

# Fin Whale (*Balaenoptera physalus*) Bones from a 5850 Year Old Shell Midden on San Miguel Island, California, USA

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## ABSTRACT

*Large cetaceans, once diverse and abundant in northeastern Pacific waters, were heavily impacted by commercial whaling in historic times. As a result, relatively little is known about the biogeography of many whale species prior to European contact. On Alta California's Channel Islands, maritime peoples hunted dolphins and porpoises for millennia, but ethnohistoric data suggest that larger cetaceans were not hunted. The Island Chumash scavenged beached whale carcasses for food and technological purposes, however, and the bones of large whales are relatively common in many Channel Island shell middens. Cetacean bones from such sites provide unique opportunities to document the ancient distribution and human use of larger whale species, but many bone fragments are not identifiable to the genus or species level. Here, we report genomic data for two whale bones recently recovered from a ~5850 year old shell midden on San Miguel Island. Both provided aDNA identified as fin whale, the second largest of the great whales, a species rare in California's coastal waters during the 20<sup>th</sup> century, but found in growing numbers in the area today. Our analysis provides one point in space and time for the distribution of fin whales in the past, but a wider identification of whale bones from coastal archaeological sites can potentially expand such data for numerous whale species, adding significantly to an understanding of their distributions, ecology, and utility for humans in the past.*

**Keywords** cetaceans, aDNA, historical ecology, whale bone artifacts, salvage archeology, California Channel Islands

*The systematic destruction of the great whales was a stupendous act of modern ecological folly that rivals the extirpation of the once vast herds of American bison in efficiency, speed, and last-minute second thoughts that marginally spared the species. ... It is therefore remarkable that so little serious attention has been paid until quite recently to the ecological consequences of the relatively sudden removal of whales in terms of their past role as both keystone predators in food chains and as once-superabundant prey and carrion. (J. B. C. Jackson 2006:27)*

Worldwide, nearly all large cetacean species went through major population bottlenecks caused by widespread commercial whaling activities from the 17<sup>th</sup> century through the mid-20<sup>th</sup> century. As a result, the original population size, distribution, and ecology of many large whale taxa were altered significantly, leaving gaps in our knowledge of their deeper biogeographic history. The study of fossil whales, logbooks and other historical accounts can fill some of these knowledge gaps (e.g., Scammon 1874). Original population sizes remains poorly known for most species (Best 1993; Clapham et al 2002) but new methodologies such as genomic analysis of surviving populations offer new insights into pre-whaling population size and structure (e.g., Palumbi and Roman 2006; Roman and Palumbi 2003). Monitoring of their behavior, ecology and recovery under legal protections implemented in the late 20<sup>th</sup> century offers new insights into their functional role in marine ecosystems (Estes et al. 2006). Nonetheless, much remains to be learned about the deeper history of many large whale species around the world.

Coastal shell middens around the world provide a wealth of information on ancient marine ecosystems, the biogeography of extant, extinct, and endangered species, and human articulation with coastal ecosystems and populations (Erlandson and Rick 2010). To understand the historical ecology of marine ecosystems, archaeologists can tap a wide variety of data from modern ecological studies, historical and ethnographic accounts, and biological, geochemical, genomic, and other techniques. Such tools have been particularly effective in documenting the deep history of human use of fish, shellfish, birds, pinnipeds, and small cetaceans, the remains of which are often abundant and relatively well-preserved in coastal shell middens. They have more rarely been applied to the remains of large whales, whose dietary significance may be under-represented in most coastal middens due to the differential transport of meat and blubber vs. bones (Smith and Kinahan 1984). Along with their dietary contributions, the bones of large whales were often used by coastal peoples for architectural and other technological purposes. Unfortunately, these human uses often leave whale bones found in archaeological sites fragmentary, modified, or consisting of elements (ribs, etc.) that are difficult to identify to species or even genus (Buckley et al. 2014; Monks et al. 2001; Seersholm et al. 2018:7773).

