Chapter 7
Novel Research Techniques Provide New Insights to the Sea Turtle Life Cycle

Maria Ângela Marcovaldi, Alexsandro S. Santos, Paulo H. Lara, and Milagros López-Mendilaharsu

Abstract The recent increase in the knowledge of the complex life cycle of sea turtles in the world has been possible by the use of novel technologies, such as satellite telemetry and molecular analyses. These technological advances have also provided the opportunity to assess future impacts of climate change. In this chapter, you will find a brief description of these techniques and an overview of the most relevant results obtained through scientific research of sea turtles in Brazil.

7.1 Introduction

Sea turtles have complex life histories that span many decades, habitats, and kilometers. Their *highly migratory behavior* makes them a *shared resource among many nations*. Similar to other species of marine mega vertebrates, sea turtles are an important conservation concern as the result of a range of past and ongoing threats. Direct exploitation (Marcovaldi and Marcovaldi 1999, Frazier 2003), incidental capture in fisheries (Domingo et al. 2006, Sales et al. 2008), habitat degradation (Santos et al. 2005, Tourinho et al. 2010) and fluctuating environmental conditions due to climate change (Hawkes et al. 2009) are among the main threats to sea turtle populations. Therefore, for an effective mitigation of direct threats, there is an acute need to understand how these animals use dynamic seascapes (Godley et al. 2008).

Among the seven species of sea turtles found around the world, five of them occur along the Brazilian coast (Marcovaldi and Marcovaldi 1999). All five species are threatened and included in the Brazilian Red List of Threatened Species (ICMBIO 2011), and in Appendix I in the CITES convention (CITES 2016). These species include the loggerhead sea turtle (*Caretta caretta*; Fig. 7.1a), hawksbill sea turtle (*Eretmochelys imbricata*; Fig. 7.1b), olive ridley sea turtle (*Lepidochelys olivacea*; Fig. 7.2a), leatherback sea turtle (*Dermochelys coriacea*; Fig. 7.2b) and

---

M.Â. Marcovaldi (✉) • A.S. Santos • P.H. Lara • M. López-Mendilaharsu
Fundação Pró Tamar, Rua Rubens Guelli, 134 sala 307, Salvador, Bahia, Brazil
e-mail: neca@tamar.org.br; alex@tamar.org.br; paulo.lara@tamar.org.br; milagros@tamar.org.br

M.R. Rossi-Santos, C.W. Finkl (eds.), *Advances in Marine Vertebrate Research in Latin America*, Coastal Research Library 22,
DOI 10.1007/978-3-319-56985-7_7

Fig. 7.1 Loggerhead sea turtle (**a**) and hawksbill sea turtle (**b**)

green sea turtle (*Chelonia mydas*; Fig. 7.2c). In 1980, the Sea Turtle Conservation Project—today known as TAMAR—was created to identify the species occurring in Brazil, their main breeding sites and threats to their survival (Marcovaldi et al. 2005). Prior to the creation of TAMAR, sea turtle populations in Brazil were heavily exploited through incidental take in fisheries, illegal poaching and hunting of turtle eggs and nesting females, resulting in a significant decline in turtle numbers. Exploitation for consumption is now regulated, but new threats have emerged and even increased, such as coastal development, intensified fishing, pollution, diseases and climate change (ICMBIO 2011). Hence, TAMAR adopted as its *modus operandi* an adaptive threats management framework to organize and orient priority research themes (da Silva et al. 2016).

Recent technological advances in genetics, telemetry, biochemical markers and stable isotope analysis are increasing our knowledge of the distribution and behavior of sea turtles. In the present chapter, we intend to review the most relevant information gained through research studies on (1) satellite telemetry, (2) conservation genetics and (3) climate change impacts.

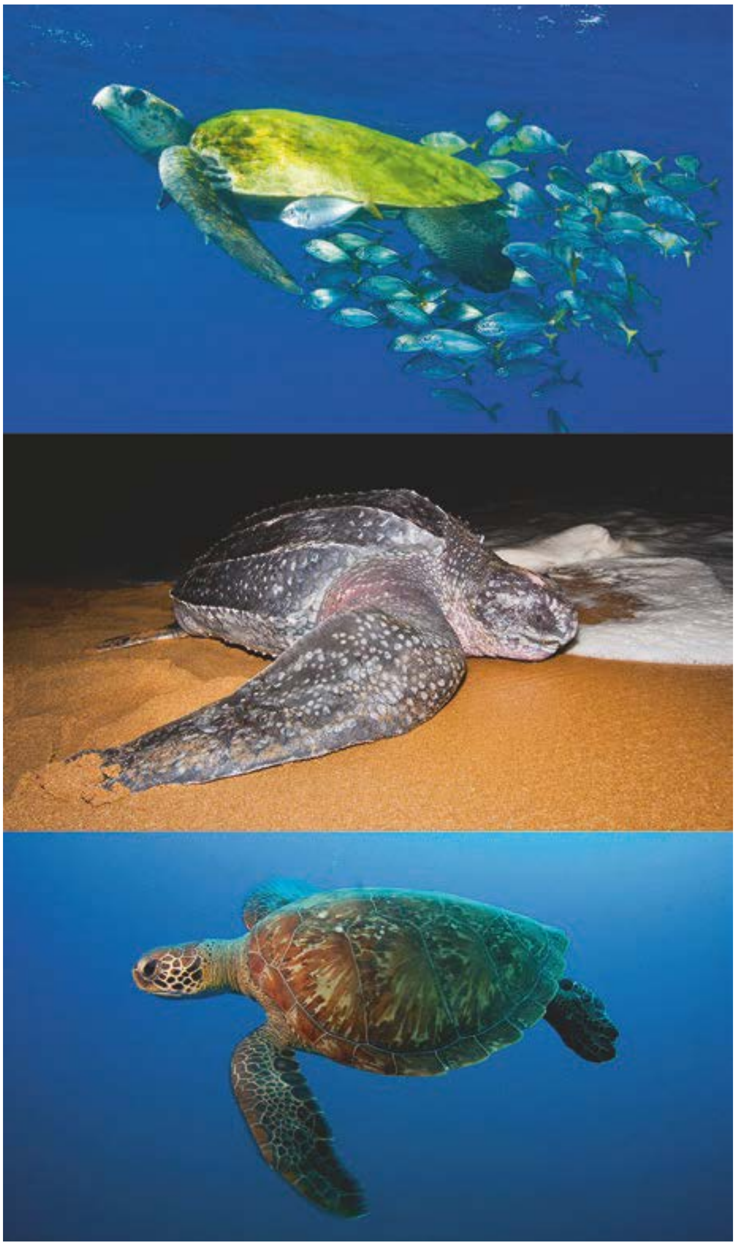


Fig. 7.2 Olive ridley sea turtle (**a**) leatherback sea turtle (**b**) and green sea turtle (**c**)

7.2 Satellite Telemetry

Understanding the spatial behavior of marine turtles during their migrations and prolonged movement phases is central to elucidating key aspects of their complex life cycle and ecology. The development of satellite telemetry in the late 1980s allowed the first in-depth studies of animal movement patterns (Duron-Dufrenne 1987, Fancy et al. 1988). Since then, continuing improvements to the satellite network, transmitter miniaturization, and new deployment techniques have expanded the range of species that can be studied with satellite-tracking (Coyne and Godley 2005). In this way, satellite-tracking studies have become particularly prevalent in recent decades and has led to substantial progress in the field, as this technique allows the reconstruction of the actual routes followed by marked individuals (Godley et al. 2008). Adult females, for example, can migrate thousands of kilometers between breeding sites and feeding grounds, thus satellite telemetry provide the opportunity to map migratory routes and identify foraging and high-use areas.

7.2.1 Migratory Destinations and Foraging Areas of Adult Females

Initial studies using satellite telemetry in Brazil began in 2000–2001. Satellite transmitters were deployed on eight loggerhead-nesting females in Espírito Santo, and eight green turtles from foraging areas in Ceará, including juvenile and adult turtles. In the case of the loggerheads, it was not possible to determine any general pattern after they left the nesting beaches, as most of the transmissions were relatively short in duration (Lemke et al. 2003). On the other hand, green turtles remained in coastal areas; some exhibited high fidelity to their foraging areas while others displayed medium and long distance movements (Godley et al. 2003).

Between 2005 and 2006, 15 satellite transmitters (Fig. 7.3) were fitted to hawksbill sea turtles (*E. imbricata*) and 10 to loggerhead sea turtles (*C. caretta*) along the northern coast of the State of Bahia. After the inter-nesting period, all females migrated to distant feeding grounds up to 2000 km away from the beaches (Marcovaldi et al. 2010, 2012).

