

ARTICLES

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Southernmost Reports of the Hawksbill Sea Turtle, *Eretmochelys imbricata*, in Temperate Waters of Argentina and Evidence of a Hybrid Origin Supported by Mitochondrial DNA Analysis

The Hawksbill Sea Turtle, *Eretmochelys imbricata* (Linnaeus 1766), is the most tropical of all sea turtle species, distributed along the central region of the Atlantic, Pacific, and Indian oceans (Mortimer and Donnelly 2008; Witzell 1983). The species lives in close association with hard-substrate communities such as coral reefs, foraging primarily on sponges, and may also occur in coastal lagoons and bays (Meylan 1988; Plotkin 2003).

For a long time, hawksbills, in contrast to the other species of sea turtles, were thought to not undertake extensive migrations (Carr et al. 1966; Van Dam and Diez 1998; Witzell 1983). However, satellite tracking and mark-recapture studies have provided information about movements of the species, which are on the scale of hundreds of kilometers (Bellini et al. 2000; Marcovaldi et al. 2012; Parker et al. 2009; Tröeng et al. 2005; Van Dam et al. 2008; Whiting and Koch 2006).

The main nesting areas are located between the Tropics of Cancer and Capricorn (Pilcher 1999; Pilcher and Ali 1999; Witzell 1983). In the western Atlantic Ocean, they are found in the southeastern United States, along the entire Central American coast, through the Greater and Lesser Antilles, southward to Brazil (Beggs et al. 2007; Bjørndal et al. 1985; Blumenthal et al. 2009; Lagueux et al. 2003; Lara-Ruiz et al. 2006; Marcovaldi and Chaloupka 2007; Meylan and Redlow 2006; Richardson et al. 2006; Tomás et al. 2010; Tröeng et al. 2005; Van Dam et al. 2008; Fig. 1). In the southwestern Atlantic, the nesting and feeding grounds of hawksbills are mainly along the northeastern coast of Brazil, the Atol das Rocas and Fernando de Noronha archipelagos, and the Arvoredo and Abrolhos islands (Marcovaldi and Chaloupka 2007; Marcovaldi et al. 1999; Proietti et al. 2012; Sanches and Bellini 1999; Fig. 1). The southernmost recorded feeding ground is in Mostardas (30.88027°S, 50.60666°W) on the coast of Rio Grande do Sul, Brazil, where a live juvenile was found (Valls et al. 2011).

Genetic analyses of hawksbills based on a short mitochondrial DNA (mtDNA) fragment (384 bp of the control region) were used to characterize several Atlantic nesting areas (Bass 1999; Bass et al. 1996; Bowen and Karl 1996; Bowen et al. 2007; Blumenthal et al. 2009; Browne et al. 2007; Diaz-Fernandez et al. 1999) and some feeding areas in the Caribbean (Bowen et al. 1996; Browne et al. 2007; Tröeng et al. 2005; Fig. 1). Recently, genetic studies based on longer mtDNA sequences (760 bp) in western

Atlantic nesting areas identified 47 polymorphic sites that determined a total of 25 haplotypes, improving the ability to detect population structure in hawksbills and suggesting probable hybridization events (Lara-Ruiz et al. 2006; Leroux et al. 2012; Vilaça et al. 2013). Specifically, Caribbean feeding grounds showed the likelihood of transoceanic migrations (Bass et al. 1996; Bowen et al. 2007; Velez-Zuazo et al. 2008). Monzón-Argüello et al. (2010) demonstrated the occurrence of young hawksbills from the Caribbean nesting areas in feeding grounds off Cape Verde, corroborating mark-recapture results (Bellini et al. 2000; Marcovaldi and Filippini 1991).

The Hawksbill Sea Turtle is classified as Critically Endangered by the IUCN (Mortimer and Donnelly 2008). The most serious problem this species encounters is harvest by humans. Hawksbills have largely been exploited for their shells, which are used for decorative purposes (Meylan and Donnelly 1999). Effective conservation relies on accurate knowledge of the population distribution, including characterization of nesting and feeding areas and migration patterns. The analysis of hawksbill turtles in the southwestern Atlantic including southernmost reports in

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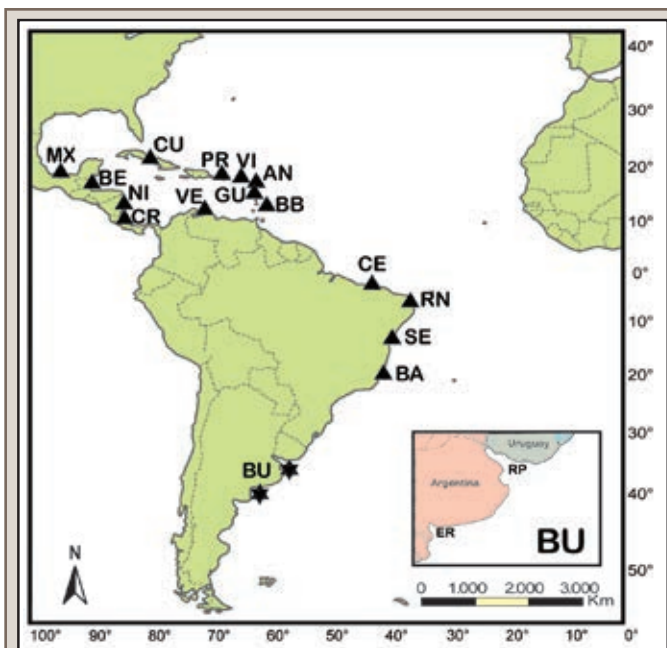


