
UNCOVERING AGING PATTERNS ACROSS CAPTIVE AND WILD SEA TURTLES*

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A driving force behind centuries of biological inquiry has been the profound desire to understand the ecological and evolutionary mechanisms shaping aging patterns in nature. At the heart of this fascination lies the challenge of unravelling how trait assemblages define a species' position in life history space, and how this position presupposes a species' susceptibility to the negative effects of aging, i.e., senescence. Protective phenotypes (e.g., shells and venom) and specialized life modes (e.g., flight and fossoriality) have emerged as key drivers of macroevolutionary patterns that reduce aging rates, yet empirical tests have been strongly biased toward birds, mammals, and terrestrial ectotherms. Marine ectotherms, despite their ecological importance, remain critically understudied. Here, we synthesize a combined 130 years of census data from wild and captive sea turtle populations across three continents to provide an unprecedented view of aging in this group. Using long-term nesting records for more than 1,800 first-time breeding female green (*Chelonia mydas*) and loggerhead (*Caretta caretta*) turtles from Cyprus, Australia, and the Cayman Islands, we show that sea turtles exhibit negligible but positive actuarial senescence. Across populations, individuals maintain high reproductive viability late into their lives, a finding consistent with other studies on testudines. Captive green turtles had lower aging rates compared to their wild counterparts, with wild loggerheads having similar aging rates to wild green turtles. These findings establish a new empirical baseline for aging in highly fecund long-lived marine ectotherms and emphasize the exceptional capacity of sea turtles to sustain reproduction across extended lifespans, with broad implications for both evolutionary theory and conservation biology.

BASK ME A QUESTION: HONU (*CHELONIA MYDAS*) BASKING TRENDS AT LALO

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Throughout the global range of the green sea turtle, basking on land is an uncommon behavior. One of only a small number of locations where this behavior is documented is in Hawai'i, USA. In Hawai'i, green sea turtles, or honu, are known to frequently haul out on beaches and bask diurnally and also nocturnally. There are a number of theories on why honu utilize basking, ranging from thermoregulation to predator avoidance or even aiding in digestion. A particular area where honu bask in large numbers is at their nesting beaches at Lalo (French Frigate Shoals) in the remote Papahānaumokuākea Marine National Monument, approximately 700 km from the main Hawaiian Islands. At Lalo basking behavior is documented in adults of both sexes as well as occasionally juveniles.

Field biologists at Lalo conduct unique surveys during the nesting season that allow them to tag, measure, and collect tissue samples from basking individuals. This also allows for robust data collection on breeding adult males, which is extremely rare across all sea turtle species. Basking surveys also provide a unique form of re-sight data, helping aid in population monitoring and sex ratio estimations. Aggregations of basking honu allow for the rare opportunity to rapidly collect data on a large number of individuals. These aggregates can even exceed 300 honu on a 0.5 km area of beach. These surveys have revealed interesting trends including the relationship between the number of male and female basking honu, what percentage of turtles display basking behavior, and how this information pertains to the number of nesting individuals. Additionally basking surveys have helped reveal more details on when honu arrive, when they disperse, when their numbers peak at the nesting grounds and also how tidal events can influence the number of basking turtles.

TIMING MATTERS: SEASONAL MIGRATION AND ADAPTIVE GENOMIC PATTERNS IN GREEN TURTLES (*CHELONIA MYDAS*) FROM POILÃO ISLAND, WEST AFRICA*

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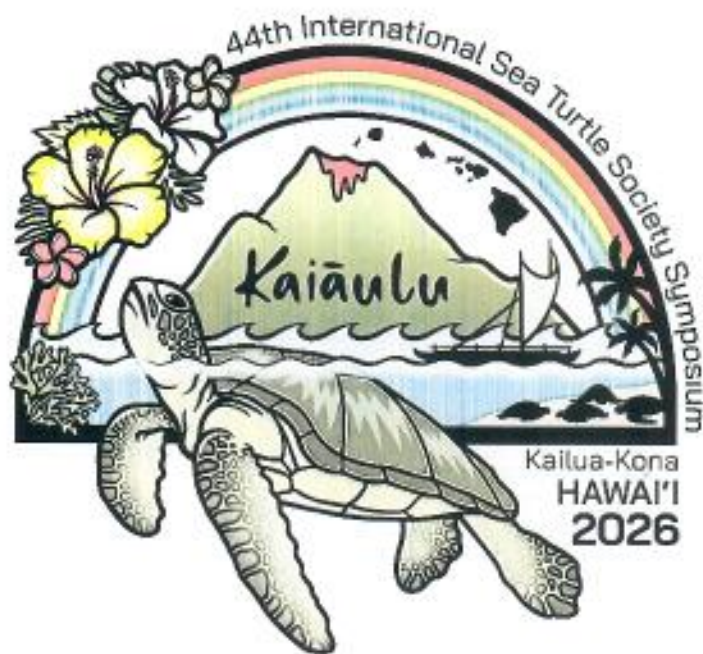
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Sea turtles are highly migratory, with adults cyclically moving between breeding and foraging areas that are often hundreds to thousands of kilometers apart. Variations in migratory patterns have been described in some sea turtle populations. However, genomic and temporal differences within the same population, which play a significant role in explaining migratory patterns in other seasonal migrant species, remain largely unexplored. Additionally, differences in breeding timing can also lead to genetic divergence within seasonal migrant species, have not yet been reported for sea turtles. Advances in genomics allow comparative analyses that can potentially identify genes linked to adaptive behavioral/physiological changes driven by seasonal environmental conditions. This is highly relevant in the face of climate change, as the existence of environmental-associated loci may be key for local adaptations. Poilão Island, Guinea-Bissau, one of the world's largest green turtle (*Chelonia mydas*) rookeries, hosts year-round nesting, with most activity concentrated during the wet season (June to October) and with fewer turtles nesting at distinct periods during the dry season (November to January and January to April). We tracked post-nesting females from Poilão during the main nesting season (from 2018 to 2021; n = 44) and during the dry season (2023 to 2025; n=20), to understand if migration destination varied depending on breeding seasonality. We found that green turtles from the main (wet) nesting season either migrate north, to Mauritania (1000 km north), Senegal and The Gambia (300-400 km north), or stay within 40-90 km of the nesting site, in the Bijagós Archipelago. However, turtles nesting in the early dry season migrated about 2,000 km southeast to forage offshore near Accra, Ghana, while turtles from the late dry season crossed the Atlantic, travelling almost 3,000 km westward to forage in Brazil. These novel insights suggest that Poilão hosts at least three groups of green turtles with distinct breeding phenology and migratory behaviors. To understand the potential genetic and ecological differentiation of the three groups of green turtles breeding in Poilão, we performed a comparative genomic analysis using whole genome sequencing of individuals from each group

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