Conservation Genetics of the Critically Endangered Kemp's Ridley Sea Turtle: An Opportunity for Urgent Bi-national Research

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Introduction
- The Kemp's Ridley sea turtle (Lepidochelys kempi) is listed as Critically Endangered by the IUCN.
- It has the most restricted distribution among the seven species of marine turtles (Gulf of Mexico and Atlantic US coast).
- 90% of the nesting occurs in a short stretch (~78 miles) of the Texas coast (Figure 1).
- In the US, most nesting occurs in the Texas coast, with Padre Island National Seashore (PINS) hosting the highest number of nests (6200 between 2013 and 2014).
- Nonnursery users of the entire Gulf of Mexico coastline, in the US and Mexico, are important for migration and foraging of this species.
- This sea turtle has been the focus of decades of bi-national Mexico-US conservation efforts that began after this species experienced dramatic population declines.
- Since the late 1990s, after decades of bi-national conservation efforts, the species was progressively rebounding successfully (Figures 2 and 3).
- Unfortunately, in 2013, the year of the BP oil spill in the Gulf of Mexico, the population experienced a severe reduction in the number of nests in both Texas and Mexico (Figure 2).
- There is deep concern about the future of this species, and data to inform and assist bi-national conservation management and conservation measures are urgently needed.
- Genetic studies will provide useful information that can greatly enhance the conservation of this important sea turtle.

Objective
To use genome information to determine the current genetic variability of the Kemp's Ridley, as well as signatures of past bottlenecks, effective population size, number of breeders per reproductive season, levels of population differentiation, and estimation of the number of breeders through genome identification, in this species.

Materials and Methods
- Blood and skin samples were collected from individuals in the Texas coast and the main nesting locations in ‘Tampalajá’ and ‘Cáscara’ in Mexico (Figure 4).
- To understand the genetic diversity and structure of the population, we used the whole-genome restriction-site-associated DNA sequencing (WGS-RAD-seq) method (Puritz et al. 2012) to survey the genome of the Kemp's Ridley for single nucleotide polymorphisms (SNPs).
- Quality control and SNP discovery using Tassel (10,000 SNPs discovered). We analyzed these SNPs to infer population structure, genetic diversity, and breeding relationships among the populations.
- Conducted population genetics analyses using SNPs and microsatellite information.

Preliminary Results
- The analysis revealed all necessary steps for sampling, genotyping, and SNP discovery (10,000 SNPs discovered) (Figure 5).
- The analysis revealed the genetic diversity and structure of the population, and the relationships among the populations.
- Conducted population genetics analyses using SNPs and microsatellite information.

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Samples
- We have collected samples in the Texas coast and Tampalajá from three nesting seasons: 2010, 2014 and 2016 (Figure 1; Table 1).

Table 1. Location and sample size of Kemp’s Ridley sea turtle in three nesting seasons.

<table>
<thead>
<tr>
<th>Nesting Season</th>
<th>Sample Size</th>
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<tbody>
<tr>
<td>2010</td>
<td>100</td>
</tr>
<tr>
<td>2014</td>
<td>120</td>
</tr>
<tr>
<td>2016</td>
<td>130</td>
</tr>
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Figure 1. Sampling sites of Kemp’s Ridley sea turtle in Texas, Tampalajá, and Veracruz.

Figure 2. Haplotype diversity of Kemp’s Ridley sea turtle in Tampalajá.

Figure 3. Nesting counts of Kemp’s Ridley sea turtles in Tampalajá.

Figure 4. Reliable and with variation collected at adult females and adult males.

Figure 5. SNPs found using the WGS-RADseq technique in 44 individuals, 16 females and 28 males, collected in Texas in 2016. A total of 190,000,000 reads was obtained with an average of 20,000,000 reads per sample.

References

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