Fig. 7.3 Hawksbill sea turtle carrying a satellite transmitter at the nesting beach

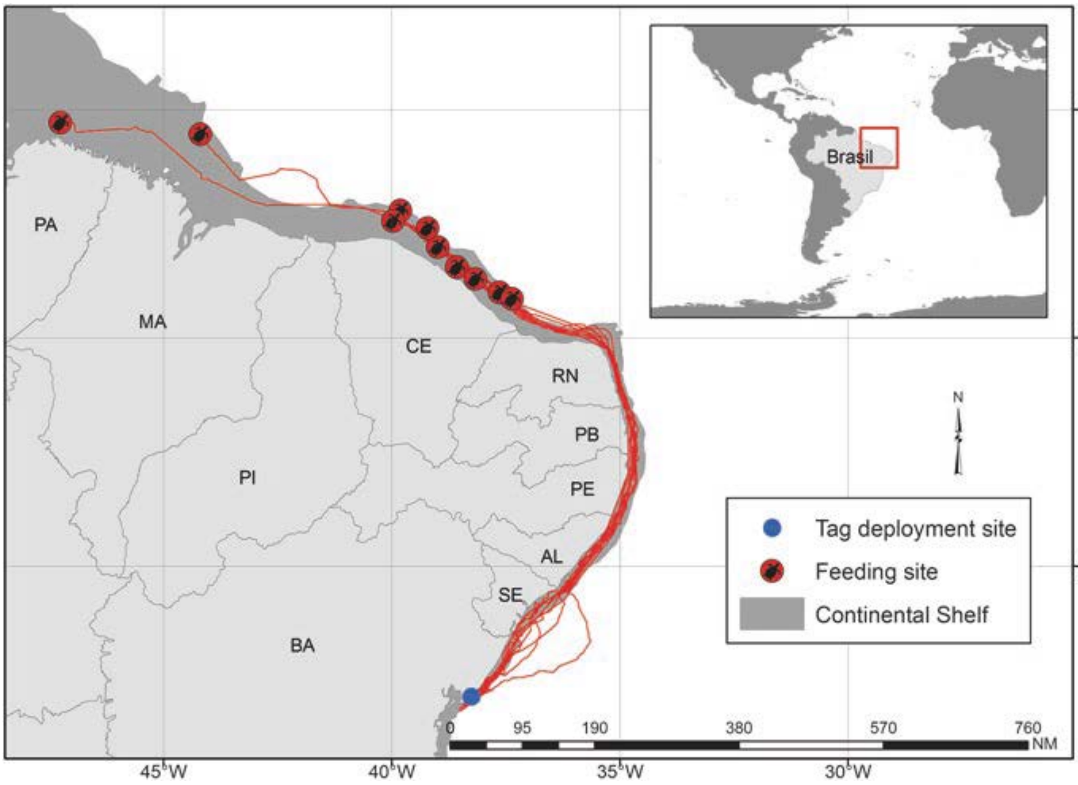


Fig. 7.4 Post-nesting migrations and feeding grounds of 10 loggerhead female turtles satellite-tracked from nesting beaches along the northern coast of Bahia State, Brazil

Study results revealed important aspects of the habitat use and identified a migratory corridor along the northeastern coast of Brazil. Main foraging areas of loggerheads turtles were located along the northern coast of Brazil, especially off the coast of Ceará (Fig. 7.4). Exceptionally long battery life of satellite transmitters allowed tracking nesting females through an entire remigration interval (i.e. round-trip migrations from foraging areas and breeding grounds). After a second post-nesting migration, five loggerhead turtles returned to the same foraging area indicating strong philopatry to specific foraging areas (Fig. 7.5). Concerning hawksbill sea turtles, some individuals migrated northwards and remained in feeding grounds between the States of Rio Grande do Norte and Pará, like the loggerheads, while others moved toward coral reef areas along the coast of Alagoas and southern Bahia (Fig. 7.6) (Marcovaldi et al. 2012).

In the State of Sergipe, 10 olive ridley female turtles (*L. olivacea*) were fitted with satellite transmitters. During the breeding season, the females remained along the coast of Sergipe and their locations overlapped with the area of operation of the shrimp trawl fleet, a major threat to this population. After leaving the nesting area, most of them migrated along the continental shelf towards feeding grounds along the northern, north-eastern and south-eastern coasts of Brazil, while two females migrated to oceanic waters near the equator (Fig. 7.7) (Da Silva et al. 2011).

Finally, four female leatherback sea turtles (*D. coriacea*) were tracked by satellite telemetry. Three turtles were tagged on nesting beaches in Espírito Santo state,

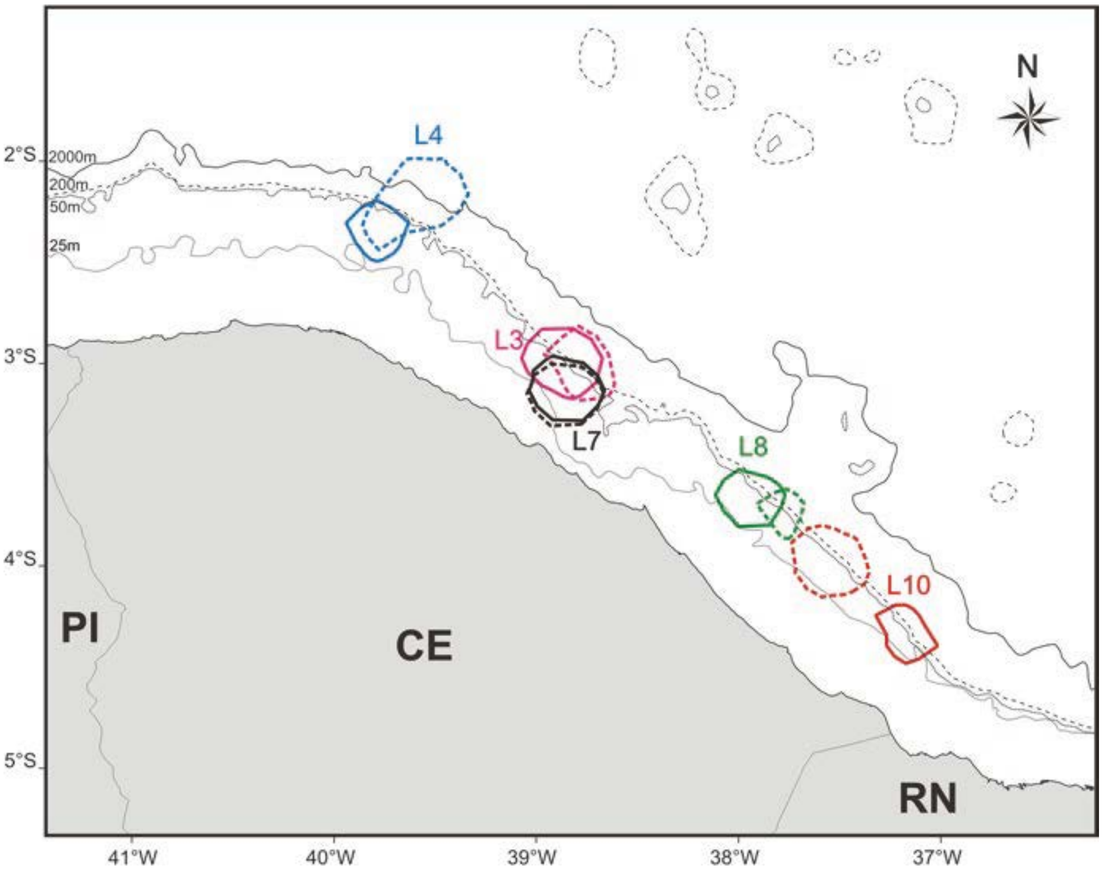


Fig. 7.5 Kernel-estimated home-range utilization 50% distributions of feeding areas of the five tracked loggerhead turtles following their first (*solid perimeter*) and second (*broken perimeter*) post-nesting migration. State abbreviations—*PI* Piauí, *CE* Ceará, *RN* Rio Grande do Norte (Data from Marcovaldi et al. 2010)

and one was incidentally capture in a driftnet off the coast of São Paulo State. Tracking in the breeding area revealed that between successive egg-laying trips, the turtles spread out and move up to 160 km off the coastline. The post-nesting migrations helped to identify foraging grounds between the South of Brazil and the Rio de la Plata estuary (Fig. 7.8) (Almeida et al. 2011). The overlap between the high-use areas of these animals and large-scale fishing zones was highlights as a major threat to these turtles.

