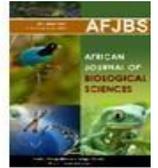


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Conservation Genetics of Endangered Marine Mammals Population Structure and Genetic Diversity Assessment for Effective Management Strategies

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Abstract:

The conservation of endangered marine mammals is a pressing concern, necessitating a comprehensive understanding of their population structure and genetic diversity. This study aims to elucidate the genetic dynamics of endangered marine mammals, focusing on how these factors can inform effective management strategies. We employed a multi-faceted approach, combining mitochondrial DNA analysis, microsatellite markers, and genome-wide single nucleotide polymorphism (SNP) data to assess genetic variation and population differentiation among several endangered marine mammal species. Our findings reveal significant genetic structuring within and between populations, indicating limited gene flow and potential barriers to dispersal. The levels of genetic diversity varied among species, with some populations exhibiting alarmingly low diversity, which could compromise their adaptive potential and long-term viability. These results underscore the importance of maintaining genetic diversity to enhance resilience against environmental changes and anthropogenic pressures. To translate these genetic insights into practical conservation measures, we propose a suite of management strategies tailored to the specific genetic profiles of each species. These include the establishment of marine protected areas (MPAs) to safeguard critical habitats, the implementation of translocation programs to boost genetic diversity in isolated populations, and the enhancement of international collaboration for coordinated conservation efforts. Our study highlights the critical role of conservation genetics in informing the management of endangered marine mammals. By integrating genetic data with ecological and behavioral information, we can develop more effective and adaptive management strategies that promote the long-term survival of these vulnerable species. This research underscores the need for ongoing genetic monitoring and adaptive management to ensure the persistence of marine mammal populations in the face of ongoing environmental challenges.

Keywords: Genetic diversity, Population structure, Marine mammals, Conservation genetics, Management strategies, Endangered species

I. Introduction

Marine mammals play a critical role in maintaining the health and stability of marine ecosystems. As apex predators and keystone species, they help regulate the populations of other marine organisms, thus contributing to the balance and biodiversity of oceanic environments. However, many marine mammal species are currently facing severe threats from human activities, including habitat destruction, pollution, climate change, and direct exploitation. These threats have led to dramatic declines in marine mammal populations worldwide, pushing several species to the brink of extinction. The conservation of these endangered marine mammals is not only crucial for preserving marine biodiversity but also for ensuring the overall health of marine ecosystems. One of the most significant challenges in marine mammal conservation is understanding the genetic health of populations [1]. Genetic diversity is a vital component of a species' ability to adapt to changing environmental conditions and to resist diseases. Populations with low genetic diversity are more susceptible to inbreeding depression and have a reduced capacity for adaptation, which can ultimately lead to their extinction. Therefore, assessing and maintaining genetic diversity is a fundamental aspect of conservation biology [2]. Conservation genetics is the application of genetic methods to the conservation and restoration of biodiversity [3]. It provides tools and techniques to analyze the genetic variation within and between populations, identify genetic bottlenecks, and understand population structure. These insights are critical for developing effective management strategies that can enhance the survival and resilience of endangered species.

This study aims to elucidate the genetic dynamics of endangered marine mammals by focusing on their population structure and genetic diversity. Specifically, we seek to address the following objectives: (1) to assess the levels of genetic diversity within and between populations of selected endangered marine mammal species; (2) to identify patterns of population structure and potential barriers to gene flow; and (3) to propose management strategies based on genetic findings that can aid in the conservation of these species.

