Determining Phylogeny of *Salminus brasiliensis* Using COI Gene

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Introduction and Goals

- Neotropical system
  - Biodiverse and a large source of speciation.
- Golden Dorado (*Salminus brasiliensis*)
  - Large, predatory species that is of high recreational value
  - Its genus has a history of taxonomic uncertainty

The goal of this project is to characterize the COI MT gene variation of Golden Dorado across the two major water basins in South America.

- COI gene
  - Marker commonly used for DNA barcoding
  - Used in this project to determine the phylogeny of *S. brasiliensis.*

Due to a history of isolation between Golden Dorado populations, I hypothesize that we will detect genetic differences based on the water basin they inhabit.

Materials and Methods

Legend:
Blue polygon – Amazon River Basin
Pink polygon – La Plata River Basin
Blue stars – Bolivian GD samples
Pink Stars – Argentinian GD samples

Figure 1: Map highlighting the study area of this project. The polygons highlight each river basin, while the stars show the sample collection sites.

- Samples were collected both from the Amazon and the La Plata River Basins.
- In total, 25 samples were collected for this project.

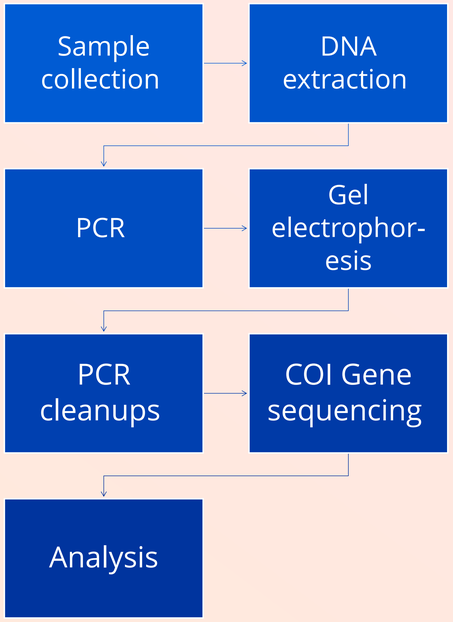

Figure 2: Workflow of methods used in this project.

Results

- A working thermocycler profile was created after several weeks of PCR troubleshooting. We obtained successful amplification of the target COI gene sequence as visualized using gel electrophoresis. Bands on the gels were consistently bright and at the correct base pair length (*see figure 5*). Expected PCR product size is 460 – 669bp.

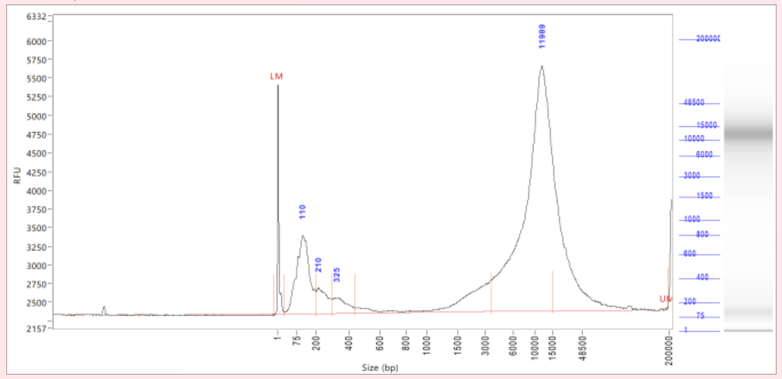

Figure 3: A successful fragment analyzer run of a GD sample used in this project. Fragment sizes larger than 1000 bp (largest peak) indicate high molecular weight and large fragment DNA obtained from fin clip sample.

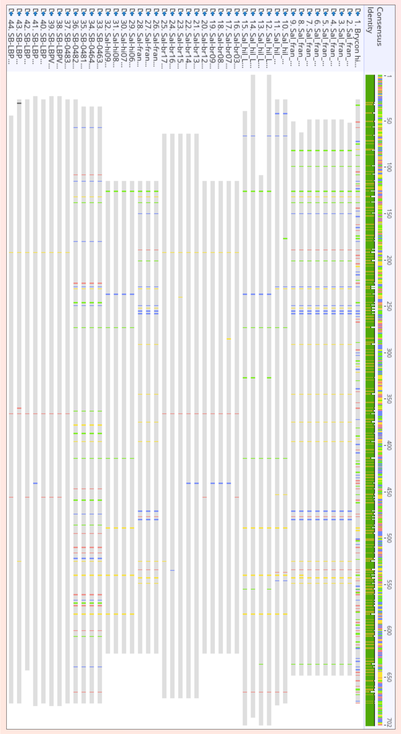

Figure 4: A GD MT DNA sequence alignment that shows multiple similarities in Golden Dorado from similar locations. 44 sequences were used. Sequences were downloaded from NCBI (Rosso et al., 2018).

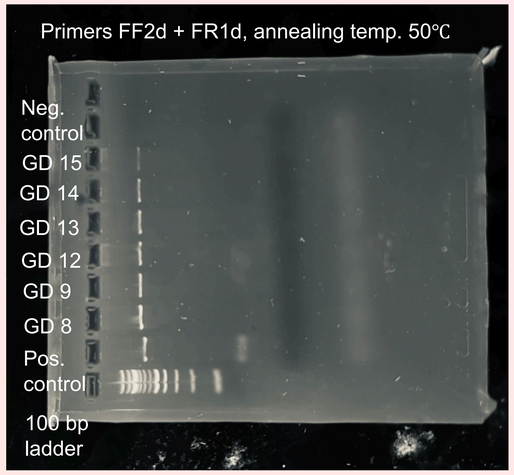

Figure 5: An agarose gel using PCR product from Bolivian Golden Dorado samples. This gel shows successful amplification (note the bright bands at correct bp length).

Next Steps

- Once PCR cleanups have been performed on all PCR products, the products will be sent to Molecular Biology Core Labs in Worcester, MA to sequence the COI gene.
- Returned sequences will be aligned using the computer software Geneious Prime.
- Alignments will be analyzed for haplotype diversity within and between the two groups.
- Results will be shared with collaborators in Bolivia.

Literature Cited

Rosso JJ, Rueda EC, Sanchez S, et al. Basin-scale distribution and haplotype partitioning in different genetic lineages of the Neotropical migratory fish Salminus brasiliensis. Aquatic Conserv: Mar Freshw Ecosyst. 2018;28:444-456. https://doi.org/10.1002/aqc.2830

Acknowledgements

I would like to thank the CAFE Summer Scholars Program for funding this project. I'd also like to thank Nadia Fernandez and Dr. Lisa Komoroske for guiding and supporting me throughout this project and the other work I conduct in the Molecular Ecology and Conservation Lab.