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de Aves and their average residence time. The best-fitting model indicated that adult survival was lower for turtles arriving for the first time than for those returning in successive years, probably due to a high rate of tag loss during the first year. Survival varied considerably among years, with a mean annual probability of 0.83 for returning turtles (95% CI 0.51–0.98). This value is similar to survival estimated in Tortuguero, Costa Rica (0.85; 95% CI 0.83-0.87), the only other population in the Caribbean that has demographic estimates based on long-term capture histories, but is much lower than estimates in Australia (0.95; 95% CI 0.92-0.98). Also, Isla de Aves had a remigration interval of 1-3 years, (X: 2.37, SD: 1,10), which was similar to the interval estimated for Tortuguero, Costa Rica (X: 2.95, SD 0,88), but shorter than estimates from Australia (5-7 years). Fluctuations in adult annual survival may be due to turtle fishing in Nicaragua, the Dominican Republic, the Lesser Antilles and the Gulf of Venezuela, where females from Isla de Aves are known to feed. Such fishing pressures do not exist in Australia. The frequency of hurricanes across the Caribbean also explained a small but significant proportion of variation in adult survival (F= 4.638; p=0.04508 R2=0.16). However, although population size varied among years (100-1,453 females), we observed an apparent increase between 1979 and 2008. Thus, although we were able to document the effect of threats on adult survivorship, it appears that the Isla de Aves population may be stable at present or even growing. Management actions to grow this population further will need to be tailored not only to local nesting trends but also to regional climatic cycles and distributed anthropogenic threats and natural conditions in foraging grounds.

GENETIC STOCK STRUCTURE OF HAWKSBILL NESTING POPULATIONS IN THE EASTERN PACIFIC

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The use of molecular genetic techniques plays a critical role in the understanding and management of global sea turtles populations. Due to strong philopatry demonstrated by the taxon, mitochondrial DNA (mtDNA) continues to provide a useful genetic marker for evaluating population structure and phylogeography. We used mtDNA to conduct the first-ever genetic survey of hawksbill nesting stocks in the eastern Pacific Ocean. We analyzed a total of 61 tissue samples collected between 2008 and 2011 from four rookeries across the region. Despite small sample sizes for some rookeries, our initial findings provide novel insights into population structuring and the evolutionary origins of hawksbill turtles in the eastern Pacific. Three previously identified haplotypes and two new ones were found with overall frequencies of 78.7% and 21.3%, respectively, the latter only evident in Central American nesting stocks. Significant differentiation was found between rookeries in Central and South America, providing evidence for stock structuring in the eastern Pacific. One haplotype predominated at all four nesting sites. This and the other two previously identified haplotypes occur in the Indo-Pacific. From a phylogeographic perspective, the prevalence of Indo-Pacific derived haplotypes in eastern Pacific nesting stocks suggests eastern Pacific populations radiated out of the western Pacific, an assertion previously postulated, but which has remained unconfirmed until now. Furthermore, the existence of new haplotypes exclusive to the eastern Pacific suggests the populations have been separated sufficiently long to accumulate new mutations in the mtDNA control region at the regional population level. We also found potential evidence for fine scale genetic

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segregation between nesting habitat types, possibly maintained by behavioral differences. Nonetheless, additional studies are needed to confirm this hypothesis. Our findings have important implications for hawksbill management strategies on both regional and global scales. Additional research with larger sample sizes and variable markers will prove crucial to gaining further understanding of hawksbill stock structuring and genetic diversity in the eastern Pacific.

LAGUNA MADRE RECRUITING CLASS OF 2012

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Endangered sea turtle conservation efforts share the common and very vital goal of increasing populations to self-sustainable numbers. With a large effort being carried out towards all species of sea turtles in the Gulf of Mexico, a better understanding of nesting grounds, their relationship to juvenile foraging grounds and population trends can bolster or increase conservation efforts. The Laguna Madre is and has been a viable and flourishing marine ecosystem for many decades. It is an area that provides great foraging grounds for Atlantic green sea turtles (Chelonia mydas) of all sizes. Many nearby beaches in Northern Mexico have reported increases in Atlantic green nesting. Looking at nesting data totals from Mexico and straight carapace length from stranding reports in the Laguna Madre, collected over the past 6 years, will allow for the analysis of possible shifts in the average size of the Lower Laguna Madre Population. A shift to a smaller average size in the Lower Laguna Madre green sea turtles' population, coupled with an increase in Northern Mexico nesting, could represent more recruitment in the Lower Laguna Madre population and may represent a growing population of green sea turtles in the Western Gulf of Mexico. Results show a noticeable increase in the number of nesting green sea turtles along with a decrease in the average carapace length of Lower Laguna Madre juvenile green sea turtles. This decrease in the average carapace length is a great indicator of positive recruitment. This recruitment of juvenile green sea turtles is a positive step in the recovery of the threatened Atlantic Green population in the Western Gulf of Mexico.

BAYESIAN FRAMEWORK TO INTEGRATE TRADITIONAL ECOLOGICAL KNOWLEDGE INTO ECOLOGICAL MODELING: A CASE STUDY WITH SEASONALITY OF MARINE TURTLES IN FRENCH GUIANA

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Indigenous groups offer alternative knowledge and perspectives based on their own locally developed practices of resource use. This Traditional Ecological Knowledge (TEK) has been acquired from long-term observations and uses of natural systems. Some promote the use of TEK in scientific research, however the methodology to integrate such knowledge in ecological models is not straightforward. We advocate the use of Bayesian framework to integrate TEK as a prior for analysis. We exemplified such a use of TEK to analyze the seasonality of marine turtles in French Guiana. We show that TEK can resolve some situations in which the parameter fit was not possible. On the other hand, TEK could be biased and it is safer to have data with enough information to prevent this bias to influence strongly the posteriors. The construction of ecological model to be used with TEK will be discussed.



PROCEEDINGS OF THE THIRTY-THIRD ANNUAL SYMPOSIUM ON SEA TURTLE BIOLOGY AND CONSERVATION



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5 to 8 February, 2013 Baltimore, Maryland, USA

Compiled by: Tony Tucker, Lisa Belskis, Aliki Panagopoulou, ALan Rees, Mike Frick, Kris Williams, Robin LeRoux, and Kelly Stewart

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