Which Whales Are Hunted? A Molecular Genetic Approach to Monitoring Whaling

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In recognition of the global overexploitation of whale populations, the International Whaling Commission (IWC) voted in 1982 to impose an indefinite moratorium on commercial hunting. Although the moratorium has been in effect since 1986, whaling never actually ceased. Some IWC members have continued to hunt whales under scientific permit and for aboriginal or subsistence use. As a result, a commercial market for whale products has been sustained. Are the whale products available today exclusively from species hunted or traded in accordance with international treaties? A recent spot check of Japanese retail markets shows that they are not and suggests that the existence of legal whaling serves as a cover for the sale of illegal whale products.

In developing a Revised Management Procedure for future harvests, the IWC has carefully selected a catch-limit algorithm to maintain abundant stocks above 54% of their preexploitation numbers (*1*). By contrast, little attention has been given to the problem of illegal hunting of the many depleted stocks of whales. This omission is a particular concern given the magnitude of illegal whaling that can go unnoticed by the international community (*2*). Recent revelations of Soviet "secret" whaling in the Southern Hemisphere are staggering—from 1948 to 1973, four factory ships processed 48,477 humpback whales and reported only 2,710 (*3*). There is little doubt that this illegal hunting has contributed to the variable recovery among stocks of right and humpback whales (*4*, 5) and the absence of recovery among blue whales throughout the Southern Hemisphere (*3*).

In addition, there is increasing concern over illegal international trade in whale products and domestic sale from unregulated local whaling or fisheries by-catch. A recent attempt to export 260 tons of whale meat (reportedly in storage since 1976) from Russia to Japan was stopped by the Russian Ministry of the Environment (*6*). In October 1993, an air cargo handler in Oslo, Norway, uncovered 3.5 tons of whale meat, labeled as Norwegian shrimp, bound for export to South Korea (*7*). Baleen whales from by-catch of coastal Japanese fisheries are reportedly sold on the domestic markets without permission of government agencies (*8*). While the IWC Scientific Committee was meeting this year (May 1994), Japanese customs officials in Nagasaki intercepted 11 tons of undocumented whale meat inbound on a Korean fishing vessel (9).

The IWC's acceptance of the Revised Management Procedure at this year's meeting is generally viewed as a step toward the return to commercial whaling. If so, there is an urgent need to consider new and effective methods to verify catch records of exploited species and to interdict illegal trade of protected species. We tested the potential of molecular genetic methods for identifying the species and probable geographic source of whale products using samples purchased in retail markets throughout the main island of Japan from February to April 1993. The products were all labeled as "kujira," the Japanese generic term for whale, and ranged in quality from dried and salted strips of meat, marinated in sesame oil and soy sauce, to unfrozen sliced meat sold for "sashimi." In order to comply with restrictions on importation and exportation of whale products for scientific research (*10*), we conducted all analyses of whale tissue in situ using a portable laboratory for polymerase chain reaction (PCR). We successfully amplified, purified, and later sequenced 155 to 378 base pairs (bp; mean, 322 bp) of the mitochondrial DNA (mtDNA) control region from 16 commercial products. We focused on the control region of the mtDNA because of its high species- and population-specific variability (*4*, *11*, *12*). The "test" sequences were then aligned and compared to "type" sequences from a total of 16 cetacean species (n = 24 individuals, including representative geographical variants where available) found in our own collection (*4*) and in a complete search of GenBank (release 79) and European Molecular Biology Laboratory databases (release 36.0).

Bootstrap simulations unambiguously (>90%) grouped 14 of the test samples with a type-species sequence, providing statistical support for our species identifications (Fig. 1). Eight samples grouped with the minke whales and four grouped with fin whales. One sample of marinated meat, #19, yielded both a minke whale and a humpback whale sequence. Two samples, #13 and #28, were placed unambiguously (bootstrap value, 92%) within the family Delphinidae, which includes dolphins, pilot whales, and killer whales. One sample, #16, was placed intermediate between the sperm whale and the harbor porpoise, differing from each by >30%.

The humpback whale sequence (sample #19b) was identical to sequences we have obtained from other humpback whales sampled near the Mexican, Hawaiian, and Japanese (Ogasawara Islands) wintering grounds, suggesting a North Pacific origin. One fin whale sequence (sample WS4) was identical to fin whales sampled near Iceland (*13*) and in the western Mediterranean, suggesting that the origin of this sample was the North Atlantic. The other three fin whales, however, differed by 1.6 to 2.9% from the type sequences, possibly suggesting an origin outside of the North Atlantic. Among the nine minke whale sequences, eight were similar to type samples from

