

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

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24 mixed stock analysis.

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26 **Running head:** Shark fin trade genetic tracking

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

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INTRODUCTION

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

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

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

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

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

88 Genetic stock identification (GSI) methods employ natural spatial partitions in
89 genetic characters to estimate the stock composition of a fishery (Shaklee & Currens
90 2003). In vertebrate species where females stay close to their birthplace or home back to
91 it for parturition or spawning (“natal homing”), the mitochondrial control region (mtCR)
92 locus is often an excellent marker for reconstructing the contribution of distinct
93 spawning, rookery or nursery regions (hereafter referred to as “mitochondrial stocks”) to
94 fishery catches. GSI using mtCR sequences have been successfully used to source
95 catches of bony fish, sea turtles and marine mammals back to their stock/birthplace of
96 origin (e.g. Waldman et al. 1996, Laurent et al. 1998, Baker et al. 2000) but have never
97 been applied to sharks.

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

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

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

125

126

MATERIALS AND METHODS

127 Despite severe sampling constraints associated with limited market access, dried
128 fin samples were obtained from 11 major Hong Kong fin traders (Clarke et al. 2006) and
129 species-specific multiplex PCR confirmed that 62 fins were from *Sphyrna lewini*
130 (Abercrombie et al. 2005). Steps were taken during sampling to ensure that each fin came
131 from a different animal (e.g. by sampling the same fin type at the same trader). DNA was
132 isolated from ~ 20 mg of each dried fin sample (DNeasy kit, Qiagen, Valencia, CA,
133 U.S.A.). PCR amplification and mtCR sequencing protocols followed Duncan et al.
134 (2006), producing a partial mtCR sequence of 547 bp from the first domain for analysis.
135 Each fin was allocated to a broad geographical origin (i.e. Western Atlantic, Eastern
136 Atlantic, or Indo-Pacific) by matching its haplotype (by eye) to the geographic
137 distribution of mtCR haplotypes obtained from the combined baseline genetic datasets of
138 Duncan et al. (2006), Ovenden et al. (2009) and the present study (combined n = 452
139 wild-caught, globally distributed individuals). The evolutionary relationships of “novel”
140 market fin haplotypes not recorded in any of these three surveys to the known wild-
141 caught haplotypes were assessed using a statistical parsimony network constructed in
142 TCS 4.1 (Clement et al. 2000).

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

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

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

173

174

RESULTS

175 *Market fin haplotype composition and relationships*

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

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

190

191 *Western Atlantic stock structure*

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

199 Western Atlantic *Sphyrna lewini* are structured into at least three distinct
200 mitochondrial stocks (overall $\Phi_{ST}=0.74$, $p < 0.000001$): the “northern” (comprised of
201 U.S. Atlantic and Gulf of Mexico animals, pairwise Φ_{ST} non-significant), “central”
202 (Belize and Panama) and “southern” (Brazil) stocks (Fig. 3, Table 2). Haplotype and
203 nucleotide diversities were highest in the central mitochondrial stock ($h = 0.731$ [s.d. =
204 0.072], $\pi = 0.0035$ [0.0005]) and lower in both the northern and southern mitochondrial
205 stocks (northern: U.S. Atlantic and Gulf of Mexico; $h = 0.399$ and 0.270 [s.d. = 0.06 and
206 0.02], $\pi = 0.001$ and 0.0005 [0.0001 and 0.0001], respectively; southern: $h = 0.103$ [s.d. =
207 0.055], $\pi = 0.0003$ [0.0002]).

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211 *Mixed stock analysis*

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

221

222

DISCUSSION

223 *Market fin provenance*

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

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

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

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

251

252 *Western Atlantic mitochondrial stock structure*

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

257 populations linked by continuous coastline exhibit high connectivity. Interestingly, they
258 noted very little sharing of haplotypes between the eastern U.S., Panama Atlantic and
259 Brazil coastlines; however, their sample sizes from these regions were too limited (n=32,
260 2 and 3 respectively) to detect population differentiation. The pattern of strong
261 mitochondrial stock differentiation we observed along the Western Atlantic coastline
262 means one of two things: (1) female *S. lewini* remain close to their natal region of origin
263 (e.g. Chapman et al. 2009) or (2) females usually return to their natal region to give birth
264 (“natal homing”). Mitochondrial stock structure has also been described in several other
265 shark species (Pardini et al. 2001, Keeney et al. 2005, Stow et al. 2006, Schultz et al.
266 2008, Chabot & Allan 2009) and may prove to be a common characteristic of coastally-
267 oriented sharks in particular.