7.2.1.1 Conservation Implications

Tracking data has helped us to identify migratory corridors and high-use areas of sea turtles in Brazilian waters. In addition, these findings were essential to better understand the impacts of human activities- such as fishing- across their habitats to improve coastal management. It is recognized that satellite telemetry can be a useful tool in determining the effectiveness of current marine protected areas (MPA) boundaries and where additional protected areas should be considered (Witt et al. 2008,

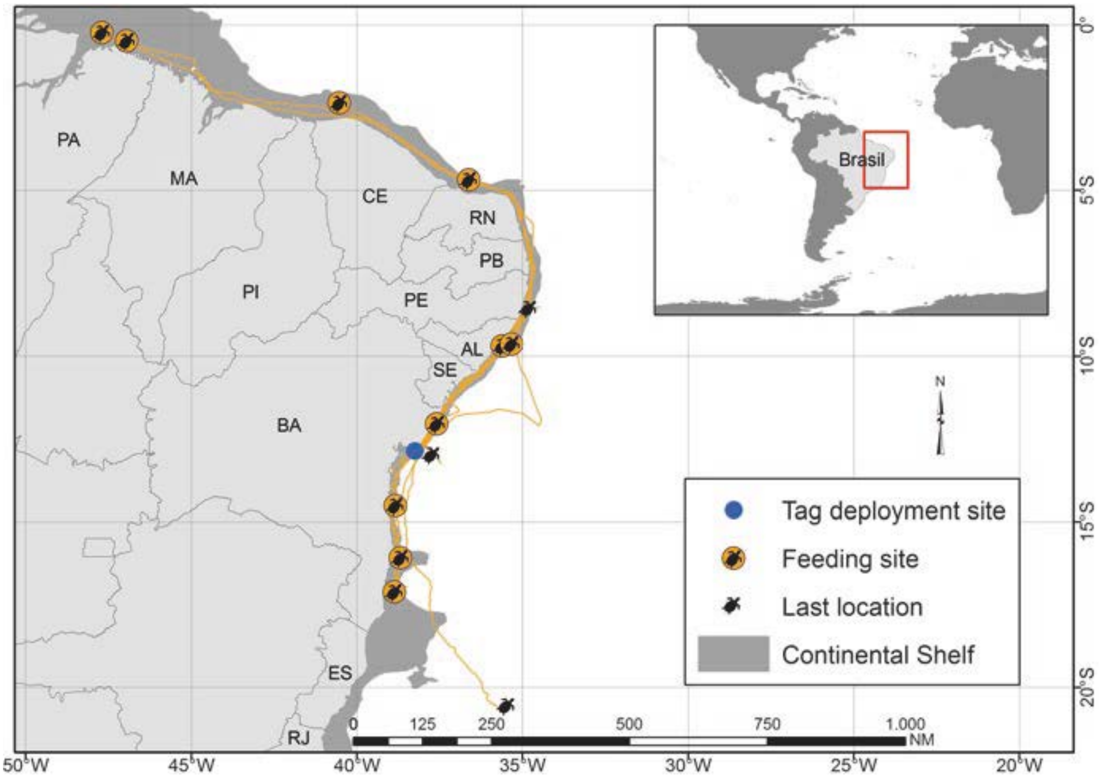


Fig. 7.6 Post-nesting migrations and feeding grounds of 15 hawksbill female turtles satellite-tracked from nesting beaches along the northern coast of Bahia State, Brazil

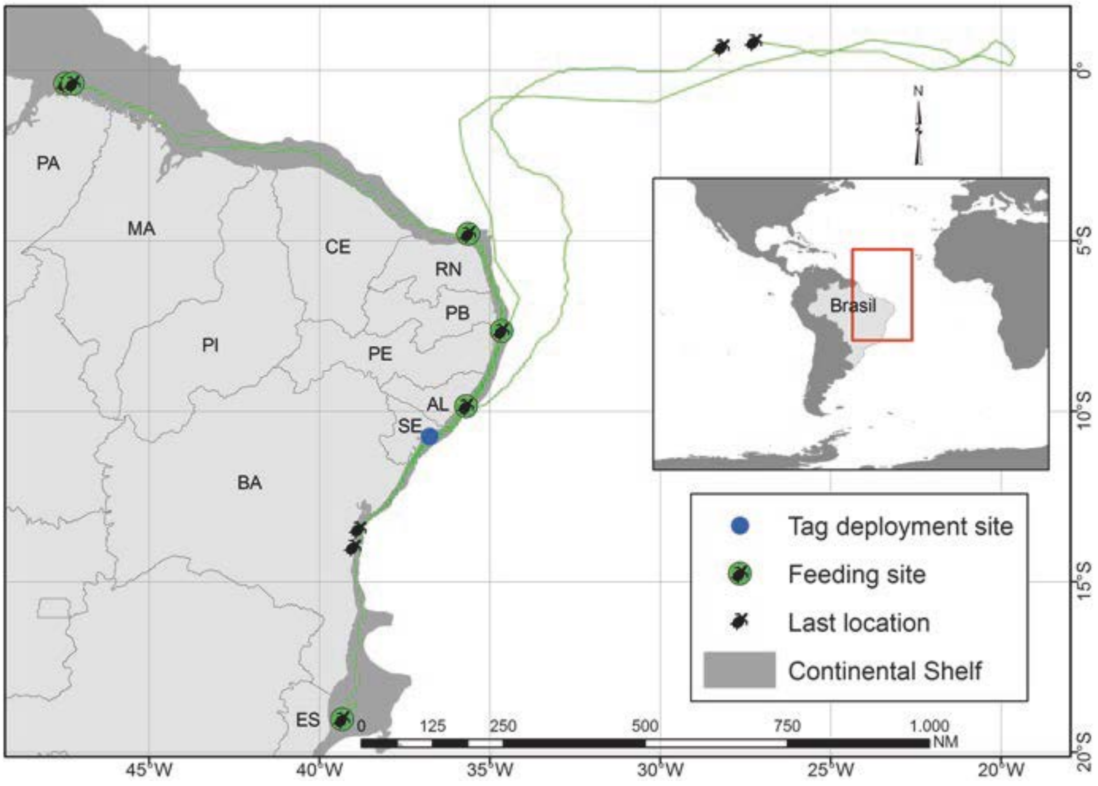


Fig. 7.7 Post-nesting migrations and feeding grounds of 10 olive ridley female turtles satellite-tracked from nesting beaches in Sergipe State, Brazil

milagros@tamar.org.br

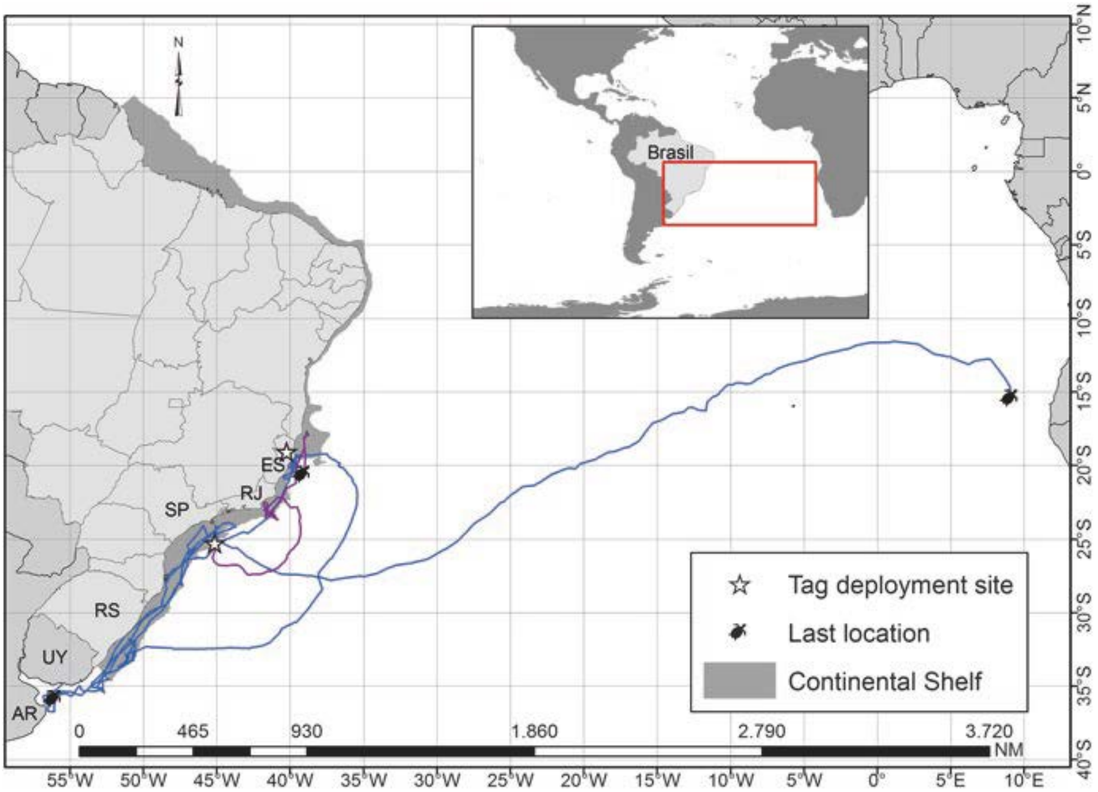


Fig. 7.8 Migration routes and high-use areas of two leatherback female turtles tracked from nesting beaches in Espírito Santo (*blue line*), and a female incidentally captured in a drift-net off the São Paulo coast, Brazil (*purple line*).

