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Origin and genetic diversity of leatherbacks (*Dermochelys coriacea*) at Argentine foraging grounds

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ABSTRACT

To conduct conservation of migratory species, such as marine turtles, is important to understand the population structure throughout the entire distribution of the species. We study the genetic composition of the leatherback turtles, *Dermochelys coriacea* foraging in waters off Argentina by analyzing 763 bp sequences of the mtDNA control region in order to determine the nesting origin of these animals. A total of 40 samples were collected from adult leatherbacks (mean 143.5; 180–123 cm curved carapace length) captured (10%) in fisheries or encountered as strandings (90%). Based on analysis of mtDNA sequences we detected 4 haplotypes, the most common ($n = 26$) being DC1.1, and the other two rarer DC1.3 ($n = 4$), DC13.1 ($n = 2$), and DC1.4 ($n = 1$). The genetic diversity was evaluated through the haplotype (0, 3712 ± 0, 1000) and nucleotide diversities (0, 000521 ± 0, 000553). Bayesian Mixed Stock Analysis (MSA) showed that the Buenos Aires foraging leatherbacks come primarily from the West African rookeries (Ghana and Gabon, mean estimate = 69% and 14% respectively). MSA results are consistent with those from mark–recapture studies, since four leatherbacks captured in Argentinean waters were adult females that were originally tagged on the nesting beaches in Gabon, West Africa. Our findings demonstrate the connection between nesting and foraging areas in the South Atlantic and illustrate the importance of the Malvinas ecoregion to the survival of migratory marine vertebrates, such as leatherbacks.

1. Introduction

The Southwest Atlantic is an important breeding and feeding area for many groups of marine vertebrates, largely due to the favorable oceanographic characteristics generated by the convergence of the Malvinas and Brazil currents (Peterson and Stramma, 1990). It is among the most productive ecoregions in the world and is home to populations of over 600 vertebrate species, including seabirds, marine mammals and sea turtles (Miloslavich et al., 2011). Most of these species exhibit seasonal migrations such as humpback whales (*Megaptera novaeangliae*), Southern right whales (*Eubalaena australis*) and Manx shearwater (*Puffinus puffinus*). The feeding habitats of right whales occur in higher latitudes where cold, nutrient rich waters generate large amounts of plankton. Calving, nursing, and breeding habitats occur in lower latitudes where warm, shallow waters are favorable for reproduction (Acevedo and Martínez, 2013; Guilford et al., 2009; Rasmussen et al., 2007; Zerbini et al., 2011). Sea turtles are an example of endangered and threatened species that have complex life cycles spread across different habitats (Wallace et al., 2013). Nesting grounds are frequently separated by thousands of kilometers from neritic and oceanic feeding grounds (Bolten, 2003a, 2003b; Musick and Limpus, 1997). Understanding the connectivity among populations using these different habitats at different life stages is important for conservation, since threats to animals at distant foraging and developmental areas will impact specific breeding populations differently (Fossette et al., 2014; Wallace et al., 2011).

The leatherback turtle is widely distributed from 71° N to 44° S throughout all oceans of the world (Eckert et al., 2012; Marquez, 1990). Leatherbacks are on the IUCN threatened species list (Wallace et al., 2013) due to dramatic population declines, particularly in Pacific populations (Mast and Pritchard, 2006; Sarti et al., 1996; Spotila et al., 1996, 2000). Adults typically undertake periodic long distance migrations from temperate foraging grounds to tropical nesting beaches to breed (Bailey et al., 2012; Benson et al., 2011; Fossette et al., 2010a, 2010b; Hughes et al., 1998; James, 2000; James et al., 2006; López-Mendilaharsu et al., 2009).

Nesting areas for leatherback turtles are distributed from southeastern USA to northern Brazil in the western Atlantic and from Mauritania to Angola in the eastern Atlantic (Barata et al., 2004; Dutton et al., 1999, 2013; Eckert et al., 2012). The largest Atlantic nesting populations occur

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in French Guiana, Suriname and Gabon (Girondot et al., 2007; Pritchard and Trebbau, 1984; Witt et al., 2009). Recent studies with satellite telemetry and mark–recapture have provided information about habitat use and movements for this species (Fossette et al., 2014). Fossette et al. (2010a, 2010b) and Witt et al. (2011) showed that the adult female leatherbacks tagged at the nesting beaches in West Africa migrate to multiple foraging areas, including waters off the coast of South America. Results of mark–recapture studies at nesting beaches in Gabon have demonstrated that tagged individuals occur in Argentinean waters, which are the most important feeding grounds in Southwest Atlantic (Billes et al., 2006; Fossette et al., 2010a, 2014; López-Mendilaharsu et al., 2009). These studies are limited to adult females tagged on nesting beaches, and it is unclear where the males and juveniles foraging off Argentina are from. Leatherback turtles feed mainly on jellyfish in this region, primarily in the estuaries of the Rio de la Plata (RP) and El Rincón (ER) at Buenos Aires (BA) province from December to March (González-Carman et al., 2011) (Fig. 1). The seasonal and regional occurrence of this species in southernmost waters is strongly associated with high-density of gelatinous organisms (Fossette et al., 2010a; López-Mendilaharsu et al., 2009; Mianzan and Guerrero, 2000). Activities of economic importance such as maritime transport, domestic and industrial waste discharge, tourism, and fishing occur in Argentinean coastal waters, potentially affecting the survival of this species (Domingo et al., 2006; González-Carman et al., 2011; López-Mendilaharsu et al., 2009; Mianzán et al., 2001).

