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Migration of hawksbill turtles *Eretmochelys imbricata* from Tortuguero, Costa Rica

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The hawksbill turtle *Eretmochelys imbricata* is a widely distributed and critically endangered species that feeds on sponges and fills an important ecological role in the coral reef ecosystem. At Tortuguero, Costa Rica, trend analyses indicate considerable decline in nesting estimated at 77.2–94.5% between 1956 and 2003, as a result of excessive turtle fishing. We analyzed flipper tag returns, satellite telemetry and genetic samples to determine movements and habitat use of adult female Tortuguero hawksbills. Tag returns and satellite telemetry show hawksbills migrate to foraging grounds in Nicaragua and Honduras. Genetic analysis indicates the hawksbills may also migrate to Cuban, Puerto Rican, and possibly Mexican waters. We conclude hawksbills represent an internationally shared resource. There is a close correlation between tag recapture sites, hawksbill foraging grounds and coral reef distribution. Caribbean coral reef decline may reduce food availability and negatively impact hawksbill turtles. Conversely, hawksbill decline may shift the balance on coral reefs by reducing predation pressure on sponges and hence make coral reefs less resilient to natural and anthropogenic threats. Strategies aiming to conserve hawksbills and coral reefs must consider both the extensive hawksbill migrations and the close relationship between the species and the coral reef ecosystem.

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The hawksbill turtle *Eretmochelys imbricata* is a species with a circumglobal tropical distribution including 110 countries and territories (Anon. 2003). The hawksbill turtle feeds primarily on several species of marine sponges and cnidarians (Meylan 1988, León and Bjorndal 2002). It fills an important ecological role in the coral reef ecosystem by influencing community diversity and structure through selective feeding, reducing the cover of certain species of sponges and cnidarians and lowering those species' ability to outcompete other reef organisms (León and Bjorndal 2002).

Humans have captured hawksbill turtles for centuries for meat, eggs and to manufacture its keratinous carapace plates into tortoiseshell items (Parsons 1972, Meylan and Donnelly 1999). The tortoiseshell trade is the major reason for the global decline observed in hawksbill nesting (Meylan and Donnelly 1999). International tortoiseshell trade is now prohibited.

In the Caribbean, genetic studies have shown that foraging populations of hawksbills comprise turtles of multiple stock origins from far ranging areas (Bass et al. 1996, Diaz-Fernández et al. 1999). Caribbean hawksbill populations have been described as declining or depleted in 22 of 26 geopolitical units for which information is available (Meylan 1999a). An overall Caribbean hawksbill decline of 95% since preexploitation is thought to be a conservative estimate (Bjorndal and Jackson 2003). As recently as 1905, one third (corresponding to

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11 schooners and sloops) of the sea turtle fishing fleet based at the Cayman Islands was exclusively dedicated to fishing hawksbill turtles (Swettenham 1906). Hawksbill turtles are still caught in many countries in the Caribbean (Lagueux 1998, Meylan and Donnelly 1999), with Cuba currently permitting the largest legal catch of 500 hawksbill turtles per year (Carrillo et al. 1999). Adult hawksbill turtles' preferred foraging habitat, coral reefs, have also declined precipitously in the Caribbean. Caribbean reefs have declined more than Australian and Red Sea reefs and many coral reefs may have been significantly degraded prior to 1900 (Pandolfi et al. 2003). In recent years, Caribbean corals have continued to decline with an estimated 80% reduction in hard coral cover during the last three decades (Gardner et al. 2003).

