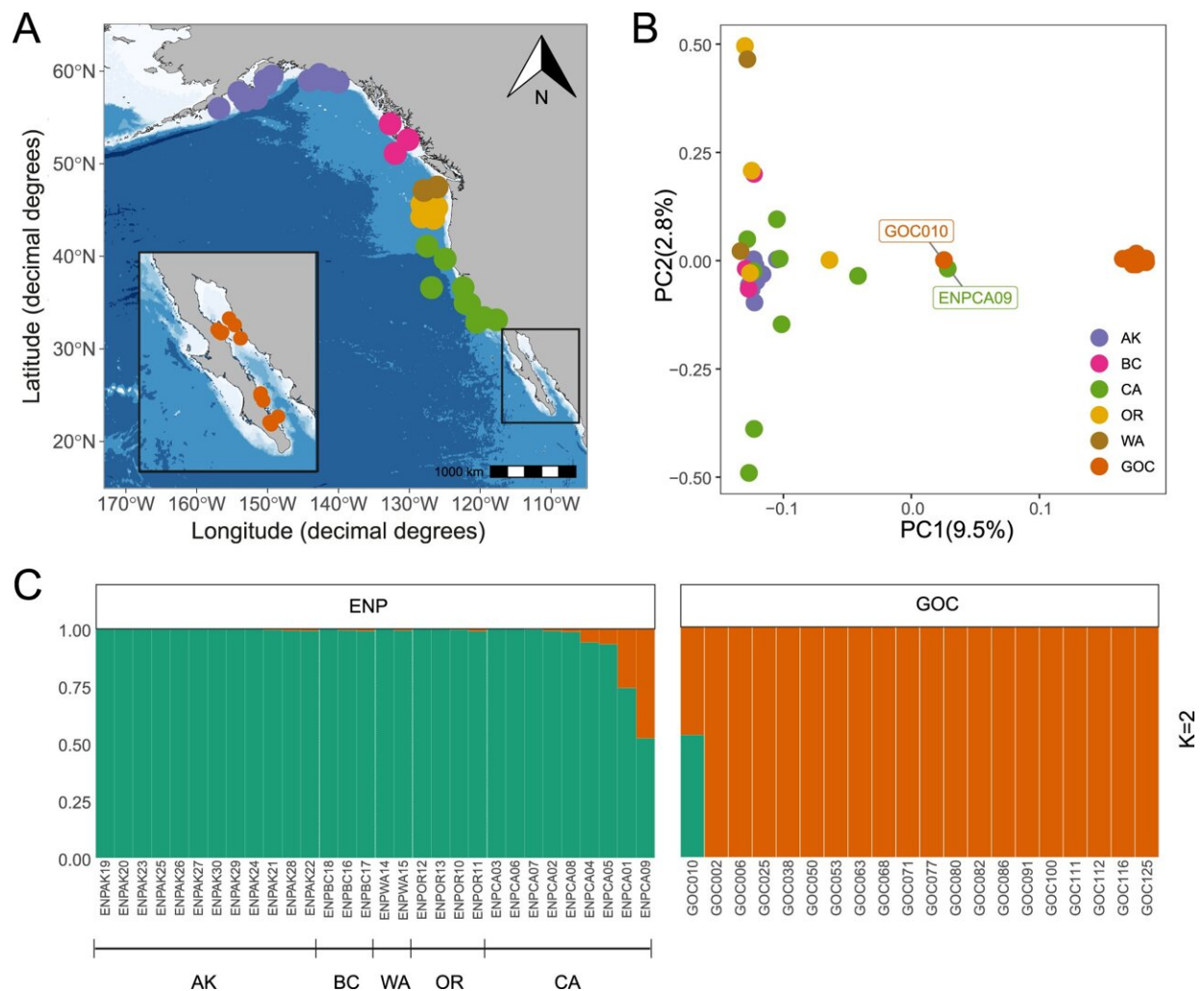


Whaling wiped out far more fin whales than previously thought

October 13 2023, by Holly Ober



Population structure and sample origins for the fin whale genomes obtained in this study. **A** Thirty skin samples were collected along Eastern North Pacific (ENP) locations near Alaska (AK), British Columbia (BC), Washington (WA), Oregon (OR), and California (CA) from 1995 to 2017. Twenty samples were

collected in seven sites within the Gulf of California (GOC) from Bahía de La Paz and Los Frailes in the southern Gulf to Bahía de los Ángeles, Puerto Refugio, and Bahía Kino around the Midriff islands. **B** PCA for 50 samples are colored by their location origin. The admixed individuals are labeled. **C** Admixture analyses supported two ancestral populations ($K = 2$). Credit: *Nature Communications* (2023). DOI: 10.1038/s41467-023-40052-z

A new genomic study by UCLA biologists shows that whaling in the 20th century destroyed 99% of the Eastern North Pacific fin whale breeding, or "effective," population—29% more than previously thought.

But there is also some good news: Genes among members of this endangered species are still diverse enough that current conservation measures should be enough to help the [population](#) rebound without becoming inbred. The study also found that the health of this group is essential for the survival of highly isolated, genetically distinct fin whales in the Gulf of California.

