New Count of Old Whales Adds Up to Big Debate

A new census of past whale populations has produced a controversial result. The study, using genetic markers, suggests that some whale populations were once about 10 times larger than previously suspected. The results hint that overhunting is the culprit and that the ocean can sustain more of the leviathans than previously thought. But some scientists question the findings, which have implications for international management practices: If the results are true, goals for whale recovery efforts should be set higher, the authors of the new work say.

Whale populations are known to be volatile; they have risen and plummeted with changes in market demands, hunting technology, and ocean conditions. To gauge populations, researchers traditionally relied on the sometimes spotty logbooks compiled by whaling captains over the last few centuries. Such records helped the International Whaling Commission peg the past North Atlantic population of humpback whales at about 20,000, for example, which is twice the current number.

But according to an analysis on page 508, North Atlantic humpbacks once numbered 240,000. Marine conservation biologists and geneticists Joe Roman of Harvard University and Stephen Palumbi of Stanford University used a small section of mitochondrial DNA (mtDNA) to reconstruct whale history. They compiled a database of mtDNA samples from humpback, minke, and fin whales mostly in the North Atlantic, with some data coming from the Southern Hemisphere and the Antarctic.

The team then compared the genetic distance between humpback and fin whales, which diverged at the genus level between 6 million and 10 million years ago, to estimate how quickly mtDNA had mutated. They also measured the genetic diversity within each species of whale. Given those numbers, they could calculate how many breeding females would have been necessary to accumulate the genetic variability observed in the mtDNA samples. (mtDNA is passed down through eggs, not sperm.) A final calculation, based on the proportion of a whale population that consists of breeding females, produced an estimate of the total population.

Roman and Palumbi calculate that fin whales in the North Atlantic once numbered about 360,000 individuals. That’s about six times more than previously thought. The North Atlantic minke whale population was once 265,000, or about twice today’s population. The results “require a fundamental rethinking of the oceans” and their capacity to support large numbers of whales, says Palumbi.

Although the researchers admit that these populations might have only existed hundreds of thousands of years ago, they speculate that huge numbers of whales roamed the oceans until relatively recently, when industrialized hunting began taking its toll.

But many geneticists and whale biologists object. “The proposed reduction in abundance could have happened at any point in evolutionary time,” says Per Palsbøll, a whale population geneticist at the University of California, Berkeley. That calls into question the work’s relevance to present management efforts, he says, “since the abundance estimate may relate to a rather different time period with a different climate and ecological conditions.”

Another key uncertainty is tied to setting the molecular clock of mtDNA. Karen Martien, a conservation geneticist and fisheries biologist at the Southwest Fisheries Science Center in La Jolla, California, disagrees with Roman and Palumbi’s estimated mtDNA mutation rates. “Some [mtDNA] base pairs might have mutated multiple times,” she says, but the researchers would register only one mutation, which would artificially inflate population estimates.

Palumbi acknowledges that the piece of mtDNA they used is “particularly badly behaved,” and the two researchers plan to use other genetic loci to confirm their findings, as well as data from Southern Hemisphere populations of whales. Nevertheless, Palumbi says that mutation rates would have to be five times higher and the duration of a generation at least twice as long to make the genetic analysis fit with conventional population estimates.

But some researchers aren’t ready to abandon estimates based on logbook records. “From what we know of the recent history of these populations, we simply cannot reconcile [Roman and Palumbi’s] figures with anything that’s even remotely realistic,” says Phillip Clapham, a whale biologist at the Northeast Fisheries Science Center in Woods Hole, Massachusetts.

Precipitous population drops are well documented in other large mammals, such as brown bears, points out Peter Beerrli of Florida State University in Tallahassee, who developed the population estimate model used by Roman and Palumbi. The team’s mutation rate is reasonable for mammals, he says, but other variables are uncertain enough to have thrown off their confidence intervals. Still, he believes “the numbers are not that wrong.”

—NAOMI LUBICK

www.sciencemag.org  SCIENCE  VOL 301  25 JULY 2003  451