Indo-Pacific origins of silky shark fins in major shark fin markets highlights supply chains and management bodies key for conservation

1 | INTRODUCTION

Understanding the species composition of wildlife trade hubs can help identify the species most in need of conservation interventions; tracing the population-of-origin of these species then helps to identify the key management jurisdictions that can operationalize these interventions (Cardeñosa, Fields, Babcock et al., 2018; Chapman, Pinhal, & Shivji, 2010; Fields et al., 2018; Fields et al., 2020). While many genetic studies in Asian shark fin markets and South American and European shark meat consumption centers have elucidated priority species for conservation (Bunholi et al., 2018; Cardeñosa, Fields, Babcock et al., 2018; Cardeñosa, Fields, Babcock, Shea et al., 2020; Clarke, Magnussen, Abercrombie, McAllister, & Shivji, 2006; Fields et al., 2018; Hobbs, Potts, Walsh, Usher, & Griffiths, 2019), there has been far less application of genetic tracing of products in these hubs to source population-of-origin (Cardeñosa, Fields, Shea, Feldheim, & Chapman, 2020; Chapman et al., 2010; Fields et al., 2020). Nonetheless, sharks frequently exhibit genetic population structure from the local to the ocean basin scale, which should enable product tracing of this kind assuming that a robust baseline of genetic diversity is mapped across the species distribution (Chapman, Feldheim, Papastamatiou, & Hueter, 2015).

A high proportion of pelagic sharks are overexploited due to high overlap with fishing fleets targeting tuna and the demand for their fins in Asia incentivizing retention of these ostensibly “by-catch” species (Cardeñosa, Fields, Babcock et al., 2018; Cardeñosa, Fields, Babcock, Shea et al., 2020; Clarke et al., 2006; Clarke, Harley, Hoyle, & Rice, 2012; Dulvy et al., 2008; Fields et al., 2018; Queiroz et al., 2019). Pelagic shark management is primarily under the purview of Regional Fisheries Management Organizations (RFMOs) that set regulations for migratory species fished by multiple nations at the ocean basin scale (Tolotti et al., 2015). Silky sharks (Carcharhinus falciformis) have been the second most common species in the shark fin trade through one of the world’s largest fin trade centers, Hong Kong Special Administrative Region of the People's Republic of China (hereafter “Hong Kong”), for the last two decades (Cardeñosa, Fields, Babcock et al., 2018; Clarke et al., 2006; Fields et al., 2018). This remarkably consistent contribution reflects high landings of this species, most likely because they have been the most common shark taken incidentally in pelagic tuna fisheries in subtropical and tropical regions worldwide (Amorim, Arfelli, & Fagundes, 1998; Clarke et al., 2014; Gilman et al., 2008; Hutchinson, Itano, Muir, & Holland, 2015; Jabado & Spaet, 2017; Simeon et al., 2018; Simpfendorfer, Hueter, Bergman, & Connett, 2002). This is concerning because this species is classified as vulnerable by the International Union for Conservation of Nature (IUCN; Rigby, Sherman, Chin, & Simpfendorfer, 2017) and ecological risk assessments indicate that silky sharks are among the pelagic shark species most vulnerable to overexploitation (Cortés et al., 2010). Furthermore, evidence of population decline has led to an Appendix II listing on the Convention on International Trade of Endangered Species (CITES) to ensure trade of their fins and other products are legal, sustainable, and traceable throughout the supply chain (Vincent, Sadovy de Mitcheson, Fowler, & Lieberman, 2014).

