Tracking the fin trade: Genetic stock identification in Western Atlantic scalloped hammerheads sharks (*Sphyrna lewini*)

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ABSTRACT: Location or stock-specific landings data are necessary to improve management of shark stocks, especially those imperiled by overexploitation to supply the international shark fin trade. In the current absence of catch monitoring directly at extraction sites, genetic stock identification of fins collected from major market supply chain endpoints offers an overlooked but potentially useful approach for tracing the fins back to their geographical or stock of origin. To demonstrate the feasibility of this approach, we used mitochondrial control region (mtCR) sequences to trace the broad geographical origin of sixty two Hong Kong market-derived *Sphyrna lewini* fins. Twenty-one percent of these fins were derived from the Western Atlantic, where this species is listed as “Endangered” by the International Union for the Conservation of Nature (IUCN). We also show that *S. lewini* mtCR sequences are geographically segregated in the Western Atlantic (overall $\Phi_{ST} = 0.74$, $n = 177$ sharks), indicating that breeding females either remain close to or home back to their natal region of origin for parturition. Mixed stock analysis simulations show that it is possible to estimate the relative contributions of these mitochondrial stocks to fin mixtures in globally-sourced trade hubs. These findings underscore the feasibility and utility of genetic stock identification of market-derived shark fins to obtain essential data on exploitation levels not otherwise available to productively inform stock assessment and management of *S. lewini* and potentially other fished shark species.

INTRODUCTION

Strong demand for shark fins is arguably the major driver of shark mortality globally, with estimates of between 26 and 73 million sharks killed annually to supply the fin markets (Clarke et al. 2006). In the context that most shark fisheries are unregulated, this high level of exploitation is thought to have generated unsustainable fishing pressure on many shark stocks worldwide (Bonfil 1994, Rose 1996, Clarke et al. 2006).

A central goal of most fisheries management and conservation is to manage the resource on a stock-specific basis to preserve the diversity and evolutionary potential of the species as a whole (Dizon et al. 2002). Achieving these stock-specific management goals for sharks has been difficult for several reasons. For one, few shark stocks have been fully delineated using genetic data even though this is an integral part of stock assessment (FAO 2000, Heist 2005). Another serious problem is that many countries lack the resources, infrastructure or political will to effectively monitor their shark fishery landings at local extraction sites. There remain, therefore, glaring deficiencies in the species and stock-specific catch data required for reliable, quantitative shark stock assessments (Bonfil 1994, FAO 2000, ICCAT 2005). In the absence of traditional monitoring at extraction sites, surveying the major market supply chain endpoints has been proposed as a valuable alternative to derive data on species and stock exploitation levels (Clarke et al. 2006, Baker 2008).

One shark species whose stocks are of particular concern is the scalloped hammerhead, *Sphyrna lewini*, in the Western Atlantic. Fins from this mainly coastal, globally distributed, large hammerhead species fetch premium market prices due to their large size and high “fin needle” content ($US 100 -120kg $^{-1}$; Abercrombie et al. 2005),

and this species appears to have collapsed in the western North Atlantic and Gulf of Mexico due to overexploitation (Baum et al. 2003, Myers et al. 2007). Correspondingly, Western Atlantic *S. lewini* have been listed as "Endangered" (EN A2bd+4bd) since 2006 on the International Union for the Conservation of Nature's (IUCN) Red-List of Threatened Species.

An estimated 1-3 million *S. lewini* and its congener *Sphyrna zygaena* are killed annually worldwide to supply the fin trade (Clarke et al. 2006), but the stock-specific contributions of each species to this total remains unknown. Hammerhead sharks are not currently included on any international management or trade agreements (e.g. CITES), which means that *S. lewini* will primarily be assessed and managed under the auspices of domestic fishery regulations or regional fisheries management organizations. This regional level of management underscores the need for geographical origin and/or stock-specific landings data for *S. lewini*, and indeed threatened shark species generally.

Genetic stock identification (GSI) methods employ natural spatial partitions in genetic characters to estimate the stock composition of a fishery (Shaklee & Currens 2003). In vertebrate species where females stay close to their birthplace or home back to it for parturition or spawning ("natal homing"), the mitochondrial control region (mtCR) locus is often an excellent marker for reconstructing the contribution of distinct spawning, rookery or nursery regions (hereafter referred to as "mitochondrial stocks") to fishery catches. GSI using mtCR sequences have been successfully used to source catches of bony fish, sea turtles and marine mammals back to their stock/birthplace of origin (e.g. Waldman et al. 1996, Laurent et al. 1998, Baker et al. 2000) but have never been applied to sharks.