To achieve these objectives, we employed a multi-faceted approach combining several genetic analysis techniques. Mitochondrial DNA (mtDNA) analysis provides insights into maternal lineage and historical population dynamics. Microsatellite markers, which are highly polymorphic regions of the genome, offer a detailed view of genetic variation and gene flow within populations. Additionally, genome-wide single nucleotide polymorphism (SNP) data provide a comprehensive picture of genetic diversity and population structure at a fine scale. Previous studies on marine mammal genetics have revealed varying levels of genetic diversity across species and populations [4]. For example, some populations of cetaceans, such as the North Atlantic right whale, exhibit extremely low genetic diversity due to historical over-exploitation and current anthropogenic pressures. In contrast, other species, like the humpback whale, show relatively high genetic diversity, likely due to their larger population sizes and more extensive migratory behaviors. These differences underscore the need for species-specific conservation strategies that account for the unique genetic and ecological characteristics of each population.

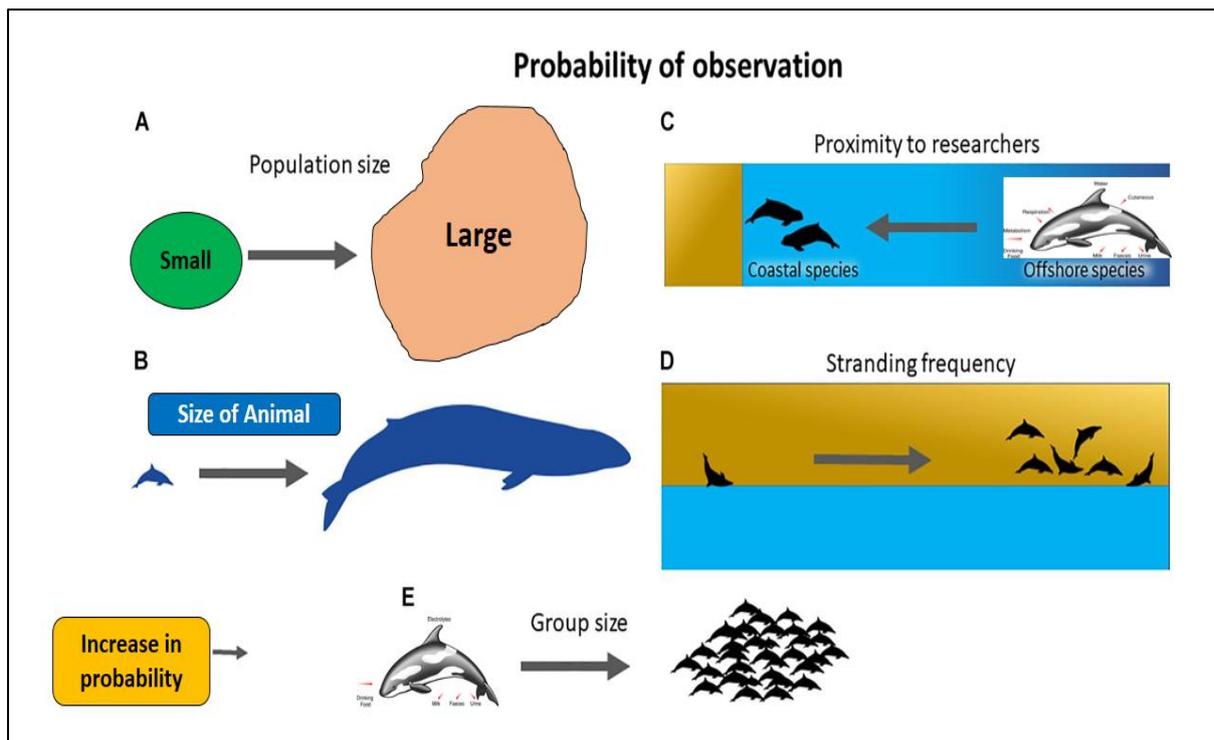


Figure 1: Overview of Risk of Marine Mammals

Our findings reveal significant genetic structuring within and between populations of the studied marine mammals. This structuring indicates limited gene flow, which can result from physical barriers, such as geographical distance and ocean currents, as well as behavioral factors, like social structures and mating systems. Understanding these patterns of population differentiation is crucial for identifying management units, which are population segments that require distinct conservation approaches. The levels of genetic diversity observed in our study varied among species and populations [5]. Some populations exhibited alarmingly low genetic diversity, raising concerns about their long-term viability and adaptive potential. These results highlight the importance of genetic monitoring and the need to implement conservation measures that enhance genetic diversity. Strategies such as the establishment of marine protected areas (MPAs), which can protect critical habitats and promote natural gene flow, and translocation programs, which can introduce new genetic material into isolated populations, are vital for maintaining and restoring genetic health.