Today many marine mammal species and populations are recovering under legal protections such as the 1972 Marine Mammal Protection Act and related conservation efforts. Understanding the biogeography, genetic diversity, ecology, and demography of marine mammal populations in the past is critical to such conservation, restoration, and management efforts (see Braje and Rick 2011; Erlandson et al. 2014; Estes et al. 2006; Palumbi and Roman 2006). For some pinnipeds, the deeper time perspectives offered by archaeological records has identified anomalies in the distributions of ancient populations or species versus those found historically or among post-bottleneck recovering populations (e.g., Rick et al. 2009, 2011). For large cetaceans of the eastern Pacific, only limited archaeological data are currently available with which to map the ancient distribution and abundance of various species (see Huelsbeck 1994; Monks et al. 2001; Wellman et al. 2017). Here we help address that gap through the aDNA analysis and specific identification of two whale bones recently recovered from a 5,850 year old shell midden on San Miguel Island.

## BACKGROUND

Humans have hunted or scavenged large whales for millennia. Some Middle Stone Age and Late Stone Age shell middens in South Africa have produced barnacles (e.g., *Coronula* spp.) that live only on whales, for instance, suggesting that early *Homo sapiens* scavenged whale blubber and meat from beached whales, then transported such resources back to nearshore camps (Kandel and Conard 2003).

Archaeological and ethnohistoric data document that later peoples in various parts of the world, including the Arctic and Northwest Coast of North America, systematically hunted whales (see Drucker 1951; Huelsbeck 1994; Monks et al. 2001; Wellman et al. 2017), possibly beginning ~3,000 or so years ago.

California's Channel Islands, with a history of human occupation spanning at least 13,000 years, have been a particularly rich source of archaeological data used to reconstruct the historical ecology of marine ecosystems of the Southern California Bight (e.g., Braje et al. 2017; Erlandson et al. 2014; Rick et al. 2015). Today the waters of the Santa Barbara Channel and larger Southern California Bight are home to at least 27 cetacean species, nearly one-third of all extant cetaceans worldwide. Among the larger cetaceans, gray, blue, fin, humpback, minke, sperm, pilot whales, and orcas have all been seen in Santa Barbara Channel waters ([NPS webpage](#)). Smaller cetaceans (dolphins and porpoises) were actively hunted and consumed by Channel Island peoples since at least the Middle Holocene and for these considerable faunal data are available on the species hunted (e.g., Glassow et al. 2008; Porcasi and Fujita 2000). We know comparatively little about the deep history of most of the larger cetacean species in the area, however, many of which were hunted to the brink of extinction by historical commercial whaling.

The Island Chumash fished, foraged, and hunted in Channel Island waters for millennia, including the hunting of pinnipeds, sea otters, porpoises, dolphins, and large pelagic fish such as swordfish, tunas, and sharks. There is no convincing archaeological or ethnohistoric evidence that the Chumash hunted large cetaceans (Heizer 1974), but they reportedly utilized the carcasses of dead whales for food, fuel, technological, and ritual purposes. In fact, the bones of large whales are relatively common constituents found in Island Chumash archaeological sites, often used as house supports (ribs), bowls or seats (vertebrae), burial associations (scapula and other elements), platters (vertebral epiphyseal plates), and other purposes. The earliest whale bone from a Channel Island archaeological site from a small shell midden (CA-SMI \_\_\_ ) on San Miguel Island dated to ~10,000 years ago (cal BP) and reportedly consists of a fragment of a petrosal bone from an unidentified large whale (Watts 2013:41).

Unfortunately, even for later sites we know very little about the species of whales utilized by the Chumash. Humpback (*Megaptera novaeangliae*) and California gray (*Eschrichtius robustus*) whales are among the most abundant larger cetaceans in the area today and might be expected to be the most common species represented in archaeological sites. Today two of the largest baleen whale species, the blue whale (*Balaenoptera musculus*) and fin whale (*B. physalus*), are also regularly seen in Santa Barbara Channel waters, although both were fairly rare until relatively recently. Historical accounts (e.g., Scammon 1874) also indicate that these large cetaceans were present along the California Coast during the early years of commercial whaling in the area.

CA-SMI-526 is a very large shell midden formed on a long linear dune near Point Bennett on the northwest coast of San Miguel Island (Figure 1), the westernmost of the Northern Channel Islands. Although most of the site appears to be relatively stable today, its northern end overlooks a rocky coastline where marine erosion and strong northwesterly winds have exposed a series of shell midden strata divided by dune sands and paleosols representing episodes of dune building and relative landform stability, respectively. Because expanding pinniped populations on San Miguel Island have been implicated in the destruction of several coastal shell middens (see Braje et al. 2011), the areas where they haulout on land have been actively monitored by archaeologists and biologists for the past decade.

