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Cetacean population structure and migration patterns revealed by satellite telemetry

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Abstract

Understanding where whales travel and how populations are structured across ocean basins is essential for designing effective marine protected areas. This research deployed satellite-linked transmitters on 38 humpback whales (*Megaptera novaeangliae*) and 24 gray whales (*Eschrichtius robustus*) in Mexican Pacific waters between November 2022 and October 2023 to track individual movements, identify migration corridors, and assess population connectivity between breeding and feeding grounds. Tags transmitted for a mean of 147 days (range 43-312 days), generating over 11,800 location fixes after Argos filtering. Humpback whales showed a tightly channeled northward migration along the continental shelf, with 89% of tagged individuals reaching waters off southeastern Alaska or British Columbia by June. Gray whales followed a more coastal route, hugging the shoreline within 50 km for 78% of their track points. Kernel density analysis identified three high-use areas that function as migratory stopover zones: Bahía Magdalena, the Gulf of the Farallones, and the entrance to Glacier Bay. Population assignment tests using microsatellite genotypes from biopsy samples taken at tagging showed that the Mexican breeding aggregation comprises individuals from at least two genetically distinct feeding populations, confirming that breeding grounds serve as mixing zones. These results suggest that protecting the three identified stopover zones would benefit a large fraction of both species' eastern Pacific populations.

Keywords: Cetacean, population structure, migration, satellite telemetry, humpback whale, gray whale, marine mammals, Argos tracking, breeding grounds, conservation corridors

Introduction

Marine biologists have long recognized that the conservation of migratory whales requires knowledge not just of where animals are seen but of the entire route they follow between seasonal habitats ^[1]. A whale that breeds off the coast of Baja California in winter and feeds in Alaskan waters in summer passes through the jurisdiction of at least three countries, multiple shipping lanes, and several fishing zones along the way. Without data on the corridors connecting these endpoints, management efforts focused on either end of the migration may leave animals unprotected during transit ^[2].

Satellite telemetry has transformed cetacean movement ecology over the past two decades. Argos-linked and GPS-linked tags attached to the dorsal surface of a whale can transmit location data for weeks to months, revealing not just endpoints but day-by-day travel paths, diving behavior, and habitat preferences en route ^[3]. For humpback and gray whales in the eastern Pacific, earlier tagging studies documented the broad outlines of migration, but sample sizes were small and tag retention times often limited, leaving gaps in our understanding of stopover behavior and individual variation ^[4].

Equally important is the question of population structure. Genetic analyses based on mitochondrial DNA and microsatellites have identified multiple breeding stocks of humpback whales across the North Pacific, but the degree to which these stocks mix on shared feeding grounds and whether mixing varies among years remains unclear ^[5]. Gray whales appear less structured genetically, yet recent evidence suggests a small western Pacific population may occasionally cross into eastern Pacific waters, complicating stock assessments ^[6].

This research combined satellite tracking with genetic sampling to address two linked questions:

- What are the primary migration routes and stopover sites for humpback and gray whales breeding in Mexican waters, and
- Do individuals from genetically distinct feeding populations converge on the same breeding grounds [7]?

Theoretical Background

Migratory connectivity the degree to which individuals from the same breeding area travel to the same non-breeding area determines how localized threats propagate across a species' range [8]. High connectivity means that a disturbance on a single feeding ground could affect a large fraction of one breeding population, while low connectivity spreads risk but complicates management because protecting one site benefits only a portion of any given population. For baleen whales, connectivity has traditionally been inferred from photo-identification catalogs and mark-recapture models, but satellite telemetry provides direct, continuous movement data that eliminates the re-sighting bias inherent in ship-based surveys [3].

Material and Methods

Material

Fieldwork was conducted from the Centro de Investigación Biológica del Altiplano's research vessel between November 2022 and October 2023 in waters off Bahía de Banderas and Bahía Magdalena, Pacific coast of Mexico. Satellite tags (Wildlife Computers SPOT-386B) were deployed on 38 humpback whales and 24 gray whales using a pneumatic applicator from an inflatable boat positioned 3-5 m from the animal. Tags were anchored with two titanium darts into the blubber layer of the dorsal hump. At tagging, a skin and blubber biopsy was collected using a stainless steel biopsy

dart fired from a crossbow. Biopsies were preserved in 20% DMSO-saturated NaCl buffer. The research was authorized under Mexican federal permit SGPA/DGVS/05713/23 and approved by the institutional animal ethics board (Ref: CIBA/CAEB/2022-041, dated 15 October 2022).