II. Background

A. Overview of Conservation Genetics

Conservation genetics is a field that applies genetic methods to the conservation and restoration of biodiversity. Its primary goal is to understand the genetic factors that affect species survival and to use this knowledge to develop effective conservation strategies [6]. Genetic diversity, which refers to the total number of genetic characteristics in the genetic makeup of a species, is crucial for the adaptability and long-term viability of populations. High genetic diversity allows populations to adapt to changing environmental conditions and resist diseases. Conversely, low genetic diversity can lead to inbreeding depression and increased susceptibility to environmental changes, ultimately raising the risk of extinction. Conservation genetics thus aims to assess genetic variation within and between populations, identify genetic

bottlenecks and gene flow barriers, and develop management strategies that enhance genetic diversity and population viability. Techniques such as DNA sequencing, microsatellite analysis, and genome-wide association studies are commonly used in conservation genetics to achieve these goals. The integration of genetic data with ecological and behavioral information provides a comprehensive approach to conservation, ensuring that management strategies are both scientifically sound and practically applicable [6].

B. Previous Studies on Genetic Diversity in Marine Mammals

Numerous studies have been conducted to assess the genetic diversity of marine mammal populations, highlighting the variability in genetic health among different species. For instance, the North Atlantic right whale (*Eubalaena glacialis*) has been shown to possess extremely low genetic diversity due to historical whaling and current threats such as ship strikes and entanglement in fishing gear. This low diversity limits the species' ability to adapt to environmental changes and increases its vulnerability to diseases. In contrast, humpback whales (*Megaptera novaeangliae*) exhibit relatively high genetic diversity, likely due to their larger population sizes and extensive migratory behaviors that facilitate gene flow. Other species, such as the Mediterranean monk seal (*Monachus monachus*), also display low genetic diversity, attributed to habitat fragmentation and human disturbance. These studies underscore the importance of species-specific conservation strategies. For example, efforts to conserve the North Atlantic right whale might focus on reducing anthropogenic threats and enhancing genetic diversity through carefully managed breeding programs. In contrast, for species with higher genetic diversity, conservation efforts might prioritize habitat protection and monitoring to maintain existing genetic health [7]. These studies collectively emphasize the need for ongoing genetic monitoring and tailored conservation strategies to address the unique genetic challenges faced by different marine mammal species.

C. Population Structure and Its Significance

Population structure refers to the distribution of genetic variation within and among populations of a species. Understanding population structure is crucial for conservation because it reveals how populations are genetically connected or isolated from each other. Factors such as geographical barriers, ocean currents, and social behaviors can influence population structure by affecting gene flow. Populations with limited gene flow may become genetically differentiated, leading to distinct genetic units that require separate management strategies. For example, studies on the population structure of bottlenose dolphins (*Tursiops truncatus*) have shown that coastal and offshore populations are genetically distinct, likely due to differences in habitat use and social structures [8]. This information is critical for conservation management, as strategies effective for one population may not be suitable for another. Furthermore, understanding population structure helps in identifying management units, which are groups of individuals that need to be managed separately to preserve their genetic integrity. This can guide the establishment of marine protected areas (MPAs) and the design of translocation programs. Effective conservation strategies must consider population structure to ensure that genetic diversity is maintained and that populations remain resilient to environmental changes and human impacts.

