communities due to their cultural practices and identities and livelihoods (Nelms et al. 2021; van Oppen and Coleman 2022; Cammen et al. 2016). These omics approaches have been used to assess genetic diversity, population structure and inbreeding; to evaluate population and species viability; and to guide evidence-based management such as the design of marine protected areas and the management of coastal development (Barceló et al. 2021; Reeves et al. 2022; Kardos et al. 2023). The field has also incorporated more recent advances in genomic methodologies, including whole-genome sequencing (WGS), environmental DNA (eDNA), museomics and epigenomics, which have enabled detailed investigations into adaptive divergence, local adaptation and evolutionary resilience (Kardos et al. 2023; Foote et al. 2016; Nigenda-Morales et al. 2023).

Although genomics has become a powerful tool in conservation, its application to marine mammals presents distinct challenges. As highly mobile, often elusive and long-lived non-model species, marine mammals typically lack well-developed genomic resources. Despite these constraints, recent advances in sequencing and assembly technologies have markedly improved genome availability, with chromosome-level reference genomes now available for 31 of 94 cetacean species, 3 of 37 pinniped species and 2 of 5 sirenians (no chromosome-level reference genome for polar bear or sea otter to date) (Supple and Shapiro 2018; Alvarez-Costes et al. 2025; Morin et al. 2025). These resources facilitate deeper insights into our understanding of marine mammal genetic health and evolutionary potential, while also offering new opportunities to inform effective management of vulnerable populations (Funk et al. 2019; Morin et al. 2024). Fostering collaboration with Indigenous communities is crucial for inclusive and impactful genomic research in marine mammal conservation, recognizing that marine mammals represent kin (often elders) and spiritual entities, and provide resources for creating both functional and treasured items. Data derived from treasured species are often considered as sacred as the species themselves, reflecting many Indigenous Peoples' view of DNA as demonstrating ancestral links to the environment (Collier-Robinson et al. 2019; Mead 2010; Kukutai and Black 2024; Ramos et al. 2025). Due to this connection, marine mammal genomics is of interest to many Indigenous Peoples, and time is of the essence, as knowledge passed down through generations risks being lost over time, particularly amid the face of the fundamental ecosystem changes of the Anthropocene. Indigenous Ecological Knowledge has long enriched ecological research and its conservation applications for marine mammals (Huntington 1998; Hovelsrud et al. 2008; Reeves et al. 2023; Humphries et al. 2025; McGrath et al. 2025); however, engaging and actively involving Indigenous communities requires more than goodwill. The marine mammal genomics field would therefore benefit from a detailed, practical 'how-to' framework to ensure that collaborations are genuine, culturally safe and mutually beneficial.

The emerging role of genomics in marine mammal conservation has been acknowledged by ongoing workshops at the Society for Marine Mammal (SMM) biennial meetings. Cammen et al. (2016) showed the transformative potential of next-generation sequencing and omic technologies in marine

mammal conservation following the 2013 and 2015 meetings. Subsequent SMM Marine Mammal Genomics workshops in 2019 and 2024 highlighted breakthroughs in reference genome construction, functional genomics, and long-read and single-cell sequencing that enable critical insights into adaptive capacity, genetic load, resilience and the cultural dimensions of marine mammal genomics. Here, we synthesize recent advances in marine mammal omics, underlining their direct applications in conservation science and species management. Drawing on collective experiences upholding the *mana* (inherent prestige and value, Māori concept) of our Indigenous community partners, we provide a framework for working alongside Indigenous communities. By exploring cutting-edge technologies, knowledge integration and emerging methods, this review aims to highlight omics tools and evolving fields, charting a course forward for omics-driven strategies that will safeguard marine mammals into the future, along with their unique cultures, through culturally grounded conservation.

3 | Working With Indigenous Communities and Knowledge Systems in Marine Mammal Conservation Genomics

In this section, we discuss the ethical and cultural obligations marine mammal geneticists have when working with Indigenous communities. We also summarize resources on how to engage respectfully, including when integrating IEK, to support both biodiversity conservation and the communities we work alongside (United Nations 1992; Shaw et al. 2024). We acknowledge with humility that most of the author team has undertaken academic training in formerly colonizing or colonized, high-income nations, and only a few identify as Indigenous. However, we echo the sentiments of other scientists working alongside Indigenous Peoples, that it is critically important to share our learnings to reduce the collective impact our scientific community has on Indigenous communities (Kater 2022).

3.1 | Colonization and Underrepresentation of Indigenous Perspectives in Marine Mammal and Genomic Sciences

Colonization has had severe negative impacts on Indigenous People through death, disease, displacement from their ancestral lands, and further intergenerational trauma resulting from loss of language and culture, and disruption of environmental knowledge transmission, including about marine mammals. Ongoing consequences, including structural racism and scientism, have further sidelined Indigenous People from research (Ani 2016; McAllister et al. 2019; Asai 2020; Tseng et al. 2020; Naepi et al. 2021). Furthermore, commercial hunting of marine mammals, alongside political pressure and legislation (e.g., laws protecting marine mammals) due to the 1970s environmental movement, have restricted many Indigenous practices including direct subsistence takes of marine mammals, and the relationships with, and observations of, living and dead animals required to sustain IEK (Eichstaedt 1998; Kitossa 2000; Marsh et al. 2022). As IEK often relies on active practices to sustain transmission (Hikuroa 2017; Molnár and Babai 2021), this has further prevented intergenerational knowledge transfer

(Haggan and Neis 2007; Fernández-Llamazares et al. 2021; Marsh et al. 2022).

3.2 | Indigenous Ecological Knowledge in Marine Mammal Conservation Science

Surviving IEK is not only part of Indigenous Peoples' cultural identity but provides powerful insights to conservation of the co-existence with biodiversity (Marsh et al. 2022), based on observations and experiences inextricably linked to the environment. While much existing scientific research highlights nature's contributions to humans, people's reciprocal contributions to nature are rarely acknowledged (Ojeda et al. 2022). In contrast, IEK systems are based on long-term, relational observations within ecosystems, often highlighting similarities across taxa and other facets of the environment, whereas science focusses on differences. This means IEK can offer insights that are temporally and spatially extensive, often complementing Western science to enhance conservation and management. For example, Iñupiat communities in Alaska co-manage bowhead whale harvests through the Alaska Eskimo Whaling Commission and the International Whaling Commission, combining local knowledge with scientific monitoring to ensure sustainable take and population health (Huntington 1989; Huntington et al. 2021), similar to the Inuit-led management of beluga whale (*Delphinapterus leucas*) populations in Canada (Huntington 1998; Breton-Honeyman et al. 2021). Elsewhere in the Northern Hemisphere, organizations such as the North Atlantic Marine Mammal Commission (NAMMCO) acknowledge the rights and needs of Indigenous and local coastal communities to sustainably harvest marine mammals based on the best available scientific evidence and user knowledge, ensuring Indigenous and conservation priorities. In the Southern Hemisphere, in regions that include Australia, First Nation rangers work collaboratively with Indigenous People to identify core use zones by dugongs (*Dugong dugon*) for management (Bayliss and Hutton 2017). These examples show that Indigenous-led monitoring and governance to improve conservation outcomes for marine mammals while strengthening intergenerational knowledge transmission, cultural sovereignty and adaptive responses to ecological change; however, additional work is needed to inform best practices for integrating IEK into formal management policies and stock assessments.