## METHODS

### Field Methods

Emergency salvage excavations at CA-SMI-526N were prompted by the recent destruction of the site by the activities of California sea lions (*Zalophus californianus*) hauling out on the site surface. A visit by DeLong and Erlandson in 2017, identified remnants of a dense “red abalone midden” (see Glassow 2016) eroding from a paleosol deeply buried in a sand dune well below a dense Late Holocene midden that caps the dune. Two  $^{14}\text{C}$  dates on red abalone shells collected from the red abalone midden demonstrate that it was deposited ~5,850 cal BP or 3900 B.C.E. Consultations between DeLong and Erlandson, Laura Kirn of Channel Islands National Park, and the Elders Council of the Santa Ynez Indian Reservation, led to a plan to salvage a sample of the red abalone midden before it was completely destroyed. Salvage investigations in February 2018 included the excavation of three contiguous 1 x 1 m test units, oriented in a 1 x 3 m long trench that penetrated a shell midden deposit that ranged from 5 to 20 cm thick (Figure 2). Two cetacean bones were recovered from this trench from a shell midden deposit densely strewn with hundreds of large red abalone (*Haliotis rufescens*), California mussel (*Mytilus californianus*), owl limpet (*Lottia gigantea*), sea urchin (*Strongylocentrotus* spp.), and other shell fragments, as well as the bones of fish, birds, and other marine mammals. One large slab of whale bone found at the base of the midden in Units 1 and 2 was too fragmentary to identify to element or species. A second specimen was found in Unit 3 and is a small portion of an epiphyseal plate—probably used as a platter or serving plate—from the vertebral disc of a large whale.

### DNA Extraction and Analysis

To try to identify the species represented by these two bone whale fragments, we sent small samples of each specimen to the National Marine Fisheries Service’s Southwest Fisheries Science Center (SWFSC) for aDNA analysis. At the SWFSC’s Ancient DNA Lab, aDNA extractions were performed on both pieces of bone using the methods of Morin et al. (2006) and Höss and Pääbo (1993), modified as described in Hofreiter et al. (2004). PCR reactions were performed in 50ul volumes containing 1X NH4 PCR buffer (16 mM (NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub>, 67 mM Tris-Cl (pH 8.8 at 25°C), 0.01% Tween-20; Bionline USA Inc., Randolph, MA), 300 nM of each primer, 150uM each dNTP (dA, G,C, TTP), 2.5 mM MgCl<sub>2</sub>, 2.5 units of TAQ polymerase (Biolase, Bionline USA Inc., Randolph, MA), and 5–10uL of DNA. PCR cycling conditions included initial denaturing for 2 minutes, 30 seconds at 94°C, 45 cycles of 94° for 30 seconds, 48° for 45 seconds, and 72° for 90 seconds, followed by a final extension period of 72° for 10 minutes.

Because of the degradation of the aDNA, PCR was performed by amplifying three overlapping sections of the mitochondrial control region using several primer pairs, each approximately 200-270 base pairs in an attempt to obtain a final sequence of 400bps. The PCR product was generated using the primers pairs TRO-A3, AD1-DL1, and D-A3r from Robertson et al. (2007). PCR amplification was successful for only the two latter primer pairs. The amplified product was sequenced in both directions using the same primers on the Applied Biosystems Inc. (ABI) 3130 Genetic Analyzer using standard protocols and ABI BigDye Terminator v3.1 chemistry. Sequences were aligned and edited by eye using Sequencher (v4.8, Gene Codes Corp., Ann Arbor, MI) to create a consensus sequence. A 204bp sequence was obtained from each sample. The sequences were identical to each other and checked for species identification in GenBank.

## RESULTS

The aDNA sequences extracted, amplified, and analyzed from the samples of two whale bones from CA-SMI-526N were both identified as fin whale (*Balaenoptera physalus*), with a 100 percent match to several fin whale sequences submitted to GenBank. It seems likely that both fin whale bones are from the same individual, but genomic analysis was not detailed enough to determine this with certainty. Currently, we have no way of knowing if these fin whale bones are the result of human harvest of the meat, bone and blubber of stranded fin whales, or just the use of skeletal elements found on San Miguel Island beaches.

