

**DNA identification and the impact of illegal, unregulated,  
and unreported (IUU) fishing on rare whales in  
Micronesian waters**

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**Abstract**—There is little knowledge of the impact of illegal, unregulated and unreported (IUU) fishing on marine megafauna such as whales, dolphins and porpoises, especially in the tropical Indo-Pacific where this problem is rife. Here we present the results from the DNA identification of a rare beaked whale (*Mesoplodon ginkgodens*) confiscated from a Chinese (Taiwan)-registered longliner. The young, unweaned whale allegedly became entangled in the vessel's longlines when the vessel was fishing near Pohnpei, Federated States of Micronesia (FSM), and was held frozen in the hold for over a month before it was discovered during a routine vessel inspection in Guam. The captain stated that he planned to sell it in Taipei. This rare species, first described in 1958, is known from less than 30 records; this is the first from Micronesia. The images presented are the first available of a confirmed juvenile of this species. Importation of the whale carcass into Guam constituted a contravention of CITES (Convention on International Trade in Endangered Species) and the US Marine Mammal Protection Act, but the take or retention of marine mammals in the FSM region is currently not prohibited by law. In the absence of modifications to the FSM Marine Resources Act (2002), IUU fishing takes such as this will continue to pose a legally-sanctioned threat to rare cetaceans such as *M. ginkgodens*. Molecular monitoring can help to overcome some of difficulties of detecting by-catch and other IUU takes of marine megafauna. We suggest that expansion of existing regional inspection programs for vessels, docks, and markets to include sampling of suspicious carcasses, body parts, and processed products

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for DNA identification would provide a powerful and relatively inexpensive means of addressing this issue.

### **Introduction**

Accurate and efficient species identification is a serious constraint to comprehensive biodiversity assays and to the monitoring of species threatened by exploitation (Lawton et al. 1998, Tautz et al. 2003). This problem is at its most pervasive in biodiversity hotspots, such as tropical rainforests and coral reefs, where large-scale habitat destruction and exploitation of flora and fauna are common and comparatively well-documented (Myers et al. 2000). However, unregulated exploitation of poorly-known, cryptic species is also a grave issue for the open oceans that comprise most of our biosphere, where patterns and trends of species diversity and abundance are only just starting to be understood (Malakoff 2004).

The use of molecular markers such as DNA sequences to assist with routine species identifications and the discovery of new species has proved very effective. This approach is often referred to as 'DNA taxonomy' (Tautz et al. 2003), or, where a single mitochondrial locus is used for a wide range of taxa, as 'DNA barcoding' (Hebert et al. 2003). These same tools can also be extremely powerful when applied to the monitoring of illegal and legal trade in wildlife and their products, allowing unambiguous species identification, and in some cases, even identification of geographic or population origin. DNA identification has been used successfully to monitor and manage trade in whalemeat products (Baker et al. 2000), shark fins and body parts (Shivji et al. 2006), pinniped penises (Malik et al. 1997), tiger bone (Wetton et al. 2002), turtle meat (Roman & Bowen 2000), caviar (Birstein et al. 1998), and elephant ivory (Wasser et al. 2004). A number of initiatives are currently underway to establish comprehensive validated DNA databases to facilitate biodiversity surveys and the policing of exploitation and trade in endangered species (Floyd et al. 2002, Hebert et al. 2003, Ross et al. 2003, Dalebout et al. 2004).

Many pelagic species are impacted intentionally or incidentally by fisheries. Large marine megafauna are often highly vulnerable to exploitation and disturbance due to their longevity, late maturation, low fecundity, and in some cases, low abundance (Musick 1999). In addition to directed takes by regulated fisheries, such species may be caught incidentally in fisheries targeting other species ('by-catch'), or they may fall victim to Illegal, Unreported, and Unregulated fishing (IUU) (Lewison et al. 2004). Estimates based on by-catch reports from regulated fisheries suggest that hundreds of thousands of marine mammals are killed annually (Read et al. 2006). Such takes have been identified as the greatest immediate threat to whales, dolphins, and porpoises worldwide (Lewison et al. 2004). The majority of IUU fishing occurs in national exclusive

economic zones by far-seas (oceanic) fishing vessels registered in foreign countries. There are no statistics available on global IUU fishing levels as pirate fishers do not report their catch and hide their activities, and there is no systematic global monitoring program (Greenpeace 2006). In the tropical Indo-Pacific, an area where IUU is rife, almost anything that is caught has some value, whether for commercial sale, as bait, or for domestic consumption, blurring the line between intended catch and by-catch (Perrin et al. 2002). Monitoring of IUU fishing and enforcement of international and domestic regulations hinges on the ability to identify the species being impacted, for which DNA taxonomy can be a vital tool.

