

($n=24$ in total), including phenotypic variables (i.e. nesting phenology, non-breeding area, body-size, clutch size, reproductive output) and environmental variables (i.e. sea surface temperature at foraging and breeding grounds, oceanic currents at the time of migration, and foraging ground productivity). Through genomic scans of over 25 million SNPs along the genome, and a functional enrichment analysis, we were able to determine whether specific biological functions or pathways are overrepresented among the candidate genes, providing new insights into potential adaptive differences between groups. By combining satellite tracking with ecological and genomic data, our integrative approach has allowed us to better understand the interplay of breeding phenology, migratory movements and genomic variation within one of the world's most important green sea turtle rookery.

DYNAMIC FORAGING LANDSCAPES SHAPED BY BODY SIZE AND GENETICALLY INFERRED NATAL ORIGIN OF GREEN TURTLES IN OKINAWA

Tomoko Hamabata¹, Junichi Okuyama², Nao Yoshida², Kiyoshige Kobayashi³, Yoshimitsu Tsukakoshi⁴, Hideaki Nishizawa⁵, Takeru Nakagawa⁵, Kotaro Ichikawa⁶

¹Advanced Institute For Marine Ecosystem Change, Tohoku University, Japan

²Fisheries Technology Institute, Japan Fisheries Research and Education Agency

³Port of Nagoya Public Aquarium, Nagoya Port Foundation

⁴Sea Turtle Museum of Kumejima

⁵Graduate School of Informatics, Kyoto University

⁶Field Science Education and Research Center, Kyoto University

Seagrass meadows along the Okinawan coast are key foraging habitats for green turtles (*Chelonia mydas*), supporting individuals from multiple natal origins and contributing to coastal ecosystem productivity. These habitats are also crucial for understanding population connectivity and the ecological role of coastal ecosystems under changing oceanographic conditions. Previous studies have shown regional variation in the composition of natal origins and body-size distributions among foraging grounds in Japan. For example, around the Yaeyama Islands of the southern Ryukyus, turtles originating from lower-latitude regions outside Japan are disproportionately represented in smaller size classes relative to individuals of the local Ryukyu origin. Building on these findings, this study investigates whether size-based and natal-origin patterns are consistent across other foraging grounds in Okinawa. We analyzed green turtles from seagrass beds around Kume Island ($n = 162$) and the Miyako Islands ($n = 150$), integrating these data with previously published samples from the Yaeyama Islands ($n = 102$). Natal origin was inferred at the individual level using mtDNA control-region haplotypes and genome-wide nuclear variants, together with straight carapace length (SCL) as a proxy for growth stage. Individuals were assigned to three natal regions: the Ogasawara Islands, the Ryukyu Archipelago, and the lower-latitude Northwest Pacific outside Japan (including Southeast Asia, Micronesia, and the Marshall Islands). Our analyses revealed clear differences in natal-origin composition among the three foraging grounds. Turtles originating from the lower-latitude Northwest Pacific were most frequent in the Yaeyama Islands, located at the upstream end of the Kuroshio Current. However, their contribution did not decrease monotonically with downstream distance: the proportion of lower-latitude individuals in the Miyako Islands was comparable to that observed in Kume Island, despite Miyako being geographically adjacent to Yaeyama. Furthermore, size-specific histograms constructed for each natal origin revealed clear, origin-dependent constraints on body-size distributions: Ryukyu-origin individuals were concentrated in smaller size classes in Kume and Miyako, and lower-latitude individuals consistently peaked at 45–50 cm across all sites. These results demonstrate that the structure of foraging aggregations cannot be explained by geography or current flow alone, but instead reflects a complex coupling between natal origin, growth stage, and habitat selection. By enabling

individual-level natal assignment, we move beyond population-level averages and reveal fine-scale, size-dependent structuring within foraging aggregations in the Northwest Pacific.