Fin whales, the second largest whale (and animal) on earth, are found in oceans virtually worldwide. They can live more than 90 years, reaching lengths of ~26 m and weights of 80 tons or more. One of the baleen whales (Balaenoptera), the fin whale is a filter-feeder, primarily eating small schooling fish, squid, and crustaceans. Other than humans, the only known predator of fin whales is the orca or killer whale. Historically, Scammon (1874:35-36) described fin (a.k.a. finback) whales as being relatively common along the Pacific Coast of North America, especially during the summer months, and noted that they could sometimes be found in groups of 15-20 individuals. He also noted that although they sometimes approached ships, they were very difficult to capture due to their speed and unpredictable movements. Because of their size and speed, it seems unlikely that the Island Chumash or other indigenous peoples would have hunted fin whales from their much smaller boats. Today, there are an estimated 9,000 fin whales in the waters off of California, Oregon, and Washington (Nadeem et al., 2016). They were heavily hunted commercially during the mid-20<sup>th</sup> century and are still listed as an endangered species.

Documenting that fin whales were present in coastal California and Santa Barbara Channel waters 5,850 years ago currently provides the earliest evidence for human use of their skeletons (and potentially the meat of stranded individuals) known from the Pacific Coast of North America and potentially the world (see Buckley et al. 2014). Because fossil whale bones post-dating the end of the Last Interglacial are likely to be found along ancient shorelines (or deeper waters), the specimens from CA-SMI-526 also provide valuable points in space in time for the known distribution of Fin whales along the Pacific Coast of North America in the deep past, well before their decimation by commercial whaling in historic times.

## DISCUSSION AND CONCLUSIONS

Fin whale bones have recently been identified via aDNA analysis in a Maori midden in New Zealand (Seersholm et al. 2018) and through ZooMS analysis in North Atlantic collections from archaeological sites in Iceland and Scotland (Buckley et al. 2014). To our knowledge, however, the only other fin whale bones identified in an archaeological site along the Pacific Coast of North America are from the Ozette site, a Makah whaling village located on Washington's Olympic Peninsula, where they comprised a very small percentage (<1%) of a large assemblage dominated by gray and humpback whale remains (Huelsbeck 1994). In another large assemblage, this one from the British Columbia Coast, Monks et al. (2001) morphologically identified 89 elements from large whales, including humpback (78%), gray (14%), right (*B. glacialis*; 5%), and minke whales (2%). At the Par-Tee site (35CLT20) on the northern Oregon coast, Wellman et al. (2017) used aDNA analysis to identify 28 of 30 tested whale bone samples: 17 (60.7%) as gray, 9 as humpback (32.1%), and one each (3.6%) as orca (*Orcinus orca*) and minke (*B. acutorostris*) whales. These Northwest Coast examples all come from areas where whaling was integral to

indigenous cultures (B.C. and WA) or where ethnographic and archaeological data suggest that people hunted whales opportunistically prior to European contact (OR; Losey and Yang 2007; Sanchez et al. 2016).

As such, these Northwest Coast assemblages may be heavily selected culturally, favoring those species of medium-sized whales that could be hunted in relatively small boats paddled by human hunters armed with indigenous technologies that were ingenious but much less deadly than the explosive harpoons of later commercial whalers. In this sense, whale bones from Channel Island archaeological sites—and other coastal areas around the world where whale carcasses were obtained primarily via scavenging rather than active hunting—may more closely represent the natural diversity and demography of large whale taxa that lived and died in nearby waters. Further analysis of archaeological whale bone assemblages from such areas is needed to determine if this hypothesis is true.

With the rapid advances taking place in genomic, isotope, trace element, and other scientific analyses of bones from archaeological sites, it should soon be possible to gain much more detailed insights into the historical ecology and more recent evolutionary history of whale species around the world. For now, we hope this paper helps to inspire further application of- genomic and other analytical methods (i.e., Buckley et al. 2014) that can identify archaeological whale remains.