FIG. 1. The map shows the nesting grounds of Hawksbill Sea Turtles throughout the Atlantic Ocean. Individuals collected off the coast of Buenos Aires (BU) in Argentina are symbolized by stars (RP, Rio de la Plata estuary; ER, El Rincon estuary, inset map). References and abbreviations for nesting colonies (indicated by triangles) considered possible sources of turtles found in Argentina are: Cuba (CU), Puerto Rico (PR), Virgin Islands (VI), Antigua (AN), Guadeloupe (GU), Barbados (BB), Venezuela (VE), Costa Rica (CR), Belize (BE), Nicaragua (NI), Mexico (MX) and States of Bahia (BA), Rio Grande do Norte (RN), Sergipe (SE), and Ceara (CE) (Lara Ruiz et al. 2006; Leroux et al. 2012; Vilaça et al. 2013).



FIG. 2. Photo of the Hawksbill Sea Turtle found in San Clemente del Tuyú, Buenos Aires, Argentina.

temperate waters improves our understanding of this aspect of their biology.

In recent years, the Regional Program for Sea Turtle Research and Conservation of Argentina (PRICTMA) has analyzed the presence of sea turtles in the temperate waters of Argentina, identifying life-history stages as well as the genetic diversity and probable origin of individuals (Prosdocimi et al. 2012). Previously, Green (*Chelonia mydas*), Loggerhead (*Caretta caretta*), and Leatherback (*Dermochelys coriacea*) sea turtles have been confirmed in Argentinean feeding grounds (Gonzalez Carman et al. 2011). Here

we report analyses of the southernmost records of Hawksbill Sea Turtles in the southwestern Atlantic along the Argentina coast using morphological and mtDNA markers. An extension of the distribution range for this critically-endangered species can reveal novel potential habitats. Such critical information can be combined with knowledge of the species' life cycle in the Southern Hemisphere to further conservation efforts.

Materials and Methods.—Beaches and ports along 2800 km of the maritime and fluvial coast of Argentina were regularly surveyed by PRICTMA from 2009 to 2010. Turtles found were weighed, measured, and sampled for genetic analysis according to Bolten (1999) and Dutton (1996). The specimens for this study were identified as *Eretmochelys imbricata* following morphological keys of Pritchard and Mortimer (1999). To classify individuals in life stages, we considered the criteria of Sanches and Bellini (1999) and Vélez-Zuazo et al. (2008). Turtles below 35 cm curved carapace length (CCL) were considered "small" (juveniles with little swimming capacity and hence subject to being dispersed by oceanic currents), whereas turtles with a CCL 35–65 cm were considered "large" (juveniles that probably have a capacity to swim independent of oceanic currents).

A DNAeasy Tissue Kit was used for DNA extractions, following the manufacturer's instructions for animal tissues (Qiagen, Inc.). A 760 bp mtDNA control region fragment was amplified in both directions using primers LCM15382 (5'-GCT TAA CCC TAA AGC ATT GG-3') and H950 (5'-GTC TCG GAT TTA GGG GTT TG -3'; Abreu-Grobois et al. 2006). Polymerase chain reaction (PCR; 1.5 mM MgCl₂, 1× PCR Buffer, 200 μM each dNTPS, 0.5 μM each primer, 0.6 U Taq from Invitrogen Life Technologies, 1 μl template DNA and H₂O to a total volume of 50 μl) was carried out under the following conditions: 10 min at 95°C, 35 cycles of 1 min at 94°C, 30 cycles of 1 min at 50°C, and 1 min at 72°C, followed by 5 min at 72°C (Shanker et al. 2004), using a MGW Biotech Primus PCR System. The samples were purified and sequenced using the MACROGEN, Inc. (Seoul, South Korea) sequencing service.

Sequences were edited and aligned using the Bioedit V 7.0 (Hall 1999) and Clustal programs (Higgins and Sharp 1988). Polymorphic sites were identified using GENALEX 6 (Peakall and Smouse 2006).

To infer the possible origin of the turtles, we compared our results with data from 13 Caribbean and Brazilian nesting beaches: Cuba (CU), Puerto Rico (PR), Virgin Islands (VI), Antigua (AN), Guadeloupe (GU), Barbados (BB), Venezuela (VE), Costa Rica (CR), Belize (BE), Nicaragua (NI), Mexico (MX), and the Brazilian states of Bahia (BH), Rio Grande do Norte (RN), Sergipe (SE), and Ceara (CE) (Lara Ruiz et al. 2006; Leroux et al. 2012; Vilaça et al. 2013; Fig. 1, Table 1).