Given the high market value of fins from *Sphyrna lewini* and its IUCN Endangered status in the Western Atlantic, we wished to determine if GSI methods could be used to determine whether fins from *S. lewini* originating in this region occurred at detectable frequencies in the contemporary fin market. Findings from a global population genetic study of this species (Duncan et al. 2006) suggests this may be feasible: *Sphyrna lewini* mtDNA lineages exhibit strong population structure on a global scale and no mtCR haplotypes were shared between the Atlantic and the Indian or Pacific oceans, although some Indo-Pacific haplotypes were closely related to Atlantic haplotypes. Correspondingly, the first objective of our study was to see if mtCR sequences could be used to trace *S. lewini* dried fins collected in one of the world's largest fin markets (Hong Kong) back to a broad geographical origin.

Western Atlantic stock assessments performed to inform management and conservation efforts require that the stocks being assessed are clearly defined, and also hinge upon the collection of landings and trade data on a finer geographic scale. Duncan et al. (2006) included Western Atlantic *Sphyrna lewini* in their global study, but their sample sizes from this region were too small to examine finer scale stock delineation. Therefore, the second objective of our study was two-fold: (1) to better delineate geographic structuring of *S. lewini* mtDNA lineages within the Western Atlantic and (2) to determine whether it would be feasible to use mtCR sequence data to source fins in the market to their natal region of origin on a finer geographic scale within the Western Atlantic. Mixed stock analyses (MSA) have been developed for the latter application and carry a level of error that is inversely related to the intensity of stock structure in the species of interest (Waldman et al. 1996, Laurent et al. 1998, Baker et al. 2000, Bowen et

al. 2007). We therefore used a simulated MSA to determine whether *S. lewini* mtCR sequences are sufficiently structured in the Western Atlantic to permit accurate reconstruction of individual mitochondrial stock contributions to the globally sourced fin mixtures found in major markets.

MATERIALS AND METHODS

Despite severe sampling constraints associated with limited market access, dried fin samples were obtained from 11 major Hong Kong fin traders (Clarke et al. 2006) and species-specific multiplex PCR confirmed that 62 fins were from *Sphyrna lewini* (Abercrombie et al. 2005). Steps were taken during sampling to ensure that each fin came from a different animal (e.g. by sampling the same fin type at the same trader). DNA was isolated from ~ 20 mg of each dried fin sample (DNeasy kit, Qiagen, Valencia, CA, U.S.A.). PCR amplification and mtCR sequencing protocols followed Duncan et al. (2006), producing a partial mtCR sequence of 547 bp from the first domain for analysis. Each fin was allocated to a broad geographical origin (i.e. Western Atlantic, Eastern Atlantic, or Indo-Pacific) by matching its haplotype (by eye) to the geographic distribution of mtCR haplotypes obtained from the combined baseline genetic datasets of Duncan et al. (2006), Ovenden et al. (2009) and the present study (combined n = 452 wild-caught, globally distributed individuals). The evolutionary relationships of “novel” market fin haplotypes not recorded in any of these three surveys to the known wild-caught haplotypes were assessed using a statistical parsimony network constructed in TCS 4.1 (Clement et al. 2000).

For finer-scale *Sphyrna lewini* stock delineation within the Western Atlantic, we combined the Western Atlantic mitochondrial DNA sequences from Duncan et al. (2006) (total n = 37; distribution: U.S. Atlantic n = 16; U.S. Gulf of Mexico n = 16; Panama Atlantic n = 2; Brazil n = 3) with new sequences that we generated (n = 140). We thus analyzed mtCR sequences from a total of 177 wild-caught animals sampled from four locations: U.S. Atlantic (n = 53), U.S. Gulf of Mexico (n = 45), Central American Caribbean (n = 22) and Brazil (n = 57), providing wide coverage of the species' Western Atlantic range. DNA isolation and mtCR sequencing protocols employed for these samples were the same as those used for the market-derived fin samples. Genetic diversity indices were calculated in DnaSP 4.0 (Rozas et al. 2003). Genetic differentiation (Φ_{ST}; Jukes-Cantor distances) between the sampling sites and test of their significance was calculated in Arlequin 2.001 (Schneider et al. 2000), using AMOVA. A statistical parsimony network was constructed for the observed Western Atlantic haplotypes in TCS 4.1 (Clement et al. 2000).