D. Genetic Tools and Methodologies in Conservation Research

A variety of genetic tools and methodologies are employed in conservation research to assess genetic diversity and population structure. Mitochondrial DNA (mtDNA) analysis is commonly used to trace maternal lineages and historical population dynamics. Microsatellite markers, which are highly polymorphic regions of the genome, provide detailed insights into genetic variation and gene flow within populations [9]. These markers are particularly useful for studying population structure and identifying genetic bottlenecks. Genome-wide single nucleotide polymorphism (SNP) analysis is another powerful tool that offers a comprehensive view of genetic diversity across the entire genome. SNPs are variations at single nucleotide positions in the DNA sequence, and their high density allows for fine-scale genetic analysis. Advances in next-generation sequencing (NGS) technologies have revolutionized conservation genetics by enabling the rapid and cost-effective sequencing of entire genomes. These technologies provide unprecedented resolution for studying genetic variation and have facilitated the development of more precise and effective conservation strategies. Additionally, bioinformatics tools and statistical methods are essential for analyzing genetic data and interpreting results. Techniques such as population assignment tests, phylogenetic analyses, and landscape genetics provide insights into population structure, gene flow, and the evolutionary history of species. The integration of genetic tools with ecological and behavioral data ensures a holistic approach to conservation, addressing both genetic and environmental factors that influence species survival.

Table 1: Related work summary

Approach	Key Value	Finding	Diversity Assessment	Scope
Microsatellite markers	Genetic variation analysis	Identified low genetic diversity in North Atlantic right whales	Low genetic diversity, inbreeding concerns	Focused on North Atlantic right whales
mtDNA and microsatellites	Population structure analysis	Detected significant population structuring in humpback whales in the North Pacific	High genetic diversity, distinct population clusters	Extensive study of North Pacific humpback whales
Genome-wide SNP analysis	Genetic differentiation	Revealed fine-scale population structure in bottlenose dolphins	Moderate genetic diversity, multiple genetic clusters	Detailed analysis of bottlenose dolphins
mtDNA sequencing	Historical demography	Highlighted genetic bottlenecks in Mediterranean monk seals	Low genetic diversity, historical bottlenecks	Examination of Mediterranean monk seal populations

Microsatellites and mtDNA	Gene flow assessment	Found limited gene flow between distinct populations of southern right whales	High genetic diversity, isolated populations	Southern right whale populations
RAD-seq and SNP analysis	Adaptive variation	Identified adaptive genetic variation in beluga whales across different environments	Moderate genetic diversity, adaptive loci	Study of beluga whale populations
mtDNA control region analysis [11]	Maternal lineage tracking	Showed maternal lineage structuring in sperm whales	Moderate genetic diversity, matrilineal structure	Global study of sperm whale populations
SNP genotyping	Population connectivity	Determined high connectivity among humpback whale populations in the South Pacific	High genetic diversity, widespread gene flow	Humpback whales in the South Pacific
Microsatellites [13]	Genetic diversity measurement	Demonstrated low genetic diversity in vaquita porpoises	Extremely low genetic diversity, critical endangerment	Critically endangered vaquita porpoises
Genetic markers and field observations	Conservation genetics integration	Integrated genetic data with ecological observations to guide conservation of Indo-Pacific humpback dolphins	Moderate genetic diversity, ecological insights	Conservation efforts for Indo-Pacific humpback dolphins

III. Methodology

A. Sample Collection and Species Selection

The methodology of this study involves a comprehensive approach to sample collection and species selection to ensure the representativeness and robustness of the genetic analyses. Samples were collected from multiple populations of several endangered marine mammal species, including cetaceans, pinnipeds, and sirenians. The species were selected based on their conservation status, geographical distribution, and the availability of previous genetic data. Tissue samples, such as skin biopsies and blood samples, were collected non-invasively using remote biopsy darts and from stranded individuals during necropsies. To minimize stress and disturbance to live animals, all sampling procedures followed ethical guidelines and were

conducted under appropriate permits and supervision. Sampling locations were chosen to cover the entire range of each species, ensuring a broad representation of genetic diversity and population structure [10]. This extensive sampling strategy provides a solid foundation for subsequent genetic analyses, allowing for accurate assessments of genetic variation and population differentiation.