Shillinger et al. 2010). A factor of great importance is that the breeding and foraging grounds of most turtles tracked are located within Brazilian territorial waters. This provides a good starting point to ensure the long-term protection of this important portion of sea turtle's life cycle, as many political and national conservation measures are already established.

7.2.2 First Satellite Tracks of Neonate Sea Turtles in the South Atlantic

The "lost years" refers to the time after turtles' hatch and head to the sea where they remain for many years before returning to near-shore waters as large juveniles. The time period is often referred to as the "lost years" because not much has been known about where the young turtles go and how they interact with their oceanic environment. Satellite tracking devices attached to oceanic-stage sea turtles in the North Atlantic have provided new information on the so-called 'lost years' of this species (Mansfield et al. 2014).

Currently, TAMAR in collaboration with NOAA and the University of Central Florida are working to understand the migratory behavior and dispersal patterns of oceanic-stage loggerheads in the South Atlantic Ocean. For this, nineteen neonate

Fig. 7.9 Juvenile loggerhead turtle tracked using a solar-powered satellite tag

loggerhead sea turtles were satellite tagged using modified small-scale solar-powered satellite tags. Turtles were lab-reared until reaching a minimum size (>10 cm) to ensure the tags were <3–5% of the turtles' weight (Fig. 7.9). Then they were released at different times throughout the nesting season to coincide with changes in the current pattern along the coast of Praia do Forte (e.g. southern direction in early/mid season and northern direction in late season). Oceanographic drifters were released along with the turtles to collect concurrent information on current patterns, and to examine the probability that turtles were passively drifting with the prevailing ocean currents. Except for two turtles that transmitted for less than 5 days, the transmission duration of the tags varied from 1 to 4 months (n = 17). Throughout the tracking period the turtles traveled between 500 and 5000 km (e.g. as far as the island of Barbados in the Caribbean). Initially, all turtles followed a general circulation pattern observed with initial drifter trajectories following large-scale current patterns. While some of the turtles traveled along the continental slope (north or south depending on the prevailing current pattern), others also moved to oceanic waters. As a result young turtles in the South Atlantic appear to be influenced by seasonal changes in current regimes—possibly impacting the connectivity of Brazilian turtles in the western Hemisphere (ISTS).

7.3 Conservation Genetics

Maintaining genetic diversity is an important component of conservation. Conservation genetics aims to assess genetic status of populations and propose measures for maintaining genetic diversity to prevent risks that could affect

Fig. 7.10 Tissue sample collection from a green turtle for molecular genetic analyses

persistence of populations. However, in conservation, the application of molecular markers can also contribute to the understanding of evolutionary history, demography and ecology of endangered species (Vilaça et al. 2016).

Molecular genetic studies (Fig. 7.10) have improved our knowledge on sea turtle life history, in aspects such as sea turtle phylogeography, gene flow, dispersal, feeding groups, migratory behavior, mating systems, sex ratios of breeding populations, reproduction biology, hybridization, conservation and management (Vilaça et al. 2016).

Because sea turtles occupy broad geographic ranges including nesting and foraging areas utilized by adults, and in some cases geographically distinct ontogenetic habitats (Musik and Limpus 1997), defining the scale of management units (MUs) is challenging (Hamann et al. 2010). Furthermore, sea turtles exhibit complex population structure often influenced by sex-biased gene flow among nesting stocks, and varying degrees of overlap during post-hatchling migrations, in developmental habitats and on adult foraging grounds (Bowen and Karl 2007).

Thus, different molecular analyses can be applied to determine genetic stock structure for different demographic segments of a population (Wallace et al. 2010). Maternally inherited mitochondrial DNA (mtDNA) is useful for resolving nest site fidelity and homing behavior (Bowen et al. 2004). In addition to defining nesting populations, this genetic marker is also useful for resolving maternal origin of both males and females at various life stages and feeding habitats (Bowen and Karl 2007). Nesting females typically demonstrate philopatry to nesting areas. However, males do not restrict mating efforts to their ancestral breeding area, and apparently copulate with females from other regional nesting populations (FitzSimmons et al. 1997, Roberts et al. 2004). Because nuclear DNA (nDNA) reflects contributions of both males and females, analyses of nDNA markers (e.g. microsatellites) can resolve breeding or reproductive stocks that encompass multiple mtDNA-defined nesting stocks (Bowen and Karl 2007, Carreras et al. 2007).

Since the genetic differentiation of rookeries, by use of mtDNA, detailed studies using mixed stock analysis (MSA) - a method borrowed from fisheries research, to determine natal origins of foraging grounds- have aimed to explain the processes that generate the composition of turtles at mixed foraging areas (Jensen et al. 2013).

Genetic tools have also proven useful in answering questions about the reproductive behavior of sea turtles. Since the first study that documented multiple paternity in loggerhead turtles (Harry and Briscoe 1988), researchers have used dozens of microsatellite loci to understand mating systems in all species of sea turtles, and even so, questions remain regarding sperm storage and possible fitness benefits of different mating strategies (Phillips et al. 2013). Furthermore, a combination of mtDNA and microsatellite data has been used to document several cases of hybridization in sea turtles (Vilaça et al. 2012). Molecular genetic studies of sea turtles exist within broader genetic fields that are constantly evolving. New tools and techniques in this field promise to overcome some of the limitations of past studies (Jensen et al. 2013).

In the present section, we review key genetic studies for sea turtles populations in the Southwest Atlantic, including information on genetic composition of rookeries and foraging aggregates. For this purpose, we organized some of the most relevant results by species, as well as hybridization cases.

7.3.1 Loggerhead, **Caretta caretta**

Reis et al. (2009) assessed the genetic composition of Brazilian loggerhead rookeries and foraging aggregates based on mtDNA control region. The authors analyzed 329 samples from Brazilian rookeries (Rio de Janeiro, Espírito Santo, Bahia and Sergipe) and an oceanic foraging ground (Elevação do Rio Grande—ERG). Four distinct loggerhead haplotypes (380 bp fragment) were observed among the 204 turtles sampled from Brazilian rookeries: CC-A4 (86.3%), CC-A24 (6.4%), CC-A25 (0.5%), and CCxLO (6.8%) (Fig. 7.11). Results showed that endemic haplotypes (CC-A4, CC-A24, CC-A25), found only in Brazilian rookeries, create a unique Brazilian haplotype profile and suggest the existence of two genetic stocks: the northern stock (Sergipe and Bahia rookeries), and the southern stock (Espírito Santo and Rio de Janeiro rookeries). The CCxLO haplotype, only found in Sergipe, was attributed to specimens considered hybrids because they have the typical olive ridley mtDNA haplotype, but the external morphology of loggerheads or a mixture between loggerhead and olive ridley turtles.

When considering longer mtDNA fragments, CC-A4 haplotype was subdivided into three variants (Shamblin et al. 2014). Therefore, based on these results, Shamblin et al. (2014) proposed the recognition of three stocks in Brazil: Northern coast (Sergipe and Bahia), Espírito Santo, and Rio de Janeiro. In light of the subdivision of CC-A4 obtained with the longer control region fragments, an analysis with

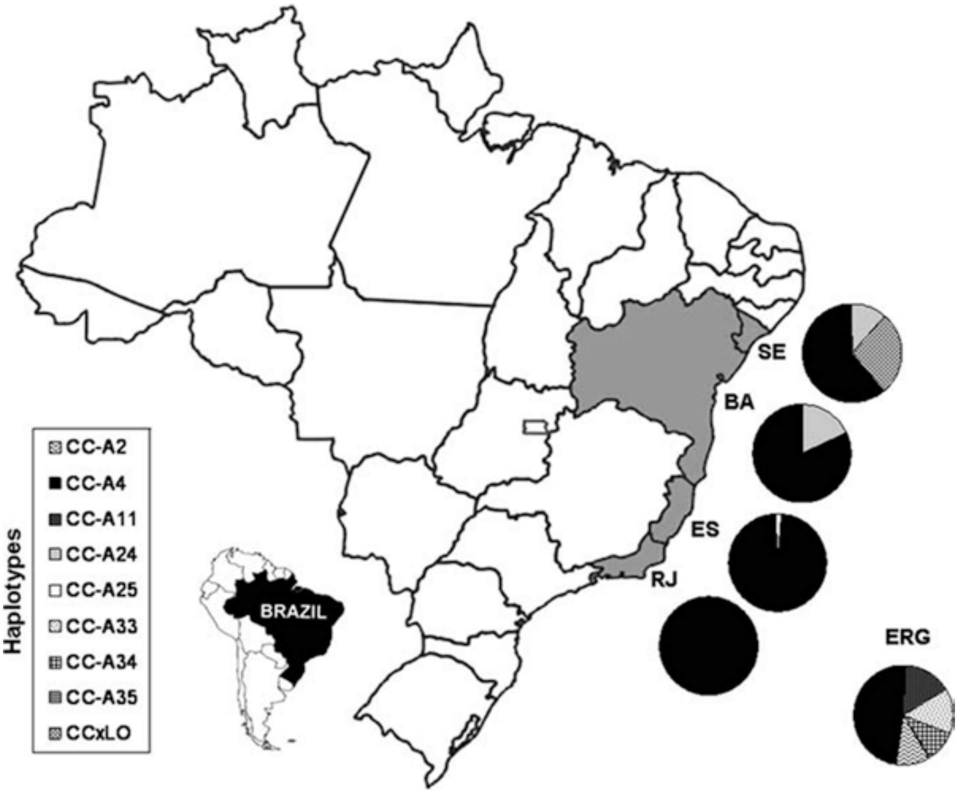


Fig. 7.11 Surveyed locations on the Brazilian coast and loggerhead turtle mtDNA haplotype frequencies for rookeries of Rio de Janeiro (*RJ*), Espírito Santo (*ES*), Bahia (*BA*) and Sergipe (*SE*), and for the foraging aggregation of Elevação do Rio Grande (*ERG*). Colors in the circles represent the different mtDNA haplotypes (Data from Reis et al. 2009)