In Costa Rica, observations on hawksbill use date back at least to 1799 when Miskito Indians and pirates traded shell for food along the Caribbean coast (de Acosta 1799). In 1881, a Swedish explorer visiting the beach of Cahuita, 115 km south of Tortuguero (Fig. 1), observed ca 20 hawksbill turtles awaiting slaughter and stated that the hawksbill turtle represented the most valuable fishing resource on the coast (Bovallius 1888). In 1923, the US Consul in Limón, 80 km south of Tortuguero (Fig. 1) estimated an annual take of 750 hawksbill turtles in the local fishery (Meily cited in Tressler 1923). A small fishery for hawksbill turtles operated off Tortuguero (Fig. 1) until 1973 (Carr and Stancyk 1975). Data on hawksbill nesting at Tortuguero Beach (10°35.51′N. 83°31.40′W–10°21.46′N, 83°23.41′W) have been collected during research activities primarily aimed at green *Chelonia mydas* and leatherback *Dermochelys coriacea* turtles, since 1956 (Carr et al. 1966, Campbell et al. 1996, Troëng et al. 2004). Publications of Tortuguero research results have reported on hawksbill ecology and migrations (Carr et al. 1966, Carr and Stancyk 1975), and on their reproductive biology (Bjorndal et al. 1985). There was a significant decline in the number of nesting hawksbill turtles recorded at Tortuguero between 1972 and 1991 and the population is believed to have continuously declined between 1956 and 1991 (Bjorndal et al. 1993).

Research to quantify the movements and habitat utilization of reproductively active turtles is urgently needed to identify areas and habitats critical to hawksbill survival. Results from such research will help the development of conservation strategies needed to recover depleted hawksbill populations so they can fulfill their ecological role in Caribbean marine ecosystems.

Flipper tags and recapture data can be used to determine hawksbill movements but only provides start and end points for migrations. Satellite telemetry can be employed to determine the exact routes taken by individual turtles but high costs limit the sample size in satellite telemetry studies. Molecular genetics can also be used to elucidate movements and habitat utilization of sea turtles. Flipper tagging, telemetry and genetics by themselves have limitations, but combined together offer new opportunities for insights into the migrations and habitat use of elusive creatures such as hawksbill turtles (Dutton in press). The objectives of this paper are to combine multiple approaches to determine the nesting trend, migratory routes and habitat use of the hawksbill

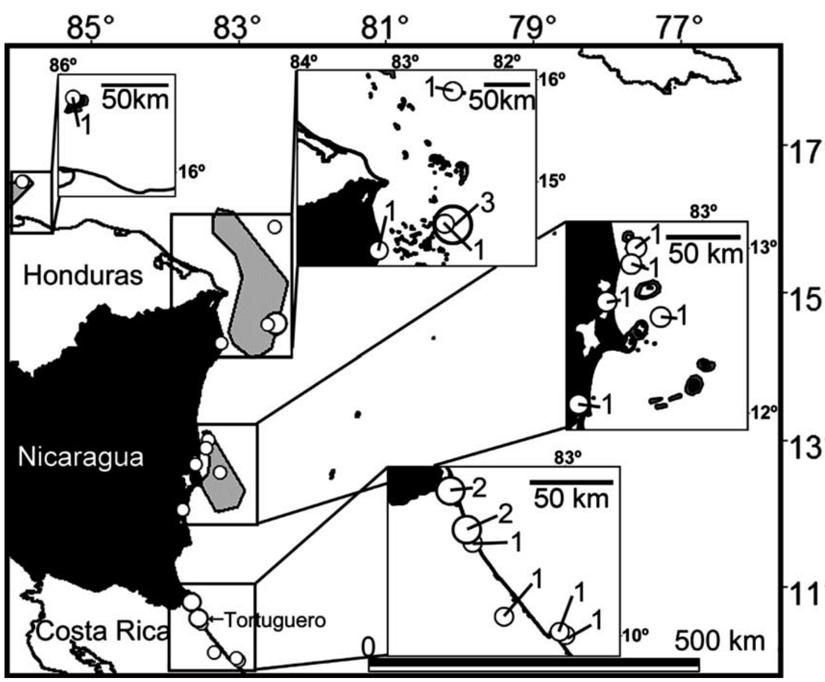


Fig. 1. Recaptures of hawksbill turtles tagged at Tortuguero. Open circles indicate recapture locations, coral reef concentrations indicated in grey (Bay Islands, Honduras; eastern Honduras/northern Nicaragua; central Nicaragua). Close-ups show recapture locations, number of hawksbills captured at each site and coral reefs in grey.

turtles nesting at Tortuguero, Costa Rica and to discuss ecological and management implications.