3.3 | Ways to Address the Imbalance: Advice for Working With Indigenous Communities

Given the innate importance of marine mammals to Indigenous Peoples and the legacy of science's use by colonizers, we have an obligation to work alongside Indigenous communities to conduct ethical and effective marine mammal genomic science. This is especially so given samples used in omics research (e.g., tissue or cells) and the resulting data derived from culturally treasured species, such as marine mammals, can be considered sacred by Indigenous Peoples (Collier-Robinson et al. 2019; Ramos et al. 2025). Here, we build on previous guidance (e.g., Morin et al. 2020) to provide advice to those beginning to think about how they might engage with Indigenous communities (summarized in Figure 1):

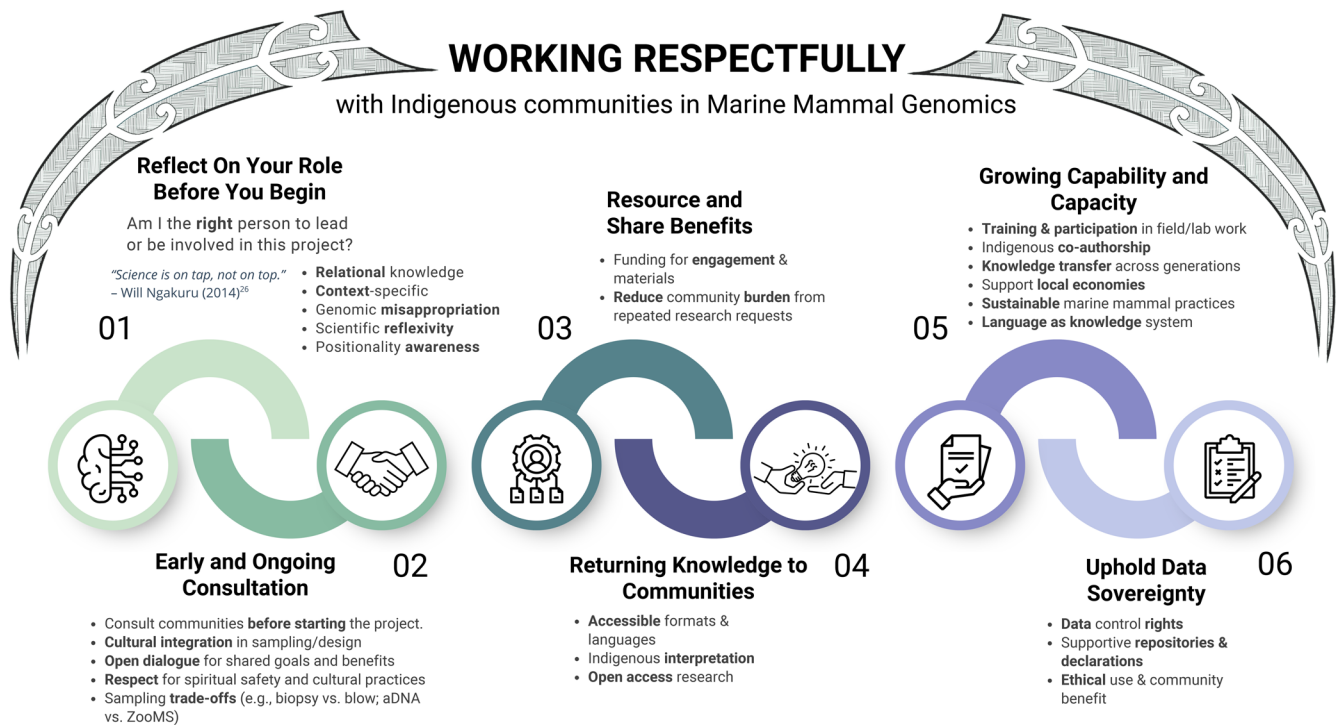


FIGURE 1 | Workflow for integrating Indigenous Ecological Knowledge into marine mammal genomics. Top design was illustrated by Alana Alexander.

1. *Before starting, ask: am I the right person/scientist to lead/ be involved in this project?* Indigenous perspectives often center ‘knowledge as belonging’ (Hikuroa 2017; Woodward et al. 2020), yet genomics has a legacy of separating IEK and samples from their contexts by misappropriation (Hudson et al. 2020; Halmai et al. 2025). We do not have the inherent right to pursue research that intersects with Indigenous interests or appropriates IEK (Smith 2021). Additionally, there is a need for individuals to assess their own intent, and this obligation extends beyond the individual to include stakeholder and institutional roles. We encourage everyone to consider whether their involvement is appropriate, whether Indigenous leadership or co-leadership that enables the IEK practitioner voice is more suitable (when lacking), and how institutional responsibilities can support, not override Indigenous authority, priorities and decision-making.
2. *Early consultation to incorporate customs, values and knowledge into sampling and design:* Consultation with local Indigenous groups before projects begin allows for open dialogue, incorporation of different knowledge systems and sharing of aspirations between parties (Shaw et al. 2024). This enables the development of a mutually acceptable plan for achieving research aims, managing risks, sharing research benefits and caring for resultant data. For example, IEK may guide field work and practices to support spiritual safety (e.g., Hudson et al. 2021; Taiuru 2022), particularly if it occurs alongside cultural hunting (Sudlovenick et al. 2025). Technical discussions might include trade-offs between additional information gained from more invasive sampling methodologies, both for live animals (e.g., biopsy vs. blow sampling or eDNA) and precious marine mammal resources such as seal pelts and whale bone tools (historical/ancient DNA) (Marsh et al. 2022).
3. *Resourcing and benefit-sharing:* Indigenous communities must be resourced to reduce the cumulative impact of engaging with multiple scientific teams (Hudson et al. 2021; Smith 2021). Intersecting with resourcing, equitable sharing of benefits arising from genomics research is both a moral imperative and a legal one (e.g., the Nagoya Protocol, 2010). However, we acknowledge Indigenous communities may not engage due to a lack of capacity and need to prioritize other matters (e.g., health or education). In addition to financial resourcing, identifying and creating other opportunities to share benefits with Indigenous communities is critical (Scholz et al. 2022), and can include the following:
 - a. *Returning knowledge to communities:* returning research findings to communities has historically been neglected by many genomicists (Arango-Isaza et al. 2023). However, sharing research outcomes with those with inherited responsibilities to marine mammals is part of ethical and respectful science. Sharing can also help reduce educational inequities that influence who becomes a researcher and therefore shape research directions (Smith 2021; Arango-Isaza et al. 2023). Interpretations of research should be tailored to the audience, including non-specialized vocabulary free of genomics jargon, using local languages or

dialects, culturally relevant analogies and with delivery via different media (Arango-Isaza et al. 2023; Shaw et al. 2024). However, we should not assume community members cannot understand our research, so it is also important to share the primary research alongside guiding materials. Additionally, genomics researchers should recognize the risk of ‘flattening’ Indigenous languages and culturally specific concepts into simplified scientific or English-language equivalents, and support Indigenous-led approaches to language and knowledge sharing.

- b. Growing capability and capacity: providing Indigenous community members opportunities to participate in field and laboratory research can address educational inequities in genomics research, and build local capability and capacity (e.g., Ramos et al. 2025, and references within). Observing biopsy and drone-based blow sampling can demystify these approaches, so first-hand experience can guide decision making. Including Indigenous coauthors on manuscripts acknowledges the important contributions of place-based and cultural knowledge (e.g., Reeves et al. 2023; McGrath et al. 2025) but should not replace explicit resourcing of Indigenous community members.
- c. Rebuilding IEK, practices and economies: supporting Indigenous ways of being is vital to biodiversity conservation and sustainable development (United Nations 1992; Shaw et al. 2024). Economically supporting young people to remain in their communities (i.e., paid research positions) can enhance intergenerational transmission of IEK (Aswani et al. 2018). Genomics can also be used to support Indigenous Peoples in sustainable interactions with marine mammals, such as managing subsistence harvests and tourism (Bayliss and Hutton 2017; Frost et al. 2021; Shaw et al. 2024). It is also important to acknowledge the centrality of Indigenous language to IEK, with multiple examples in genomics and molecular ecology research (e.g., Ramos et al. 2025) including Ramari’s beaked whale, the only whale named after an Indigenous woman (Carroll et al. 2021).

4. Data sovereignty:

Indigenous Peoples have the right to protect and manage their cultural knowledge and genetic resources (Article 31 of United Nations Declaration on the Rights of Indigenous Peoples, United Nations 2007). Indigenous Data Sovereignty specifies Indigenous control of data so that data utilization is consistent with Indigenous ethics, and benefits from the data accrue to Indigenous communities. It is important to note that Indigenous Data Sovereignty does not preclude the storage of data in open repositories consistent with the FAIR principles (Jennings et al. 2023); rather, it affirms Indigenous authority over how data are accessed and used. In practice, this often requires Indigenous approval or engagement prior to data reuse, ensuring that research proceeds with consent, accountability and benefit-sharing. Readers are encouraged to learn about Indigenous perspectives on open data (Ramos et al. 2025) and to review examples of marine mammal genomics datasets stored on repositories that support Indigenous Data Sovereignty (Foote et al. 2023; Reeves et al. 2023;

Alvarez-Costes et al. 2025; McGrath et al. 2025) and/or other methods for declaring Indigenous interests in data (Liggins et al. 2021; Mc Cartney et al. 2022).