larger sample sizes from the Brazilian rookeries is necessary to better resolve the number of MUs and their boundaries.

Mixed Stock Analysis (MSA) indicated a major contribution to the ERG foraging aggregation from Brazil (mean 59.5%). However, the ERG aggregation is a mixed stock with haplotypes from worldwide rookeries such as northwestern Atlantic, Mediterranean, Western Australia, Queensland, and New Caledonia (Fig. 7.12). However, the MSA results must be interpreted with care, since this analysis assumes that all source rookeries are known, but African and Indo-Pacific rookeries have been very poorly surveyed (Shamblin et al. 2014).

7.3.2 *Green Turtle,* Chelonia mydas

The genetic structure of nesting populations of green turtles nesting at the three known rookeries in Brazil were assessed: Trindade (n = 99), Rocas Atoll (n = 37), and Fernando de Noronha (n = 16) (Fig. 7.13). This study, based on short mtDNA control-region haplotypes suggested genetic structuring of green turtle populations, with haplotype frequencies significantly different between Trindade and the other

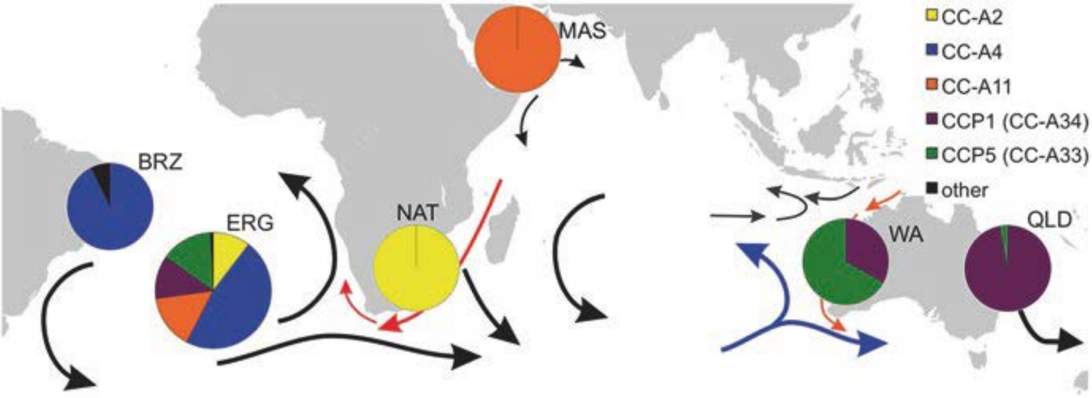


Fig. 7.12 Loggerhead turtle haplotype distribution for an oceanic foraging aggregation and major Indian Ocean rookeries. Control region haplotype (380 base pair) frequencies for the oceanic juvenile foraging aggregation from the Elevação do Rio Grande (*ERG*) and adjacent ridge and slope of the continental shelf in the South Atlantic Ocean and the regional management units (RMUs) in the South Atlantic, Indian, and South Pacific Ocean basins. Colors within the circles represent the different loggerhead haplotypes. *BRZ* is combined Brazilian rookeries; *NAT* is Natal, South Africa (Shamblin et al. 2014); *MAS* is Masirah Island, Oman (Shamblin et al. 2014); WA is Western Australia (FitzSimmons et al. 1996), *QLD* is Queensland, Australia rookeries (Boyle et al. 2009). The *arrows* indicate directionality of major surface currents: *orange* represents the Leeuwin Current; *blue* indicates the Western Australia Current, and *red*, the Agulhas Current (Data compiled by Shamblin et al. 2014)

two rookeries, and no significant difference between Rocas Atoll and Fernando de Noronha (Bjorndal et al. 2006).

Later, the stock structure of the Brazilian rookeries was reexamined using the mitochondrial short tandem repeat (mtSTR) marker and expanded control-region sequences. Results revealed significant structure between Rocas Atoll and Fernando de Noronha separated by only 150 km, indicating that these rookeries are discrete populations with respect to female natal homing (Shamblin et al. 2015).

Although feeding grounds (FGs) in Brazil were differentiated among them, intra-regional structure was less pronounced. Ascension was the primary natal source of the study FGs, with Surinam and Trindade as secondary sources (Naro-Maciel et al. 2012).

7.3.3 *Hawksbill,* Eretmochelys imbricata

Hawksbill turtles from the two main rookeries in Brazil (Bahia and Pipa) are inserted within the Southwest Atlantic Regional Management Unit (RMU) (Wallace et al. 2010). The two rookeries are related, even though they belong to different genetic stocks. By using sequences of the mtDNA control region and autosomal genes Vilaça et al. (2013) revealed striking differences between the two Brazilian nesting sites studied.

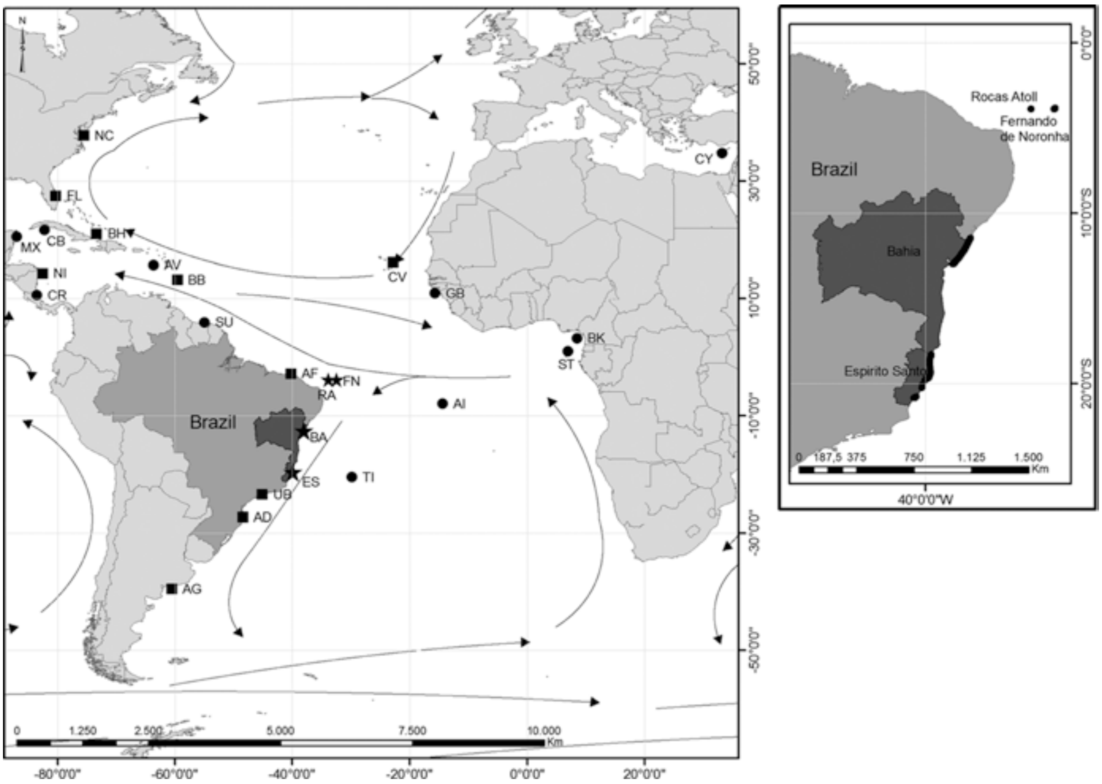


Fig. 7.13 Map of the Rocas Atoll (*RA*), Fernando de Noronha (*FN*), Bahia (*BA*), and Espirito Santo (*ES*) study sites (*symbolized by stars*) with respect to general oceanic circulation patterns shown as arrows, and other *C. mydas* groups previously subject to genetic analysis. Abbreviations for other FGs (*symbolized by squares*) are as follows: Almofala (*AF*); Argentina (*AG*); Arvoredo (*AD*); Bahamas (*BH*); Barbados (*BB*); Cape Verde (*CV*); Florida (*FL*); Nicaragua (*NI*); North Carolina (*NC*); Rocas Atoll (*RA*); and Ubatuba (*UB*). Rookeries that were assessed (*symbolized by circles*) were: Hutchinson Island, Florida, USA (*FL*); Quintana Roo, Mexico (*MX*); Aves Island, Venezuela (*AV*); Matapica, Surinam (*SU*); Lara Bay, Cyprus (*CY*); Cuba (*CB*); Tortuguero, Costa Rica (*CR*); Ascension Island, UK (*AI*); Poilão, Guinea Bissau (*GB*); Bioko Island, Equatorial Guinea (*BK*); Sao Tome (*ST*); Trindade Island, Brazil (*TI*); and Rocas Atoll, Brazil (*RA*). The inset map shows the sample collection sites (Adapted from Naro-Maciel et al. 2012)