Over the last two decades, studies of intraspecific genetic variation using molecular markers have been useful in the analysis of the population structure and phylogeography of sea turtles (Avise, 2007; Bowen et al., 2004, 2005; Fitzsimmons et al., 1997; Lara-Ruiz et al., 2006; Lee, 2008). Mitochondrial DNA (mtDNA) in particular has been used to identify the origin and stock composition of foraging populations and infer migratory routes (Bass et al., 2006; Bolker et al., 2007; Bowen et al., 1994, 2007; Jensen et al., 2013; Luke et al., 2004; Naro-Maciel et al., 2007).

Previous studies using short mtDNA sequences (496 bp) have characterized nesting colonies from the Atlantic, Pacific and Indian Oceans and one feeding area in the Atlantic (Brazil) and demonstrated low variation (Dutton et al., 1999, 2007; Vargas et al., 2008). Recent studies using longer (763 bp) sequences have revealed additional variation in the mtDNA control region that has improved the ability to detect population structure in leatherback (Dutton et al., 2013).

In the present work we analyzed mtDNA sequences (long sequences, 763 bp) and morphometric data obtained from leatherback foraging aggregations in Argentine waters in order to improve our knowledge about the migratory patterns of this species. Our specific objectives were to i) determine the life history stage, ii) analyze the genetic diversity, and iii) to estimate the nesting stock composition of leatherback turtles in foraging areas of Argentina. Understanding which nesting colonies use these southernmost feeding areas will help determine which nesting populations are potentially impacted by threats, such as fishing and pollution, great distances away.

2. Materials and methods

2.1. Sample collection

A total of 40 leatherback turtles were sampled by Regional Program for Sea Turtle Research and Conservation of Argentina (PRICTMA)

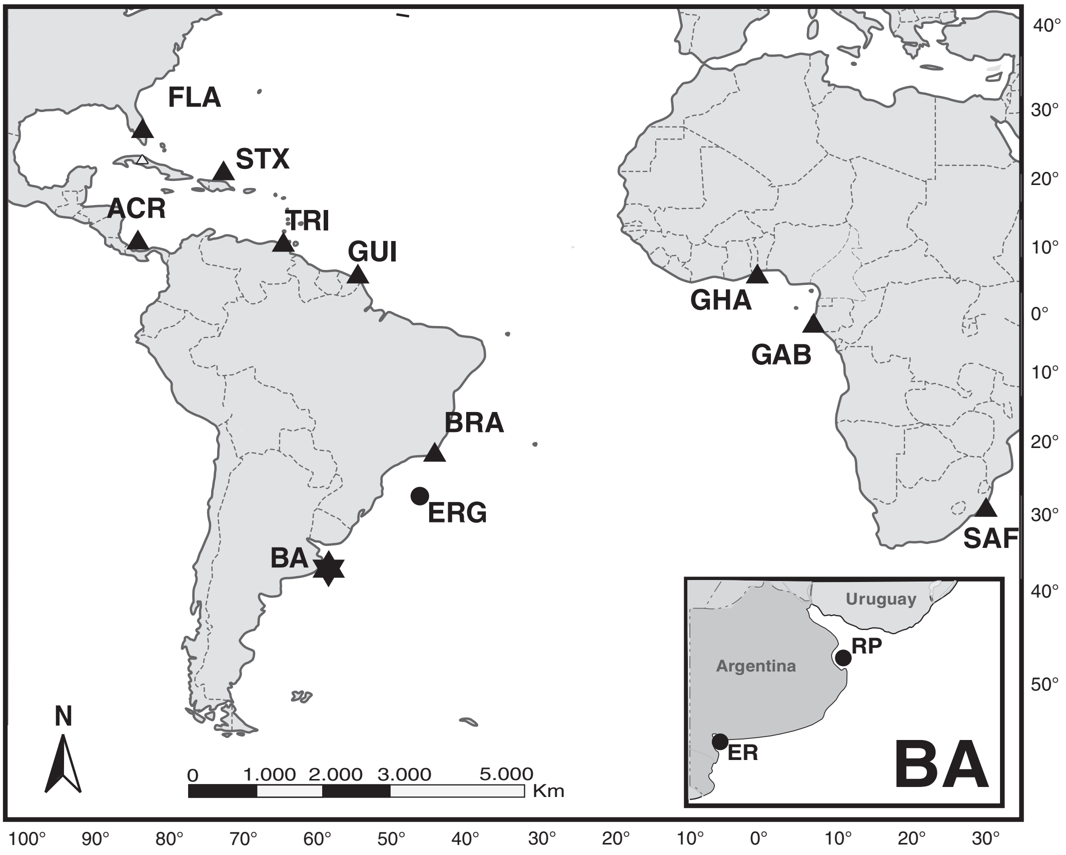

Fig. 1. Map showing locations of the main nesting populations throughout the Atlantic (east and west) and the feeding grounds in our study in the western Atlantic. Rio de la Plata (RP) and El Rincón (ER) estuaries (see inset) are located in Buenos Aires (BA) province, Argentina (symbolized by stars). Nesting colonies, considered possible sources of turtle feeding at BA (indicated by triangles) are as follows: ERG (Elevação do Rio Grande), ES (Espirito Santo), TR (Trinidad), GUI (French Guiana and Suriname), FL (Florida in the United States), STX (St. Croix in the U.S. Virgin Islands), GHA (Ghana), GAB (Gabon) and SAF (South Africa) in South West Indian Ocean. Elevação do Rio Grande (ERG) feeding grounds are indicated by circles (Dutton et al., 2013; Vargas et al., 1999).