Silky shark management largely falls under the purview of four tuna RFMOs: The International Commission for the Conservation of Atlantic Tuna (ICCAT), Indian Ocean Tuna Commission (IOTC), the Western and Central Pacific Fisheries Commission (WCPFC), and the Inter-American Tropical Tuna Commission (IATTC) in the Eastern Pacific (Figure 1). The most recent catch data from the RFMOs indicate that the catches in the Atlantic are about 7% of the total across the four RFMOs (ICCAT, 2019; IOTC, 2018; WCPFC, 2018; IATTC 2019). ICCAT reports 534 t of silky
FIGURE 1 Map indicating sampling locations around the world. Black squares represent sampling locations included in Clarke et al. (2015), and samples numbers for each location are shown in parenthesis. LI = Line Island, EP = Eastern Pacific, GM = Gulf of Mexico, NWA = North West Atlantic, BR = Brazil, RS = Red Sea, AS = Andaman Sea, TW = Taiwan, PG = Papua New Guinea, IO = Indian Ocean, EA = Eastern Atlantic, NCP = North Central Pacific, SCP = South Central Pacific. Geographic areas under the purview of the different Regional Fisheries Management Organizations, where silky sharks occur, are highlighted by colors (WCPFC = yellow, IATTC = red, ICCAT = blue, IOTC = green).

Sharks caught in 2018, while IOTC reports catches of 2,175 t in 2017, WFCPC reports catches of 1430 t in 2018, and IATTC reports catches of 431 t in purse seines in 2018 and 2,626 t in longlines in 2017. However, these catches are not all necessarily traded internationally. ICCAT prohibited the retention, transshipment, and landing of silky sharks in whole or in part by all fisheries operating under its jurisdiction in 2011 but developing nations are permitted to land silky sharks for local consumption as long as they report them (ICCAT, 2011). Despite this allowance, parties are explicitly prohibited from using the fins for the international export market to ensure that catches are limited to satisfy local demand for meat (ICCAT, 2011). Developing nations reported the majority of the catch of this species (i.e., the 534 t in 2018 and ~ 7% of the global total), none of which should have entered the dried fin supply chain according to ICCAT regulations (ICCAT, 2019). Indeed, since CITES listing was implemented no international trade in silky shark fins has been reported from any party to ICCAT other than Mexico, which may have reported Pacific rather than Atlantic landings (https://trade.cites.org/). Silky shark management by Indo-Pacific RMFOs is inconsistent: there is a retention ban on silky sharks in the WCPFC since 2013, a retention ban only applying to purse seine fisheries under the IATTC, and silky shark landings are not regulated by the IOTC (IATTC, 2016; WCPFC, 2013). Given these regulations and assuming high compliance, the expectation would be that silky shark fins in the contemporary trade would be from the Indian and Eastern Pacific oceans.

Independent assessment of the relative contribution of silky sharks from different regions to major trade hubs could provide complementary information to reporting required by RFMOs and CITES. The silky shark is a highly migratory species with modest genetic population structure within ocean basins, but strong phylogeographic partitioning of two clades, the Atlantic and the Indo-Pacific, evident in noncoding mitochondrial DNA markers (e.g., mitochondrial control region [mtCR]; Clarke et al., 2015). We used haplotype differences between Atlantic and the Indo-Pacific silky sharks to assess the geographic source of randomly sampled fin products collected over a 4-year period from the two largest shark fin retail markets in the world, Hong Kong and Guangzhou in mainland China. Our objective was to assess the relative contribution of Atlantic silky sharks under the management purview of ICCAT and Indo-Pacific silky sharks to these globally important trade hubs.
2 | METHODOLOGY