STABLE ISOTOPE RATIOS THROUGHOUT THE DECOMPOSITION OF KEMP'S RIDLEY (*LEPIDOCHELYS KEMPII*) SEA TURTLES

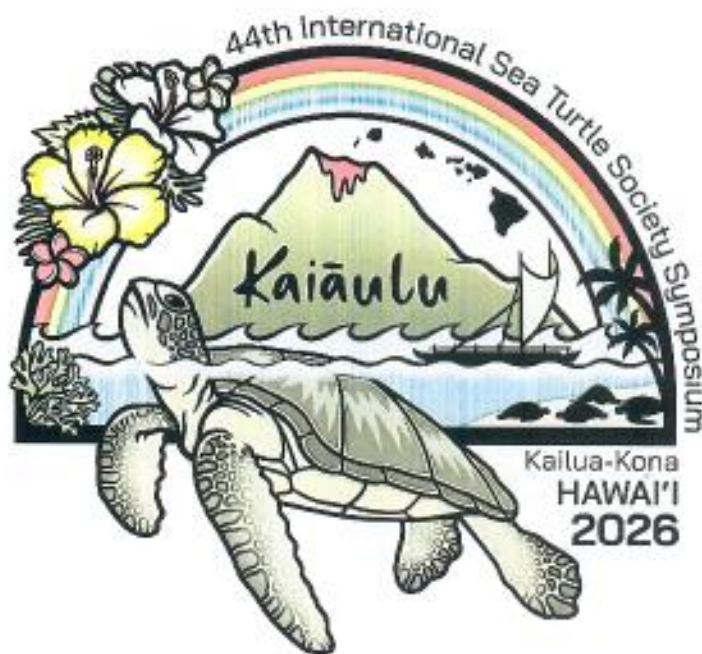
Jessica Hufham^{1,2}, Jamie Clark^{1,2}, Matthew Ramirez^{1,2}

¹Department of Biology and Marine Biology, University of North Carolina Wilmington, Wilmington, North Carolina, United States of America

²Center for Marine Science, University of North Carolina Wilmington, Wilmington, North Carolina, United States of America

Stranded sea turtles can provide a vast amount of ecological data that are otherwise difficult to collect from these migrating threatened and endangered species. For example, stable isotope analysis (SIA) is a critical tool in population ecology and is often applied on collected tissues from stranded or deceased sea turtles to illuminate various aspects of an animal's life history, such as foraging and movement patterns. While collecting these samples, it is important to acknowledge the range of body conditions responders encounter while working with stranded sea turtles. For deceased sea turtles, the decomposition process may alter stable isotope values as tissues break down. Previous research in sea turtles and other marine megafauna suggest that stable isotope ratios in skin and muscle are largely invariant over long periods of the decomposition process, but no study has evaluated this process in sea turtle carcasses subject to field conditions that mimic the natural stranding process (e.g., tidally influenced). Stable carbon ($\delta^{13}\text{C}$) and nitrogen ($\delta^{15}\text{N}$) isotope ratios were analyzed from seven decomposing Kemp's ridley (*Lepidochelys kempii*) sea turtles who stranded in the state of North Carolina. For this study, carcasses were secured within fine mesh cages, positioned along three inundation levels in the intertidal zone of a marsh at the University of North Carolina Wilmington's Center for Marine Science. Skin samples were retrieved at low tide with a 5mm punch from the back of the neck, if available, on known decomposition intervals (Day 0, 1, 3, 5, 7, 9, 11, 13) over the span of 13 days. All turtles fully decomposed naturally within this time period. The epidermis layer was separated, freeze dried, and ground into a homologous powder. Samples were then run on a Thermo Delta V Plus continuous-flow mass spectrometer paired with a Costo 4010 elemental analyzer to quantify $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values. We will use time series statistical analysis to identify significant breakpoints in each turtles' isotopic record over time, providing clarity on how stable isotope data change in relation to stranding conditions. By examining SIA values through the decomposition process, this study can help validate under what conditions researchers can obtain reliable and accurate SIA data from dead stranded turtles.

PROCEEDINGS OF THE FORTY-FOURTH SYMPOSIUM ON SEA TURTLE BIOLOGY AND CONSERVATION



February 28 – March 6, 2026
Kailua-Kona, Hawai'i, USA

Compiled by:
Paul A. Whittock, Lisa C. Belskis, & Joseph B. Pfaller

June 2026