Fisheries Research 164 (2015) 130–134

Contents lists available at ScienceDirect

Fisheries Research

journal homepage: www.elsevier.com/locate/fishres

Short Communication

DNA barcoding reveals targeted fisheries for endangered sharks in Indonesia

Andrianus Sembiring[a,g], Ni Putu Dian Pertiwi[a], Angka Mahardini[a], Rizki Wulandari[a], Eka Maya Kurniasih[b], Andri Wahyu Kuncoro[c], N.K. Dita Cahyani[a], Aji Wahyu Anggoro[a], Maria Ulfa[d], Hawis Madduppa[b], Kent E. Carpenter[e], Paul H. Barber[f], Gusti Ngurah Mahardika[a,*]

[a] *The Indonesian Biodiversity Research Centre, The Animal Biomedical and Molecular Biology Laboratory of Udayana University, Jl Sesetan-Markisa 6, Denpasar, Bali, Indonesia*
[b] *Faculty of Fisheries and Marine Science, Bogor Agricultural University, Jl Rasamala, Bogor, West Java, Indonesia*
[c] *Marine Science Department, Faculty of Husbandry, Fisheries, and Marine Science, University State of Papua, Jalan Gunung Salju Amban, Manokwari, Papua, Indonesia*
[d] *Flora and Fauna International, Jl Cumi-Cumi 15, Banda Aceh, Sumatra, Indonesia*
[e] *Department of Biological Sciences, Old Dominion University, Norfolk, VA 23529, USA*
[f] *Department of Ecology and Evolutionary Biology, University of California Los Angeles, Los Angeles, CA 90095-7239, USA*
[g] *Master program in Environmental Sciences, Udayana University, Jl P.B. Sudirman, Denpasar, Bali, Indonesia*

ARTICLE INFO

Article history:
Received 9 October 2014
Received in revised form 4 November 2014
Accepted 9 November 2014
Handling Editor Prof. George A. Rose
Available online 11 December 2014

Keywords:
Shark
DNA barcoding
Indonesia

ABSTRACT

Sharks are apex predators and keystone species that have a profound influence on the ecology and food-web dynamics of coral reefs and epipelagic marine ecosystems. However, sharks are being heavily overfished compromising the health of the world's reefs and pelagic environments. Although Indonesia is the world's largest and most diverse coral reef ecosystem, information on the exploitation of sharks in this region is scarce. Results of DNA barcoding of shark fin revealed two alarming findings: (1) a rarity of reef sharks that should dominate Indonesia's coastal ecosystems, and (2) a fishery that targets endangered sharks. The diversity and number of threatened species recovered in this study highlights the urgent need for improved regulation and control of Indonesia's shark fishery.

1. Introduction

As apex predators, many sharks are keystone species that have a significant influence on the ecology and food-web dynamics of coral reef and epipelagic ocean ecosystems (Ferretti et al., 2010; Myers et al., 2007). However, shark populations have declined globally by up to 90% (Myers et al., 2007), largely as a result of a multi-billion dollar industry that harvests hundreds of millions of sharks annually (Chapman et al., 2013) and life history traits such as low fecundity, late maturity, and a long gestation period that make shark populations particularly sensitive to overfishing and habitat degradation (Baum et al., 2003). Global shark fisheries are largely driven by the demand for shark fins, a key ingredient in the Asian delicacy, shark fin soup.

The Convention on International Trade in Endangered Species of Wild Fauna and Flora (CITES) currently lists many sharks as Appendix I (species threatened with extinction) or Appendix II (species where trade must be regulated to prevent over-utilization). A further 60 sharks and rays are listed as "vulnerable" or "near threatened" (Camhi et al., 2009). While CITES designation should promote regulation of international trade in shark products, the primary commodity resulting from shark fisheries are fins. Whole sharks are rarely landed at commercial ports (Clarke et al., 2006; Liu et al., 2013) throughout much of the world; instead sharks are "finned" at sea, a process by which fins are removed and bodies discarded, and then fins dried for sale to wholesalers (Fig. 1). This process is common whether sharks are the targeted fisheries species or the result of by-catch (Afonso et al., 2012). Dried fins typically lack key diagnostic features, making identification of fins to species, and therefore regulation of trade in fins, extremely challenging. While DNA barcoding based on a short fragment of the mitochondrial cytochrome oxidase I (*COI*) gene has been used to

---

[*] Corresponding author at: The Indonesian Biodiversity Research Centre, The Animal Biomedical and Molecular Biology Laboratory of Udayana University, Jl Sesetan-Markisa 6, Denpasar, Bali 80226, Indonesia. Tel.: +62 361 8423061; fax: +62 361 223791.
E-mail address: gnmahardika@indosat.net.id (G.N. Mahardika).

http://dx.doi.org/10.1016/j.fishres.2014.11.003
0165-7836/

Fig. 1. Photographs of shark and shark-fin sample collection. Sun-dried fins (left) in Bali, November 1, 2011; whole shark and elasmobranch auction at the harbour in Lombok (right), July 12, 2012.