To assess the utility of using mixed stock analysis (MSA) for reconstructing individual Western Atlantic stock contributions to market-derived mixtures of *Sphyrna lewini* fins, we ran simulations in a commonly-used (e.g. Bowen et al. 2007) MSA program (Statistics Program for Analyzing Mixtures (SPAM 3.7b): www.cf.adfg.state.ak.us/geninfo/research/genetics/genetics.php). The SPAM program randomly resamples the baseline mitochondrial haplotype frequency of each Western Atlantic mitochondrial stock delineated in this study to construct mixtures (n = 100 animals) with a known (i.e. user-specified) contribution from each stock. The program then uses maximum likelihood (1000 iterations) to reassign each individual in the mixture

to its most probable mitochondrial stock of origin and thus reconstruct the contribution of each stock to the mixture. The accuracy of future "blind" (i.e. stock contribution unknown) MSA given the level of structure observed is assessed by the level of concordance obtained between the mean estimated contribution of each mitochondrial stock to the mixture and their known, user-specified contributions. We ran multiple simulations using a wide range of user-specified contributions from each mitochondrial stock (i.e. ranging from equal to various combinations of highly skewed contributions).

RESULTS

Market fin haplotype composition and relationships

The 62 Hong Kong market-derived *Sphyrna lewini* fins were composed of eighteen mtCR haplotypes (Table 1). Fifty-seven of these fins matched a known mtCR haplotype from the combined global dataset of Duncan et al. (2006) and the present study (see next paragraph). Of the five fins with "novel" haplotypes, three (GenBank accession numbers GU014384, GU014386 and GU014387) had haplotypes very closely related to Indo-Pacific haplotypes (Fig. 1), indicating an Indo-Pacific origin for these fins. The two remaining novel fin haplotypes (accession numbers GU014385 and GU014388) were within one substitution of haplotype 13 (West Africa) and haplotype 26 (Caribbean; GU014389) (Fig. 2), respectively, but at least six mutational steps from any known Indo-Pacific haplotype, supporting their Atlantic origin. Thus, all the market derived fins could be traced to capture origins in the either the Atlantic or Indo-Pacific regions (Table 1). Overall, the 62 *S. lewini* fins originated from the Indo-Pacific (~65%) and both sides

of the Atlantic basin (combined total ~34%), with a likely ~21% contribution (13 fins) from the Western Atlantic region (Table 1).

Western Atlantic stock structure

Eight mtCR haplotypes separated by up to six mutational steps were found among the 177 wild-caught *Sphyrna lewini* sampled from the Western Atlantic (Fig. 2); three of these haplotypes (H26-H28) were novel (i.e. not found in Duncan et al.'s [2006] global survey; GenBank accession numbers GU014389, GU014390, GU014391). None of the Western Atlantic haplotypes were recorded in the Indo-Pacific by Duncan et al. (2006; n=228) or Ovenden et al. (2009; n=47). Similarly, none of the Indo-Pacific haplotypes were recorded in our survey of Western Atlantic animals.

Western Atlantic *Sphyrna lewini* are structured into at least three distinct mitochondrial stocks (overall Φ_{ST} =0.74, $p < 0.000001$): the "northern" (comprised of U.S. Atlantic and Gulf of Mexico animals, pairwise Φ_{ST} non-significant), "central" (Belize and Panama) and "southern" (Brazil) stocks (Fig. 3, Table 2). Haplotype and nucleotide diversities were highest in the central mitochondrial stock (h = 0.731 [s.d. = 0.072], π = 0.0035 [0.0005]) and lower in both the northern and southern mitochondrial stocks (northern: U.S. Atlantic and Gulf of Mexico; h = 0.399 and 0.270 [s.d. = 0.06 and 0.02], π = 0.001 and 0.0005 [0.0001 and 0.0001], respectively; southern: h = 0.103 [s.d. = 0.055], π = 0.0003 [0.0002]).

Mixed stock analysis

Mixed stock analysis simulations executed using a range of user-specified stock contributions indicated sufficient structure within the Western Atlantic to allow accurate mitochondrial stock-specific landings reconstructions to be made (Table 3). The mean simulation recovered contributions of each mitochondrial stock were very close to the user-specified contributions with narrow deviation around the mean. This close concordance was true regardless of the degree of skew and relative contributions of the northern, central or southern *Sphyrna lewini* mitochondrial stocks used in the mixture (Table 3). We observed haplotypes typical of each stock in the 13 fins collected in the Hong Kong market that originated in the Western Atlantic (Table 1).

DISCUSSION

Market fin provenance

Our survey of a reasonably large and broadly distributed sample of wild-caught Western Atlantic *Sphyrna lewini* showed no sharing of haplotypes between the Western Atlantic (n=177) and Indo-Pacific (n=275), consistent with Duncan et al.'s (2006) findings based on a smaller (n=37) Western Atlantic sample set. This strong signal of ocean basin-based mitochondrial "endemicity" (or likely near-endemicity) suggests that allocation of most market-derived fins to at least an ocean-basin origin will be reasonably robust. Indeed, we were able to exactly match 57 of the 62 market fins to either an Atlantic or Indo-Pacific haplotype.