5. *Communicating genomic aims and utility in Indigenous partnerships*: Successful communication requires shifting focus away from technical complexity and toward outcomes that matter to communities. This can be supported through simplified jargon-free proposals, workshops or meetings and the use of infographics and accessible language to foster shared understanding (Alvarez-Costes et al. 2025; Arango-Isaza et al. 2023; Shaw et al. 2024), while still facilitating access to more technical knowledge streams given the diverse skillsets present in communities. Effective communication must be grounded in trust, which is built through sustained relationships, careful listening, transparency and time invested in developing local capacity. Trust is strengthened through consistent engagement during project development, meaningful opportunities for participation such as involvement in fieldwork or necropsies, and continued recognition beyond research outputs, including inclusive media engagement and the creation of community-focused or educational resources (as evident in the below case studies). Such practices support reciprocal, long-term partnerships rather than transactional research relationships.

3.4 | Moving Toward Research Co-Designed With Indigenous Communities

Producing co-designed and co-led research with Indigenous communities takes time, trust and supporting the community’s interests rather than pursuing only researcher-led questions (Smith 2021). Collaborative projects can demonstrate the innate strengths of Indigenous-led approaches (e.g., Woodward et al. 2020) alongside the skillsets of community members (Smith 2021). This relationship building requires long-term resourcing of both communities and researchers, a challenge under many science funding systems, particularly for early career researchers. However, combining different ways of knowing, including philosophies tying humans to the environment (Smith 2021), with the relatively new field of genomics, will lead to excellent collaborative research on culturally significant marine mammal species. We present a detailed workflow (Figure 1), which visually summarizes the steps and considerations needed to engage with Indigenous communities and integrate IEK into marine mammal genomics, emphasizing respectful collaboration and equitable sharing of benefits throughout the research process, including in the emerging technologies and analyses highlighted in this review.

4 | Trends in Marine Mammal Genomics

Early marine mammal genetic research largely focused on protein electrophoresis and restriction fragment analysis (e.g., Bonnell and Selander 1974; Arnason et al. 1984; Baker et al. 1990; Amos et al. 1991; Palsbøll et al. 1997), followed by a major transition to mitochondrial DNA and/or small panels of microsatellite markers (e.g., Lyrholm et al. 1999; Bérubé and Aguilar 1998; Pichler et al. 2001). With more affordable high-throughput sequencing

technologies, it has become possible to sequence whole genomes and generate large-scale population datasets. These advances have greatly increased the resolution at which researchers can investigate populations, shaping the field of marine mammal genomics.

To highlight shifting priorities, technological advances and emerging focal areas shaping the discipline, we built on Cammen et al. (2016) by conducting a review of peer-reviewed marine mammal genomics literature to update trends in publication rates, research aims and methodological approaches. We searched the Web of Science database using the topic term 'genom*' and each of the following terms: 'marine mammal', 'pinniped', 'seal', 'sea lion', 'sea otter', 'whale', 'dolphin', 'polar bear', 'manatee', 'dugong', 'cetacean', 'porpoise', 'walrus', 'Steller's sea cow', identifying 1353 records on 11 March 2025. We note that we assumed all omics papers would have included the term 'genomics'. We excluded 55% of the search results that were not directly related to genomic studies with marine mammals. The remaining 613 were categorized by main research aim and primary research methodology (Table S1) based on Cammen et al. (2016).

Our review revealed a marked increase in the number of omics publications per year, particularly since 2012 (Figure 2A). This growth was accompanied by a notable rise in the relative proportion of WGS studies (Figure 2B), likely driven by the declining cost of sequencing per megabase over time (Figure 2C). Despite the growing adoption of WGS, mitogenome studies remain widely used, reflecting their continued relevance for specific research aims, management and resource-limited contexts. The COVID-19 pandemic disrupted output, with a sharp decline in publications across all six categories in 2020 (fitness, microbiome, resource development, population genomics and demography, phylogenomics, evolutionary adaptation and genome evolution; Figure 2).

5 | Emerging Fields in Marine Mammal Genomics

The emerging fields highlighted in this section were chosen based on presentations, discussions and collaborative insights shared by researchers from various disciplines during the Genomics Workshop at the Society of Marine Mammalogy 2019 and 2024 meeting. Collectively, these topics represent the directions of ongoing marine mammal genomics research.

5.1 | Reference Genomes

Reference genomes provide critical 'genomic infrastructure' without which many of the other types of 'omics' studies would not be possible. The field of reference genome generation has progressed substantially, primarily due to the integration of long-read and short-read sequencing technologies and the establishment of consortia dedicated to reference genome assembly (e.g., <https://www.cetaceangenomesproject.org>). Currently, high-quality reference genomes have been generated for approximately one-third of all known cetacean species (Morin et al. 2025). New opportunities to investigate the genomic foundations of speciation and adaptation in marine mammals will be

Genomic Research Designed to Support Indigenous Stewardship

The genome assembly of the hourglass dolphin (*Cephalorhynchus cruciger*, previously known as *Lagenorhynchus cruciger*) presented by McGrath et al. (2025) integrates genomics with cultural recognition, conservation stewardship and Indigenous data sovereignty (Case Study 1, Figure 3). The hourglass dolphin is recognized as a *taonga* species (species that are deeply treasured, culturally significant and spiritually important) to iwi Māori of Aotearoa New Zealand, and in particular to Ōraka-Aparima Rūnaka (local indigenous community) for the individual utilized for the reference genome. Hāru-a-tai McGrath et al. (2025) intentionally employed a cost effective, portable Oxford Nanopore sequencing as a long-read sequencing technology available within Aotearoa New Zealand. Having this methodological choice enabled Indigenous governance and control of genomic data, including the decision for the sample and data to remain within Aotearoa New Zealand. The high-quality reference genome reported by McGrath et al. (2025) provides a critical conservation resource for a poorly studied Southern Ocean species, enabling future assessments of population history, adaptive potential and vulnerability to climate change. Importantly, this case study demonstrates that integration between Indigenous values and genomics can occur through research design choices that prioritize stewardship, sovereignty and long-term conservation outcomes. As such, this study demonstrated how genomic practice itself can be oriented toward conservation frameworks that respect Indigenous relationships with marine species.

Alvarez-Costes et al. (2025) generated reference genomes for Hector's and Māui dolphins, which are two subspecies of the Aotearoa New Zealand endemic dolphin, *Cephalorhynchus hectori*. This species is of significant conservation and cultural importance to Indigenous communities (Case Study 2, Figure 3). Iwi were consulted prior to the generation of the reference genomes by Alvarez-Costes et al. (2025) and again following data generation to seek approval for publication. The study also incorporated principles of Indigenous data sovereignty and community benefit, including the development of a plain-language guide to the genomics resources to support accessibility and understanding beyond the scientific community.

unlocked as this is expanded to include all cetaceans, pinnipeds, sirenians and other marine mammals, by ongoing efforts from the Vertebrate Genome Project, Darwin Tree of Life, DNAzoo and individual research groups (Dudchenko et al. 2017; Rhie et al. 2021; Darwin Tree of Life Project Consortium 2022).

Although the number of species with reference genomes available is increasing, reference bias can impact analyses when substantial genetic variation exists across a species' range (Chen et al. 2021). Pangenome analyses can address this issue by