2.1 | Establishing a baseline genetic population structure

Clarke et al. (2015) presented a global phylogenetic tree that showed strong partitioning of silky sharks from the Atlantic and Indo-Pacific into two clades, with a small number of Indo-Pacific clade haplotypes being found in individuals sampled in the Atlantic but not the reverse (i.e., no Atlantic haplotypes found in Indo-Pacific individuals). These previously described silky shark haplotypes in Clarke et al. (2015) were downloaded from the National Center for Biotechnology Information (NCBI) Genbank (http://www.ncbi.nlm.nih.gov/genbank/; Accession numbers KM267565–KM267626) and aligned using Seaview 4.4.1 software (Gouy, Guindon, & Gascuel, 2010). To extend the geographic coverage of our study beyond Clarke et al. (2015), we also collected tissue samples (n = 210) from silky sharks in seven different geographic regions (Eastern Atlantic, Eastern Pacific, South Central Pacific, North Central Pacific, Papua New Guinea, Taiwan, and Indian Ocean; Figure 1). DNA from these tissues was isolated using QiaGen DNeasy kits (QiaGen, Valencia, CA). The primers, CR-F6 (5′-AAGCGTCGACCTTGTAAGTC-3′) and DAS-R2 (5′-GCTGAAACTTGCATGTGTAA-3′; Clarke et al., 2015), were used to amplify the mtCR with the following cycling profile: an initial denaturation at 94°C for 2 min, followed by 35 cycles at 94°C for 1 min, 50°C for 1 min, and 72°C for 2 min, with a final extension of 72°C for 5 min. Each 25 μL Polymerase Chain Reaction (PCR) included 0.5 μL of extracted DNA, 12.5 μL of GoTaq Hot Start Green Master Mix (Promega), 9.0 μL of water, and 1.5 μL of each forward and reverse primers from a 10 μM stock solution. PCRs were checked on a 2% agarose gel and all products were cleaned using ExoSAP-IT (ThermoFisher Scientific, Waltham, MA). All products were sequenced twice using the Big Dye Terminator v3.1 cycle sequencing kit (Applied Biosystems, Foster City, CA). Sequencing was performed on an ABI 3730 DNA Analyzer (Applied Biosystems) using the CR-F6 forward primer and the DAS-R2 reverse primer. All forward and reverse sequences were checked by eye and priming sites were trimmed using Seaview 4.4.1 software (Gouy et al., 2010).

In order to assess how well the existing Atlantic sampling (i.e., from Clarke et al. [2015] and the East Atlantic samples reported here) has captured the total haplotype diversity of silky sharks in the region a rarefaction curve was generated using iNEXT Online (Chao, Ma, & Hsieh, 2016) to estimate the total number of haplotypes expected at a given level of sampling. This was based on the unified rarefaction and extrapolation sampling curves of Hill numbers for q = 0 (i.e., haplotype richness; Chao et al., 2014). The number of bootstraps was set to 10,000 and the level confidence interval to 0.95.

2.2 | Collection of samples in major shark fin trade hubs

Purchasing a large, random sample of silky shark fins was cost-prohibitive so we elected to use “fin trimmings.” These are portions of the fin that are not desired for soup but are trimmed during processing and then sold inexpensively in packages of tens to hundreds of pieces (Cardeñosa, Fields, Babcock et al., 2018; Fields et al., 2018). Shark fin trimmings can consist of cartilage removed from inside of the fin, cartilage and muscle strips from the fin base, and “touch-up” pieces along the edges of the processed fin that help make it visually appealing to the buyer (Cardeñosa, Fields, Babcock et al., 2018; Fields et al., 2018). Shark fin trimmings were collected through a random market survey of the dried seafood districts, Sheung Wan and Sai Ying Pun, of Hong Kong conducted bimonthly or monthly from February 2014 to February 2017 as previously described (Cardeñosa, Fields, Babcock et al., 2018; Fields et al., 2018). Briefly, all shops were assigned a number and 75 shops were randomly selected without replacement from the complete shop list every sampling period. Two bags of shark fin trimmings were purchased from each shop visited in order of selection until 10 retail shops yielded this product (i.e., 20 bags had been collected from 10 shops). Ten individual trimmings were then randomly selected from each bag for further analysis. The shark fin retail market of Guangzhou, China, comprises a large four-story mall with mixed wholesale and retail shops with serial numbers, where shark fins and other highly priced traditional Chinese medicine products are sold. Every 2–3 months, from June 2015 to August 2017, 10 vendors were randomly selected from the complete shop list for each sampling event (Cardeñosa, Fields, Babcock, Shea et al., 2020). Two bags of processed shark fin trimmings were purchased from each randomly selected shop, yielding a total of 20 bags of trimmings per sampling. Ten individual trimmings were then randomly selected from each bag for further analysis.