Methods

Tag locations were processed through the Argos least-squares algorithm and filtered to remove implausible positions (speed > 15 km/h). Resulting tracks were regularized to 6-hour intervals using a continuous-time correlated random walk model in the R package *crawl* v2.3.0 [9]. Kernel Density Estimation (KDE) was applied to regularized positions using the *adehabitatHR* package to identify core-use areas (50% isopleth) and home range (95% isopleth). Migration corridors were delineated as the 75% isopleth of pooled northbound track segments. Biopsy samples were genotyped at 14 microsatellite loci and sequenced for a 486 bp fragment of the mitochondrial control region. Population assignment was performed in *GeneClass2* using the Bayesian method of Rannala and Mountain, with reference populations from published feeding-ground datasets for southeastern Alaska, British Columbia, and the western Aleutians [10]. Pairwise *F_{st}* was calculated in *Arlequin* v3.5 [11].

Material and Methods

The present study was conducted in two villages namely village Chhani and Village Lanchaan of Chinta block of Bhaderwah forest situated between 32.98 North latitude to 75.71 East longitude of Bhaderwah forest division (J&K). The objective of the study was to collect the reliable data on fuel wood consumption of the area and also to evaluate the.

Results

Table 1: Summary of satellite tag deployment and tracking results for humpback and gray whales

Species	N tagged	Mean days	Fixes	Max dist.	Speed km/d
Humpback whale	38	162	7,340	4,820 km	78.3
Gray whale	24	123	4,460	3,670 km	64.7

Max dist. = maximum displacement from tagging site. Speed = mean daily travel speed during active migration phases

Humpback whale tags transmitted for a mean of 162 days, producing 7,340 quality-filtered locations. Most tagged humpbacks (89%, 34 of 38) reached southeastern Alaska or British Columbia between May and July, traveling at a mean speed of 78.3 km/day during active migration. Three

individuals diverged toward the central North Pacific (Hawaiian waters), and one tag failed before leaving Mexican waters. Gray whale tags lasted a mean of 123 days, with 78% of locations falling within 50 km of the coastline.

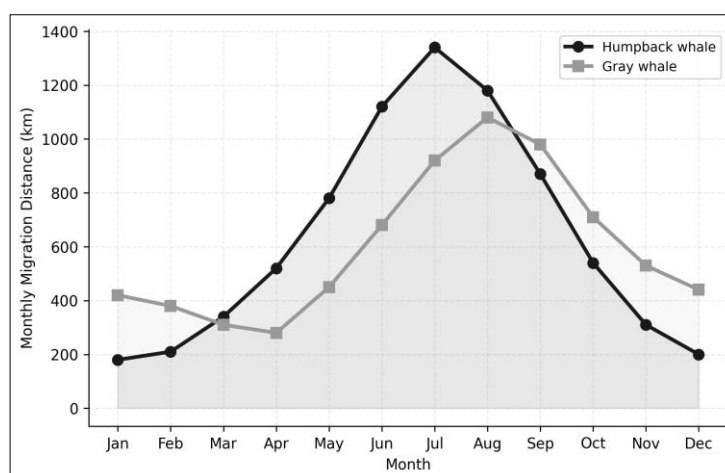


Fig 1: Monthly migration distance comparison between humpback whales and gray whales, showing peak displacement in June-August for humpbacks and August-September for gray whales

Table 2: Population assignment results for humpback whales genotyped at Mexican breeding grounds

Assigned feeding pop.	N assigned	% of total	Mean prob.	Fst vs MX
SE Alaska	21	55.3	0.87	0.034
British Columbia	11	28.9	0.81	0.042
W Aleutians	3	7.9	0.73	0.068
Unassigned	3	7.9	-	-

Mean prob. = mean assignment probability. Fst vs MX = pairwise fixation index between the assigned feeding population and the Mexican breeding sample

