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Xochitl de La Rosa and professors Luis A. Hurtado and Mariana Mateos are studying conservation genetics aspects of the Kemp's ridley sea turtle with cutting edge genomics methodologies. The Kemp's ridley is the world's most endangered sea turtle, and has one of the smallest distributions among sea turtles, confined mainly to the Gulf of Mexico. Most (> 90%) of the Kemp's Ridley nesting occurs along a short (~78-mile) shoreline stretch in the Mexican border state of Tamaulipas, where the 16-mi long Rancho Nuevo site alone hosts the highest number of nests per season (~80%). In the US, most nesting occurs on the Texas coast, with Padre Island National Seashore (PAIS) hosting the highest number of nests (~1000 between 2002 and 2015). After experiencing a severe and sustained bottleneck that put this species on the verge of extinction, it appeared to be rebounding successfully, following decades (since 1978) of Mexico-US bi-national efforts aimed at its recovery. Unfortunately, nesting was severely reduced by ~ 35% during 2010, the year of the BP Deepwater Horizon oil spill in the Gulf of Mexico, as compared to 2009. Although nesting rebounded in 2011 and 2012 to levels similar to 2009, nesting declined drastically again during 2013 and experienced a further drop during 2014. Should nesting continue to decline, long-term species recovery efforts will be compromised.

Therefore, there is deep concern about the future of the Kemp's ridley, and data to inform and assess bi-national management and conservation measures are urgently needed. Population genetics information crucial to the long-term conservation of the Kemp's ridley, including baseline data required for monitoring its future status, is lacking.



Sampling for genetic analysis project in the Sanctuary Playa de Rancho Nuevo (in the image Xochitl de la Rosa from College Station Texas A & M, and Victor Ontiveros from Universidad Autonoma de Tamaulipas).

These studies, however, have been severely limited, due to: (1) the complex logistics associated with sampling in the remote main nesting beaches and the burden of securing related permits; and (2) the paucity of informative genetic markers. Last year, we used cutting edge genomics methods and discovered >30,000 single nucleotide polymorphisms (SNPs) that represent genome-wide variation in the Kemp's ridley. We will apply this powerful technique to hundreds of specimens we sampled during 2014 and 2015, as well as new samples we will collect in the next nesting seasons. This conservation genomics study will gather important baseline information for long-term monitoring of this critically endangered sea turtle, including estimations of genomic diversity, effective population size, number of breeders, assessment of levels of population differentiation, and detection of genomic signatures of bottlenecks. The research involves collaborations from multiple institutions and agencies in Mexico and the US and is funded by grants from Texas Sea Grant and the TAMU-CONACyT Program.

The governmental institution in Mexico in charge of conserving the most representative ecosystems of Mexico and its biodiversity is the **Comisión Nacional de Áreas Naturales Protegidas** (CONANP) <http://www.conanp.gob.mx/>.



Protected turtle nest nursery in the Sanctuary Playa de Rancho Nuevo (in the image Xochitl de la Rosa from College Station, Texas A&M, and Victor Ontiveros from Universidad Autonoma de Tamaulipas).

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