Methods

Nesting trend

The Caribbean Conservation Corporation (CCC) Tortuguero Tagging Database contains all hawksbill nesting and tagging data collected at Tortuguero since 1956. Meylan (1999a) reported on hawksbill nesting at Tortuguero from 1972 to 1998 but the method for deriving annual nest estimates is unclear. We estimated the hawksbill nesting trend using three methodologies including those suggested by Carr and Stancyk (1975) and Bjorndal et al. (1993). In the two latter cases, we calculated overall trends using linear regression of annual estimates to determine the change in nesting abundance between the start and the end of the time interval analyzed (Zar 1999). We also estimated the nesting trend by calculating the number of hawksbill encounters (nesting and no-nesting emergences) recorded per night and km of regular beach patrols during the months of July and August each year from 1956 to 2003. During 1956–1959, 3.2 km of beach was regularly patrolled, during 1960–1964, 6.4 km were patrolled and during 1965–2003, 8.0 km of beach was patrolled at night. We considered the number of nights patrolled during July and August each year to be equal to the number of nights with at least one sea turtle encounter as recorded in the CCC Tortuguero Tagging Database. We used a nonparametric regression model with Markov field random smoothness priors and a Bayesian smoothing spline in the program BayesX to calculate nesting trends with 95% credible intervals (Fahrmeir and Lang 2001, Balazs and Chaloupka 2004).

Flipper tag returns

The CCC Tortuguero Tagging Database includes information on 397 hawksbill turtles tagged with metal flipper tags after completing nesting at Tortuguero, from 1956 to 2003. The flipper tags have a unique tag number and a carry a message rewarding the finder for returning the tag to Univ. of Florida, USA. If the exact tag recapture location was not reported, we estimated a position based on the description of the recapture site. Carr et al. (1966), Carr and Stancyk (1975), Bjorndal et al. (1993) and Meylan (1999b) have previously reported a total of 11 international tag returns from Tortuguero hawksbill turtles from Honduras ($n = 2$), Nicaragua ($n = 8$) and Panama ($n = 1$). Careful examination of the tag return record from Panama (Bjorndal et al. 1993, Meylan 1999b) revealed uncertainty about the species involved and the record was therefore eliminated from our analysis.

Satellite telemetry

In July 2000, we fitted two hawksbill turtles with satellite transmitters after completed nesting. Transmitters were attached to the carapace according to Balazs et al. (1996) and with the transmitter antenna in a posterior position. We added a roll of kevlar anterior to the antenna to protect its base. The Argos satellite system provided location and time data. Transmitters were equipped with sensors providing mean dive time and the number of dives during the past 12 h. Submergence events exceeding 10 s were recorded as dives. We filtered data to ensure high quality information for analyses. We used only location class 3, 2, 1 and A data for calculations of travel speed as suggested by Hays et al. (2001). If the first set of latitude and longitude positions indicated a travel speed of > 5 km h^{-1}, we used the second set of positions. We removed all data points indicating unrealistic travel speeds of > 5 km h^{-1} from further analysis. We divided all remaining data points into activity categories based on turtle movements. We assumed turtles were internesting when we observed nesting or location data indicated nesting occurred after release. Post-nesting migrations started when turtles began to move rapidly in the direction of benthic foraging grounds. Shallow water feeding/resting began once post nesting migrations were complete and continued until the transmitters stopped transmitting. For each category we calculated mean travel speed and dive times. We used spatial information from Spalding et al. (2001) to determine the distribution of Caribbean coral reefs.

