

NEW GENETIC INSIGHTS INTO THE NORTH PACIFIC LOGGERHEAD'S KEY FORAGING GROUND

Hugo David Gallardo Sánchez¹, Omar Horacio Sol Torres¹, Luz Estrella Hernández Hernández², Alan Alfredo Zavala Norzagaray², Alonso Aguirre⁶, César Paúl Ley Quiñónez³, Eduardo Reséndiz^{4,5}, Roldán A. Valverde^{7,8}, Fátima Yedith Camacho Sánchez², José Alberto Narváez Zapata⁹, Bryan P. Wallace^{10,11}, Miguel Ángel Reyes López¹

¹Instituto Politécnico Nacional, Mexico

²Universidad Autónoma de Tamaulipas UAM Reynosa-Aztlán, Tamaulipas, Mexico

³IPN-CIIDIR Sinaloa, Blvd. Juan de Dios Bátiz Paredes 250, Col. San Joachin, Guasave, Sinaloa, México

⁴Grupo Tortuguero de las Californias A.C., Calle Seis No. 141, Col. Azaleas, La Paz B.C.S., México

⁵Departamento Académico de Ciencia Animal y Conservación del Hábitat, Universidad Autónoma de Baja California Sur (UABCS), La Paz, México

⁶Michael Smith Natural Resources Building, Colorado State University School of Earth, Environmental, and Marine Sciences, The University of Texas Rio Grande Valley, Texas, USA

⁷School of Earth, Environmental, and Marine Sciences, The University of Texas Rio Grande Valley, Texas, USA

⁸Sea Turtle Conservancy, Gainesville, Florida, USA

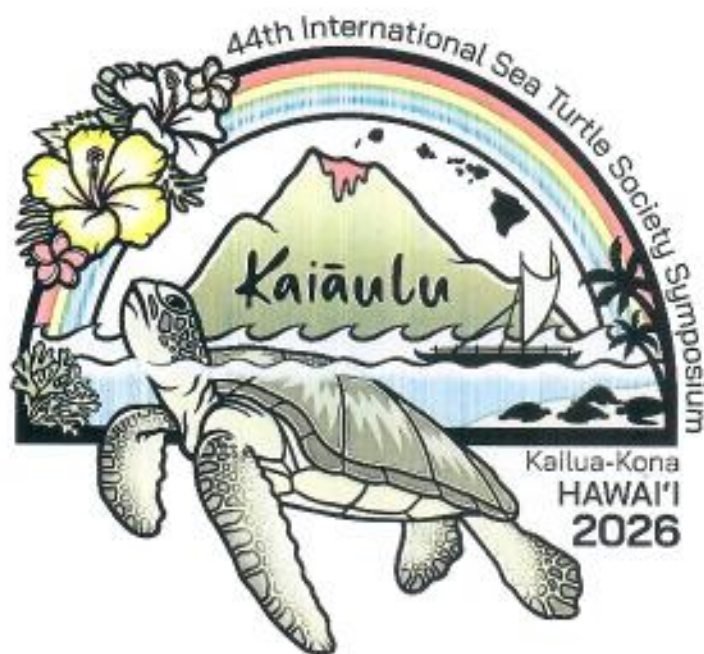
⁹Centro de Biotecnología Genómica, Instituto Politécnico Nacional, Tamaulipas, Mexico

¹⁰Ecolibrium, Inc., Boulder, CO 80303, USA

¹¹Department of Ecology and Evolutionary Biology, University of Colorado Boulder, Boulder, CO 80302, USA

The North Pacific loggerhead sea turtle (*Caretta caretta*) RMU, which nests exclusively in Japan, depends critically on the foraging ground in Baja California Sur (BCS), Mexico. This area is a hotspot for juvenile turtles, but also for bycatch mortality. Genetic characterization of this key aggregation has been severely limited, relying on a single study from 1995 and short mtDNA fragments, obscuring effective conservation and monitoring. To address this, we present a contemporary genetic analysis of the BCS loggerhead hotspot using 77 blood samples collected from juveniles at the epicenter distribution in front of Adolfo López Mateos Port. Standard genetic differentiation and diversity statistics were estimated to update the North Pacific and BCS genetic landscape employing 533 novel and worldwide mtDNA control region sequences (837 bp and 370 bp). By applying a longer, 837 bp fragment, we uncovered significantly higher haplotype diversity than previously reported with standard ≈ 350 bp markers in BCS, highlighting a critical need for standardized molecular protocols in the Pacific. Our analysis confirms the presence of key haplotypes (including CcP2.1, CcP2.3, and CcP3.1) linking this foraging ground to the nesting rookeries in Japan. This work bridges a 30-year genetic data gap and provides a crucial baseline for monitoring this vulnerable population. We propose a new, standardized haplotype nomenclature for the Pacific. Our findings form the foundation for ongoing work and underscore the immediate need for Mexico-Japan policy partnerships for addressing research gaps and informing and directing effective conservation strategies.

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