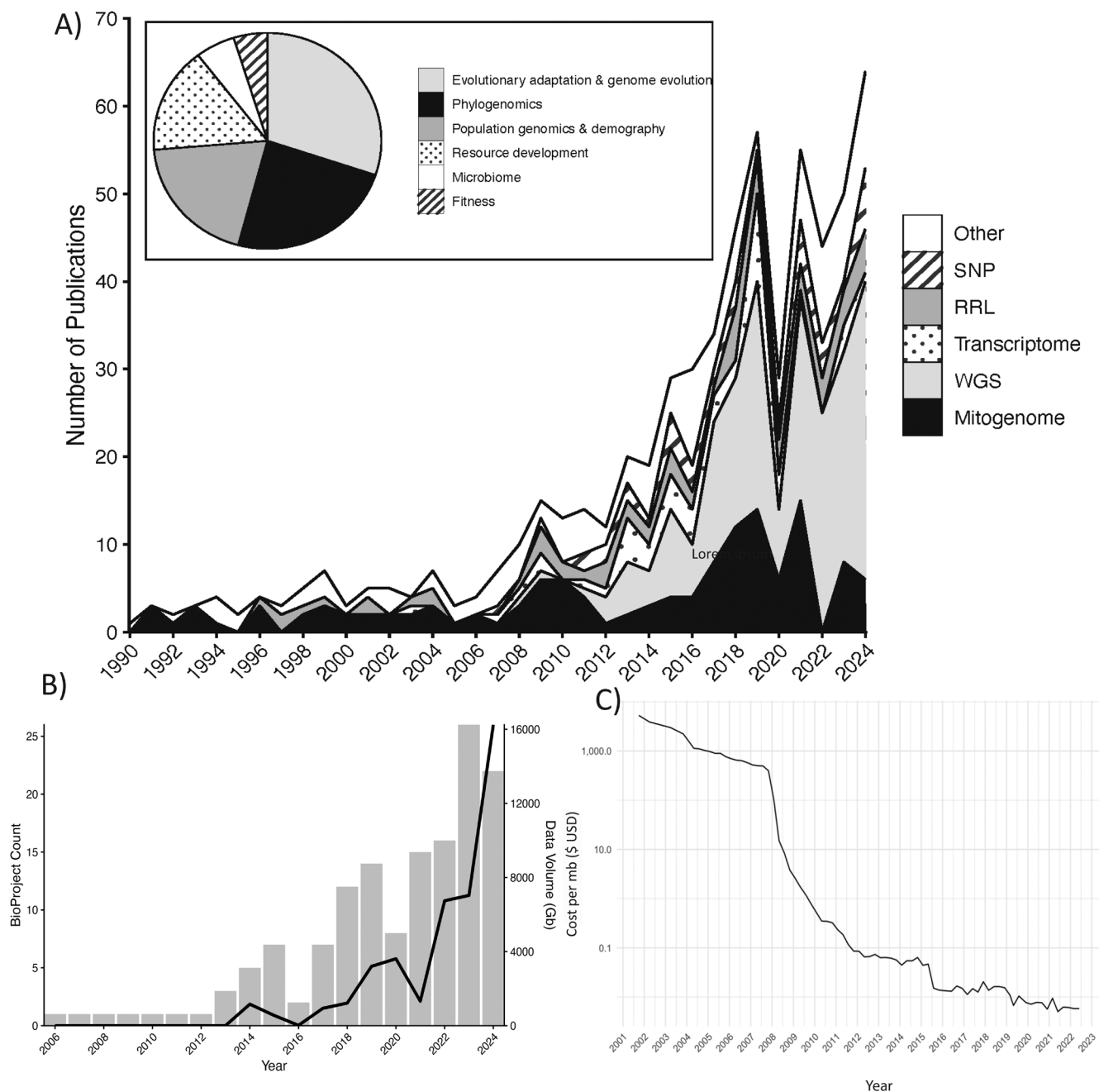


FIGURE 2 | The evolution of genomic research in Marine Mammal ecology. (A) Number of marine mammal genomics publications from 1990 to 2024, categorized by primary methodology (inset) and research aim following Cammen et al. (2016). Highlighted genomic methodologies included high-throughput SNP genotyping (SNP) and sequencing of mitogenomes (Mitogenome), whole genome sequencing (WGS), transcriptomes and reduced representation libraries (RRLs), with additional methodologies summarized in 'other'. (B) The number of BioProjects (grey bars) per year related to marine mammal genomics publications from 2006 to 2024 submitted to the online repository maintained by the National Center for Biotechnology Information (NCBI). The total corresponding data volume in gigabases (Gb) is shown with a black line. (C) Cost per megabases (Mb) (\$USD) for sequencing from 30 September 2001 to 31 May 2022. Data credit: National Human Genome Research Institute (NHGRI).

capturing genetic diversity across all studied populations, and pangenome graphs can make genome-wide variation easier to visualize and interpret (Saada et al. 2024). This marks a significant difference from traditional linear genome models and allows for the identification of structural variants and transposable elements (Secomandi et al. 2025). Although pangenomes for marine mammals have not yet been generated, this remains a promising approach for future studies.

5.2 | Environmental DNA (eDNA)

Environmental DNA refers to genetic material shed by organisms into the environment (such as via exhalation, defecation, urination, sloughed skin), which can be extracted and used for downstream analyses (Ficetola et al. 2008; Foote et al. 2012). Environmental DNA has become a valuable tool for monitoring marine mammals, enabling detection of individual species and broader biodiversity



FIGURE 3 | Case studies demonstrating the integration of Indigenous Ecological Knowledge (IEK) with research, supporting Indigenous sovereignty and stewardship. Case study numbers correspond to the order in which they are presented in the text and do not correspond to the order of photographs shown in the figure; no image was available for Case Study 4. Case Study 1 shows an hourglass dolphin (*Cephalorhynchus cruciger*) necropsy conducted by the Cetacean Ecology Research Group, Massey University in collaboration with Dr. Ramari Oliphant Stewart, highlighting co-produced research approaches. Image by Massey University, New Zealand. Case 2 shows the Hector's dolphin (*Cephalorhynchus hectori*), a species of conservation concern in Aotearoa New Zealand, image by Sebastian Alvarez-Costes. Case Study 3 shows whalers, including First Nations peoples, and killer whales cooperating during the pursuit of a humpback whale (*Megaptera novaeangliae*) in Eden, Australia (c. 1910–1920), image by Charles E. Welling, courtesy of the Eden Killer Whale Museum. Case Study 5 shows Dr. Ramari Oliphant Stewart (Ngāti Awa, Te Whānau-ā-Apanui, Rongomawahine, Ngāti Mahuta) with the skull of Ramari's beaked whale (*Mesoplodon eueu*), a species named in recognition of her knowledge and contributions, image by Tanya Cumberland.

(Székely et al. 2021; Boyse et al. 2024). However, its effectiveness (for some applications) relies on understanding the degradation and transport of DNA in aquatic environments, which affects species detectability over time and space (Collins et al. 2018; Suarez-Bregua et al. 2022). Factors such as water temperature, tides, salinity, UV exposure, microbial activity, sampling quantity and sampling depth influence eDNA persistence and must be considered when designing studies (Kelly et al. 2018).

Efforts to improve laboratory protocols and analytical models are ongoing, aiming to infer species abundance and/or biomass from eDNA samples (Shelton et al. 2016; Fonseca 2018; Kelly et al. 2019; Bizzozzero et al. 2024). Different laboratory processing approaches (metagenomic shotgun sequencing, metabarcoding, qPCR/ddPCR, hybridization capture) allow for either the detection of single (or multiple targeted) species versus descriptions of whole communities (Parsons et al. 2018; Nguyen et al. 2023). Detecting species presence through species-specific PCR amplification of the targeted (mito-)genomic region is especially useful for monitoring elusive species (Boldrocchi et al. 2024; Valsecchi et al. 2022, 2023; Wilcox Talbot et al. 2025). Alternatively, eDNA metabarcoding combined with high-throughput sequencing employs PCR primer sets designed to target entire taxonomic groups or within-species diversity (Taberlet et al. 2012; Baker et al. 2023). This method has been applied in various studies, including diet analysis, biodiversity monitoring, marine connectivity research, community network assessments and marine spatial planning (Closek et al. 2019; Djurhuus et al. 2020; Muenzel 2022; Jacquemot et al. 2024). If

sufficient DNA from a single species is retrieved (multiple individuals identified), population genetics inferences directly from eDNA are feasible (Bennington et al. 2024; Székely et al. 2021; Clem et al. 2025). Similar approaches are also utilized with exhaled respiratory vapour (blow sampling, e.g., Atkinson et al. 2021; O'Mahony et al. 2024), extended to also include low-coverage whole genomes through shotgun sequencing, however success is species dependent (O'Mahony et al. 2026).

Emerging CRISPR-based detection methods have significantly improved the accuracy and sensitivity of identifying invasive and/or elusive species compared to traditional PCR-based techniques (Nagarajan et al. 2024). These approaches leverage artificial intelligence (AI) to pinpoint specific regions, consistent with CRISPR mechanism within the mitogenome or even entire genomes, enabling the design of highly targeted CRISPR primers (Williams et al. 2019; Durán-Vinet et al. 2025). As a result, species can now be detected at much lower abundances and with greater resolution, enhancing conservation management efforts, as seen in monitoring of the African manatee (*Trichechus senegalensis*; Leugger et al. 2025).