Genetic analysis

Small tissue samples were collected and preserved from hawksbill turtles nesting at Tortuguero from 2000 to 2003 using methods described by Dutton (1996). All turtles were identified by flipper tags to avoid repeat sampling in different years. Sequences of mitochondrial (mt) DNA were amplified from DNA extracted and PCR-amplified using standard procedures (Bass et al. 1996). Samples were analyzed using LTCM1 and HDCM1 primers (Allard et al. 1994) which amplified a portion of about 550 bp, although sequences were truncated at 400 bp for subsequent analyses to homogenize sequence lengths to those reported in Bass (1999). Sequences were obtained using an automated sequencer, with all variable positions confirmed by comparing sequences from both strands. We used Bayesian mixed stock analysis incorporating Markov Chain Monte Carlo (MCMC) methods as implemented in the program BAYES (Pella and Masuda 2001) to re-estimate stock contributions at foraging areas in Cuba, Puerto Rico and Mexico. Estimates of contributions by different nesting populations to these three feeding grounds were based on haplotype frequencies reported in Diaz-Fernández et al. (1999). The baseline rookery data are the same as those used in previous mixed stock analysis feeding ground studies (Bass 1999), with our new data from the Tortuguero nesting population. Since these published rookery haplotypes are based on the shorter (ca 380 bp) sequences, we truncated our sequences and followed Bass's (1999) haplotype designations to allow the mixed stock analysis to be performed. However, we were able to further distinguish haplotypes using the longer sequences comparable to those used by Diaz-Fernández et al. (1999) for descriptive purposes, and ruled out presence of some of the additional haplotypes identified by Diaz-Fernández et al. (1999) in Cuba, Puerto Rico and Mexico (Table 2).

Results

Nesting trend

All three methodologies used suggest considerable decline in hawksbill nesting at Tortuguero (Fig. 2). The methodologies used by Carr and Stancyk (1975) and this study produced estimates of overall hawksbill decline for the time period from 1956 to 2003 of 94.5–77.2% (Fig. 2).

Flipper tag returns

Between 1956 and 2003, 20 hawksbill turtles tagged at Tortuguero were recaptured elsewhere (Fig. 1). Recaptures within Costa Rica (n = 8) most likely represent turtles caught during nesting, internesting or on their way to or from the nesting beach. The locations of all 12 international recaptures (ten previously reported by Carr et al. 1966, Carr and Stancyk 1975, Bjorndal et al. 1993, Meylan 1999b) coincide closely with the distribution of coral reefs in Honduras and Nicaragua (Fig. 1). One hawksbill was recaptured close to Guanaja Island in the Bay Islands, Honduras, six were reported from or adjacent to coral reefs in eastern Honduras/northern Nicaragua and five were report from or adjacent to coral reef areas in central Nicaragua (Fig. 1). There are no international hawksbill recaptures from sections of the Central American coast that lack coral reefs (Fig. 1).

Satellite telemetry

Hawksbill turtle a initiated migration immediately upon release but turtle b spent 28 d in nearshore areas within 30 km of the Tortuguero nesting beach (Table 1). Travel speed of turtle b during the internesting period was low. Diving behavior was characterized by dives of intermediate duration. Post nesting migrations of turtle a and b were conducted along a migratory corridor close to shore and lasted 11–26 d (Table 1, Fig. 3). Travel speed was greater during post nesting migration than during any other activities and dive times were of shorter duration (Table 1). Once post nesting migrations were complete, travel speed was reduced as the hawksbill turtles took up residence in coastal waters (Table 1, Fig. 3). Shallow water feeding/resting was characterized by dives of longer duration (Table 1). The distance traveled between the nesting beach and benthic feeding grounds was 466 km for turtle a and 314 km for turtle b