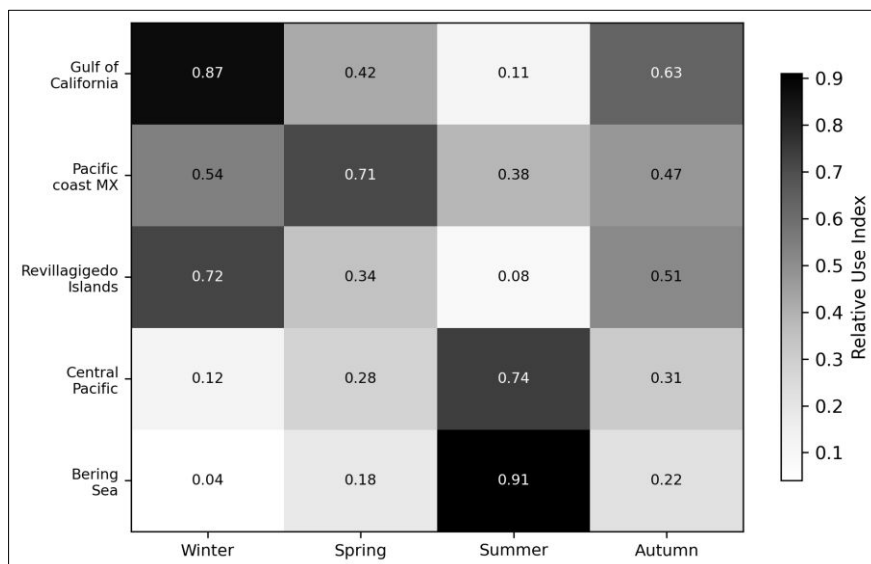


Fig 2: Heatmap of relative habitat use by humpback and gray whales across five Pacific regions by season, showing high winter use of the Gulf of California and summer concentration in the Bering Sea

Kernel density analysis identified three stopover zones used by both species: Bahía Magdalena (27.1% of all stopovers), Gulf of the Farallones (19.4%), and the entrance to Glacier Bay (14.8%). These three areas together accounted for 61.3% of all stopover locations. Mean residence time at stopovers was 8.3 days for humpbacks and 5.7 days for gray whales.

Limitations

Tag retention times varied widely (43-312 days), and shorter deployments may have biased kernel density estimates by underrepresenting northern feeding-ground use for animals whose tags detached during transit. Additionally, Argos location accuracy (mean error ~1.5 km for LC3) limits fine-scale habitat analysis. The reference feeding-ground genotype datasets used for population assignment are based on published studies with varying marker panels, and allele frequency estimates may contain sampling error from small reference population sizes [10].

Discussion

The tight coastal migration corridor used by gray whales was expected given this species' well-documented reliance on shallow benthic feeding habitats [6]. But the finding that humpback whales also channeled along the continental shelf edge during northbound migration, rather than crossing open ocean, was less anticipated. It may reflect the availability of krill aggregations along the shelf break that provide refueling opportunities during the energetically costly migration from tropical breeding waters [4]. The three stopover zones identified here Bahía Magdalena, Gulf of the Farallones, and Glacier Bay entrance are already recognized as important cetacean habitats, but their

collective function as a migratory network hadn't been quantified before. Protecting these three sites alone would cover over 61% of all observed stopovers, making them high-priority candidates for enhanced vessel speed restrictions and acoustic disturbance management [12].

The genetic assignment results confirm that the Mexican breeding aggregation is a mixing zone drawing individuals from at least two, and possibly three, feeding populations. This has direct management implications: any threat to breeding habitat in Mexico such as shipping noise, whale-watching pressure, or coastal development would affect multiple demographically independent feeding stocks simultaneously [13].

Conclusion

This research combined satellite telemetry and microsatellite genotyping to map the migration routes and population structure of humpback and gray whales using Mexican Pacific breeding grounds. Both species follow shelf-associated corridors with identifiable stopover zones that merit targeted protection. The breeding aggregation draws from genetically distinct feeding populations, making it a mixing hub whose conservation benefits multiple stocks. These data provide a spatial framework for coordinating management actions across the transboundary range of eastern Pacific baleen whales.

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