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

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

281 The strong signal of mitochondrial stock structure along the Western Atlantic
282 coastline is somewhat surprising given the lack of obvious physical barriers (e.g. deep
283 ocean expanses) to a large mobile animal, and the contrasting high mitochondrial
284 connectivity seen along continental margins in Indo-Pacific conspecifics (Duncan et al.
285 2006). However, a generally similar structuring of mtDNA lineages in the Western
286 Atlantic has been observed in other large, mobile marine vertebrates (e.g. manatees -
287 Garcia-Rodriguez et al. 1998; blacktip sharks - Keeney et al. 2005). In the absence of
288 impermeable physical barriers to female-mediated gene flow, it is possible that
289 reproductive season mismatches at different latitudes or local adaptation of individuals to
290 either tropical or warm temperate conditions may inhibit female movements or favor
291 natal homing in these species.

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

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

311

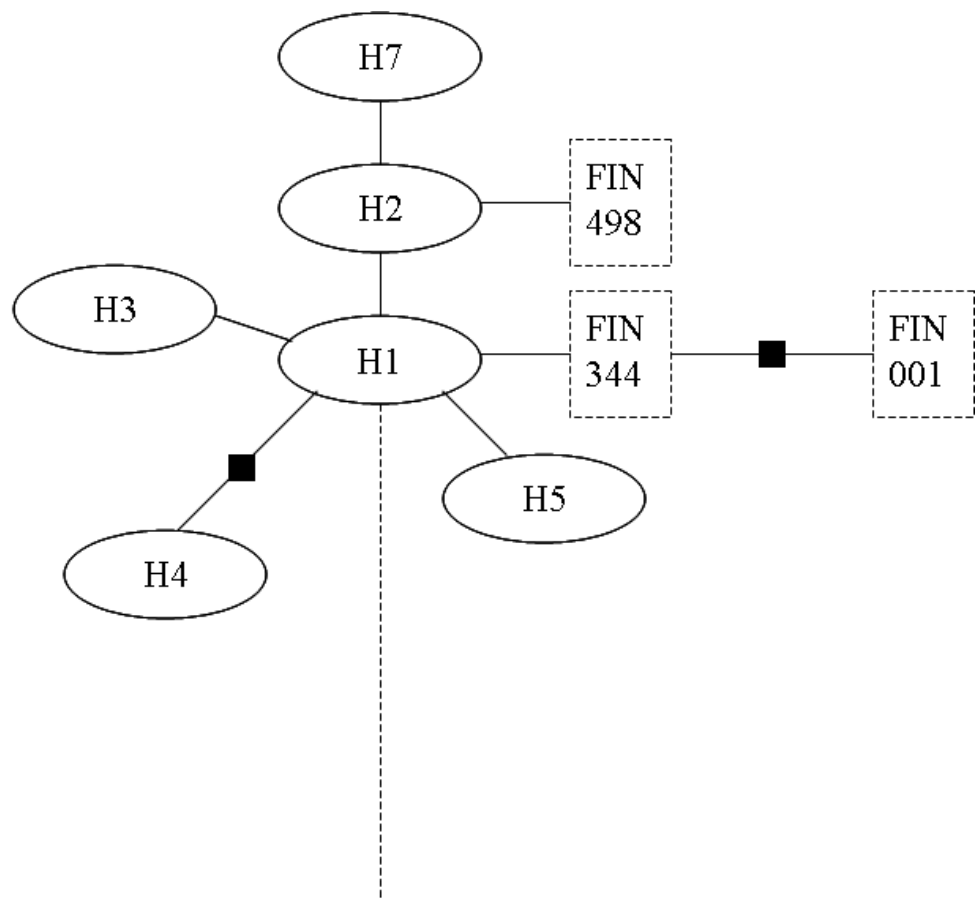
312 *Mixed Stock Analysis*

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