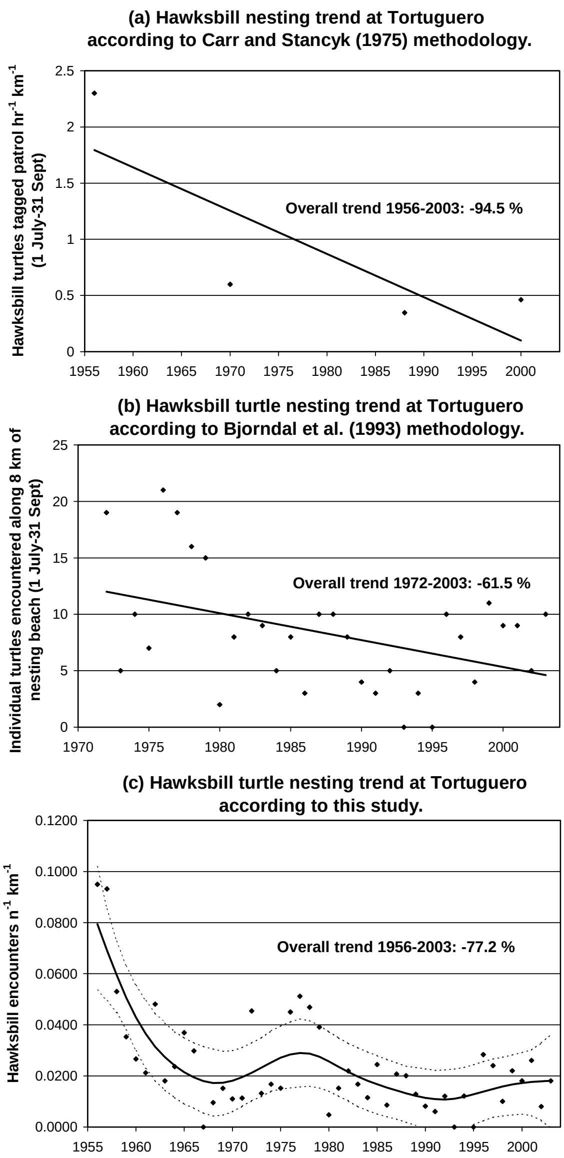


Fig. 2. Hawksbill nesting trend at Tortuguero.

Table 1. *Eretmochelys imbricata* dive times (mean ± SD) and travel speed (mean ± SD) as recorded through satellite telemetry.

Turtle	CCL (cm)	Release date in 2000	Internesting					Post nesting migration					Shallow water feeding/resting				
			Days	n	Dive time (min)	n	Travel speed ($km\ h^{-1}$)	Days	n	Dive time (min)	n	Travel speed ($km\ h^{-1}$)	Days	n	Dive time (min)	n	Travel speed ($km\ h^{-1}$)
a	86.5	19 July	0	0	N/A	0	N/A	26	28	12.3 ± 6.6	5	0.7 ± 0.3	435	563	37.2 ± 10.1	94	0.6 ± 0.8
b	85.0	20 July	28*	39	29.2 ± 11.7	17	0.8 ± 0.8	11	17	15.5 ± 6.6	1	0.9	112	144	40.3 ± 17.1	20	0.5 ± 0.4

*Turtle b was observed nesting on 16 August 2000.

compared to the direct distance between the beach and the foraging grounds of 451 km for turtle a and 270 km for turtle b. Hawksbill turtle a remained between the Miskito Cays and the northern Nicaragua mainland and hawksbill turtle b stayed in the vicinity of Man O' War Cay, in central Nicaragua (Fig. 3). The locations of the foraging grounds coincide with areas known to harbor coral reefs. Turtle b was observed again on the Tortuguero beach on 2 July 2003 but did no longer carry the transmitter.

Genetic analysis

A total of 42 samples were sequenced from Tortuguero nesters (Table 2). Comparison of haplotype frequencies with those published from other rookeries in the Atlantic shows that the Tortuguero rookery is a distinct genetic stock with relatively large contributions of haplotypes G, L and α which are rare or not reported at all in other Caribbean rookeries (Table 2). Haplotype α had previously only been identified at Caribbean foraging areas (Table 3), but was found at relatively high frequency (17%) in the Tortuguero rookery. The mixed stock analyses indicate that hawksbill turtles from the Tortuguero nesting population are present on Cuban and Puerto Rican feeding grounds, and possibly at very low frequencies in Mexican waters (Table 4).