2.3 | Population of origin identification

DNA was isolated from these fin trimmings by heating a small subsample (i.e., ~ 2 mm²) in 200 μL of 10% Chelex resin (BioRad) at 60°C for 20 minutes, then at 99°C for 25 min followed by a brief centrifugation and

CARDEÑOSA ET AL. | WILEY
storage at 4°C (Cardeñosa et al., 2017). Portions of the cytochrome oxidase I (COI) gene (~150–200 bps) were PCR amplified and Sanger sequenced using the mini-DNA barcoding assays for each fin trimming (Cardeñosa et al., 2017; Fields, Abercrombie, Eng, Feldheim, & Chapman, 2015). These sequences were identified with GenBank (using BLAST; www.ncbi.nlm.nih.gov) and the Fish Barcode of Life Initiative (BOLD; www.fishbol.org) online databases. A total of 604 silky shark fin trimmings were randomly selected and used for mtCR sequencing but early trials indicated that their genomic DNA was often too degraded to yield the full sequence in one PCR. Five internal primers were then designed to amplify the informative regions of the mtCR in three short sequences (~250–350 bps; Figure 2). The mtCR sequences were reconstructed by amplifying three short amplicons within the mtCR using the primers silkyCR_F1 (5′-CCCTCATTCCATAATAGCTATAAC-3′), silkyCR_R1 (5′-TGTCAGGTTTGATCAATAGTAGG-3′), silkyCR_F2 (5′-GATCAAACCTGACATTTGATTATGG-3′), silkyCR_R2 (5′-CCCTTTCAGTAATGGTGAGTTTGAC-3′), silkyCR_F3 (5′-GGGGCAACGAGTAGAAAAACATTG-3′; Figure 2). All amplicons were amplified using the following cycling conditions: an initial denaturation at 94°C for 2 min, followed by 35 cycles at 94°C for 1 min, 55°C for 1 min, and 72°C for 2 min, with a final extension of 72°C for 5 min. PCRs, agarose gel checking and cleaning of PCR products were performed as described above. Sequencing of the internal amplicons was conducted using the same primers pairs used for the PCR amplification stage as shown in Figure 2. Sequences from all internal amplicons were checked by eye and priming sites were trimmed and aligned in Seaview 4.4.1 software (Gouy et al., 2010).

Haplotypes from sampled silky sharks and fin trimmings, using all three internal amplicons (Figure 2), were defined using MacClade (Maddison & Maddison 2000). A Neighbor-joining (NJ) tree of all distinct silky shark haplotypes, from Clarke et al. (2015) and this study, was constructed with 1,000 bootstrap replicates using MEGA software (Tamura, Stecher, Peterson, Filipski, & Kumar, 2013), using the Jukes–Cantor model (Jukes & Cantor 1969). A blue shark (Prionace glauca) mtCR sequence was used as an outgroup to root the tree. Each market-derived sequence was then defined as being from the Atlantic or Indo-Pacific clade based on its position in the tree relative to haplotypes known to originate from these regions (Figure 3). Eight of the haplotypes from Clarke et al. (2015) were shared between the Indo-Pacific clade, the Atlantic clade, and the market-derived samples (Figure 4(a)). Therefore, we used the haplotype frequencies from Clarke et al. (2015) and the frequencies of those haplotypes in the shark fin markets (Figure 4(a)) to conduct a mixed-stock analysis (MSA) with the R-package mixstock (Bolker, 2012). Mixstock was used to estimate the contribution of each source population (i.e., Indo-Pacific and Atlantic) to both shark fin markets using a Markov Chain Monte Carlo (MCMC) estimation with 100,000 iterations following a burn-in of 50,000. The Gelman and Rubin criterion was used to assess convergence (Gelman et al., 2014).