#### ACKNOWLEDGMENTS

*First and foremost, our research was supported by our home institutions. We are deeply grateful, however, to Russell Galipeau, Laura Kirn, Bert Ho, and Ian Williams of the Channel Islands National Park for facilitating the data recovery at CA-SMI-526N. Hannah Erlich, Mark Alow Garcia, and Bert Ho assisted in our field work at the site and Terry Jones of Cal Poly San Luis Obispo loaned us field equipment for the excavation. We are also grateful for the support of the project by the Elders Council of the Santa Ynez Band of Mission Indians and Quntan Shup of Southern Owl Clan Consultants. Finally, we thank the editors and reviewers for their help in the review, revision, and publication of this paper.*

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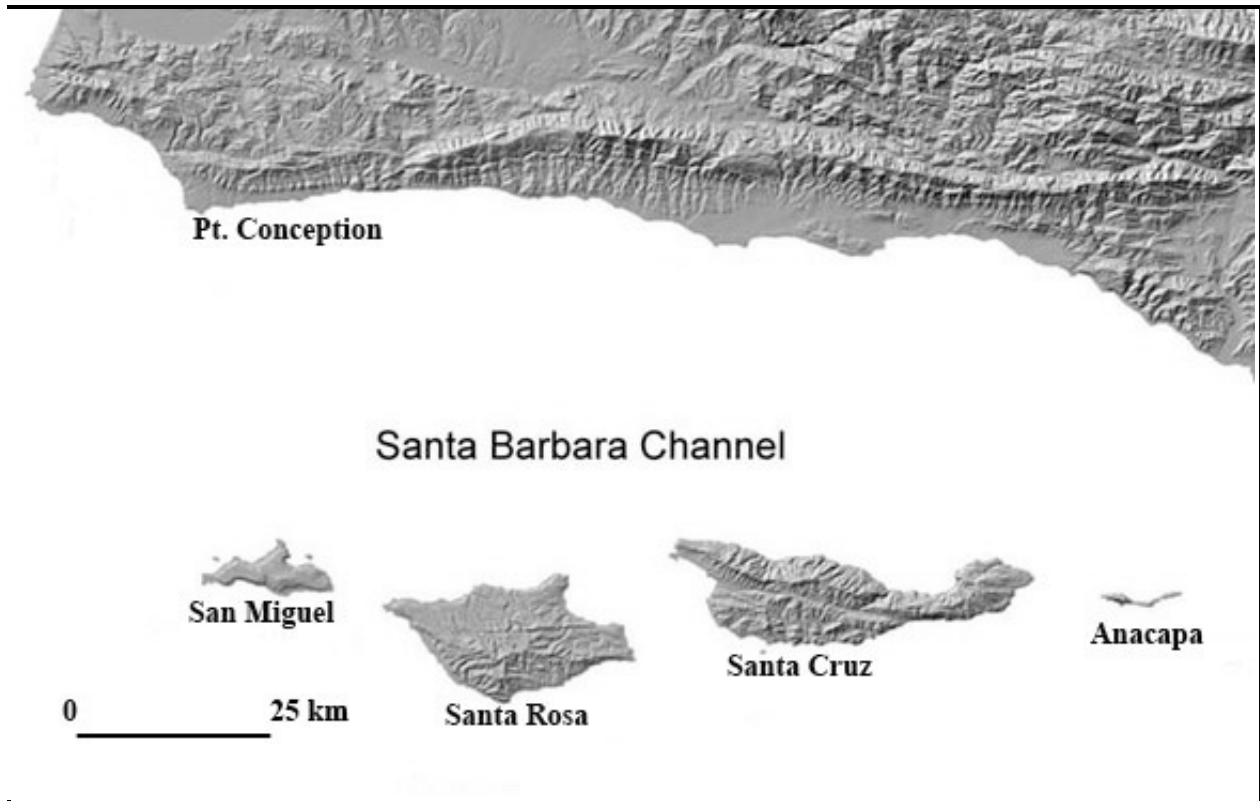


Figure 1. The general location of CA-SMI-526.



Figure 2. Unit 1 after initial cleanup (top), showing the density of red abalone and other shells exposed in the midden at CA-SRI-526N (top); and near the completion of excavation, showing a portion of an unidentified whale bone element partially exposed (upper right) at the base of the shell midden (bottom), Photos by J. Erlandson.