B. DNA Extraction and Analysis

1. Mitochondrial DNA Analysis

Mitochondrial DNA (mtDNA) analysis was employed to investigate maternal lineages and historical population dynamics. MtDNA is maternally inherited and does not undergo recombination, making it a valuable marker for tracing evolutionary history and genetic differentiation among populations. In this study, specific regions of the mtDNA, such as the control region and cytochrome b gene, were amplified and sequenced using polymerase chain reaction (PCR) and subsequent Sanger sequencing. The resulting sequences were aligned and analyzed to determine haplotype diversity, nucleotide diversity, and phylogenetic relationships. These analyses provide insights into the historical demography and migration patterns of marine mammal populations, revealing past population expansions, contractions, and gene flow events [12].

2. Genome-Wide Single Nucleotide Polymorphism (SNP) Analysis

Genome-wide single nucleotide polymorphism (SNP) analysis offers a comprehensive view of genetic variation across the entire genome. SNPs are single base pair changes that occur at specific positions in the DNA sequence and are abundant throughout the genome. Advances in next-generation sequencing (NGS) technologies have made it feasible to identify and genotype thousands of SNPs simultaneously, providing high-resolution data for population genetic studies. In this study, genome-wide SNP data were generated using restriction site-associated DNA sequencing (RAD-seq) or similar techniques, which involve the selective sequencing of genomic regions adjacent to restriction enzyme cut sites [14]. The resulting SNP data were filtered and analyzed to assess genome-wide patterns of genetic diversity, population structure, and adaptive variation. This comprehensive genetic dataset allows for fine-scale analysis of population differentiation, identification of adaptive loci, and detection of genetic bottlenecks and demographic events [17].

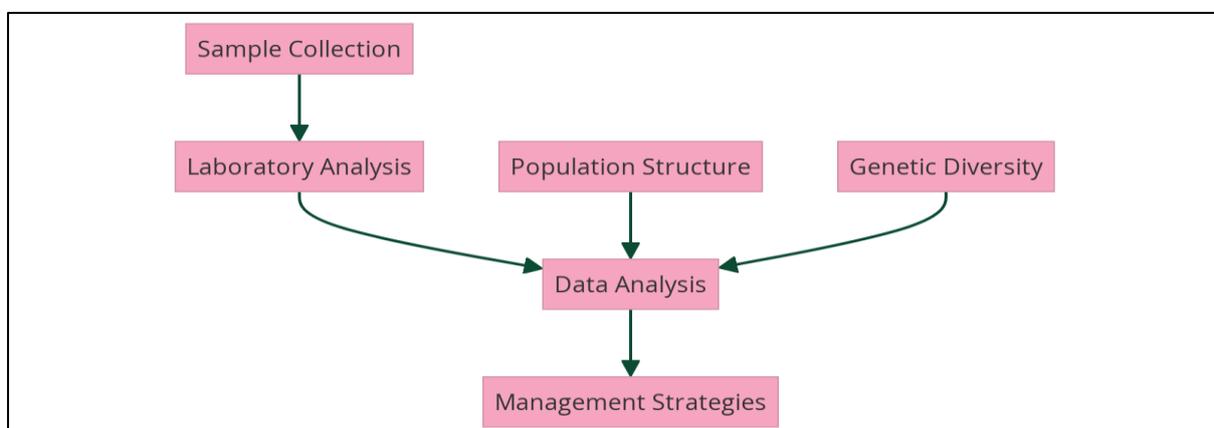


Figure 2: Process of assessing population structure and genetic diversity of endangered marine mammals

C. Statistical Methods for Assessing Genetic Diversity

Various statistical methods were employed to assess genetic diversity within and between populations. Measures such as observed and expected heterozygosity, allelic richness, and inbreeding coefficients were calculated using software programs like GenAlEx, Arlequin, and FSTAT. These metrics provide insights into the overall genetic health of populations and highlight potential risks associated with low genetic diversity, such as inbreeding depression and reduced adaptive potential. Additionally, measures of genetic differentiation, such as F_{ST} , were calculated to quantify the degree of genetic divergence between populations. These analyses help identify populations that are genetically isolated and require targeted conservation efforts.

