Evolutionary History of Two Leatherback Turtle Lineages in The Eastern Pacific: Insights from Genomics, Morphometry and Local Ecological Knowledge

Progress Report I

Figure 1. Photograph of me with a leatherback turtle.

Credits to Filiberto González.

Carlos Abraham Castillo Morales

El Colegio de la Frontera Sur

03-June-25

1. Progress

This project is a continuation of our previous work, which also received support from the Rufford Foundation. Previously, through mitochondrial DNA (mtDNA) analysis and local ecological knowledge (LEK), we found that there may be more than one group of leatherback turtles (*Dermochelys coriacea*) in the Mexican Pacific. Through LEK, we discovered that some local residents who have closely interacted with these animals recognize two varieties of leatherback turtles.

We later published our findings in a scientific article in *Scientific Reports*, and a group of Brazilian colleagues suggested that the genetic differences observed could be due to the presence of nuclear mitochondrial DNA segments (NUMTs) in the population. A NUMT is essentially a copy of an mtDNA fragment that migrates to the nucleus and inserts into the nuclear genome. Therefore, two different regions are being compared, which would explain the observed differences.

However, many questions remain unanswered, such as:

- Is the NUMT present in all individuals or only in some?
- Does this have evolutionary and/or adaptive implications?
- What are the conservation implications for leatherback turtles?
- What are the differences between the morphotypes described through LEK?
- Are there adaptive differences between each of the morphotypes?

We are currently conducting a deeper analysis using genomics, morphometrics, and LEK to determine the differences between the two groups and what these differences mean in terms of adaptation and conservation for leatherback turtles. We also aim to determine whether these differences are purely morphological or if there is a deeper underlying cause.

Fieldwork for this project began in December 2024 on the coast of Oaxaca, Mexico. We visited the communities of Barra de la Cruz and Cahuitán, two of the country's most important nesting beaches for this species. In Barra de la Cruz, we collected samples from 12 turtles, and in Cahuitán, we collected 8 samples. For each turtle, we took a tissue sample for genomic analysis and recorded morphometric measurements. Additionally, during some of the field trips, we were accompanied by a local expert who identified whether each turtle belonged to group 1 or group 2.

Figure 2. Me taking measures of a leatherback turtle.

Credits to Filiberto González

After fieldwork, we took the samples to the genetics lab at El Colegio de la Frontera Sur to extract DNA. We are currently in the process of obtaining the necessary permits to send the DNA samples for sequencing. Once we have them, we will be ready to begin the genomic analyses and continue this research.

2. Obstacles to the Original Plan

The only obstacle we've encountered so far in this project is that it was impossible to take high-quality photographs for geometric morphometric analysis. As a result, we have decided to discard the geometric morphometric analysis. However, we did take body measurements to conduct linear morphometric analysis, which should be sufficient for carrying out this project.

3. Plans for the Future

The next steps for this research are to sequence 10 whole genomes to compare them and determine whether there are genomic-level differences in this turtle population. We will also analyze the morphometric data obtained during fieldwork. Finally, we will generate 40 reduced-representation genomes (GBS) to gather data on gene flow, inbreeding, adaptive genes, effective population size, genetic diversity, and other important metrics. From all this information, we plan to publish at least two scientific articles in high-impact journals.

Figure 3. A nesting leatherback turtle.

Credits to Filiberto González