Source: Indonesian Biodiversity Research Centre.

identify fins to species (Holmes et al., 2009; Moftah et al., 2011; Pinhal et al., 2012; Wong et al., 2009), this technique is not widely used to promote regulation of shark fisheries.

Comprised of more than 17,000 islands, Indonesia is the largest geographic area and heart of the “Coral Triangle”, a six-nation region of South East Asia that is home to the world’s most diverse seas (Carpenter et al., 2011; Dubinsky and Stambler, 2011; Roberts et al., 2002). Approximately 30% of the world’s shark and ray species are present in this region (Last and Stevens, 1994) including regional endemics unique to the Coral Triangle and other broadly distributed Indian and Pacific Ocean species (Barnett et al., 2012; Bond et al., 2012; Campana et al., 2011; Nadon et al., 2012; Oliver et al., 2011). The high value of shark fins on global markets has sparked rapid growth in shark-fishing in Indonesia focused on supplying fins to growing markets in Asia. Comprised of a mixture of commercial and opportunistic artisanal fisheries, the total elasmobranch catch in Indonesia was estimated at more than 110,000 tonnes in 2007 (Camhi et al., 2009), representing the largest recorded harvest in the world (Tull, 2009). Despite the size and value of Indonesian shark fisheries, the expansive nature of Indonesia combined with the diffuse nature of the shark fin fishery means that basic fisheries data needed for effective management and regulation in Indonesia (e.g. species composition, harvest levels, etc.) is severely lacking.

2. Materials and methods

We collected 582 shark fins from traditional fish markets and shark-fin exporters across Indonesia from mid-2012 to mid-2014, including Aceh, Jakarta, West Java, Central Java, East Java, Bali, West Kalimantan, South Sulawesi, North Sulawesi, Maluku, and West Papua. Additional samples were collected from shark fin export warehouses in Cilacap (Central Java) and Tanjung Luar (West Nusa Tenggara) (Fig. 2). We sampled a thin slice of tissue from dried fins in fish markets. In export warehouses, we randomly sampled a minimum of five caudal fins from boxes of fresh fins. The total numbers of dried and fresh fins were 164 and 418, respectively. Samples were preserved in 96% alcohol for subsequent DNA analysis.

Whole DNA was extracted using a simple Chelex protocol (Walsh et al., 1991). A fragment of the mitochondrial cytochrome oxidase C subunit-1 (COI) was amplified using AmplyTaq Red$^{\mathrm{TM}}$ (Applied Biosystems) and the standard fish DNA-barcoding primers Fish-BCL and Fish-BCH (Baldwin et al., 2009). The amplification parameters were an initial denaturation of 94 °C for 15 min, 38 cycles of 94 °C for 30 s, 50 °C for 30 s, and 72 °C for 45 s, with a final extension of 72 °C for 5 min. PCR products were visualized via electrophoresis on agarose gels and ethidium bromide staining.

The COI fragment could be amplified and sequenced from all samples. The sequencing was conducted using both forward and reverse directions at the University of California Berkeley Sequencing Facility. The result was aligned using MEGA5 (Tamura et al., 2007). We then determined species identity by comparing sequences to GenBank and Barcode of Life Data Systems (http://www.boldsystems.org) databases enforcing a sequence homology threshold of >99% as previously applied (Liu et al., 2013).

3. Results

DNA barcoding of a 600–654 bp of mitochondrial *COI* gene successfully determined the species identity of 582 fins collected from markets across the Indonesian archipelago based on a 99% sequence similarity criterion in GenBank and Barcode of Life Data Systems (BOLD) databases. In total, analyses determined 40 different shark species (Table 1). Five species (silky, scalloped hammerhead, blue, big eye thresher, and thresher sharks) represented more than 50% of the total fins sampled. Silky (19.10%), scalloped hammerhead (10.50%) and blue sharks (8.20%) were the most common species recovered, followed by bigeye thresher (7.60%) and thresher sharks (7.20%). In contrast, 29 species were observed at less than 2% of the total samples, including 7 species that were represented by only one or two samples.

The vast majority of the samples (92%) were listed as “endangered” (1) “vulnerable” (12) or “near threatened” (19) while only 4 species were listed as species of least concern. The remaining 3 species are classified as data deficient. Similarly, 83% of species identified were pelagic species of shark while only 17% were reef sharks.

4. Discussion

Identification of unknown shark fins from Indonesian fish markets revealed a fishery that is heavily exploiting threatened and near threatened species. In total, 80% of the species identified are either considered “endangered” (1 sample) “vulnerable” (12 samples) or “near threatened” (19 samples). In total, 38.5% of all fins came from sharks classified as endangered or vulnerable and 54.1% of fins came from sharks listed as near threatened. In contrast, only 7.2% of fins harvested came from three species categorized