

Killer whale genetics: Redefining stock structure in a marine top predator

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Recent research sheds light on stock structure of these apex predators in the northern North Pacific Ocean, with important implications for management. Credit: Km M. Parsons, National Marine Mammal Laboratory, NOAA Fisheries

Found in every ocean around the world, killer whales are a force to be reckoned with globally. Their remarkable social bonds and sophisticated hunting techniques make them top predators in their salty domain. For many years, it was assumed that these clever, highly mobile whales bred with each other freely in the seemingly homogeneous ocean. As our

understanding of the oceans' complexity has grown, and dedicated researchers have peered ever deeper into the world of killer whales, it has become clear that the truth is far more nuanced.

As the agency responsible for conserving and managing killer whales in U.S. waters, the National Oceanic and Atmospheric Administration (NOAA) faces a major challenge – it must identify orca subpopulations, understand their needs, and develop effective and sometimes unique ways to manage them. Figuring out the patterns of similarity and relatedness coded in the whales' DNA also gives managers important insights into how these subpopulations arose, what factors shaped them, and what drove divergence in the species complex. This work has implications beyond identifying the boundaries of whale stocks. It is fundamental for evaluating the status of killer [whale populations](#).

Recent studies have shown that distinct groups of killer whales gather in the same place seasonally. Previously, scientists didn't know whether this was attributable to feeding or mating patterns. Now, [genetic evidence](#) and observations of individual whales have shown that these whales exhibit low levels of "[gene flow](#)" - breeding among subpopulations. A new paper by NOAA scientists available via Open Access in the *Journal of Heredity* ([DOI: 10.1093/jhered/est037](https://doi.org/10.1093/jhered/est037)) sheds light on these principles at work among killer whales in Alaska and the northern North Pacific Ocean.

Uncertainty about the [population structure](#) and a lack of data for the far western reaches of the North Pacific have led to very broad stock designations for killer whales in the waters of the western Gulf of Alaska, Aleutian Islands, Bering Sea, and Russia. Currently, fish-eating "resident" killer whales in the far North Pacific are considered a single stock that ranges from southeast Alaska through the Aleutian Islands and Bering Sea. Bigg's killer whales (formerly known as "transients") are currently managed as two stocks with overlapping ranges – the "Aleutian

and western" stock (Gulf of Alaska, Aleutian Islands, and Bering Sea) and the much smaller "AT1" stock which appears to range primarily throughout Prince William Sound and the Kenai Fjords.

By collecting 462 skin samples from both resident and transient wild killer whales and characterizing individual genetic variability using two different genetic markers (mitochondrial DNA and nuclear microsatellites), NOAA scientist Kim Parsons and her research partners discovered further subdivision within the whale stocks. In fact, the evidence is so strong that Parsons and her colleagues believe it's time to revise the killer whale stocks in the region. Genetic tests also indicated a lack of breeding between the two killer whale types highlighting the distinctness of the sympatric Bigg's and resident [killer whales](#) on a local scale. This finding corroborates a 2010 global genetic study of killer whales¹ and what many marine scientists suspected, based on years of studying wild orcas by tracking their movements and comparing their vocalizations, preferred prey, and social structure. Though much work remains to be done, powerful genetic tools have given us another vital piece of the puzzle.

Provided by American Genetic Association

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