Differences among Brazilian feeding aggregation sites and others around the world were also found (Vilaça et al. 2013, Proietti et al. 2014). Results from genetic analysis estimates showed that the studied Brazilian feeding aggregations are mostly composed of animals originating from the domestic rookeries Bahia and Pipa, but some contributions from African and Caribbean rookeries were also observed (Fig. 7.14).

7.3.4 Leatherback, Dermochelys coriacea

Comparing haplotypes distributions among nesting and foraging grounds, Vargas et al. (2008) revealed a major contribution to a Brazilian pelagic aggregate (Fig. 7.15) from Atlantic nesting populations (mean 96.1%) and the existence of six individuals

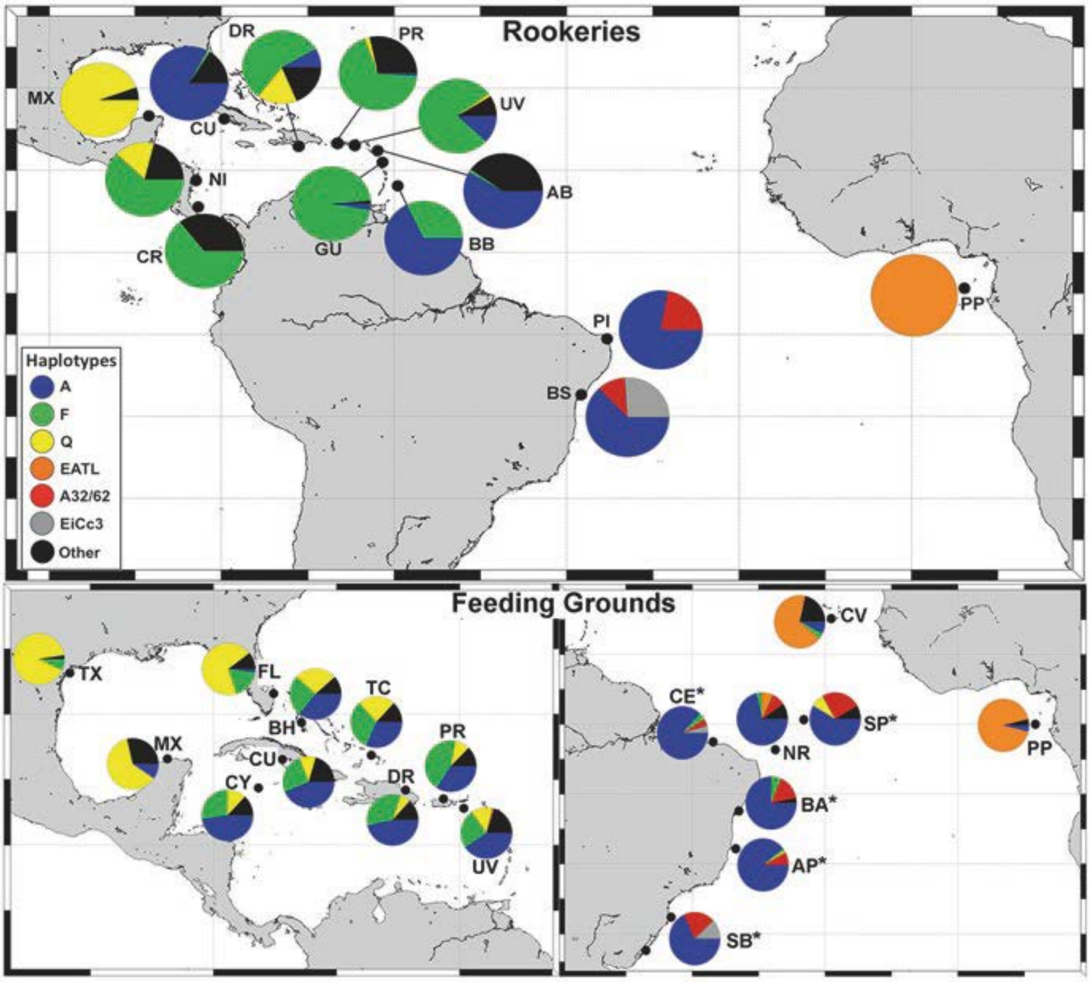
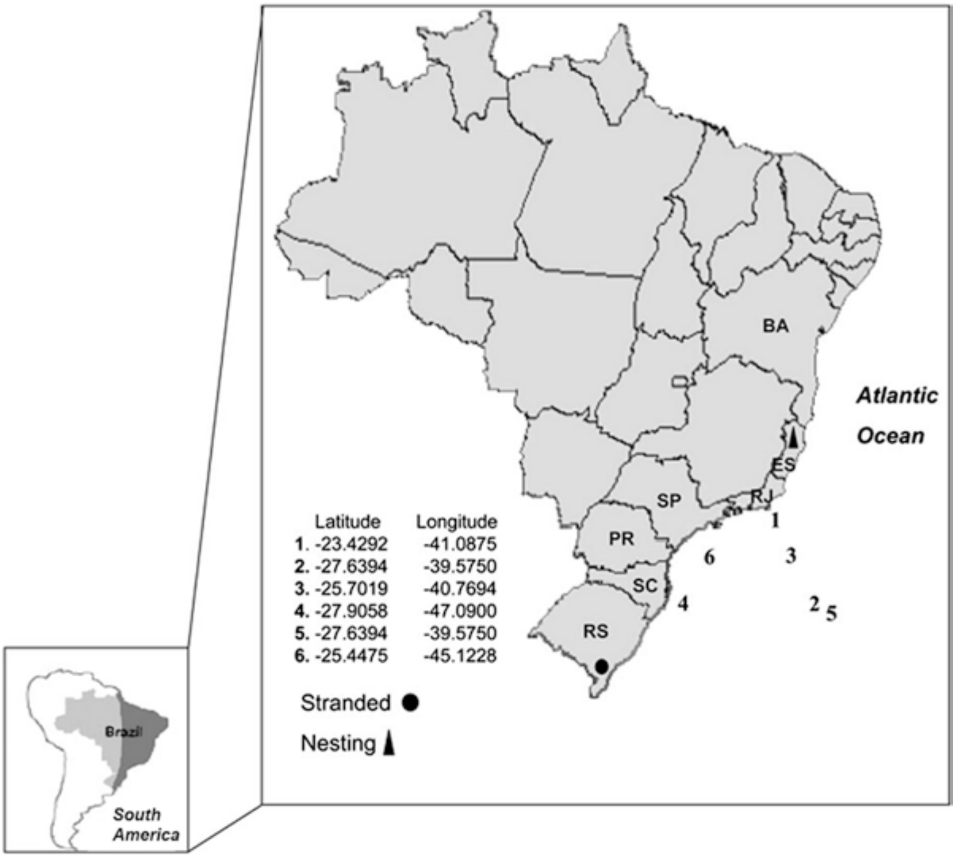


Fig. 7.14 Main haplotype frequencies of genetically described populations in the Atlantic. *study areas described in this work. Rookeries: *BS* Bahia/Sergipe, *PI* Pipa, *PP* Principe, *BB* Barbados, *GU* Guadeloupe, *AB* Antigua & Barbuda, *UV* U.S. Virgin Islands, *PR* Puerto Rico, *DR* Dominican Republic, *CR* Costa Rica, *NI* Nicaragua, *CU* Cuba, *MX* Mexico. Feeding grounds: *SP* São Pedro and São Paulo, *NR* Noronha/Rocas, CE Ceará coast, *BA* Bahia coast, *AP* Abrolhos Park, *SB* South Brazil, *PP* Principe, *CV* Cape Verde, *UV* U.S. Virgin Islands, *PR* Puerto Rico, *DR* Dominican Republic, *TC* Turks & Caicos, *BH* Bahamas, *FL* Florida, *CY* Cayman Islands, *MX* Mexico, *TX* Texas (Adapted from Proietti et al. 2014)

bearing an orphaned haplotype (Dc_A2) for leatherbacks. This haplotype was considered an orphaned haplotype because no match with nesting population were found at that moment. In a later comprehensive genetic analysis of worldwide stock structure, it was ascertained that the origins of the orphaned haplotype came from Gabon and/ or Western Africa (Dutton et al. 2013).