Of note is that seven market fins, that according to the records of the Hong Kong trader who supplied them were directly purchased from a West African source, possessed

haplotypes identical to the apparently endemic Eastern Atlantic haplotypes found in six wild-caught animals sampled there by Duncan et al. (2006). If the non-overlapping haplotype distribution between the Eastern and Western Atlantic is confirmed after increased sampling efforts in the Eastern Atlantic, this would mean the origin of at least a portion of *Sphyrna lewini* fins in trade might also be unambiguously allocated to either of these regions based on their endemic mtCR signature. The observation of non-shared haplotypes across the Atlantic is consistent with the premise that *S. lewini* movements are limited by deep ocean expanses (Duncan et al. 2006), and that female *S. lewini* show fidelity to parturition areas on their natal side of the North Atlantic, as would be expected based on the primarily coastal nature of this species (http://www.fishbase.org).

Our small genetic survey of *Sphyrna lewini* fins from the Hong Kong market revealed that the contemporary trade is sourced from the Indo-Pacific, Eastern Atlantic and Western Atlantic basins. Assuming the regional haplotype endemicity pattern distinguishing Eastern and Western Atlantic *S. lewini* is true, Western Atlantic sharks remain well represented in the Hong Kong market sample (~21% of fins), indicating that the international shark fin trade remains a threat to the endangered populations of this region.

Western Atlantic mitochondrial stock structure

The high Φ_{ST} values (Table 2) between sampling locations demonstrates that *Sphyrna lewini* mtCR lineages are further structured into at least three geographically distinct mitochondrial stocks along the eastern American continental margin. This result contrasts with Duncan et al.'s (2006) global data set findings that *Sphyrna lewini* nursery

populations linked by continuous coastline exhibit high connectivity. Interestingly, they noted very little sharing of haplotypes between the eastern U.S., Panama Atlantic and Brazil coastlines; however, their sample sizes from these regions were too limited (n=32, 2 and 3 respectively) to detect population differentiation. The pattern of strong mitochondrial stock differentiation we observed along the Western Atlantic coastline means one of two things: (1) female *S. lewini* remain close to their natal region of origin (e.g. Chapman et al. 2009) or (2) females usually return to their natal region to give birth ("natal homing"). Mitochondrial stock structure has also been described in several other shark species (Pardini et al. 2001, Keeney et al. 2005, Stow et al. 2006, Schultz et al. 2008, Chabot & Allan 2009) and may prove to be a common characteristic of coastally-oriented sharks in particular.

We note that our finding of strong mitochondrial stock structure in the Western Atlantic does not preclude male-mediated gene flow, as has been documented in some other shark species also displaying mitochondrial population differentiation (e.g. Pardini et al. 2001, Keeney et al. 2005, Schultz et al. 2008). A global survey of the geographic distribution of nuclear genetic variation in *Sphyrna lewini* based on microsatellite markers is currently underway to resolve this issue (T. Daly-Engel, University of Hawaii *pers comm*.). The absence of a nuclear genetic perspective on *S. lewini* population differentiation in the Western Atlantic not withstanding, determining the relative contribution of each mitochondrial stock to fishery landings and international trade is still valuable. Each mitochondrial lineage represents a discrete pool of birthing females and as such can be used to track the natal stock-of-origin for products in trade to improve

management and conservation practice (e.g. Waldman et al. 1996, Laurent et al. 1998, Baker et al. 2000).

The strong signal of mitochondrial stock structure along the Western Atlantic coastline is somewhat surprising given the lack of obvious physical barriers (e.g. deep ocean expanses) to a large mobile animal, and the contrasting high mitochondrial connectivity seen along continental margins in Indo-Pacific conspecifics (Duncan et al. 2006). However, a generally similar structuring of mtDNA lineages in the Western Atlantic has been observed in other large, mobile marine vertebrates (e.g. manatees - Garcia-Rodriguez et al. 1998; blacktip sharks - Keeney et al. 2005). In the absence of impermeable physical barriers to female-mediated gene flow, it is possible that reproductive season mismatches at different latitudes or local adaptation of individuals to either tropical or warm temperate conditions may inhibit female movements or favor natal homing in these species.

Our assessment of mtCR diversity in *Sphyrna lewini* from the Western Atlantic revealed relatively few haplotypes separated by a small number of mutational steps (Fig. 2), resulting in low haplotype and nucleotide diversities within each region. This low mtCR diversity may not be a function of overexploitation however, as this pattern was also typical for *S. lewini* sampled from throughout its global range (Duncan et al. 2006). The central stock from the Western Atlantic exhibited comparable haplotype and nucleotide diversity to the most diverse Indo-Pacific mitochondrial stocks examined by Duncan et al. (2006), while the northern and southern mitochondrial stocks were intermediate and among the lowest respectively.