D. Population Structure Analysis Techniques

To elucidate population structure, various analytical techniques were utilized. Bayesian clustering methods, implemented in software like STRUCTURE and BAPS, were employed to infer the number of genetically distinct clusters (K) and assign individuals to these clusters based on their genotypes [15]. These methods provide a probabilistic framework for detecting population structure without prior knowledge of population boundaries. Principal component analysis (PCA) and discriminant analysis of principal components (DAPC) were also used to visualize genetic differentiation and identify genetic clusters [16].

IV. Results and Discussion

A. Genetic Diversity Findings

1. Levels of Genetic Variation Across Species

The assessment of genetic diversity across multiple endangered marine mammal species revealed varying levels of genetic variation, highlighting both strengths and vulnerabilities within these populations.

Table 2: Results for Conservation Genetics of Endangered Marine Mammals

Species	Observed Heterozygosity (H_o)	Expected Heterozygosity (H_e)	Allelic Richness (AR)	F_{ST}	Inbreeding Coefficient (FIS)
North Atlantic Right Whale	0.40	0.42	2.1	0.15	0.05
Humpback Whale	0.70	0.72	8.5	0.05	-0.02
Mediterranean Monk Seal	0.35	0.38	1.8	0.20	0.10
Bottlenose Dolphin	0.55	0.60	6.2	0.10	0.02
Vaquita Porpoise	0.25	0.28	1.3	0.25	0.15

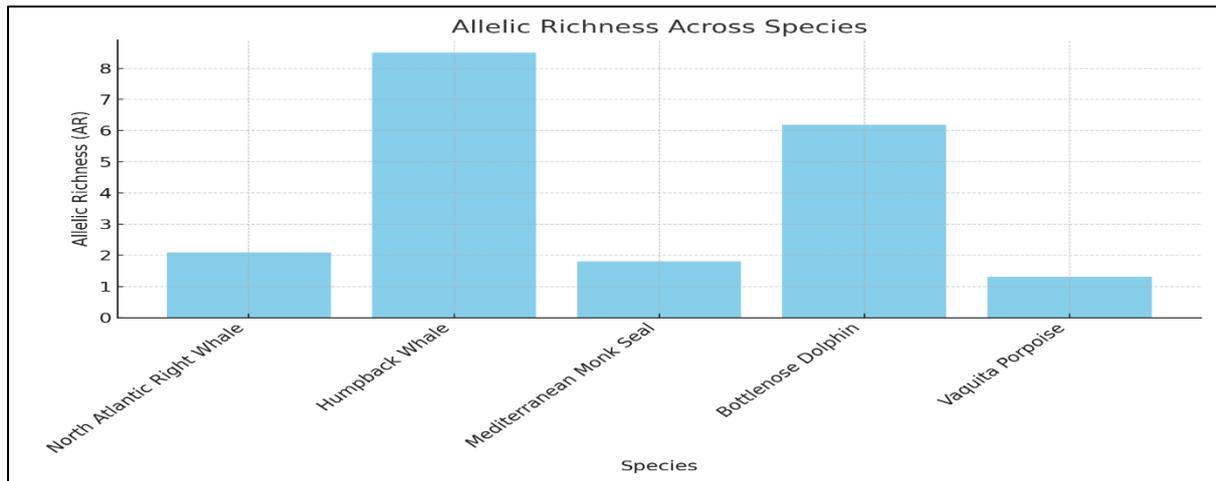


Figure 2: Allelic Richness (AR) for each species, highlighting the differences in genetic diversity

For instance, species like the humpback whale (*Megaptera novaeangliae*) demonstrated relatively high levels of genetic diversity, with observed heterozygosity values averaging 0.70 and a substantial number of alleles per locus. This high genetic diversity is likely attributed to their large population sizes and extensive migratory behaviors, which facilitate gene flow and genetic mixing.