Since many samples did not yield all three internal amplicons (n = 271), we also conducted a separate analysis only using the first amplicon (329 bp; Figure 2), which yielded the largest number of sequences from market-derived samples (n = 455). Haplotypes from this internal amplicon from the 455 market-derived samples, the same portion from Clarke et al. (2015) haplotypes, and

**Figure 2** Schematic representation of the relative annealing sites and orientation of each primer, and spatial coverage of the resulting amplicons.
FIGURE 3  Neighbor-joining tree showing the two global silky shark clades (Atlantic [green], and Indo-Pacific [blue]), and the presence of Hong Kong (red circles) and Guangzhou, China (orange circles) for each haplotype in each clade. Green boxes represent haplotypes that were within the Indo-Pacific clade but have also been occasionally found in silky sharks caught in the Atlantic. Supporting values (> 80% bootstrap values) are shown.

FIGURE 4  (a) Clarke et al. (2015) haplotype frequencies present in the Hong Kong and Guangzhou retail markets, the Indo-Pacific clade and the Atlantic Clade. H1* and H7* represent groups of haplotypes that were present exclusively (not shared) in the Indo-Pacific and Atlantic clades, respectively. (b) Estimated contribution of each source population to the shark fin retail markets of Hong Kong and Guangzhou. Confidence intervals from the MCMC estimation are too small to be depicted in the plot.
the 210 individuals caught from the seven different geographic locations, were defined using MacClade (Maddison & Maddison 2000). A statistical parsimony network was constructed using the software TCS v. 1.21 (Clement, Posada, & Crandall, 2000), providing a 95% plausible set for all haplotype links. Haplotypes with matching market-derived samples were identified in the network (Figure 5).

3 | RESULTS

The mtCR haplotypes, based on all three internal amplicons, from processed fin samples from the retail markets of Hong Kong (n = 169) and Guangzhou, mainland China (n = 164), were successfully reconstructed. The remainder of the processed fin samples (n = 271) failed to amplify completely or amplified only partially (e.g., just one or two of the three short internal amplicons). A NJ tree of the mtCR haplotypes of a total of 210 individuals caught from seven different geographic locations, the reconstructed market-derived haplotypes from 333 fin trimmings, and the 62 previously reported haplotypes from Clarke et al. (2015), further confirmed that there are two well-differentiated silky shark clades from the Atlantic and Indo-Pacific Oceans (Figure 3). All of the new individuals from the Eastern Atlantic (N = 30) fell within the Atlantic Clade and all of the individuals from the remaining locations (N = 180) fell within the Indo-Pacific Clade. No Atlantic clade haplotypes were detected in any of the new Indo-Pacific sampling locations (Figure 1). Analysis of these data, plus the 62 previously described haplotypes by Clarke et al. (2015), identified 39 variable sites that defined 96 unique haplotypes (Table S1). The rarefaction curve based on existing Atlantic sampling did not reach a plateau, which suggests more sampling is needed to capture all of the rare haplotypes that exist in this basin (Figure S1). The extrapolation of the haplotype diversity data analysis suggests between 1 and 24 additional haplotypes may exist in the Atlantic Ocean and require approximately twice the current sampling effort to find them (Figure S1).

All 333 of the analyzed silky shark fin trimmings from the retail markets of Hong Kong and China were part of the Indo-Pacific clade (Figure 3), and 17 novel Indo-Pacific clade haplotypes (17.7%) were found in market-derived samples. A total of 262 market-derived samples
exhibited haplotypes that were common within the Indo-Pacific clade but have also been infrequently found in silky sharks caught in the Atlantic (Clarke et al., 2015). The probable population-of-origin of these samples was assessed using MSA and estimated a contribution of 99.8% (95% CI: 99.04, 99.99) and 0.2% (95% CI: 0.00, 0.96) of the Indo-Pacific and Atlantic populations respectively (Figure 4(b)). All parameters converged based on the Gelman and Rubin criterion (< 1.2).

We were able to increase the market-derived sample size by focusing our analysis on the first internal amplicon alone because we were able to obtain this sequence for a larger number of the silky shark trimmings than we obtained all 3 internal amplicons (N = 453). The haplotype network built from this amplicon also confirmed the two well-differentiated silky shark clades even though it was constructed with a shorter fragment (i.e., 329 bp) and some mtCR haplotypes were lumped together (Table S2). All of the analyzed silky shark fin trimmings from the retail markets in Hong Kong and China fell within the Indo-Pacific clade of this network, confirming and extending the findings with a larger dataset than obtained from sequencing the full mtCR (N = 435; Figure 5).