Adult females are arguably a critical demographic to protect in order to sustain or rebuild shark populations (Kinney & Simpfendorfer 2008). The pattern of mitochondrial geographic structure for *Sphyrna lewini* in the Western Atlantic indicates that regional overfishing has the potential to deplete locally-breeding adult females without significant replenishment of sharks occurring from elsewhere. As such, recovery of the reportedly collapsed *S. lewini* population in the U.S. Atlantic and northern Gulf of Mexico (Baum et al. 2003, Myers et al. 2007) is unlikely to occur by immigration of adult females from the south or across the Atlantic, regardless of male patterns of movement and reproductive mixing. Instead, recovery is likely to depend on an amelioration of local-scale fishing pressure in this region.

Mixed Stock Analysis

The proper management of Western Atlantic *Sphyrna lewini* will require information about exploitation levels on adult females using specific regions to breed and individuals derived from the associated nurseries. In this context, results of the MSA simulations provide proof-of-concept that the level of mitochondrial stock structure observed may be sufficient to permit accurate reconstructions of the contribution of each stock to *S. lewini* fin mixtures found in major globally sourced markets. We did not perform MSA on the market-derived, Western Atlantic fins identified in this study due to the small sample size (13) of fins available. However, the fact that haplotypes typical of each of the three mitochondrial stocks were recovered indicates that the contemporary trade of *S. lewini* fins involves the participation of several Western Atlantic countries and the exploitation of multiple breeding grounds. These findings underscore the need for

investment in stock-specific landings and trade monitoring for a species considered endangered in this region.

Our findings for *Sphyrna lewini* also suggest that for many other coastal sharks where substantial stock structure is coming to light (e.g. Keeney et al. 2005, Stow et al. 2006, Schultz et al. 2008, Chabot & Allan 2009), surveying major market supply chain endpoints and applying genetic stock identification (GSI) methods could reveal which regions and stocks are major contributors to the trade. This information is necessary to prioritize target areas for conservation and development of much-needed stock-specific assessment and management measures. Incorporation of additional sampling (more locations, more individuals and more loci) will allow even more precise assessment of the provenance of shark fishery landings and market products. Until direct monitoring of landings at extraction sites becomes economically and politically realistic, we suggest that genetic monitoring of the market tied to knowledge of stock structure is likely to be a quicker and more efficient way of obtaining these essential data for exploited shark species.

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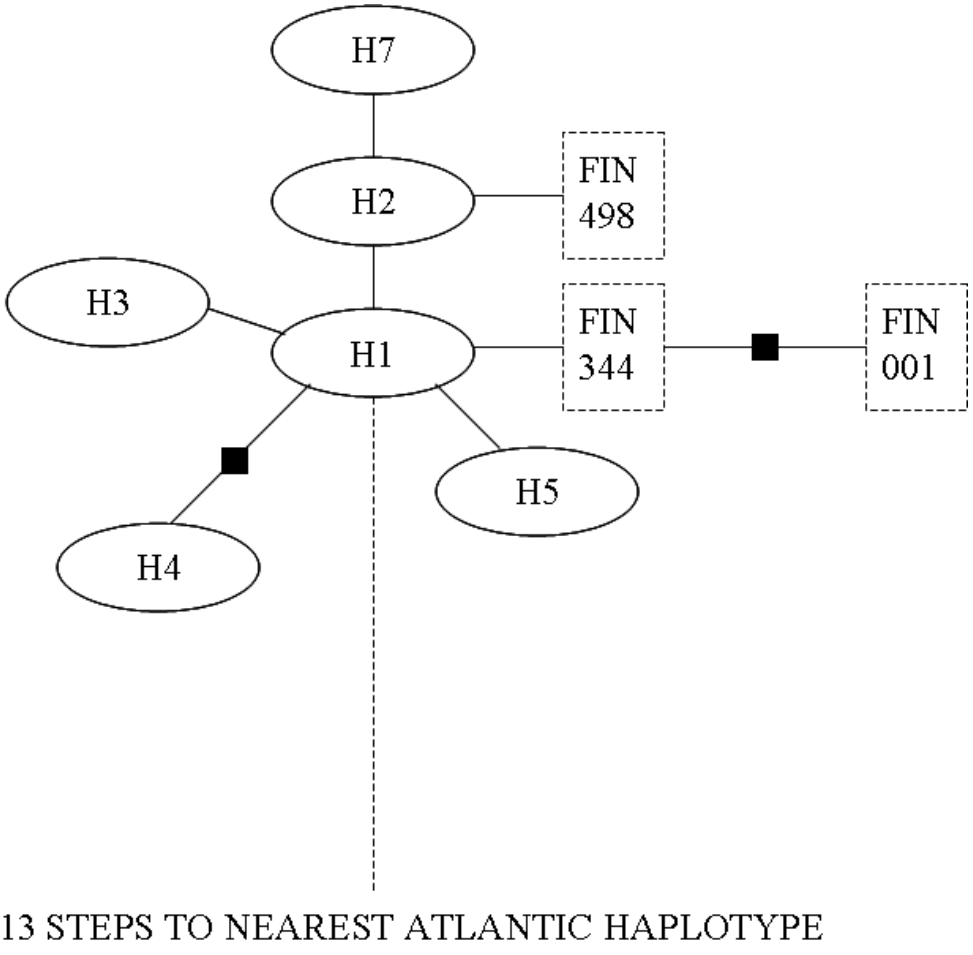
H7
H2
FIN
498
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H5
H4
13 STEPS TO NEAREST ATLANTIC HAPLOTYPE

