

**COMBINED GENETIC ANALYSIS AND DISPERSAL MODELLING REVEAL DIVERSE NATAL ORIGINS OF GREEN TURTLES FORAGING AT THE PALMYRA ATOLL NATIONAL WILDLIFE REFUGE, CENTRAL PACIFIC**

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Population connectivity and spatial distribution are fundamentally related to the ecology, evolution, and behavior of many species including cryptic marine organisms. In the marine realm the life histories of diverse taxa are shaped by movements that vary among stages, such as dispersal primarily driven by ocean currents in younger individuals, and directed migration later in life. Highly migratory and globally endangered green turtles are important elements of diverse and often distant ecosystems that may be connected in unknown and surprising ways. Genetic analysis is a powerful tool for investigating marine turtle connectivity and tracing unknown natal origins of feeding ground populations. However limitations can include high confidence intervals and incomplete sampling. Simulating hatchling dispersal within an ocean circulation model is a technique that allows us to generate spatially explicit predictions based on statistically robust sample sizes (i.e., calculating trajectories for thousands of virtual particles). Our objective was to combine these methods to determine the unknown natal origins of green turtles foraging at the Palmyra Atoll National Wildlife Refuge (PANWR), Central Pacific. We extracted hindcast output from the Global Hybrid Coordinate Ocean Model to examine how surface currents might influence the probability of green turtles from different nesting beaches reaching the PANWR foraging grounds, and used particle-tracking software to identify possible migratory corridors juvenile turtles might use to reach the PANWR. In addition, we used regional analyses of mitochondrial control region sequences from turtles collected at the PANWR during a five-year period (2008-2012). Genetic analysis revealed widespread origins ranging from the distant eastern Pacific to closer central Pacific islands. Our modeling results also indicated that turtles could potentially reach the PANWR via surface currents coming from the eastern, central, and to a lesser extent western Pacific. The emerging story of diverse PANWR origins contrasts with the more localized, self-contained Hawaiian green turtle stock, contributing to a complex model of green turtle dispersal in this region.

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**INTEGRATING DETECTABILITY AND ABUNDANCE IN ASSESSMENTS OF SEA TURTLE POPULATION TRENDS**

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Assessments of population trends based on abundance data alone, without accounting for detectability, can lead to erroneous conclusions. Population trends of threatened and endangered sea turtles worldwide are often based on counts of nests or nesting females. We analyze 39 years (1973 to 2011) of nest-count,



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Baltimore, Maryland USA

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Compiled by:

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