

Project Update: August 2016

Background

Sea turtles are particularly sensitive to population reductions, especially of juveniles mortality, because they are long-lived, slow-growing, and late to reproduce. Moreover, the high migratory behaviour of sea turtles enable juveniles to choose among oceanwide habitats and foraging strategies. Because prey availability, predation risk, and other factors often vary between habitats, differential habitat use and corresponding foraging strategies may result in differential growth, survival, and ultimately fecundity among individuals of the same species or population. Despite the demography importance of juveniles, their ecology and life history remain poorly understood. In this context, genetic studies emerge as important tools for understanding connectivity, structure and migrations of endangered populations, providing the knowledge necessary for determining adequate management strategies for the conservation of species. The loggerhead sea turtle has a worldwide tropical and subtropical distribution, but global numbers have been greatly reduced over the last decades due to exploitation for meat and eggs, fragmentation of nesting and foraging habitats, marine pollution, and especially by-catch in fisheries. In Brazil, large gaps exist in the knowledge of loggerhead sea turtles, and this work will bring valuable information of populations by identifying the genetic composition of loggerhead feeding grounds and possible losses of genetic diversity due to population decreases (bottleneck events) caused by human activities such as overexploitation and fisheries. This work will also provide the first insights on how the genetic characteristics of populations are related to foraging, habitat use and growth dynamics at different life stages. Identifying these ecological and demographic parameters are important to understand how loggerheads can respond to significant population reductions and drive population dynamics.

Project progress

- ***Field expeditions***

Twenty-six expeditions were performed from October 2015 to August 2016 along 355 km of coast, between Lagoa do Peixe (31°21'S; 051°02'W) and Chuí (33°44'S; 053°22'W), Rio Grande do Sul. During these expeditions, humeri and tissue samples were collected from 43 stranded dead loggerhead turtles, ranging from the small size of 46 cm curved carapace length (CCL) up to a maximum of 106 cm CCL.

- ***Samples from partners***

We established partnerships with two NGOs in order to increase the range and number of loggerheads turtle samples, mainly from individuals incidentally caught in fisheries. We had established partnership with Núcleo de Educação e Monitoramento Ambiental (NEMA), which provides tissue samples for DNA analysis from loggerheads caught in longline and trawling fisheries totaling 117 and 55 samples, respectively. Tissue samples collected in Santa Catarina state (n = 128) and the coast of Ceará state (n= 75) were supplied through partnership with Project Tamar-ICMBio. These samples were collected from loggerheads caught in longline and fishing weirs expeditions. Project Tamar's partnership also provides 25 humeri and tissue samples from dead loggerhead turtles found washed ashore in three states along the Brazilian coast: northern coast of Bahia, northern coast of Rio de Janeiro,

and Santa Catarina.

- **Laboratory analysis**

The laboratory activities are occurring as proposed on the project timeframe. From the 378 samples collected in fishing activities, 231 were processed to date. DNA was extracted with PureLink® Genomic DNA Kit and the mtDNA D-Loop amplified through and Polymerase Chain Reactions (PCR) using primers LCM15382/H950 and Platinum® Taq DNA Polymerase, using an Applied Biosystems Veriti 96-well Thermocycler. The obtained PCR products are currently being purified. After this phase, we will send samples for sequencing in both directions to obtain haplotype sequences for analysis of genetic diversity, population structure, and natal origins. Furthermore, each humerus was dissected and immersed in water for 2–3 weeks for complete removal of soft tissues, and then air-dried for 2 weeks. After cleaning, the medial width was measured prior to removing cross-sections for histological processing.

Next steps

The next steps in this project are: (1) finish DNA extractions and amplification of the mtDNA control of 147 samples from individuals incidentally caught in fisheries; and (2) amplify 13 nuclear DNA markers of all samples. The amplification and genotyping of nuclear markers will bring valuable information of loggerhead populations by identifying the genetic composition of feeding grounds and possible losses of genetic diversity due to population decreases (bottleneck events) caused by human activities such as overexploitation and fisheries.

Moreover, after laboratory analysis of DNA samples, we will start histological humeri processing and collection of growth lines for stable isotope analysis. By combining molecular techniques with stable isotope analysis and skeletochronology, this work will contribute towards a better understanding of how the genetic composition of loggerhead sea turtles affects trophic behaviour (i.e. feeding and habitat use) and demographic parameters (i.e. growth rates and age at sexual maturity).