Fig.1.

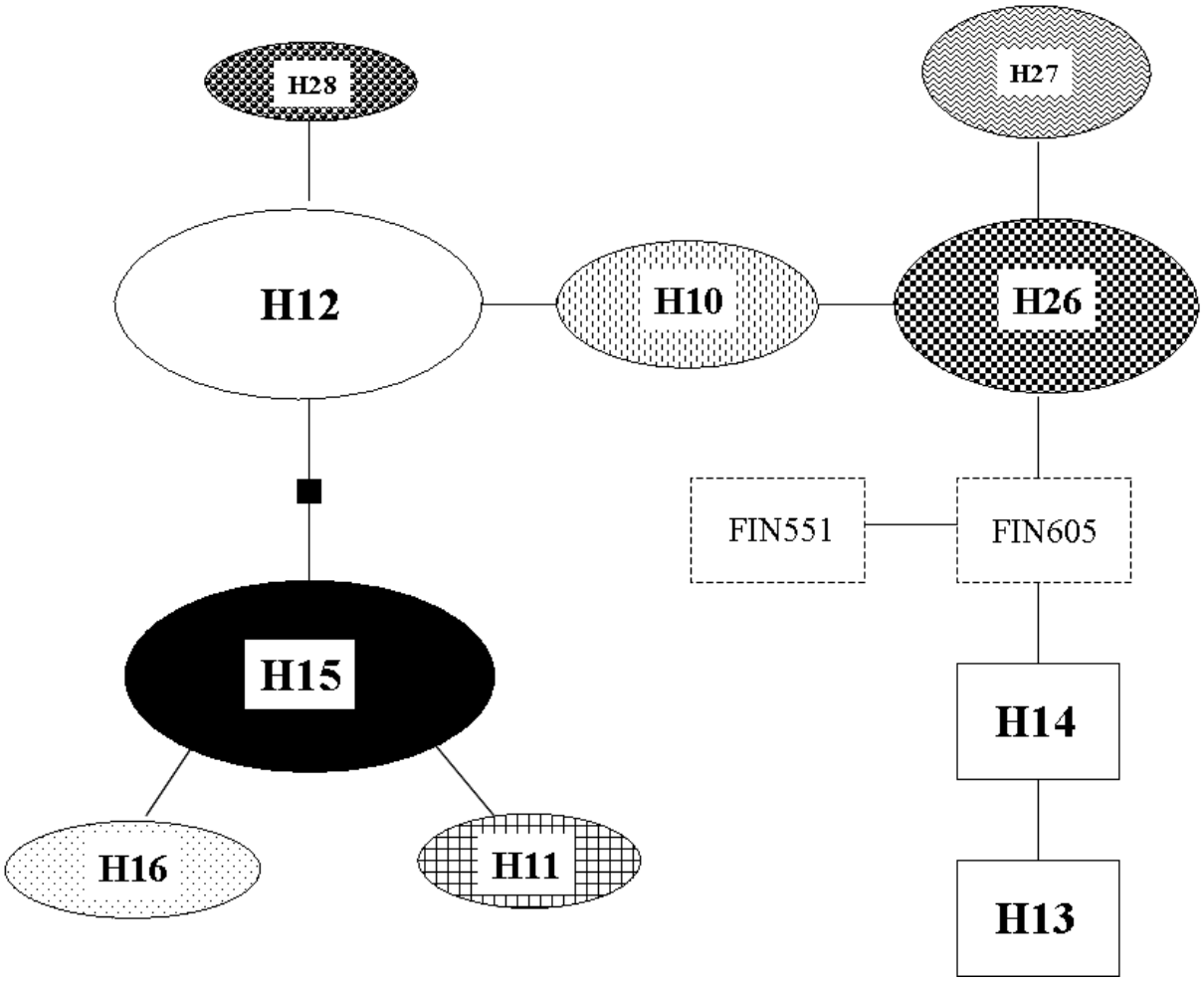

Fig. 2.