The study, [published in *Nature Communications*](#), is among the first to use whole genome information to get a picture of the size and [genetic diversity](#) of today's population. Previous studies had to rely on whaling records or mitochondrial DNA, which is inherited only from the mother, providing limited genetic information.

In the 19th century, whaling decimated most [whale species](#) around the world but left the largest ones—blue and fin whales—largely untouched. That changed with the advent of industrial whaling in the 20th century. By midcentury, close to a million fin whales worldwide had been slaughtered, at least 75,000 of these in the Eastern North Pacific.

"When you look at whaling records, you can only tell how many were killed. You can't tell how many there were to begin with," said corresponding author Meixi Lin, who worked on the project as a UCLA doctoral student and is now a Carnegie Institution for Science postdoctoral fellow at Stanford University. "We know 20th century whaling was severe, but we didn't know how severe it was for fin whales."

To find out, then-postdoctoral researcher and corresponding author Sergio Nigenda-Morales extracted DNA from [tissue samples](#) taken from wild fin whales in the Eastern North Pacific and the Gulf of California. He rounded this out with DNA provided by colleagues at the National Oceanic and Atmospheric Administration. In all, 50 whales were studied. Fin whales from the Gulf of California were included because the population there had been undisturbed by whaling, enabling researchers to assess their genetic diversity and learn how they were related to the Eastern North Pacific population.

"Getting samples from live whales is hard, because you don't know where they're going to be —and when they come up, you only have a moment to take the sample before they go back underwater," said Nigenda-Morales, now an assistant professor at Cal State San Marcos. "It is a humbling experience to conduct [field research](#) and interact with the second-largest animal on the planet."

The genome analyses revealed that the Gulf of California population diverged around 16,000 years ago, with a population that hovered around 114 adults of reproductive age. The population of breeding adults is a key indicator of a species' ability to sustain itself. The Eastern North Pacific effective population remained at around 24,000 individuals for thousands of years, until a severe decline happened between 26 and 52 years ago—a period that coincides with 20th century whaling—to only about 305 individuals.

Past ecological studies had suggested a 70% reduction in fin whale populations, while earlier [genetic studies](#) estimated a much larger pre-whaling population.

"It's usually hard to detect such strong recent reductions in the genome. But in this case, fin whales were really abundant before, which made the sudden reduction very obvious in our data. If the reduction hadn't been so strong, we wouldn't have been able to detect it," Nigenda-Morales said.

When a population suffers such a drastic decline, harmful genes left in the remaining organisms can become amplified over time as the small population size inevitably forces individuals carrying those genes to breed together. These harmful genes can reduce the health of the overall population and cause it to die out. Genetic diversity is still high among Eastern North Pacific whales, meaning that multiple versions of many genes are still plentiful and harmful genes have not yet become common.

"Most of this variation originated long, long ago, so genetic diversity in the small number of surviving individuals comes from their ancient history," said co-author Kirk Lohmueller, a UCLA professor of ecology and evolutionary biology.

Luckily, thanks to the slow pace of fin whale reproduction, the population reduction caused by whaling at its strongest point lasted for only two fin whale generations—a 50-year span—and ended with the implementation of the international whaling moratorium in 1985. Since then, the population has slowly recovered, and harmful genes have not had time to pile up.

However, [computer simulations](#) show that if the population remains at its current size, the diversity will begin to vanish. The study's authors write that the most important thing governments can do to aid fin whale

recovery is to continue to enforce the whaling ban so that fin whales have time to increase their numbers.

The future of [fin whales](#) in the Gulf of California also depends on the recovery of the Eastern North Pacific population. The genomic analysis showed that many harmful genes have become common in the former group, and that the only source of new genetic variants is the occasional Eastern North Pacific whale who wanders into their territory about once in every three generations. This infusion of new genetic material, however, has been enough to keep the population going.

For now, current protections for both populations appear sufficient, though they will need to remain in place for a long time. But climate change, ship strikes and other human-caused disturbances could jeopardize the species' recovery. The authors expect that ongoing research will help identify additional conservation measures.

"With improvement in computational models, we can incorporate factors like [climate change](#) and relate the risk of extinction from human-mediated processes with what's happening at the genomic level," said Lohmueller. "Continuing to develop such models is as important as collecting more data."

Nigenda-Morales and Lin undertook the research as doctoral students of UCLA professor and senior author Robert Wayne, who continued working on the project until he passed away late last year. The authors have dedicated the paper to him.

More information: Sergio F. Nigenda-Morales et al, The genomic footprint of whaling and isolation in fin whale populations, *Nature Communications* (2023). [DOI: 10.1038/s41467-023-40052-z](https://doi.org/10.1038/s41467-023-40052-z)

Provided by University of California, Los Angeles

Citation: Whaling wiped out far more fin whales than previously thought (2023, October 13)
retrieved 27 April 2024 from

<https://phys.org/news/2023-10-whaling-fin-whales-previously-thought.html>

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.