5.3 | Ancient DNA and Sedimentary Ancient DNA

Ancient DNA (aDNA) originates from sources that are decades to thousands of years old and is typically highly fragmented, with average lengths of 51–164 bp due to degradation caused by environmental factors (e.g., temperature, humidity, UV)

and biotic processes (e.g., bacterial decomposition), which is also tissue-dependent (Knapp and Hofreiter 2010). Sources of aDNA in marine mammal studies have included subfossil or historical bone, teeth, baleen, scrimshaw, fur and whiskers, with age able to be verified through radiocarbon dating (Post and Kompanje 1995; Pichler et al. 2001; Seersholm et al. 2016; Biard et al. 2017). To date, the oldest recovered marine mammal genome is a bottlenose dolphin (*Tursiops truncatus*), sequenced to 3× depth of coverage and dated to 5979–5626 calendar years ago (Louis et al. 2023). The highest quality historical genome comes from the now extinct Steller's sea cow (*Hydrodamalis gigas*), sequenced to 25× depth of coverage and dating to the mid-1700s (Sharko et al. 2021). Advantages of incorporating aDNA into marine mammal studies include resolving taxonomic relationships (Foote et al. 2013), tracking genetic diversity trends over time (Buss et al. 2023; Skovrind et al. 2024), detecting historical responses to climate change or anthropogenic impacts (Ruiz-Puerta et al. 2023), studying species that are locally extirpated or extinct (Sharko et al. 2021; Bro-Jørgensen et al. 2025) and origin identification of marine mammal material to historical hunting grounds and population origins (Ruiz-Puerta et al. 2023).

An alternative source of aDNA from marine mammals are marine sediment cores that have incorporated DNA sinking to the seafloor, known as sediment DNA (sedaDNA). DNA from sediments represents pelagic and benthic species communities (Sakata et al. 2020) and can provide a window into past marine ecosystem dynamics, enabling insights into the interaction of species with their environment over extended periods (Armbrecht 2020). sedaDNA detections can be interpreted as the presence of a taxon at an estimated time window and geographic location (Heintzman et al. 2023; Vogel et al. 2023, 2024). To date, only two studies have detected marine mammals in marine sediments (Zimmermann et al. 2023; Schreiber et al. 2025), however, these studies illustrate the power of this technique to track changes in marine mammal communities over time and space, complementing and refining fossil-based inferences.

5.4 | Functional Genomics

Functional genomics investigates gene and protein function and regulation at a genome-wide scale, aiming to provide systems-level insights into how genotype variation leads to phenotypic variation (Steinmetz and Davis 2004; Fields et al. 1999). Tools such as RNA-seq paired with gene ontology enrichment analyses help interpret differentially expressed genes by identifying key functions and pathways (Chen et al. 2017). Modern functional genomics combines epigenomics, proteomics, metabolomics, non-coding RNA (ncRNA) studies, regulatory network analysis and AI-driven multi-omics (Caudai et al. 2021; Przybyla and Gilbert 2022). Functional genomics holds great potential for revealing adaptation mechanisms, assessing vulnerability to changing environmental conditions, and guiding targeted conservation efforts.

Due to limited opportunity to collect appropriate samples, proteomic and metabolomic studies in marine mammals have focused on stress responses in pinnipeds. Research in northern

elephant seals (*Mirounga angustirostris*) and spotted seals (*Phoca largha*) has revealed stress-induced changes in proteins, supporting health monitoring and rehabilitation strategies (Deyarmin et al. 2020; Tian et al. 2022). In cetaceans, proteomic and metabolomic studies remain limited, although an untargeted plasma metabolomics study in bottlenose dolphins identified disrupted gluconeogenesis pathways in individuals experiencing anthropogenic stress (Deros et al. 2021). Using exhaled breath condensate from captive killer whales, Harsla et al. (2024) demonstrated the potential for shotgun metabolomic analyses and its potential for further development for cetacean health assessments. While functional genomics can reveal important physiological insights, there is a need for more coordinated large-scale sampling frameworks to inform conservation efforts across marine mammal taxa, such as generating marker panels to support health assessment (Dönmez et al. 2026).

Similarly underexplored in marine mammals are non-coding RNAs (ncRNA), despite their well-established roles in regulating gene expression and influencing diverse biological processes and diseases (Nemeth et al. 2024). A rare example is bowhead whales (*Balaena mysticetus*), for which ncRNA profiling revealed extra copies of the tumour-suppressor gene TP53, suggesting a molecular basis for their cancer resistance and longevity (Jiang and Kong 2020). This points to unique, species-specific regulatory mechanisms that warrant further study to understand resilience in long-lived marine mammals.

Most knowledge of marine mammal genetic adaptation has come from comparative genomic and transcriptomic approaches, which have identified numerous candidate genes and pathways associated with adaptation to aquatic environments. However, these approaches generally provide evidence of association rather than direct experimental validation of gene function (Whitehead 2012). Primary cell culture is a promising yet underused tool that enables functional testing of gene expression via knockdown, overexpression or CRISPR editing (Lam et al. 2020). It allows investigation of gene function across tissues and development, offering insights into regulatory elements underlying aquatic adaptations. Establishing marine mammal cell lines is difficult due to legal and logistical barriers, so experimental studies are rare. A notable exception is the vaquita (*Phocoena sinus*), with cell cultures derived from failed captive breeding (Morin et al. 2021). Other cetacean cell lines are in development at the San Diego Zoo Wildlife Alliance's Frozen Zoo.

5.5 | Epigenetics

Epigenetic monitoring tools can also be applied to various conservation contexts, such as the assessment of individuals health (e.g., Barratclough et al. 2024), the detection of signatures of selection linked to environmental conditions (Vogt 2022), and the estimation of adaptive potential and age structure of populations (reviewed in Balard et al. 2024). These types of studies typically assess epigenetic methylation, the addition of a methyl group to cytosine at CpG sites, which regulates gene expression without changing the DNA sequence. Crossman et al. (2021), for example, used a targeted

sequencing approach at CpG sites of stress-response genes in the hypothalamic pituitary adrenal (HPA) axis to quantify the cumulative effects of stress in Northern and Southern resident killer whales.

Several methods are available for estimating the proportion of genome copies for an individual that are methylated at a given site (Masser et al. 2015; Hawe et al. 2022). Recent advances allow the sequencing of thousands of CpG markers or whole epigenomes (see Laine et al. 2023; Balard et al. 2024). The widely used custom Infinium array ‘HorvathMammalMethylChip40’ (Arneson et al. 2022) estimates methylation proportions at 36,000 CpG sites that are highly conserved among mammals and has been used in multiple marine mammal species (e.g., Bors et al. 2021; Barratclough et al. 2021; Robeck et al. 2021; Peters et al. 2023; Hernandez et al. 2023; Parsons et al. 2023; Martien et al. 2026). This approach has been used to develop species-specific epigenetic clocks for various marine mammal species (Polanowski et al. 2014; García-Vernet et al. 2021; Bors et al. 2021; Mori et al. 2024), and multi-species clocks enabling age estimation in species with limited known-age samples allowing for comparative studies in conservation and health monitoring (Robeck et al. 2021, 2023; Lu et al. 2023; Parsons et al. 2023). Epigenetic ageing has provided valuable insights into population dynamics, supporting effective conservation and management (Balard et al. 2024). For instance, estimates from critically endangered Māui dolphins showed a shift toward a younger age structure over 10 years, suggesting increased offspring survival and recruitment in response to conservation protections (Hernandez et al. 2023). Epigenetic clocks have also been used to demonstrate changes in age-related mating tactics and reproductive success related to population recovery from exploitation (Eichenberger et al. 2026), highlighting how population dynamics can change with density.

Beyond epigenetic clocks, epigenetic analyses have revealed differentiation among marine mammal populations inhabiting distinct environments, supporting the idea that local ecological conditions can drive measurable epigenetic variation. For example, methylation patterns associated with ecological divergence have been identified in bottlenose dolphins (Tatsch et al. 2021), while exposure to stressors in killer whales has been linked to methylation changes in genes involved in physiological stress response (Crossman et al. 2021). Such epigenetic variations, especially in disturbed environments and in response to physiological stress, emphasize the significance of epigenetic studies for assessing human impacts and guiding conservation genomics.

6 | Evolutionary Genomic Analyses for Conservation

Analyses based on genomic and other omics tools offer novel opportunities to understand how evolutionary trajectories and adaptive potential shape conservation requirements for marine mammals. These species represent independent evolutionary radiations into the marine environment, shaped by local adaptation, gene flow, hybridization and population fluctuations, leaving detectable genomic signatures. In systems with cryptic

diversity and broad-scale connectivity, omics can reconstruct demographic histories, reveal adaptive variation and help predict responses to environmental change.