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

326 Our findings for *Sphyrna lewini* also suggest that for many other coastal sharks
327 where substantial stock structure is coming to light (e.g. Keeney et al. 2005, Stow et al.
328 2006, Schultz et al. 2008, Chabot & Allan 2009), surveying major market supply chain
329 endpoints and applying genetic stock identification (GSI) methods could reveal which
330 regions and stocks are major contributors to the trade. This information is necessary to
331 prioritize target areas for conservation and development of much-needed stock-specific
332 assessment and management measures. Incorporation of additional sampling (more
333 locations, more individuals and more loci) will allow even more precise assessment of the
334 provenance of shark fishery landings and market products. Until direct monitoring of
335 landings at extraction sites becomes economically and politically realistic, we suggest
336 that genetic monitoring of the market tied to knowledge of stock structure is likely to be a
337 quicker and more efficient way of obtaining these essential data for exploited shark
338 species.

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13 STEPS TO NEAREST ATLANTIC HAPLOTYPE

Fig.1.

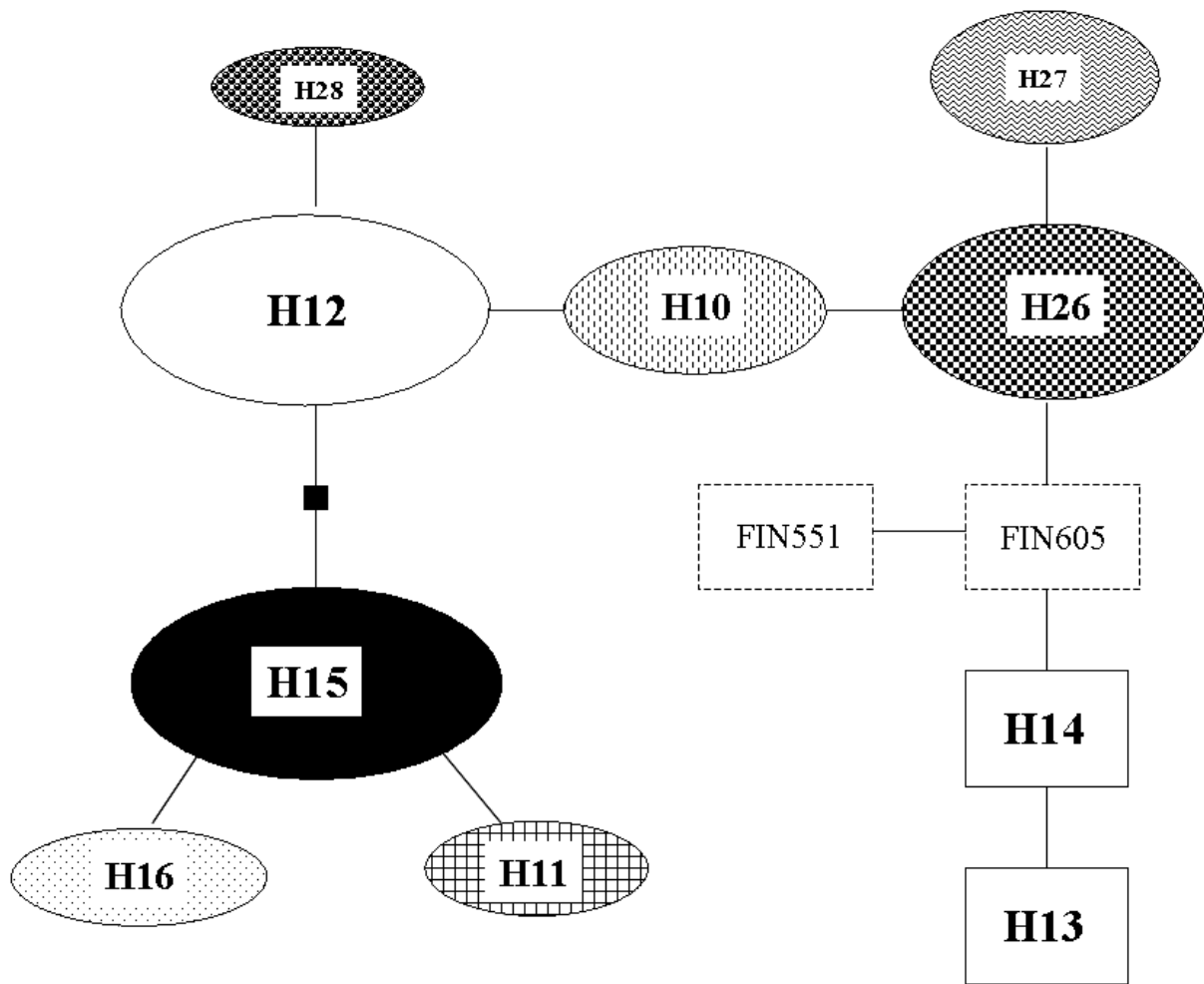


Fig. 2.