Results.—In April 2009, a live turtle was incidentally captured near Bahía Samborombón (36.24405°S; 56.97686°W) in an artisanal coastal gillnet fishery from San Clemente del Tuyú, Rio de la Plata Estuary (RP in Fig. 1 inset map; Fig. 2). In March 2010, a second turtle was found stranded dead on the coast of Monte Hermoso, El Rincon Estuary (38.99005°S; 61.27847°W; ER in Fig. 1 inset map). Morphological studies identified both specimens as large juvenile Hawksbill Sea Turtles, with CCLs of 53.0 cm and 40.8 cm and curved carapace widths of 50.5 cm and 40.3 cm, respectively.

Sequences of 760 bp in the mtDNA control region were successfully amplified from skin samples. Qualitative comparison to published data suggests that the two samples match with the Ei-BR3 haplotype, which previously had been described only from Brazilian nesting beaches (Table 1).

TABLE 1. Haplotype frequencies of mtDNA in Hawksbill Sea Turtle nesting grounds in the Atlantic based on sequences of 760 bp according Leroux et al. (2012) and Vilaça et al. (2013). N = sample size. References and abbreviations correspond with Fig 1.

Vilaça et al. 2013 nomenclature haplotype	Leroux et al. 2012 nomenclature haplotype	Caribbean Rookeries									Brazilian Rookeries			
		AN	BB	CR	CU	GU	MX	NI	PR	VI	BA	RN	SE	CE
	Ei A3	29	57							2				
	Ei A9		6	3		69			2	2				
	Ei A12			5		1								
	Ei A13				5									
	Ei A18								1					
	Ei A20								34	4				
	Ei A21								6					
	Ei A22						2							
	Ei A23						16			1				
	Ei A29				1									
	Ei A30			1	1									
	Ei A41						1							
	Ei A43						1	16	3					
	Ei A47			6										
	Ei A52			1										
	Ei A65							1						
	Ei A84							5						
Ei BR8	Ei A1	42			62	2			3	8	53	21	1	1
Ei BR17	Ei A2			11				19						
Ei BR13	Ei A11	1	21	33	1	2		54	60	50				
Ei BR2													22	
Ei BR3													21	1
Ei BR4													291	
Ei BR16													16	
Ei BR9													4	
Ei BR10													9	
N		72	84	60	70	74	20	95	109	67	119	27	4	2

Discussion.—The present study details the southernmost records of Hawksbill Sea Turtles in the western Atlantic. Results presented here also provide insight into the morphological and genetic characterization of hawksbills at temperate latitudes, while improving knowledge of the distribution of the species. Indeed, genetic analysis based on 760 bp mtDNA sequences revealed that both specimens from Argentina correspond to the haplotype Ei-BR3 that has been detected only in Brazilian rookeries (Vilaça et al. 2013). Our results suggest that Brazilian nesting colonies might be a main contributor of hawksbills along the Argentinean coast.

Population genetic analysis of nesting beaches in the State of Bahia, Brazil, based on the same mtDNA fragment showed that the third most frequent haplotype (42%) was Ei BR3. This haplotype is phylogenetically close to haplotypes described for *C. caretta* (CC A4), suggesting the existence of hybridization in nature (Lara-Ruiz et al. 2006). Studies of several nesting areas in Brazil using nuclear markers support this view and suggest that hybridization is a recent phenomenon, spanning about two generations or 40 years (Vilaça et al. 2012, 2013). Postulated hybridization events at sea turtle nesting beaches in Brazil might be related to overhunting and environmental changes associated with coastal modifications (Vilaça et al. 2012).

Both specimens analyzed here had the morphology of *E. imbricata*, but exhibited a mitochondrial genome similar to that of

C. caretta. Thus, a loggerhead female \times hawksbill male hybridization event would explain the origin of specimens detected in Argentina. The suspected hybrid nature of the turtles phenotypically identified as hawksbills also might explain the occurrence of individuals of a species with a tropical distribution at temperate latitudes. That both specimens were large juveniles with probable capacity to swim independently of oceanic currents suggests that they did not arrive along the Argentine coast by chance. Indeed, satellite telemetry found that female hybrids derived from an *E. imbricata* \times *C. caretta* mating could migrate to feeding areas of either progenitor species (Marcovaldi et al. 2012). Our results identify *E. imbricata* \times *C. caretta* hybrids along Argentine coasts, a feeding ground of *C. caretta* (Prosdociimi 2012).

The detection of hybrid individuals of hawksbills in the western Atlantic indicates the need for increased sampling effort in geographical regions not yet analyzed to study hybridization in this critically-endangered species. Moreover, genetic studies using uniparental and biparental markers are required to clarify the genetic structure and demographic history of hawksbill populations necessary to delineate effective global conservation strategies.

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