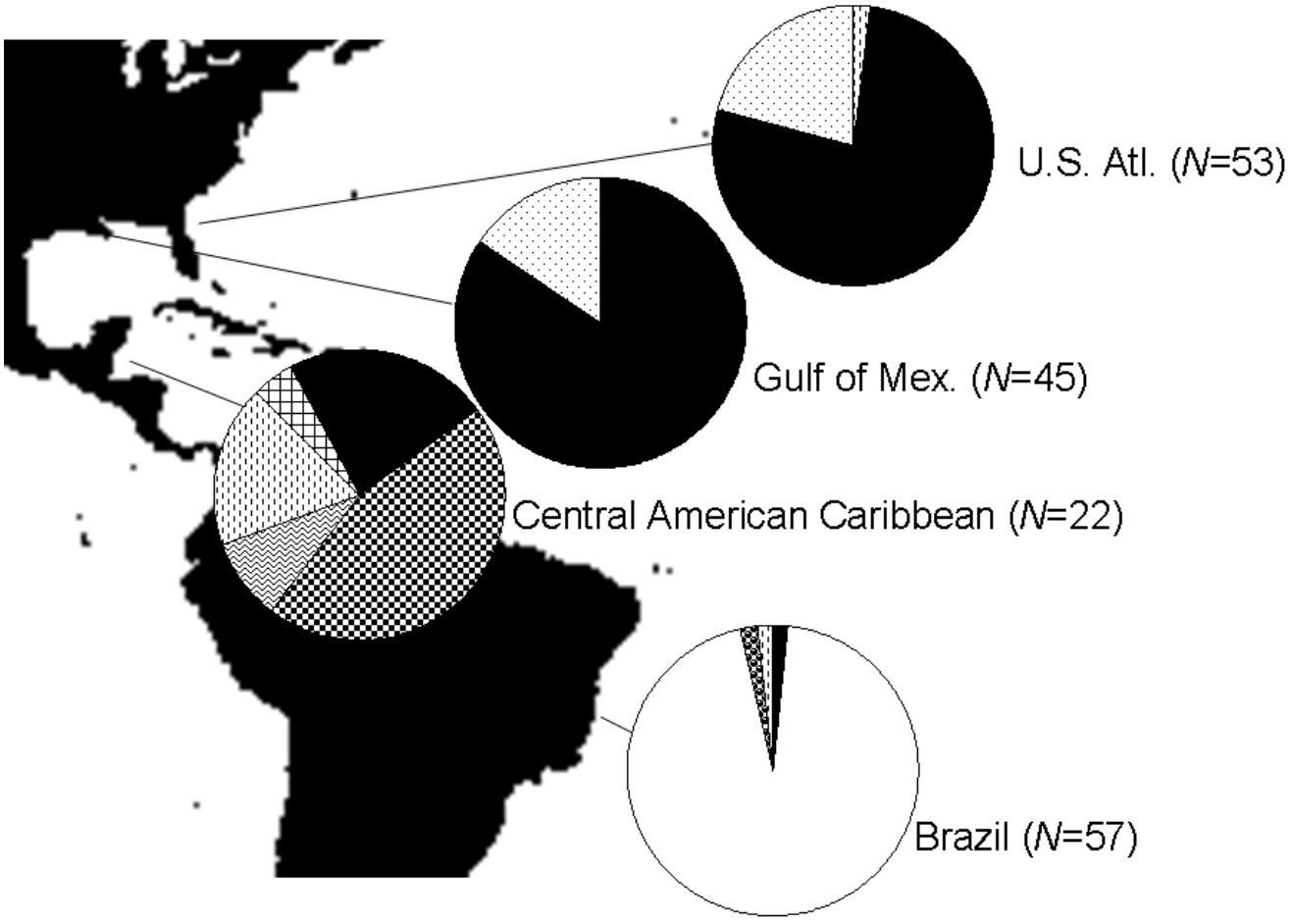
U.S. Atl. (N=53)
Gulf of Mex. (N=45)
Central American Caribbean (N=22)
Brazil (N=57)

Fig. 3.

Figure Legends

Fig. 1: Mitochondrial control region (mtCR) haplotype network for *Sphyrna lewini* sampled in the Indo-Pacific by Duncan et al. (2006), with haplotypes (in ovals) numbered to match their designation in that study. The small square represents an inferred mutational step. FIN001, FIN498 and FIN344 (dashed boxes) represent three Hong Kong market fins with novel haplotypes closely related to the Indo-Pacific haplotypes, but at least 14 mutational steps from any known Atlantic haplotype.