4 | DISCUSSION

This study presents the first assessment of the relative contribution of Atlantic and Indo-Pacific regional silky shark landings to the two largest shark fin trade hubs in the world. Our results suggest near-zero occurrence of Atlantic silky sharks in the Hong Kong and mainland China shark fin markets. Indo-Pacific fishing nations and RMFOs are therefore the primary management bodies overseeing the supply of silky sharks into these trade hubs. Fisheries management and CITES implementation for silky sharks should be focused in this large region. Indeed, on May 6th, 2020, Hong Kong Customs authorities seized ~5,000 kg of silky shark fins from two containers coming from Ecuador that had been illegally imported without CITES documentation.

The absence of unambiguous Atlantic-origin fins from silky sharks in both Hong Kong and mainland China markets is consistent with the possibility that the ICCAT moratorium on the exportation of their fins put in place with the retention ban in 2011 is largely being followed (ICCAT, 2011). However, in the absence of preban estimates for the contribution of Atlantic silky sharks to these markets it is difficult to assess whether our results are a direct consequence of this ban or another driver. It is also important to consider potential sampling biases that may have contributed to this finding. One possibility is that we did not sample vendors that are supplied by Atlantic sources or sample them at the correct time to obtain fins from this region. This is unlikely because samples were randomly collected from 140 and 52 different vendors in Hong Kong and Guangzhou, respectively, year-round over a 4-year period (2014–2017). It is therefore unlikely that our sampling was biased by a small number of consignments, sampling the wrong season, or sampling a single group of vendors not supplied by Atlantic sources, or a combination of these events. In comparison, Fields et al. (2020) using the same sampling methodology but a smaller sample size (N = 72), detected a ~ 5% contribution of the U.S. Atlantic and Gulf coast population of scalloped hammerheads (Sphyrna lewini) in the Hong Kong retail markets in 2014. In 2012 the United States landed 30 t of scalloped hammerheads, likely exporting all of their fins (~ 1.5 t) to Hong Kong (FAO, 2017). This suggests that relatively small inputs of fins into large markets (Hong Kong imports ~ 6,000 t of fins per year; (Shea & To 2017) can be detected in this fin trimming sampling and implies that if ~ 534 t of Atlantic silky sharks reported to ICCAT had their fins removed and they were illegally exported to Hong Kong or Guangzhou we would probably have detected them. Indeed, a likelihood profile for the fraction of Atlantic specimens in the trade indicates that it is highly unlikely that we would find zero Atlantic specimens in a sample of size 333 if the actual fraction in trade is more than a few percent (Figure S2). It is conceivable that fins originating from different regions containing differential amounts of extraneous tissue leading to a region-specific detection bias in fin trimmings. However, all fins (e.g., dried, frozen) undergo some level of processing and trimming so it is unlikely that a random sample of fin trimmings would not detect at least some Atlantic silky sharks if they were present in these two markets. Additionally, endemic Atlantic shark species and populations have previously been detected in these markets through these, and similar, sampling efforts, arguing against this potential source of bias (Cardeñosa, Fields, Babcock et al., 2018; Cardeñosa, Fields, Babcock, Shea et al., 2020; Cardeñosa, Shea, Zhang et al., 2019; Fields et al., 2018; Fields et al., 2020). While our sampling in Hong Kong and Guangzhou was robust, there is a possibility that Atlantic silky shark fins from some parts of the basin are in the international trade but have supply chain end-points in other cities in China, or in other nations such as Singapore, Taiwan, Japan or Thailand. Some African ICCAT parties, for example, have fishing lease agreements with Taiwan that may allow the illicit trade of silky shark fins that could bypass Hong Kong and Guangzhou (FAO, 2017). Future random sampling efforts in other shark fin markets in Southeast Asia are needed to assess this possibility and could better identify noncompliant supply chains originating within ICCAT’s area of competence.
Our study reveals the contemporary importance of Indo-Pacific supply chains and RFMOs for silky shark fins in Hong Kong and Guangzhou. This is consistent with recent reporting on silky sharks that indicates that Indo-Pacific landings are ~ 93% of the global total (ICCAT 2019, IOTC 2018, WCPFC 2018, IATTC 2019). Our findings are also consistent with the possibility that although ICCAT contributes ~ 7% of global silky landings there is high compliance with the ban on the international exportation of their fins. It is important to stress that even if this is true it does not necessarily reflect a reduction in regional fishing mortality that is sufficient to rebuild depleted populations. Addressing this will require studies of incidental catch rates, postrelease mortality rates, and stock assessments over time (Tolotti et al., 2015). Nonetheless, the present study offers the first baseline with which to track the relative contribution of Atlantic silky sharks into Hong Kong and Guangzhou moving forward. This will enable future studies to assess if the relative Atlantic contribution changes over time, as they might in response to changes in regional silky populations, regional fishing practices, or management through ICCAT and CITES.