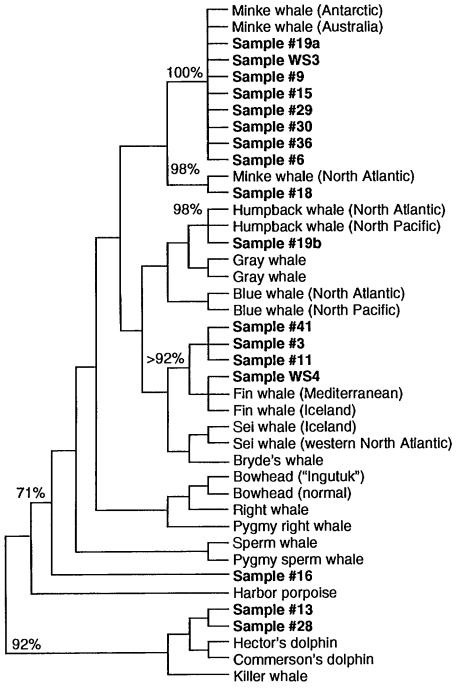

Fig. 1. Phylogenetic relationship of mtDNA control region sequences from "test" samples (#1 to #19b, shown in bold) of whale products from the Japanese retail market and "type" samples of whales and dolphins from our own laboratory or from GenBank (*11*, *23–26*). Sequences are homologous to positions 15,891 to 16,318 with respect to the mtDNA of the fin whale (*13*). Phylogenetic reconstruction of type and test sequences was performed with PAUP (*27*). Bootstrap values for the groupings of type and test sequences are shown along branches (*28*). Type and test sequences have been deposited in GenBank under accession numbers L35607 to L35633.

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Australia and the Antarctic (*14*), whereas sample #18 was most similar to a North Atlantic minke whale (*11*). Because minke whales from different oceans are known to be genetically distinct (*11*, *15*, *16*), it is likely that the sources of these products were the Southern Hemisphere and the North Atlantic, respectively.

To evaluate the legality or illegality of the baleen whale products (*17*), we reviewed the postmoratorium catch reports of the IWC (*18*). Several hundred Southern Hemisphere minke whales have been taken by Japan under scientific permit every year since 1987 and can be sold on the domestic market. Except for aboriginal catches by Greenland and Denmark, North Atlantic minke whales have been hunted only by Norway, which killed 95 during 1992 under scientific permit. Export of these products, however, has been prohibited by national policy, and the last recorded export of minke whales from Norway was in 1986 (*19*). Except for aboriginal catches by Greenland and Denmark, North Atlantic fin whales have not been hunted since 1989, when Iceland killed 68 under scientific permit. Fin whales from oceans other than the North Atlantic have not been hunted legally since the 1986 moratorium. Hunting of humpback whales in the North Pacific has been prohibited by international agreement since 1966 (*20*).

This review of recent whaling activity indicates that products available currently on the Japanese retail market may include species that have been imported illegally and others that have been hunted or processed illegally (*21*). An alternative interpretation is that fin whale, sold as unfrozen lean meat, has been in storage for at least 4 years, North Atlantic minke whale, sold as "sashimi," has been in storage (outside of the country of origin) for at least 7 years, and humpback whale meat has been in storage for 27 years.

These results demonstrate the inadequacy of the current system for verifying catch reports and trade records of commercial and scientific whaling. Systematic molecular genetic testing of commercial products (even those that have been smoked, marinated, or otherwise processed) should be integrated into requirements for future whaling under conditions for monitoring and observation by the IWC. The effectiveness of such a system would be improved by standardized labeling of retail whale products by species, geographic source, and processing date. Provided that tissue samples are made available from all whales caught under the Revised Management Procedure, it should be possible to obtain representative mitochondrial and nuclear (*22*) genetic information from all exploited stocks. Alternatively, tissue samples could be collected by biopsy sampling, as we have done (*4*). Genetic information from these samples could then be deposited in international genetic databases and would allow unambiguous identification of whale products of unknown origin.

Arguments about sustainable whaling are based on the tacit assumption that only abundant species will be killed and that depleted or endangered species will continue to enjoy protection. Without an adequate system for monitoring and verifying catches, however, history has shown that no species of whale can be considered safe.

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21. Experimental contamination can be excluded for all odontocetes, all minke whales, and most fin whales, because these were not identical to "type" sequences from our laboratory. For the two samples that were identical to sequences from our laboratory (WS4 and #19b), contamination is extremely unlikely. All field reagents were new, all equipment was decontaminated, nonaspirating tips were used for micropipetting, and no contamination appeared in the negative controls. Contamination after the amplified samples were returned to the laboratory can be excluded: Reamplifications from the magnetic beads always gave the same results.
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28. A 550-bp fragment of the mtDNA control region (*4*) was amplified in situ from 4 mg of ethanol preserved tissue with the use of Genereleaser (Bioventures, Inc.) and a portable thermal cycler (MJ Research, Inc.). After amplification by standard methods (*29*), double-stranded DNA was bound to streptavidin-coated beads (Dynal Corp.), washed to remove all unbound DNA, and returned to the laboratory for solid-phase sequencing (*30*).
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31. For collection of whale products we thank three agents who have asked to remain anonymous. For access to "type" samples or sequences we thank T. Albert, A. Baker, J. Calambokidis, S. Dawson, J. Mead, G. Notarbartolo-di-Sciara, C. Potter, R. Paterson, P. Rosel, L. Slooten, A. van Helden, and M. Zanardelli. For technical assistance and review we thank A. Perry, B. Bowen, R. Brownell, D. Taylor, and M. Donoghue. This project was conceived and coordinated by S. White and D. White of Earthtrust, Hawaii, and managed by D. Hack. MJ Research, Inc., donated a PTC-150 portable MiniCycler. Funding was provided by Earthtrust, the U.S. National Science Foundation, the University of Hawaii Foundation, and the University of Auckland.