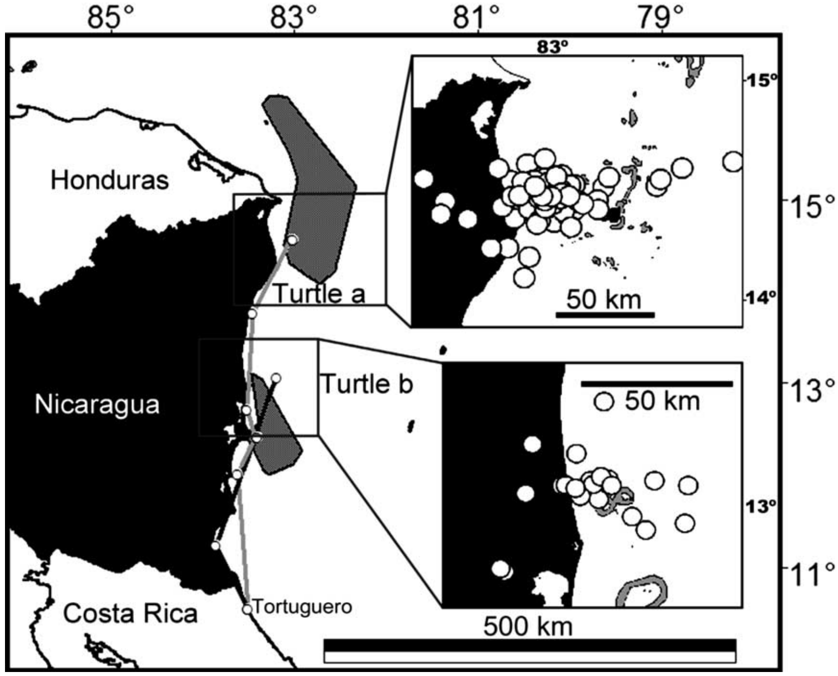
Discussion

Nesting trend

Several methods can be used to calculate trends once annual nesting values have been estimated. Linear regression is one of the two methods recommended for trend analysis in the 2000 IUCN Red List Criteria (Anon. 2001). A serious limitation of linear regression is that the resulting trend is continuous and does not detect short-term changes in nesting abundance (Fig. 2a). The nonparametric regression model is more flexible in this respect (Fig. 2c). For example; the nonparametric regression model suggests that hawksbill nesting increased at Tortuguero during the mid/late 1970s (Fig. 2c), possibly as a result of increased survival rates for adult females following the end to major fishing adjacent to the nesting beach in 1973.

All trend estimation methods concur that hawksbill nesting has declined dramatically at Tortuguero since sea turtle monitoring efforts began in 1956. The historical levels of exploitation of Caribbean hawksbill turtles (Parsons 1972, Meylan 1999a) mean that the nesting decline most likely began prior to monitoring efforts, so our trend estimates must be considered conservative. The decline in hawksbill nesting stands in sharp contrast to the encouraging nesting trend observed for green turtles

Fig. 3. Post nesting movements of two hawksbill turtles from Tortuguero. Open circles indicate satellite telemetry location data points, coral reef concentrations indicated in grey (eastern Honduras/northern Nicaragua; central Nicaragua). Close-ups show location data points as open circles and coral reefs in grey.



at Tortuguero since 1971 (Troëng and Rankin 2005). The reduced hawksbill population may remain small and declining due to continued legal and illegal, directed and incidental take of hawksbill turtles in countries where reproductive animals forage. Also, hatching and emergence success for hawksbill nests (37.9 and 37.5% in 2002) is lower than for green turtle nests (57.4 and 54.9% in 2002) at Tortuguero (Harrison et al. 2003). In addition to human take of juvenile and adult hawksbill turtles, depredation of nesting females by jaguars *Panthera onca* (Troëng 2000) may also prevent population recovery.