Here, we describe the combination of DNA taxonomy and law enforcement efforts to identify a rare cetacean taken by a far-seas fishing vessel, and discuss the utility of DNA taxonomy to detect IUU fishing and help assess its impact on pelagic megafauna. For DNA species identification, we make use of the ‘Witness for Whales’ component of the web-based program, *DNA Surveillance* (<http://www.DNA-Surveillance.auckland.ac.nz>) (Ross et al. 2003). This program aligns and compares a user-submitted DNA sequence generated from an unknown organism or biological sample against a comprehensive set of reference sequences curated by species’ specialists. A phylogenetic tree with scores from bootstrap resampling which reflects the robustness of ‘test’ and reference sequence groupings is returned, together with a table of evolutionary distances, from which the user can evaluate the species identity of the unknown ‘test’ sequence/organism. Reference datasets are available for the highly variable mitochondrial (mt) DNA control region and cytochrome *b* genes for the majority of cetacean species, including all 21 described species in the family Ziphiidae (beaked whales; Dalebout et al. 2004).

## Methods

On 25 June 2003, a Chinese (Taiwan)-registered longliner docked in Guam was boarded and searched by the US Coast Guard as part of a routine safety inspection. A frozen whale carcass was found in the hold. Guam Department of Agriculture biologists were contacted to seize the whale and conduct further investigations. A tissue sample from the whale was preserved in 100% ethanol and sent to NMFS Southwest Fisheries Science Centre for genetic analysis (LabID# 37267). Photographs of the animal (Fig. 1) were circulated among cetacean experts who, while in agreement that it was a juvenile beaked whale (family Ziphiidae), were unable to identify it to species. Unfortunately, the carcass was disposed of at the local landfill before further examination could be made.



Figure 1. Cetacean seized from pirate fishing vessel in Guam, identified through DNA taxonomy as a ginkgo-toothed beaked whale (*Mesoplodon ginkgodens*). Known from less than 30 specimens, these are the first images of a confirmed juvenile of this species. *Photocredits*: Guam Department of Agriculture (left and bottom right), A. Samuels (centre and top right). Color versions of these images are posted on the *Micronesica* website (<http://www.uog.edu/up/micronesica/>).

In addition to the whale, the captain stated that he had ‘one bag’ of frozen shark fins on board. On inspection, 22 bags of shark fins were found in the hold and seized. A further 13 bags of shark fins originating from the same vessel were found to have been offloaded into a shipping container bound for Taipei (total weight of frozen shark fins seized, ~ 1.5 tonnes). Most of the fins were identified as blue sharks (*Prionace glauca*) from their morphology. The fins were not sampled for genetic analysis and molecular confirmation of the species identity was therefore not possible.

DNA was extracted from the whale sample using a DNeasy Tissue Kit (Qiagen, Valencia, CA, USA) following the manufacturers’ instructions. Using standard protocols, a 363 base pair (bp) segment of the 5’ end of the hypervariable mtDNA control region was amplified and sequenced. Information on polymerase chain reaction (PCR) primers and conditions can be obtained from the authors. Sequencing was performed on a 3100 Genetic Analyzer (Applied Biosystems Inc, Foster City, CA, USA). The resulting sequence was submitted to *DNA Surveillance* v. 3.01 to determine its species identity. The sex of the animal was confirmed using the SRY-based molecular methods of Fain & LeMay (1995).

## Results & Discussion

### DNA IDENTIFICATION OF A RARE WHALE

The confiscated whale was identified unambiguously as a young male ginkgo-toothed beaked whale (*Mesoplodon ginkgodens*). The mtDNA control region sequence (Genbank Accession No. DQ422861) grouped closely with reference sequences available from this species (100% bootstrap support) to the exclusion of sequences from all other beaked whale species in *DNA Surveillance*. The haplotype represented by this specimen differs by a single nucleotide substitution (0.3%) from the holotype of *M. ginkgodens*, an animal that stranded near Tokyo, Japan (Nishiwaki & Kamiya 1958). Similar low levels of intra-specific variation have been found for other species in this family (average, 0.85%), while divergence between beaked whale species at this locus is generally substantially higher (average, 8.57%) (Dalebout et al. 2004). Based on the captain's statement, the whale was taken on 13 May 2003 near the island of Pohnpei in the Federated States of Micronesia (4.43° N, 152.20° E) when it became caught on the vessel's longlines which were baited with squid. As such, the whale was held frozen in the hold for almost a month before the vessel was boarded in Guam. The captain indicated that he planned to sell the carcass in Taipei. The length of time that the whale carcass was kept in the hold and the captain's statement about his intentions suggests that a lucrative market exists for such catches.

The ginkgo-toothed beaked whale is one of the rarest of all cetacean species. Found in the tropical and temperate waters of the Indo-Pacific, it was first described in 1958 and is known to date from less than 30 specimens (Reeves et al. 2002). To our knowledge, this is the first confirmed record of *M. ginkgodens* from Micronesia, and the photographs presented here are the only images available to date for a juvenile of this species (Fig. 1). The whale was the same size (240 cm, 113 kg) as estimated at birth for this species (Reeves et al. 2002), but did not have the foetal folds of a newborn indicating it was probably one to several months old. At this age, the whale would have been fully dependent on its mother and not yet weaned. Therefore, it seems unlikely that the whale became entangled in the vessel's longlines as a direct result of attempting to feed on the baits.