Later, Vargas et al. (2013) reanalyzed samples from a previous study and estimated the contribution of source rookeries to a Brazilian feeding ground, using population genetic measures and mixed stock analysis MSA, including two previously genetic undescribed rookeries: Gabon and Guadalupe/Martinique. Results of the MSA indicated major contribution to the Brazilian pelagic aggregate from Gabon (78%), the largest population of leatherbacks in the world.



	Latitude	Longitude
1.	-23.4292	-41.0875
2.	-27.6394	-39.5750
3.	-25.7019	-40.7694
4.	-27.9058	-47.0900
5.	-27.6394	-39.5750
6.	-25.4475	-45.1228

Fig. 7.15 Approximate location of sampling sites along the Brazilian coast (*RS*—Rio Grande do Sul State, *SC*—Santa Catarina State, *PR*—Paraná State, *SP*—São Paulo State, *RJ*—Rio de Janeiro State, *ES*—Espírito Santo State, and *BA*—Bahia State) and geographic coordinates for six sampling sites of pelagic (stranded/incidentally caught) animals (Adapted from Vargas et al. 2008)

7.3.5 Olive Ridley, Lepidochelys olivacea

The olive ridley sea turtle is widespread on tropical and subtropical oceans and is considered the most abundant sea turtle. In the Atlantic Ocean, this species has limited distribution and nesting has been reported mainly in Guinea Bissau, Suriname, French Guiana and northeastern Brazil. Hahn et al. (2012) characterized the genetic diversity and population structure of the olive ridley nesting populations in the Brazilian coast based on 92 samples sequenced for the mtDNA control region and 67 samples genotyped for 15 microsatellite loci. Although three mtDNA haplotypes were found, two previously unknown but very rare, the Brazilian nesting population presented one of the lowest mtDNA diversity known for the species. mtDNA data indicated a population expansion following a population decline in the past while microsatellite data suggested a scenario of demographic stability, supporting the scenario of colonization of Atlantic Ocean via a founder effect. Since this data could not find significant genetic differences between the studied olive ridleys nesting areas in the Brazilian coast, conservation strategies should consider the Brazilian olive ridleys as a single interbreeding population. (Hahn et al. 2012).

7.3.6 Hybrids

Vilaça et al. (2012) analysed nuclear markers to investigate the pattern of hybridization involving three species of sea turtles: hawksbill (*E. imbricata*), loggerhead (*C. caretta*) and olive ridley (*L. olivacea*). Results indicated that most of the individuals in the crossings olive ridley x hawksbill and olive ridley x loggerhead are F1 hybrids, whereas loggerhead x hawksbill crossings present F1 and backcrosses with both parental species. It is a remarkable find, because most of the nesting sites surveyed worldwide, including some in northern Brazil, presents no hybrids, and rare Caribbean sites present no more than 2% of hybrids. Thus, a detailed understanding of the hybridization process is needed to evaluate natural or anthropogenic causes of this regional phenomenon, which could be an important factor affecting the conservation of the Brazilian population. Of special interest is the high occurrence of loggerhead x hawksbill hybrids (42%), which display loggerhead mtDNA haplotypes but are characterized morphologically as hawksbills. The occurrence of several nesting individuals with identical mtDNA from another species may also suggest a long history of introgression between species producing likely F2 or further generation hybrids (Vilaça et al. 2012).

7.4 Climate Change Impacts

Sea turtles will be affected by changes to multiple climatic processes (e.g., increased air and sea temperature, sea level rise, precipitation, and storm activity) at all life stages and at different temporal and geographical scales (Fuentes et al. 2011, Hawkes et al. 2009). In addition, sea turtles will be affected indirectly by increased atmospheric CO_2 concentrations and declines in ocean pH. Arguably, the more detectable impacts of climate change to marine turtles will occur during their terrestrial reproductive phase (egg laying, egg incubation, and hatchling success) because there are clear, and relatively straightforward, effects of increased temperature, sea level rise, and cyclonic activity on nesting sites and reproductive output (Fuentes and Abbs 2010, Fuentes et al. 2009).

Successful incubation of sea turtle eggs occurs within a narrow thermal range of 25–33 °C. Incubation above the thermal threshold will result in hatchlings with higher morphological abnormalities and lower hatching success. Additionally, all species of sea turtle have temperature-dependent sex determination (TSD) (Mrosovsky and Yntema 1980). Warmer temperatures, above the pivotal temperature—where a 1:1 sex ratio is produced—yield more females while temperatures below the pivotal temperature shift the ratio towards more males. Consequently, projected increases in temperature are expected to result in highly female-biased populations, reduced hatching success and alteration of incubation duration (Fuentes et al. 2011). Potential consequences include a reduction in effective population size, the inability to find mates leading to reduced fecundity or female infertility, and

Fig. 7.16 Biologist collecting information on sand temperature in the field with a temperature datalogger

under more extreme climate projections, the potential for production of single sex cohorts. These changes are likely to reduce the viability of turtle populations (Fuentes et al. 2012). Consequently, knowledge of the primary sex ratio of populations with TSD is key for providing a baseline to inform management strategies and accurately predict how future climate changes may affect turtle populations. However, there is a lack of robust data on offspring sex ratio at appropriate temporal and spatial scales to inform management decisions. Today, with the advance of technology, electronic devices for temperature measurement (i.e. dataloggers; Fig. 7.16) allow monitoring temperature variations of beaches and nests. The use of such equipment in research studies makes possible the understanding of the potential impacts of climate change on populations of sea turtles and their habitats in Brazil.

Studies developed in the 1990s determined the pivotal temperature—the one that produces the sex ratio 1: 1—for loggerhead (Marcovaldi et al. 1997) and hawksbill for Brazilian populations (Godfrey et al. 1999). The conversion of this temperature to the pivotal incubation duration, which is the amount of days that the eggs incubated at constant pivotal temperature take to hatch, provide a method to estimate hatchling sex ratios (Marcovaldi et al. 1997), relatively easy to perform during fieldwork, creating the first baseline for these studies in Brazil.

Recent studies using long temporal coverages allowed us to estimate natural sex ratios to provide a baseline in advance of climate change and to assess management practices to inform future management decisions. Therefore, one of our first goals was to determine the historical variability of incubation duration and subsequent sex ratio produced at loggerhead and hawksbill nesting sites (Marcovaldi et al. 2014, 2016).

7.4.1 Hawksbill Nesting Grounds

We estimated the primary sex ratio of hawksbill hatchlings from incubation duration of 5514 in situ nests from 10 nesting beaches from two regions in Brazil over the last 27 years. A strong female bias was estimated in all beaches, with 96% and 89% average female sex ratios produced in Bahia (BA) and Rio Grande do Norte (RN). Both inter-annual (BA, 88–99%; RN, 75–96% female) and inter-beach (BA, 92–97%; RN, 81–92% female) variability in mean offspring sex ratio was observed (Figs. 7.17 and 7.18).

7.4.2 Loggerhead Nesting Grounds

The primary sex ratio of loggerhead hatchlings was estimated from incubation duration of 27,697 in situ nests from 21 nesting beaches used by two subpopulations of loggerhead turtles in Brazil over the last 25 years. A strong female bias (94%) was observed in all the areas used by the northern loggerhead stock, Sergipe (SE) and Bahia (BA), whereas a more balanced sex ratio (53% female) was estimated at the regions used by the southern loggerhead stock, Espírito Santo (ES) and Rio de Janeiro (RJ). Both inter-annual (SE: 83–99%, BA: 79.–98%, ES: 33–81%, RJ: 18–81%) and inter-beach variabilities (SE: 91–98%, BA: 89–96%, ES: 47–69%, RJ: 28–55%) in mean female offspring were observed (Fig. 7.19).

7.4.3 Conclusions

These findings provide evidence of bias in the production of female offspring in Brazil and significantly identify the beaches and months where males are produced. Identify and enhance the protection of male-producing beaches has been highlighted as high priority to mitigate potential impacts from projected increases in temperature on marine turtles (Hawkes et al. 2007, Fuentes et al. 2012, Marcovaldi et al. 2014).

This outcome has prompted us to explore the thermal profile of nesting areas used by loggerheads and hawksbills. For this, we deployed 60 data-loggers in 2013 along the whole extent of nesting areas and environments used by these species. Thermal profile will be monitored over the course of several years and will be used to estimate the current sex ratio being produced at each location. This data will be coupled with climate models to predict future sex ratio and thus help prioritize management in light of global warming.