Flipper tag returns

International tag recapture sites coincide with coral reef areas. Recaptures from mainland locations (n = 1 in northern Nicaragua, n = 2 in central Nicaragua) most likely represent animals captured on nearby coral reefs but reported from adjacent villages and towns. The recapture rates observed for Tortuguero hawksbill turtles (5%) is lower than that observed for Tortuguero green turtles (Troëng et al. unpubl.). Possible explanations for the difference in recapture rates include different tag retention rates, fisheries pressures and legal status. Pre-1998, hawksbill turtles were tagged with Monel 49 tags from National Band and Tag Company that have a higher tag loss than the Inconel 681 tags used since 1998 (Troëng et al. 2003). In Nicaragua, fishing effort is directed towards the more abundant green turtles. Hawksbill turtles are predominantly caught opportunistically in nets set for green turtles and other fisheries such as diving for lobsters (Lagueux 1998). Fishermen catching hawksbill turtles opportunistically may be unaware of the tag reward or unwilling to report the capture. Some Caribbean countries still permit green turtle fishing but strictly prohibit the take of hawksbill turtles. This could contribute to underreporting by fishermen not wanting to admit to capturing hawksbill turtles.

One lesson from reanalyzing the Tortuguero hawksbill nesting and tagging data is that the management of tagging data is dynamic. As individual sea turtles are observed again when they return to nest, interpretation of previous years' data may change. We therefore suggest regular reanalysis of the nesting and tagging data to ensure that the population range and trend estimates are based on the best available information.

Satellite telemetry

The hawksbill satellite telemetry provided relatively few good quality location data points in comparison with a similar study on green turtles (Troëng et al. unpubl.). The hawksbill's smaller size and the posterior location of the antenna may result in the transmitter seldom emerging for long enough to allow the satellite to establish a high quality fix. An anterior antenna position may increase the proportion of good quality data points but does not provide equal protection and may result in a shorter transmitter lifespan. The strength and weakness of the different antenna positions should be considered in future studies and the position that

Table 2. Reported *Eretmochelys imbricata* mtDNA haplotype frequencies for nesting beaches in the Caribbean. Haplotypes reported in Díaz-Fernández et al. (1999) have been converted to and combined with those of Bass (1999).

Haplotype	Costa Rica	Belize	Mexico	Puerto Rico	US Virgin Islands	Antigua	Barbados	Brazil	Cuba
A				1	3	9	11	4	62
B						4			
C						2			
D							1		
E							3		
F	27	11		13	28				1
G	3	1							
H		1							
I		1							
J				2					
K				1					
L	4			1					
M				2					
N				12					
O				2					
P			3						
Q			64						
R								6	
S								2	
T								1	
U								1	
α	7								
CU2									5
D11			1						
CU3									1
CU4	1								1
Reference	This study	Bass (1999)	Bass (1999), Díaz-Fernández et al. (1999)	Bass (1999), Díaz-Fernández et al. (1999)	Bass (1999)	Bass (1999)	Bass (1999)	Bass (1999)	Díaz-Fernández et al. (1999)

generates data that will fulfill research objectives should be used.

Bjorndal et al. (1985) estimated the mean internesting period for hawksbill turtles in Tortuguero to 16.8 d with half of the observed intervals (n = 20 of 40) falling between 14 and 16 d. This suggests that hawksbill turtle b returned to nest twice before traveling to benthic feeding grounds in Nicaragua although it was only observed once on the beach (Table 1). The internesting area was limited to waters within 30 km of the Tortuguero nesting beach. If this is representative for Tortuguero hawksbills, then Costa Rica recaptures of tagged turtles were not only from internesting animals but most likely include turtles on their way to or from the nesting beach. Both hawksbill turtles followed through satellite telemetry shared a migratory corridor as they moved north towards benthic feeding grounds in Nicaragua (Fig. 3). Seven of ten post nesting green turtles tracked by satellite from Tortuguero used the same nearshore migratory corridor (Troëng et al. unpubl.). The close correlation between coral reefs and the distribution of tag recaptures and foraging hawksbill turtles along the Central American coast emphasizes the hawksbill turtle's ecological role (Fig. 1, Fig. 3).

Table 3. Reported mtDNA *Eretmochelys imbricata* haplotype frequencies for Caribbean feeding grounds.