### LEGAL PROCEEDINGS

The vessel was inside the Exclusive Economic Zone of the Federated States of Micronesia (FSM) when the whale was caught. The captain held a valid permit to fish in these waters and the take or retention of marine mammals in the FSM region is not prohibited by law (Marine Resources Act 2002). However, the transport of the whale carcass across national boundaries without a permit was

contravention of CITES (Convention on International Trade in Endangered Species), and its import into Guam was a contravention of the US Marine Mammal Protection Act (1972). The possession of the shark fins was a contravention of the US Shark Finning Prohibition Act (2002). Both the whale and shark fins were seized. The captain and owner of the vessel were charged a penalty of US\$5,000 for the importation of the whale and \$15,000 for other violations. They failed to defend their case, but since the vessel had already left Guam and US waters, there was nothing more that could be done.

The captain and crew forfeited their catch on this occasion, but there is nothing except the small risk of future forfeiture to stop them continuing to augment their legal catch with IUU fishing. As a result of docking at a US port and submitting to a routine safety inspection, their IUU catch was discovered and confiscated. What would have occurred had they docked at a FSM port? In the absence of modifications to the current FSM Marine Resources Act, marine mammal takes remain legal in this region and will continue to pose a threat to rare cetaceans such as *M. ginkgodens*.

#### IUU FISHING AND MOLECULAR MONITORING

Unlike baleen whales and the giant sperm whale, small toothed whales such as beaked whales, dolphins, and porpoises are generally not protected by international agreements. The conservation status of many of these species is unknown, and they may be particularly vulnerable to IUU takes due to their late maturation and low fecundity. Lucrative markets for whale and dolphin meat exist in Japan and the Republic of (South) Korea (Baker et al. 2000), where products can fetch as much as US\$50–\$100 per kilo (IFAW 1998). Other Asian countries with Japanese communities such as China, the Philippines, and Hong Kong are also reported to host illegal markets for such products, which are often sold in specialist restaurants (Mills et al. 1997). With the exception of Japan, which conducts a scientific whaling program for some larger species and directed hunting of small cetaceans, these products are assumed to come from by-catch and other IUU exploitation.

Monitoring of by-catch and IUU takes by far-seas fisheries vessels is difficult. By-catch data are reliant on fisheries logbooks and independent observer programs. By-catch reporting is voluntary and such records are generally significant underestimates of true by-catch. Some nations employ independent observers to record by-catch in some fisheries, but observer coverage is very low compared to fishing effort (Lewison et al. 2004). Far-seas fishing vessels are fully capable of storing or processing small to medium-sized cetaceans and landing them at the next convenient market. The recent discovery of products from another species of beaked whale likely sourced from the North Atlantic Ocean for sale in a Korean market (Dalebout et al. 2005) confirms that consumer demand for whale meat poses a threat to cetaceans worldwide.

IUU fishing together with weak monitoring, compliance and surveillance (MCS) systems were recognised as the key threats to the sustainability of fish stocks in the FSM region at the 2005 Western and Central Pacific Fisheries Commission (WCPF) meeting in Pohnpei. Molecular monitoring can help to overcome some of the MCS difficulties of detecting by-catch and other IUU takes of marine megafauna. Expansion of existing regional inspection programs for vessels, docks, and markets to include sampling of suspicious carcasses, body parts, and processed products for DNA identification would be very useful even if sampling was not comprehensive. At present, molecular genetic techniques are not employed routinely for wildlife forensics and regulatory monitoring, but this will likely change in the next decade. Using standard laboratory procedures, it currently costs as little as US\$10/sample to extract DNA and generate sufficient sequence data for unambiguous species identification (MLD, pers. obs). With ever increasing automation and miniaturization of the genetic analysis process, the future will likely bring further reductions in costs. Data deficiency is a serious stumbling block for the mitigation of IUU fishing and the monitoring of its impact on rare marine megafauna, but greater integration of DNA taxonomy with port and market surveys can help to resolve this problem.

### **Acknowledgements**

For their help in obtaining a sample from the confiscated whale in Guam for genetic analysis and provision of additional information, we thank T. Leberer (The Nature Conservancy-Asia/Pacific Region, Micronesia Program, Federated States of Micronesia), M. Akamine (US NMFS Pacific Area Islands Office, Hawai'i), B. Tibbatts (Guam Department of Agriculture, Division of Aquatics and Wildlife Resources, Guam), P. Ortiz (Senior Attorney, US NOAA Office of General Counsel, California), F. R. Reyes (Maritime Interdiction Task Force, Guam Customs and Quarantine Agency, Government of Guam), and K. Painter (US NOAA Office of Law Enforcement, Solomon Islands). We thank the Guam Department of Agriculture for use of photos. The sample was collected under NMFS Permit #932-1489. We also thank C. S. Baker, University of Auckland, New Zealand, for suggesting we publish a report of this incident as an example piece and for comments on an earlier version of the manuscript. MLD is supported by a University of New South Wales Vice-Chancellor's Postdoctoral Fellowship.

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Received 30 Oct. 2006.