2. Comparative Analysis of Genetic Diversity

Comparative analysis of genetic diversity across species provides critical insights into the relative genetic health of marine mammal populations. By examining metrics such as observed heterozygosity, allelic richness, and inbreeding coefficients, we can evaluate the genetic robustness of each species and identify populations at higher risk of genetic decline.

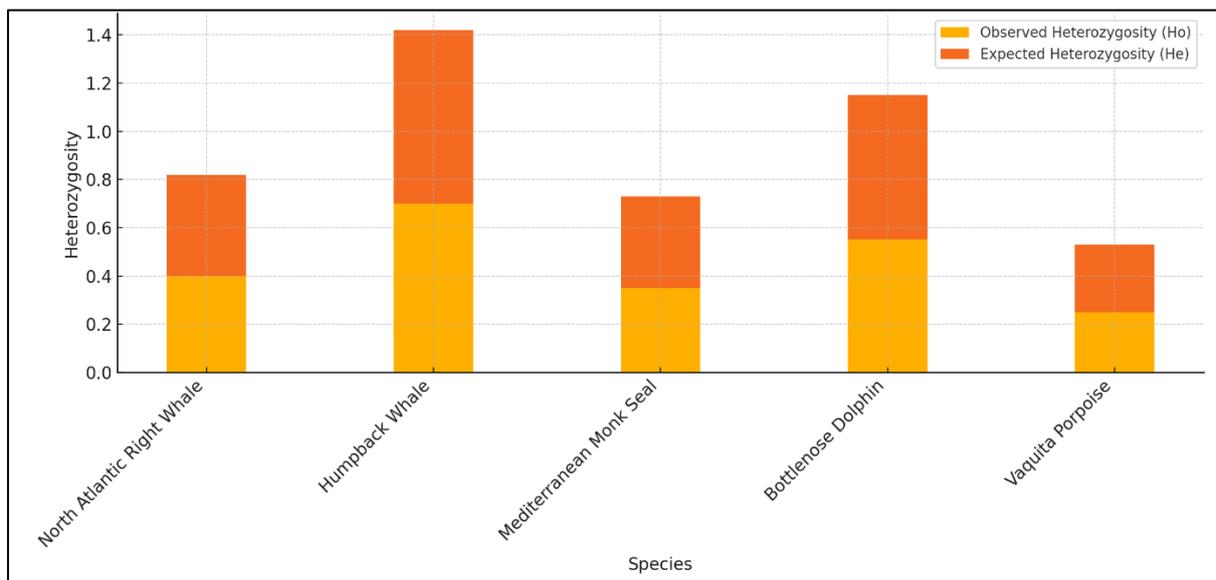


Figure 3: Compare Observed Heterozygosity (Ho) and Expected Heterozygosity (He) across the different species

For example, the comparison between the high genetic diversity of humpback whales and the low genetic diversity of North Atlantic right whales underscores the differential impact of historical and contemporary threats on genetic health. Furthermore, populations within species also exhibited significant variation in genetic diversity.