Haplotype	Cuba	Puerto Rico	Mexico
A	92	31	
B	1	1	1
F	53	44	2
G	1	1	
L	3	2	
N	13	5	
P			2
Q	22	11	13
α	5	3	
CU2	11		
CU3	6		
a	3		
b		4	
d		1	
f		1	
h		1	
l	1		
m	1		
n	2		
o	2		
p	1		
q			3
zz		1	
Pac	1		
Reference	Díaz-Fernández et al. (1999)	Díaz-Fernández et al. (1999)	Díaz-Fernández et al. (1999)

Genetic analysis

The genetic analyses indicate presence of hawksbill turtles from the Tortuguero nesting population in feeding grounds located in Cuba and Puerto Rico, and possibly Mexico (Table 4). However, hawksbill turtles carrying Tortuguero tags have not been reported from

Table 4. Estimates of contribution to feeding grounds of *Eretmochelys imbricata* from Tortuguero based on Bayesian analysis from MCMC resamplings of four stock mixtures composed of hawksbills from eight potential source nesting stocks. Median and 95% confidence limits (2.5 and 97.5% quantiles) are shown.

Feeding grounds	Mean (%)	Standard Deviation	Median (%)	2.5–97.5% quantiles	MCMC Sample
Cuba	14.44	6.780	13.35	4.12–28.74	7436
Puerto Rico	20.41	12.30	17.16	4.61–52.51	14700
Mexico	0.62	1.55	0.00	0.02–5.62	716

these countries (Fig. 1). The small sample size of tagged hawksbill turtles and tag loss could help explain the disparity between tag returns and the results of the genetic analyses. If a majority of Tortuguero hawksbill turtles migrate to foraging grounds in Nicaragua and Honduras, the probability of tagged individuals being recaptured in other countries may be small, particularly if dispersal to the more distant foraging areas occurs mainly in juveniles. It may be that hawksbill turtles with Tortuguero tags will be recaptured in Cuba, Puerto Rico and Mexico once more hawksbill turtles have been tagged with Inconel tags. It is also likely that the estimates of the Tortuguero hawksbill nesting population's contribution to feeding grounds in other countries may change as larger genetic samples from more hawksbill nesting populations in the Caribbean become available. There is a need to expand genetic studies to include many other rookeries, larger sample sizes, and additional sequence data before definitive foraging ground mixed stock analysis can be done. It is possible that as new baseline data become available, other source stocks may be identified as contributors to the foraging populations we examined here. A significant finding from our study is the presence of a haplotype at relatively high frequency in Tortuguero that had previously only been found at the feeding grounds. This new information tends to further support the possibility that Tortuguero turtles find their way to the foraging grounds around Cuba and Puerto Rico. Evidence for their presence in Mexican waters is less compelling when the margin of error is taken into account (Table 4).

Conclusions

In our study, tag returns, satellite telemetry and results of genetic analysis contribute to the conclusion that hawksbill turtles represent an internationally shared resource. The close correlation between hawksbill foraging grounds and coral reefs as demonstrated by tag recaptures and satellite telemetry has implications for both hawksbill turtles and coral reefs. Caribbean coral reefs are under unrelenting threats such as overfishing, sedimentation, eutrophication and high water temperatures and have declined considerably (Gardner et al. 2003). In Honduras and Nicaragua, an estimated 57–58% of reefs are considered at risk and increased sedimentation caused by deforestation is believed to impact reefs located within 25 km of the mainland (Spalding et al. 2001). The continued deterioration of coral reefs may negatively impact hawksbill food availability (Meylan 1988) and cause further decline of the already heavily reduced hawksbill population. Conversely, the reduction of hawksbill turtles may have negative consequences for coral reef ecosystems in the region. Some sponges are aggressive competitors for space on coral reefs and may prevail over corals more extensively in the absence of hawksbill spongivory (León and Bjorndal 2002, Bjorndal and Jackson 2003). Although other sponge feeding species may initially fulfill the predator role, a reduction in hawksbill abundance may make coral reefs less resilient and more susceptible to natural and anthropogenic impacts (Jackson et al. 2001). It is clear that conservation strategies aimed at conserving critically endangered hawksbill turtles and coral reefs must consider both the extensive migrations of hawksbill turtles and the close relationship between the species and the coral reef ecosystem.

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