6.1 | Adaptation Genomics

Comparative genomics offers powerful insights into marine mammal evolutionary history and the genetic basis of adaptation (Nery et al. 2016; Zhou et al. 2018; Huelsmann et al. 2019; Genty et al. 2024; Roh et al. 2024; Steinbinder et al. 2024; Tian et al. 2024). The transition from land to water was accompanied by major evolutionary changes in sensory systems and physiology. For example, selection associated with the emergence of echolocation led to the loss of olfactory receptor genes in odontocetes (toothed dolphins), whereas mysticetes (baleen whales) retained these genes and their function (Kishida et al. 2015; Chikina et al. 2016; Jauhal et al. 2024). Adaptations to the hypoxic conditions experienced during diving have been revealed by signals of positive selection in genes associated with oxidative stress in cetaceans and pinnipeds (Tian et al. 2017, 2022; Guo et al. 2024; Selleguin-Veiga et al. 2024), as well as modifications to oxygen transport mechanisms, including myoglobin, that enhance oxygen storage and diving endurance (Nery et al. 2013; Yuan et al. 2021; Zhang et al. 2025). Similarly, changes in genes involved in energy metabolism and blubber development and composition suggest adaptations that minimize heat loss and maintain body temperature in aquatic environments (Wang et al. 2015; Derosus et al. 2021; Yuan et al. 2021; Noh et al. 2022; Zhang et al. 2025). More recent genomic studies have extended this framework to reveal genetic adaptation to localized environmental conditions and habitats, as well as the emergence of distinct ecotypes within marine mammal species. Selection scans have identified variants associated with metabolism (Foote et al. 2016), salinity (Celemin et al. 2025; Rosing-Asvid et al. 2023; Pratt et al. 2022; Marfurt et al. 2024), diving ability (Pratt et al. 2023; McCarthy et al. 2025) and pelage coloration (Rosing-Asvid et al. 2023). Identifying the genetic basis of these traits and recognizing locally adapted populations and distinct lineages is important for understanding the early stages of speciation and for identifying populations that may be particularly vulnerable or resilient to environmental change (Stronen et al. 2022).

Genome-wide comparisons have also revealed lineage-specific differences in genome structure, including patterns of synteny, gene family expansions and contractions. Gene family contraction, via pseudogenisation, has been observed in loci of the Major Histocompatibility Complex, which shows reduced diversity in cetaceans relative to terrestrial mammals (de Sá et al. 2019; Zhang et al. 2019). In contrast, duplications have led to expansions in gene families related to DNA repair and tumour suppression (Tejada-Martinez et al. 2021). Studies of other gene families, such as superoxide dismutase, which is critical for oxidative stress response, have revealed both conserved regions and lineage-specific duplications (Tian et al. 2021). These genomic approaches reveal the evolutionary mechanisms underlying marine mammal adaptation and the genetic variation that may shape responses to future environmental stressors. Exploring variation in gene family structure within species may

further uncover copy number differences with implications for population genetics, adaptive potential and conservation management.

6.2 | Delineating Evolutionary Units for Management

Delineating evolutionarily significant lineages and/or units is a common goal of evolutionary studies and is indispensable for effective conservation strategies (Taylor, Dussex, and van Heezik 2017; Taylor, Archer, et al. 2017; Hoelzel 2023; Morin et al. 2023). However, identifying independently evolving units can be challenging in marine mammals because many species have high dispersal potential and few obvious barriers to gene flow. Consequently, populations may retain substantial ancestral variation, experience ongoing gene flow and admixture, or, in some cases, exchange genes through interspecific hybridization and introgression (Skovrind et al. 2019; Pampoulie et al. 2021; Lopes et al. 2023; Martien et al. 2024). These processes can obscure population boundaries and complicate the identification of lineages that are evolutionarily and demographically distinct. For example, genomic analyses have revealed interspecific introgression that would not be apparent from conventional phylogenetic approaches alone (Guo et al. 2022; Lo et al. 2025), as well as the effects of sex-biased dispersal, locus-specific evolutionary histories, and incomplete lineage sorting on patterns of genomic differentiation (Lopes et al. 2020; Furni et al. 2024; Brennan et al. 2025). Thus, genomic relationships among populations or species do not necessarily reflect a single, simple history of divergence, highlighting the importance of considering multiple evolutionary processes when delineating conservation units.

Developments in genomic tools have consequently enabled high-resolution investigation of the processes that shape evolutionary distinctiveness, including ancestral and contemporary gene flow (Árnason et al. 2018; Foote et al. 2019; Westbury, Petersen, Garde, et al. 2019; Lopes et al. 2023; Autenrieth et al. 2024), genetic drift and the erosion of diversity in small populations (Crossman et al. 2024; Nigenda-Morales et al. 2023; Orton et al. 2024; Hoffman et al. 2024), the emergence and accumulation of new mutations (Suárez-Menéndez et al. 2023) and major demographic changes through time (Crossman et al. 2024; Nigenda-Morales et al. 2023). Integrating these complementary signals can provide a more comprehensive assessment of whether populations are demographically and evolutionarily distinct, rather than relying on genetic differentiation alone. Such information is particularly valuable for conservation because the recognition of independent evolutionary units can guide the maintenance of genome-wide diversity and adaptive capacity (Braulik et al. 2023; Westbury et al. 2026).

6.3 | Quantifying Inbreeding and Genetic Diversity and Predicting Their Consequence

Historically, inbreeding levels in marine mammals were difficult to quantify due to the absence of pedigrees. However, the advent of genomic tools now enables precise estimation of inbreeding

Long-Term Indigenous Observations Informing Genomic Patterns

The study of the historical Eden killer whale population in southeastern Australia provides a powerful example of how Indigenous knowledge and oral histories can guide and contextualize genomic analyses over extraordinarily long temporal scales (Reeves et al. 2023) (Case Study 3, Figure 3). The Eden killer whales cooperatively hunted baleen whales with whalers, sharing the carcass in a relationship that persisted into the 20th century. However, the Thaua people had long documented a culturally transmitted cooperative hunting relationship between killer whales and Indigenous whalers in Eden, predating colonization by millennia, and had detailed accounts of individual whale identities, behaviour and lineages.

Genomic analyses of historical and contemporary samples built directly on Thaua Ecological Knowledge, providing molecular confirmation of the fate of this killer whale lineage (Reeves et al. 2023). Indigenous accounts framed testable hypotheses about population status in killer whales, that would have been difficult to generate from genomic data alone, particularly given the scarcity of samples and limited ecological context of historical populations (Reeves et al. 2023). Genomic evidence, in turn, aligned with Indigenous narratives and helped correct earlier colonist driven interpretations of history, feeding back into the Thaua community by affirming long-held knowledge. Centering of Thaua narratives also occurred in related media, including live interviews, educational resources and other public communication articles (e.g., article: <https://theconversation.com/for-generations-killer-whales-and-first-nations-hunted-whales-together-now-we-suspect-the-orca-group-has-gone-extinct-213556>). Hence, here authors demonstrated how genomics can both advance scientific understanding and support community defined benefits when guided by Indigenous knowledge systems, including cultural recognition and correcting historical narratives.

Additionally, in Rosing-Asvid et al. (2023, Case Study 4), IEK was integrated directly into the hypothesis development and drove the project design. Long-standing Inuit observations from Greenland and Canada identified a locally distinct form of ringed seal (*Pusa hispida*) in the Ilulissat Icefjord, contradicting the prevailing assumption that Arctic ringed seals represent a single panmictic population. The study used this IEK to inform hypothesis development and to guide targeted genomic, survey and biollogging analyses of the Ilulissat Icefjord population. The resulting genetic and ecological evidence corroborated Inuit descriptions of behavioural/cultural and morphological differences. This demonstrated that IEK functioned as an independent and productive line of evidence that revealed previously unrecognized evolutionary diversity and directly informed conservation of this population.

and its consequences (Hill and Weir 2011; Kardos et al. 2015). Over the past decade, studies have uncovered high inbreeding levels across numerous marine mammal species, often linked

to severe historical bottlenecks caused by commercial hunting (e.g., de Greef et al. 2024; Hoelzel et al. 2024).