Fig. 2: MtCR haplotype network for *Sphyrna lewini* sampled in the Western Atlantic. The small square represents an inferred mutational step. Haplotypes (H10-16) are numbered according to Duncan et al. (2006); Haplotypes (H26-28) were discovered in the present study. Haplotypes contained within an oval have been recorded in the Western Atlantic, and haplotypes in the solid box have only been recorded in the Eastern Atlantic. FIN605 and FIN551 (dashed boxes) represent novel, Hong Kong market fin haplotypes that are at least six mutational steps from any observed Indo-Pacific haplotype.

Fig. 3: Map of the Western Atlantic showing mtCR haplotype frequencies of *Sphyrna lewini* sampled in the U.S. Atlantic (U.S. Atl.), U.S. Gulf of Mexico (Gulf of Mex.), Central American Caribbean and Brazil. Haplotypes are color or pattern- coded to match the haplotype network in Fig. 2. (e.g. haplotype 15 is denoted by the black slices in each pie chart and in Fig. 2).

Table 1: Mitochondrial control region (mtCR) haplotypes of 62 *Sphyrna lewini* dried fins obtained from the Hong Kong market. Haplotype (HAP 1-26) designations are those used in Duncan et al. (2006). Inferred geographic origin of each haplotype is based on Duncan et al. (2006) and the present study. The number of fins with each haplotype is shown in parentheses. The NOVEL ATLANTIC and INDO-PACIFIC categories represent haplotypes not yet observed in surveys of wild-caught animals but are closely related to known Atlantic or Indo-Pacific sequences respectively.

mtCR Haplotype (no. of fins)	**Geographic origin**	**Haplotype Source**
HAP 1 (13)	Indo-Pacific	Duncan et al. 2006
HAP 2 (14)	Indo-Pacific	Duncan et al. 2006
HAP 4 (1)	Indo-Pacific	Duncan et al. 2006
HAP 8 (1)	Indo-Pacific	Duncan et al. 2006
HAP 9 (4)	Indo-Pacific	Duncan et al. 2006
HAP 10 (3)	W. Atlantic	Duncan et al. 2006
HAP 12 (3)	W. Atlantic (Brazil)	Duncan et al. 2006
HAP 13 (1)	E. Atlantic (West Africa)	Duncan et al. 2006
HAP 14 (6)	E. Atlantic (West Africa)	Duncan et al. 2006
HAP 15 (4)	W. Atlantic (U.S.A., Caribbean, Brazil)	Duncan et al. 2006
HAP 19 (4)	Indo-Pacific	Duncan et al. 2006
HAP 23 (1)	Indo-Pacific	Duncan et al. 2006
HAP 26 (2)	W. Atlantic (Caribbean)	this study
2 NOVEL ATLANTIC (2)	N/A	this study
3 NOVEL INDO-PACIFIC (3)	N/A	this study

Table 2: Population differentiation among Western Atlantic *Sphyrna lewini* collected in four regions: U.S. Atlantic (USATL, n = 53), U.S. Gulf of Mexico (USGOM, n = 45), Central American Caribbean (CACAR [Belize and Panama], n = 22) and Brazil (BRAZIL, n = 57). Numbers above diagonal show average pairwise nucleotide divergence between populations (Jukes Cantor distance). Numbers below diagonal show pairwise Φ_{ST} between populations, with values significantly different from zero bolded ($p < 0.000001$). Only the USATL-USGOM pairwise Φ_{ST} was not significantly from zero ($p > 0.62$).

	USATL	**USGOM**	**CACAR**	**BRAZIL**
USATL	*	0.00073	0.00515	0.00410
USGOM	-0.01	*	0.00525	0.00396
CACAR	**0.68**	**0.69**	*****	0.00364
BRAZIL	**0.88**	**0.91**	**0.62**	*****

Table 3: *Sphyrna lewini* mixed-stock analysis (MSA) simulation results comparing the concordance between known, user-specified mitochondrial stock contributions and mean reconstructed mitochondrial stock contributions based on stock-specific haplotype frequencies observed in this study. N = northern stock, C = central stock, S = southern stock (see text).

User-specified contributions	**Mean reconstructed contributions (std. dev)**
33% N, 33% C, 33% S	33.2% N (5.7%), 33.4% C (5.9%), 33.6% S (4.9%)
90% N, 5% C, 5% S	90.0% N (3.2%), 4.97 % C (2.5%), 4.98% S (2.2%)
5% N, 90% C, 5% S	4.90% N (4.1%), 90.1% C (4.7%), 5.1% S (2.2%)
5% N, 5% C, 90% S	5.02% N (2.8%), 4.96% C (2.5%), 90.2% S (3.2%)

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