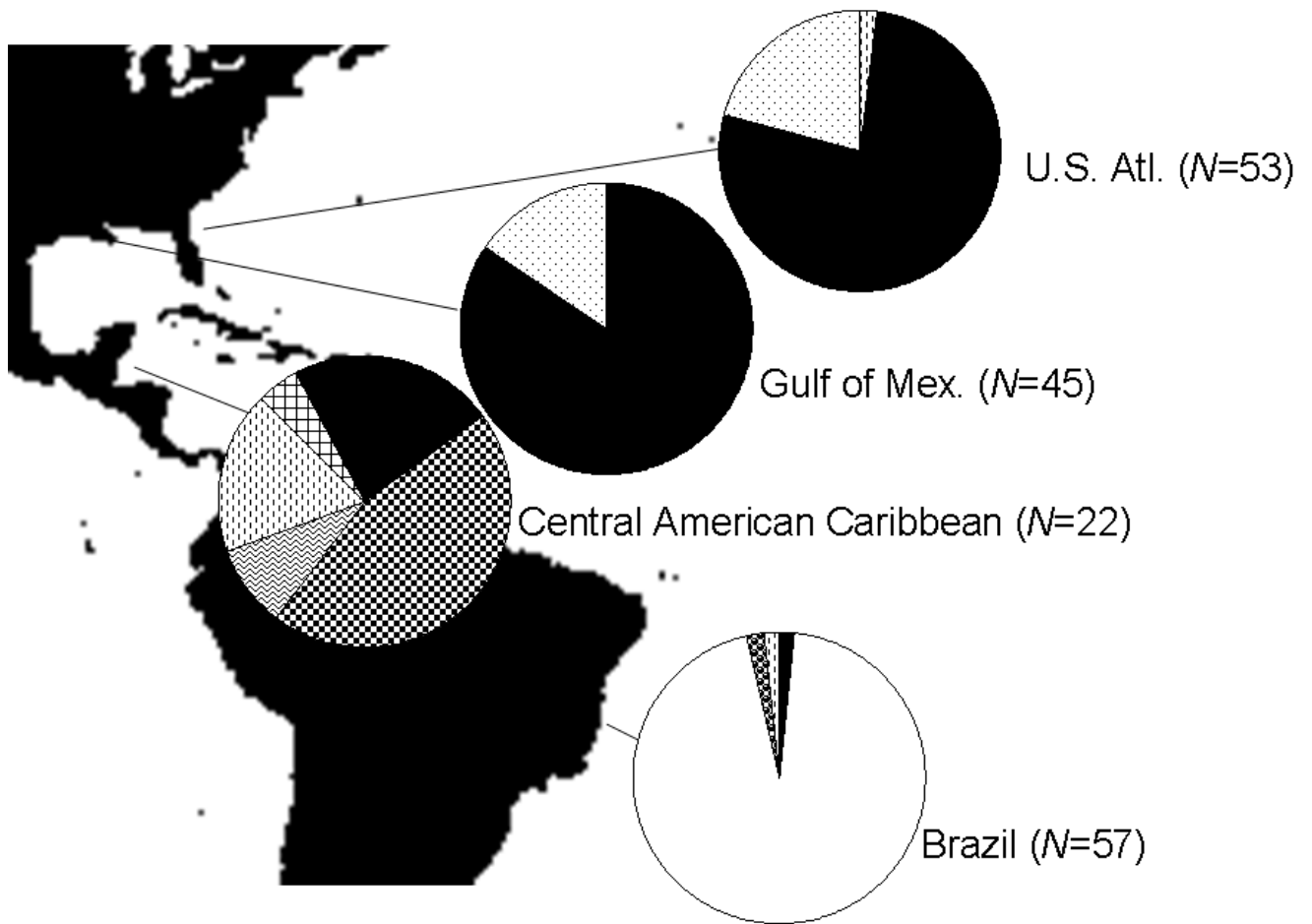


Fig. 3.

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%)

LITERATURE CITED

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