Runs of homozygosity (ROH) have emerged as a particularly powerful approach for estimating inbreeding, and can distinguish between recent inbreeding (e.g., in Antarctic fur seals [*Arctocephalus gazella*]; Humble et al. 2020) and long-term inbreeding from chronically small population sizes (e.g., vaquita *Phocoena sinus*; Robinson et al. 2022): short ROH typically reflect ancient, shared ancestry and long-term low N_e , whereas long ROH signal recent inbreeding in genetic regions that have been minimally disrupted by recombination (Kardos et al. 2016; Foote et al. 2021; Kyriazis et al. 2025). Many pinniped and cetacean populations exhibit predominantly short ROH, suggesting historical processes rather than recent consanguinity (Robinson et al. 2022; Nigenda-Morales et al. 2023; Hoffman et al. 2024). In contrast, some killer whale populations display extensive long ROH, potentially as the result of bottlenecks in the formation of new ecotypes (Foote et al. 2023; Kardos et al. 2023).

Whole-genome resequencing and ROH analyses further enable estimation of deleterious variant loads, key predictors of reduced fitness and extinction risk (Agrawal and Whitlock 2012; Kyriazis et al. 2023; Robinson et al. 2023). Inbreeding depression arises when recessive deleterious mutations become homozygous and are phenotypically expressed, reducing individual fitness (i.e., inbreeding load) (Morton et al. 1956; Caballero et al. 2017; Bertorelle et al. 2022). For instance, in Southern resident killer whales, inbreeding depression may be impeding recovery post-whaling (Kardos et al. 2023). However, in other species, such as the vaquita and northern elephant seal, there are signs highly deleterious alleles have been purged (Robinson et al. 2022; Hoffman et al. 2024). The extent of inbreeding depression differs among species and is influenced by their demographic histories (Stoffel et al. 2018; Foote et al. 2021; Robinson et al. 2022; Hoffman et al. 2024). For example, genomic erosion caused by the loss of genome-wide diversity and accumulation of deleterious mutations is a common outcome of anthropogenic pressures (e.g., hunting, habitat loss) and natural isolation (Kenyon 1969; Rocha et al. 2015; Nigenda-Morales et al. 2023). These processes can increase extinction risk by reducing adaptive potential and elevating genetic load through inbreeding (Lacy 1987; Reed and Frankham 2003; Spielman et al. 2004; Díez-del-Molino et al. 2018). While pinnipeds and sea otters often show reduced genetic diversity due to intense hunting (Stoffel et al. 2018; Bilgmann et al. 2021; Beichman et al. 2023), some mysticetes retain high diversity despite past exploitation (Crossman et al. 2024; Jossey et al. 2024). Conversely, some cetaceans exhibit low genetic diversity due to long-term isolation and small effective population sizes (Westbury, Petersen, and Lorenzen 2019; Robinson et al. 2022; Nigenda-Morales et al. 2023; Kardos et al. 2023). This evidence highlights that genomic erosion is highly context-dependent and requires species and population specific assessment to establish baselines.

Ultimately, integrating measures of ROH, genetic load and genome-wide diversity provides a powerful framework for

assessing the evolutionary and conservation consequences of demographic decline (Willi et al. 2006; Bertorelle et al. 2022). These genomic tools not only illuminate the impacts of historical exploitation and isolation but also inform targeted recovery strategies, particularly for small and vulnerable populations. Ongoing efforts should aim to link mutation load with fitness traits to predict population viability and evolutionary potential under future environmental change (Robinson et al. 2022; Kardos et al. 2024).

7 | Predictive Genomics for Conservation

Traditional conservation tools are often limited in their ability to detect early signs of population decline or loss of adaptive capacity. Consequently, there is growing interest in applying predictive genomics to conservation, with an emphasis on the need to account for evolutionary processes when forecasting species' responses (Tittensor et al. 2019; Waldvogel et al. 2020; Layton et al. 2021; Bernatchez et al. 2024). This emerging field seeks to identify genomic signatures that can forecast future viability, detect hidden genetic erosion and assess the adaptive potential of populations under changing environmental conditions. Genomic approaches already inform the management of critically endangered species (vaquita, Robinson et al. 2022; north atlantic right whale [*Eubalaena glacialis*], Orton et al. 2024), as well as endangered and vulnerable populations (Australian sea lion [*Neophoca cinerea*], Bilgmann et al. 2021; harbour porpoises [*Phocoena phocoena*], Celemin et al. 2025; killer whales, Kardos et al. 2023). These cases highlight the potential of predictive genomics to support more proactive and evolution-informed conservation strategies.

7.1 | Reconstruction and Forecasting of Demographic Histories

Demographic modelling can be used to infer historical changes in population size, migration and connectivity, revealing past bottlenecks, expansions, or long-term declines that may not be apparent from ecological data alone (Frankham et al. 2010; Shafer et al. 2015). It has been successfully applied to marine mammals, often combining different methods to ensure robust and consistent results (e.g., Bilgmann et al. 2021; Robinson et al. 2022; Nigenda-Morales et al. 2023; Crossman et al. 2024). Method selection should be carefully considered, as commonly used approaches can produce misleading inferences for structured populations subject to episodic gene flow (Mazet et al. 2016; Novo et al. 2023). This is also important to consider for cetaceans at the species level, where multiple instances of introgression have been reported (e.g., Foote and Morin 2015; Árnason et al. 2018; Westbury, Petersen, Garde, et al. 2019; Westbury, Petersen, and Lorenzen 2019; Reeves et al. 2025; McCarthy et al. 2026).

Methods based on composite likelihood and the site frequency spectrum (SFS) are particularly well-suited for large genomic datasets due to their relatively low computational costs (Gutenkunst et al. 2009; Excoffier et al. 2013; Liu and Fu 2020). Population structure, which is often shown by

marine mammals, can be incorporated with multiple populations/species in a joint SFS model. Additionally, SFS-based methods can incorporate ghost populations, that is, a lineage for which samples are not available (Slatkin 2005). For example, a study on fin whales incorporated a ghost population and demographic changes into their model, successfully detecting a whaling-induced bottleneck and thus highlighting the recent anthropogenic impacts that have shaped genetic diversity (Nigenda-Morales et al. 2023).

7.2 | Simulations for Conservation Genomics of Marine Mammals

Forward-simulations are used to explore and predict the genetic consequences of demographic scenarios. These simulations take inferred demographic parameters as input and have been used to investigate how inbreeding depression affects heterozygosity–fitness correlations (Kardos et al. 2014). In killer whales, such simulations were used to explore the genomic impacts of small population size and inbreeding (Kardos et al. 2023). These tools allow for flexible, individual-based modelling of evolutionary dynamics, including selection, recombination and non-Wright–Fisher demography (Haller and Messer 2019).

Genomic offset models are grounded in genotype–environment associations and offer a promising framework to predict the degree of genetic change required for populations or species to remain adapted under future environmental conditions. While genomic offset models are increasingly applied in terrestrial systems (e.g., Bay et al. 2018; Razgour et al. 2019; Knippler et al. 2023; Marková et al. 2023; Schmidt and Russello 2025), their use in marine ecosystems is only beginning to emerge (Layton et al. 2024). To date, we are aware of no studies that have applied genomic offset models to marine mammals.

Despite their potential, genomic offset models are inherently correlative and sensitive to the resolution of genomic and environmental data (Joost et al. 2007; Fitzpatrick and Keller 2015; Rellstab et al. 2016; Capblancq and Forester 2021; Rochat et al. 2021; Gain et al. 2023). Model assumptions, such as stable genotype–environment relationships and consistent links between genetic variation and fitness, can be affected by factors such as demographic history and population structure (Láruson et al. 2022; Lind and Lotterhos 2025). Most models rely on single-nucleotide polymorphism (SNP) data and may overlook other adaptive genomic features, including structural variants and epigenetic modifications (Heckwolf et al. 2020; Layton et al. 2021). While traditional validation approaches of genomic offset models are often infeasible in marine mammals, historical DNA combined with paleoclimate reconstructions offer a promising alternative (Atmore et al. 2022). These predictions between varying temporal datasets can then be compared with observed demographic or genetic trends to assess model performance (Layton et al. 2024). Although further validation is needed, integrating genomic offset models into marine mammal conservation may still provide insights

into adaptive capacity and help identify populations most vulnerable to future climate scenarios, supporting more climate-resilient conservation strategies.