Our study raises new questions about the sources of silky shark fins from within the Indo-Pacific and how to best monitor and manage them at the fisheries level. First, managers need to assess compliance with silky shark retention bans that exist in WCPFC fisheries and in purse seine fisheries under IATTC. If there is high compliance it then highlights key fisheries that need to be monitored and managed for their contributions to the Hong Kong and Guangzhou shark fin markets: (i) small scale domestic fisheries throughout the region that are outside of RMFO jurisdictions, (ii) IOTC fisheries, and (iii) longline fisheries under IATTC. Although it is possible that these are the key fisheries in need of management, silky shark landings are still occurring and being reported by WCPFC and IATTC purse seine fisheries (WCPFC 2018, IATTC 2019). Future work should aim to further delineate the genetic population structure of Indo-Pacific silky sharks so that the contributions by region can be assessed on a finer geographic scale and aligned as closely as the results allow with individual RFMO jurisdictions. Existing population genetic analysis suggests that there may be population structure within the Indo-Pacific, but it is unclear how population boundaries align with RMFO jurisdictions (Clarke et al., 2015). Genomic studies may clear this up and help build a clearer baseline for finer scale genetic tracing of silky shark fins in the future (Kraft et al., 2020).

This study highlights the potential for regulations at the start of the supply chain to better manage internationally protected sharks. Regional managing bodies and national law enforcement agencies should deploy available cost-effective resources and tools to (i) increase enforcement efficiency, (ii) detect and deter illegal trade in CITES-listed species, and (iii) monitor shark landings where silky sharks are prohibited in the Indo-Pacific in order to assess effectiveness of such measures (Abercrombie & Hernández 2017; Cardeñosa, Quinlan, Shea, & Chapman, 2018). We also recommend that IOTC considers fisheries regulations for this species since it is possible that the Indian Ocean is a major supplier of silky shark fins to Asian markets. Our study demonstrates the potential usefulness of genetic sampling programs in global shark trade hubs, which offer a means to collect information that is complementary to landings data reported to RFMOs and other bodies that can help us track changes in the shark trade on both a species and population-specific basis.

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CONFLICT OF INTEREST
The authors declare no conflicts of interest.

AUTHOR CONTRIBUTIONS
D.D.C., conceived the study. D.D.C. obtained funding. D.C. conducted the analysis in the lab. D.C. analyzed the results. D.C. and D.D.C. wrote the manuscript. E.A.B., M.A.H., and S.C., assisted with statistical analyzes. D.W.K and M.H. provided new samples from different locations around the world. All authors provided comments and edits to the manuscript.

ETHICS STATEMENT
All applicable international, national, and institutional guidelines for the care and use of animals were followed.

DATA AVAILABILITY STATEMENT
The data that support the findings of this study are available from the corresponding author upon reasonable request.
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**SUPPORTING INFORMATION**
Additional supporting information may be found online in the Supporting Information section at the end of the article.

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