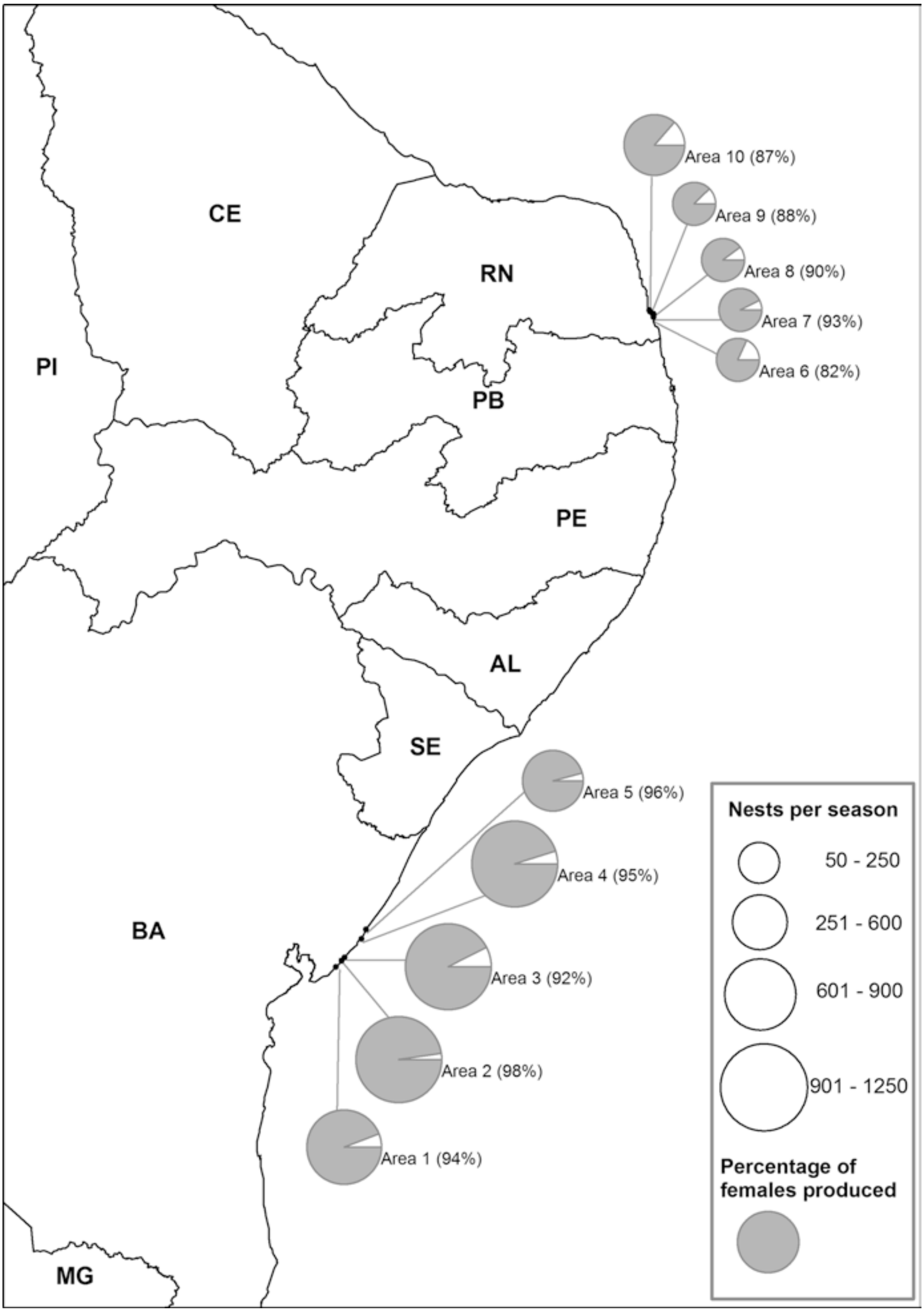


Fig. 7.17 Study sites with estimated proportion of females (*grey*) and male (*white*) hawksbill hatchlings in each area. Pie diameter is scaled according to magnitude of clutches laid each year in each area (Data from Marcovaldi et al. 2014).

milagros@tamar.org.br

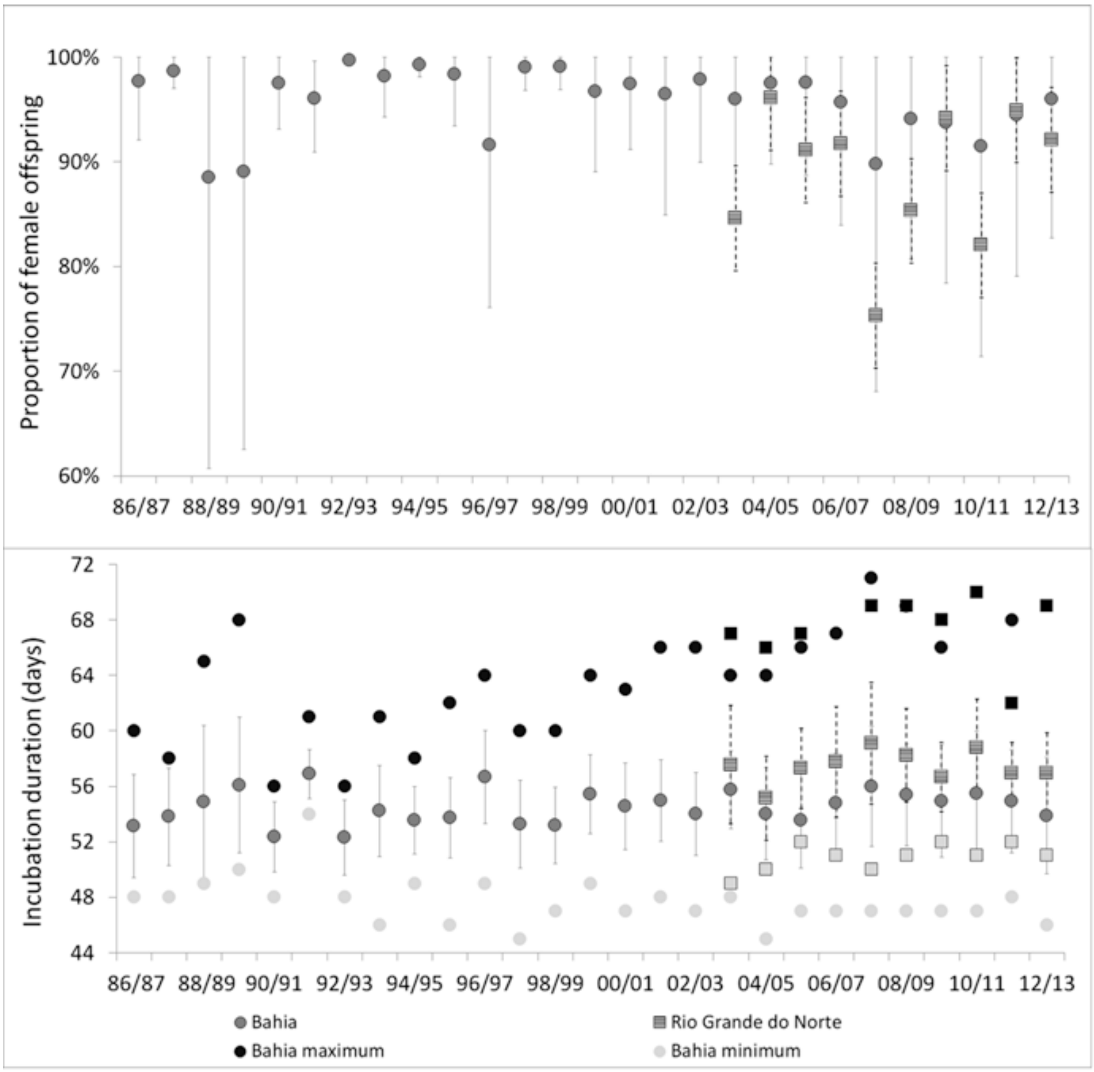


Fig. 7.18 Inter-annual (**a**) mean (SD), incubation duration of hawksbill clutches, and (**b**) mean percentage of females produced (SD) at Bahia and Rio Grande do Norte (Data from Marcovaldi et al. 2014).

7.5 Future Research and Perspectives for Sea Turtle Conservation

At the very beginning in the late 1970s, TAMAR faced a big challenge: obtain information on sea turtles occurrence along the 8.000 km of the Brazilian coastline, a mission with continental dimension. What was apparently a very basic gave us a starting point to explore a whole new universe. Collection of data, village by village, and observations in the field during the initial assessment, from 1980 to 1982, resulted in the first map of the sea turtle spatial and temporal distribution in our country and the main threats for these species (Marcovaldi and Marcovaldi 1999). As so many other sea turtle projects from other countries at that time, the key questions to be responded were related to the land part of the sea turtle life cycle.