8 | Translating Omics Into Actionable Change

Despite the growing power of genomics to inform conservation, translating these insights into real-world outcomes remains a challenge. Omics data are highly technical, and results can be difficult for non-specialists to interpret and apply. This complexity combined with limited baseline data for many threatened species can hinder the timely integration of genomic findings into conservation policy and management frameworks (Shafer et al. 2015; Taylor, Dussex, and van Heezik 2017; Taylor, Archer, et al. 2017). Structural gaps between academic researchers, resource managers and local communities can also slow the implementation of genomic tools, even when the underlying science is robust (Cook et al. 2023).

Bridging these divides requires deliberate investment in science communication and knowledge translation. Effectively communicating genomic insights in ways that are accessible, culturally relevant, and action-oriented is essential to ensure they inform on-the-ground conservation. Alongside simplifying complex results, this means producing public-friendly press releases, collaborating with media, creating visual abstracts and tailoring materials to local languages and to the values and concerns of communities (Cvitanovic et al. 2019; Dawson et al. 2021). Co-developing communication strategies with Indigenous and local communities strengthens trust, aligns conservation approaches with lived realities, and honours diverse knowledge systems (Reid et al. 2021; Latulippe and Klenk 2020). However, improving accessibility and clarity in science communication, while necessary, does not always translate into successful conservation action. Genomic insights may be well understood yet remain difficult to implement if proposed interventions conflict with local socioeconomic realities, governance structures, or culturally embedded values. Conservation outcomes therefore depend not only on how knowledge is communicated, but also on whether recommended actions are feasible, equitable and aligned with the priorities of those living alongside threatened species (Fariss et al. 2023; Delisle et al. 2018). Recognizing these realities alongside genomic evidence can foster more durable partnerships, enhance trust, and ultimately increase the likelihood that conservation strategies informed by genomics succeed over the long term.

Although translating genomic data into action requires time and effort, the benefits are profound when genomic conclusions have led to the development of conservation policy (e.g., vaquita; Robinson et al. 2022 and northern right whale; Crossman et al. 2024). Greater accessibility through multilingual abstracts, open data platforms, and community-focused outreach can democratize genomics and foster broader participation (Madliger et al. 2017; Kadykalo et al. 2021). When implemented well these efforts catalyse more inclusive, effective conservation,

encourage innovation in threat mitigation, and build long-term capacity among local and Indigenous partners.

Acknowledging Indigenous Leadership in Biodiversity Protection

Carroll et al. (2021) provide a clear example of how applied genomics can be conducted in ways that acknowledge Indigenous stewardship and expertise (Case Study 5, Figure 3). When first describing Ramari's beaked whale (*Mesoplodon eueu*) using genomic and morphological data, the authors undertook consultation with Indigenous peoples from regions where specimens originated and explicitly recognized Indigenous cultural connections in the scientific naming of the species. The common species name pays homage to Dr. Ramari Oliphant Stewart, a prominent Indigenous marine mammal expert in New Zealand, and the Khosian peoples, with the species name 'eueu', meaning 'big fish' from the Khoe language family. Although the study's primary aim was taxonomic resolution, the approach reflects an emerging model in which genomic research respects Indigenous expertise and responsibilities to biodiversity by acknowledging these linkages in species nomenclature.

de Greef et al. (2024, Case Study 6) used whole-genome sequencing of Arctic bowhead whales and narwhals to evaluate the genetic impacts of commercial whaling. Indigenous hunters contributed directly by providing biological samples through subsistence harvests, enabling genomic analyses in remote Arctic regions. Similar to Case Study 2 (ringed seals), this study demonstrates how Indigenous involvement strengthens marine mammal genomics and conservation; however, here the contribution primarily supports genomic analysis through sample provision rather than driving hypothesis formation through IEK.

9 | Future Directions

Since the last major synthesis by Cammen et al. (2016), marine mammal genomics have advanced rapidly. More species now have reference genomes and whole-genome datasets, enabling researchers to assess genetic diversity, reconstruct demographic histories, and identify signatures of local adaptation despite the status of marine mammals as non-model species. These insights are transforming our understanding of evolutionary processes and species' responses to environmental change, including differential impacts depending on marine mammal culture. High-resolution genomic data now allow us to model future scenarios, evaluate threats and forecast population trajectories under various climate and anthropogenic pressure scenarios. This predictive capacity is increasingly critical for guiding evidence-based conservation strategies aimed at long-term resilience. However, key challenges remain, for example, obtaining high-quality samples, particularly from rare or elusive species or failing to include Indigenous Ecological Knowledge. Addressing these challenges will require innovative sampling approaches, expanded international collaborations, and greater focus on underrepresented taxa. Closing these knowledge gaps will be essential for

ensuring genomic tools are applied equitably across the full spectrum of marine mammal biodiversity.

The future of marine mammal genomics is poised to be transformative. The integration of multi-omics approaches spanning genomics, transcriptomics and epigenomics, combined with AI-driven models, offers unprecedented insight into adaptation, health and ecological interactions. Cutting-edge technologies such as spatial transcriptomics, single-cell genomics and functional assays using cell lines will enable researchers to explore the molecular basis of stress responses, disease resistance and resilience in greater detail than ever before. Advances in sequencing now also allow for the detection of structural variants and transposable elements across whole genomes. These large-scale genomic rearrangements represent a major source of functional diversity, and their integration alongside SNP data will enhance our ability to identify adaptive variation and inform more effective conservation strategies. With the increasing complexity of techniques, clear science communication and translation of genomic findings will be essential to ensure research informs conservation actions across diverse interests.

Building strong, international collaborative networks remains a key priority. Coordinated responses to strandings, for example, can increase access to rare biological materials provided such efforts are undertaken in consultation with Indigenous Peoples and respect local governance systems. However, while marine mammals are deeply significant to many Indigenous communities, Indigenous concepts may also help to place marine mammals in the broader context of ecosystem health thriving through species interactions and the diversity of the biosphere, motivating more integrated and holistic research programmes. The next era of marine mammal genomics will be shaped by technological innovation, inclusive collaboration prioritizing respectful, reciprocal partnerships and the merging of diverse knowledge systems, integrating Indigenous ecological understanding with genomic tools. These efforts will be central to addressing critical questions in evolution, health and conservation, ultimately supporting the protection of marine mammal populations in a rapidly changing world.

Author Contributions

I.M.R. and S.A.-C. conceived the study. Each main section had theme leaders that were responsible for developing the core content with their team the main sections: A.A. and E.L.C. led the 'Indigenous Ecological Knowledge' section; M.L.M. and É.O.N. led the 'Trends in Marine Mammal Genomics' section; G.A.D., F.F. and S.N.-M. led the 'Evolutionary Genomics' section; and S.M.M. and S.A.-C. led the 'Predictive Genomics' section. I.M.R. and S.A.-C. synthesized these contributions into a cohesive manuscript, with input from G.G. and C.E.M. All authors reviewed and approved the final version.

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Acknowledgements

This review paper is the outcome of two international workshops on marine mammal genomics, held in 2019 and 2024, hosted by the Society for Marine Mammalogy. The 2019 workshop was organized by Andrew D. Foote and Michael McGowen, and the 2024 workshop by I.M.R., S.A.-C., C.E.M. and G.G. We thank all participants for their inspiring contributions and discussions. This research constitutes scientific contribution #385 from the Sea Research Foundation Inc. We acknowledge that some of the authorship team used AI tools to improve grammar and syntax, but not to inform any content. We acknowledge funding and collaborative support of the Minderoo Foundation in this work for I.M.R salary and its mission to protect and restore natural ecosystems for future generations. Open access publishing facilitated by Flinders University, as part of the Wiley - Flinders University agreement via the Council of Australasian University Librarians.

Funding

The 2024 workshop was generously supported by the American Genetics Association's *Special Events Awards* and the Company of Biologists' Scientific Meeting Grant.

Ethics Statement

The authors have nothing to report.

Conflicts of Interest

The authors declare no conflicts of interest.

Data Availability Statement

The data for the review component can be found in Table S1.

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Supporting Information

Additional supporting information can be found online in the Supporting Information section. **Table S1:** References identified for the literature review. Web of Science was searched on 11 March 2025 using the topic term 'genom*' combined with 'marine mammal', 'pinniped', 'seal', 'sea lion', 'sea otter', 'whale', 'dolphin', 'polar bear', 'manatee', 'dugong', 'cetacean', 'porpoise', 'walrus' and 'Steller's sea cow'. The search identified 1353 records, of which 613 were retained after excluding records not directly related to genomic studies of marine mammals. Retained studies were categorized according to their primary research aim and methodology.