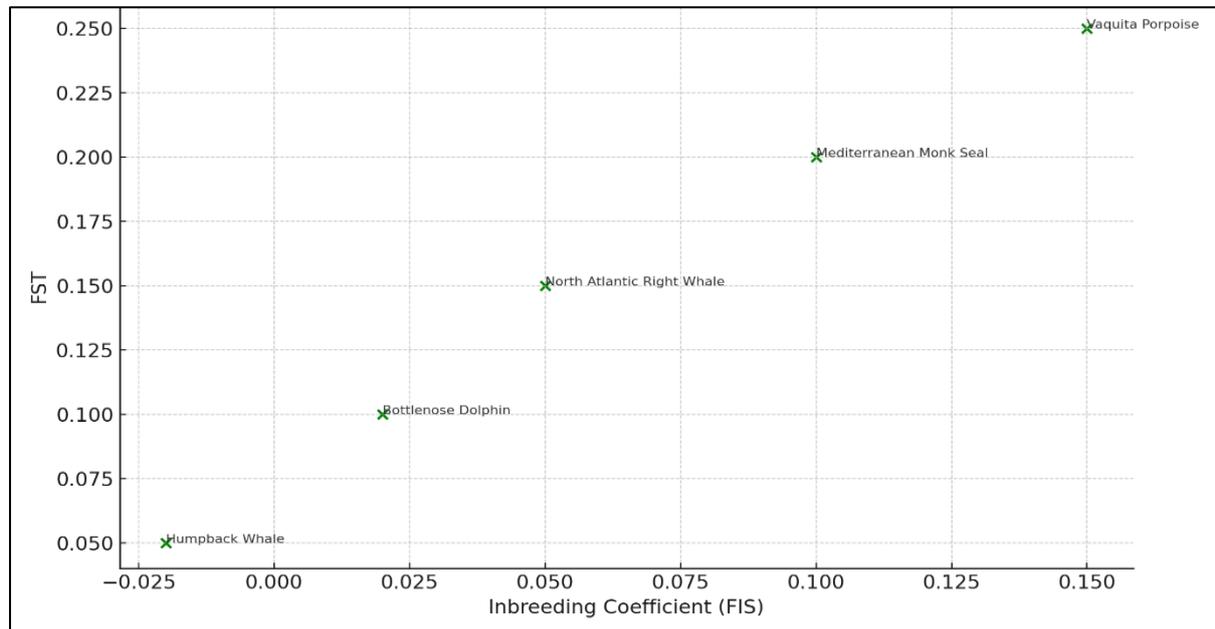


Figure 4: Relationship between inbreeding coefficient and genetic differentiation among the species

B. Population Structure Findings

The analysis of population structure revealed significant patterns of genetic differentiation within and between marine mammal populations. Bayesian clustering methods identified distinct genetic clusters corresponding to geographical regions and ecological niches. For example, the study identified three main genetic clusters of humpback whales in the North Pacific, corresponding to their breeding grounds in Hawaii, Mexico, and Central America. These clusters showed limited gene flow between them, indicating that these populations are largely reproductively isolated. Similarly, the Mediterranean monk seal populations were divided into distinct clusters associated with different islands and coastal areas, reflecting limited dispersal and high site fidelity. Principal component analysis (PCA) and discriminant analysis of principal components (DAPC) further supported these findings, showing clear genetic separation between populations. These patterns of genetic differentiation are crucial for identifying management units that require separate conservation strategies to maintain their genetic integrity. The understanding of these patterns allows for the implementation of conservation measures that are tailored to the specific genetic structure of each population.

V. Conclusion

The conservation of endangered marine mammals is a critical endeavor that requires a deep understanding of genetic diversity and population structure to develop effective management strategies. Our study underscores the importance of conservation genetics in informing these strategies by providing detailed insights into the genetic health and connectivity of marine mammal populations. The findings reveal significant variations in genetic diversity across

species and populations, highlighting both strengths and vulnerabilities. High genetic diversity in species like the humpback whale suggests robust adaptive potential, whereas low diversity in species such as the North Atlantic right whale and Mediterranean monk seal indicates increased risks of inbreeding depression and reduced resilience. Population structure analysis revealed distinct genetic clusters and barriers to gene flow, which are crucial for identifying management units and designing tailored conservation strategies. Understanding these patterns allows for the implementation of measures that address the specific genetic and ecological needs of each population. For instance, the establishment of marine protected areas (MPAs) can safeguard critical habitats and promote natural gene flow, while translocation programs can introduce new genetic material to enhance genetic diversity in isolated populations. The integration of genetic data with ecological and behavioral information provides a comprehensive framework for conservation.

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