

Morphometric data were taken from each turtle before it was tagged and released, and compiled into a database that has been maintained since the plant went on-line. From 1988 to present (a span of 25 years), green turtle (*Chelonia mydas*) capture data were analyzed to look at historical and seasonal trends in population structure, recapture rates, and fibropapilloma rates. Analysis shows that the percentage of total sea turtle captures at the plant represented by green turtles rose markedly in the late 1980's and early 1990's before leveling off. The percentage of new recruits encountered at the plant has steadily declined since the early 1990's, while the percentage of turtles that have been recaptured at the plant has steadily risen. Green turtles have also exhibited seasonal trends in which the percentage of new recruits rises during winter months and falls during summer months. The data have also shown that fibropapilloma rates are much higher in the winter months than during the remainder of the year. This long-term monitoring project will continue to provide insight into the population structure of turtles utilizing the near-shore waters adjacent to the St. Lucie power plant.

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## PHYLOGEOGRAPHY OF OLIVE RIDLEY TURTLES

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Phylogeographic studies, which consider the geographic distribution of genetic lineages, provide a powerful method to understand a species' colonization history and the interconnectedness among populations. The olive ridley turtle (*Lepidochelys olivacea*) has a global distribution across tropical and sub-tropical oceans, and is one of the most abundant marine turtle species. It is closely related to the Kemp's ridley (*Lepidochelys kempii*) and the origin of both species is believed to be related to the closure of the Isthmus of Panama during the Pliocene. Subsequently olive ridley would spread from the Pacific Ocean into the Indian, and colonized the Atlantic Ocean most recently; or a remnant population from Indian Ocean would colonized both East Pacific and Atlantic Oceans. In this study we expand our previous work by investigating new aspects of evolutionary processes and demographic history that contributed to current *L. olivacea* distribution. Using Bayesian analyses we analyzed mtDNA control region sequences from 14 rookeries (n = 541), as well as fifteen nuclear short tandem repeats (STRs) from 12 rookeries (n = 285). Bayesian analyses with the mtDNA sequences were carried out in Lamarck in two ways: 1) with 9 sets of populations: Surinam (SU), French Guiana (GF), Brazil (BR), India (IN), Sri Lanka (SL), Tiwi Island (Tis), Cape York (CY), Costa Rica (CR), Baja California (BC) and continental Mexico (ME); 2) 4 sets of populations: Indian Ocean (IN and SL), Indo/West Pacific (Australia and Malaysia), Atlantic Ocean (GB, GF, SU and BR) and East Pacific (CR, BC and ME). The results showed that genetic diversity, and consequently the Nef (females effective population size) in olive ridleys varies widely, from Nef ~17,000 for IN to Nef ~1,300 in CY (Australia); all sets of population showed sign of population growth. The unique pairs of populations with Nm values higher than one are those from the East Pacific (ME, CR, and BC) and Sri Lanka into India. Divergence times were estimated using a Bayesian approach and resulted in clade K, found only in India Ocean and the most basal lineages for olive ridley, originated around 1.6 Mya,

the East Pacific clade about 0.61 Mya, and the split between the Indo-Pacific and Atlantic lineages around 0.36 Mya. These results are mostly consistent with the recent colonization of East Pacific and the Atlantic and suggest a model of recurrent extinction/colonization for most ridley nesting sites that may be explained by climatic changes, especially during the Pleistocene. Diversification times within all five clades are very similar, ranging between 221,000 years ago and 342,000. Significant statistics for the STR data and similarly shaped star trees in each of the four major olive ridley clades suggested a population expansion, a scenario partially corroborated by the neutrality tests (Fu's FS and Tajima's D) and the Bayesian Skyline Plot (BSP) analysis which indicate a population expansion for *L. olivacea* after the last glacial maximum. These results suggest that the most recent demographic events (colonization and population expansion) for most oceanic regions may have been concurrent.

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## GENETIC STRUCTURE OF GREEN TURTLES NESTING IN THE NORTHWESTERN PACIFIC OCEAN\*

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Japan is located at the northern limit of the Pacific green turtle breeding area. The Ogasawara Islands and the Ryukyu Archipelago are the two main nesting sites of this species in Japan. Only green turtle nests are found in the Ogasawara Islands, where the number of annual nesting is estimated at more than 1,000 by beach surveys. In contrast, in the Ryukyu Archipelago the nests of three species of sea turtles (loggerheads, green turtles and hawksbills) are found. This archipelago is a long island chain lying more than 1,000 km between Taiwan and Kyushu, and contains scattered nesting rookeries of green turtles. Hence, the available data about nesting sites and the size of nesting populations are limited at several islands of the southern and northern Ryukyus. Although surveys in the central Ryukyus have been started in past years, the genetic population structure in the whole Ryukyu Archipelago is still unknown. The previous studies suggested that there were three genetically differentiated stocks nesting in the Ogasawara Islands and Yaeyama Islands, in the southern Ryukyus. These populations were also differentiated from the two neighboring populations nesting in Taiwan. In the present study we collected samples of nesting green turtles in the central Ryukyus, and analyzed them using mitochondrial DNA (mtDNA) by sequencing approximately 860 base pairs of the control region to understand the extent of genetic connectivity among the green turtle nesting populations in the northwestern Pacific Ocean. Although several haplotypes were shared with other populations, it was suggested that there were two differentiated populations in the central Ryukyus. The haplotypes detected in the central Ryukyus also belonged to three divergent clades, as was previously observed in three other Japanese populations. These clades corresponded to three of five clades detected in the populations through Australasia. Although in many rookeries the haplotypes from two divergent clades were detected sympatrically in the northern Pacific rookeries, mixtures of haplotypes from three divergent clades have been observed only in Japanese populations. Moreover, all regional populations in Japan showed high genetic diversities. These results suggested that the source of Japanese populations had their origin in the emigrations from several common populations in lower latitudes, which might have been geographically distant. Consequently, they could have maintained high genetic diversities even after they were differentiated into the small populations at the periphery of their distribution. Fifteen of 18 haplotypes, including their dominant haplotypes, have been only reported from populations in the northwestern Pacific rookeries. This suggests that the populations in this region have evolved as their own lineages after the historical immigration. Acknowledgments: This research was financially supported in part by the Global COE Program A06 to Kyoto University and the Ocean Exposition commemorative Park management Foundation. We are grateful to the International Sea Turtle Society, U.S. Fish and Wildlife Service, U.S.



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Baltimore, Maryland USA

5 to 8 February, 2013  
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Compiled by:

Tony Tucker, Lisa Belskis, Aliko Panagopoulou, Alan Rees, Mike Frick,  
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U.S. DEPARTMENT OF COMMERCE  
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