

Is there a distinct lineage of Atlantic Spotted dolphins in Southwestern Atlantic Ocean? Insights from genomics and ecological approaches

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The Atlantic spotted dolphin (*Stenella frontalis*) is endemic to tropical, subtropical and warm temperate waters of the Atlantic Ocean. The species has a complex geographical distribution, across which population structure has been recovered and it is most likely the result of distinct environmental requirements. Genetic, morphologic and ecological evidence indicate that Atlantic spotted dolphins from the Southwestern Atlantic may constitute a distinct population and deserve protection.

During the period of the project (2016 – 2017), I was able to get 108 samples of *S. frontalis* from different regions of Atlantic Ocean, including Brazil (n=80), Colombia (n=7), Guadeloupe Island (n=1), Uruguay (n=1), and Canary Island (n=19). I planned to include in my analysis samples from other regions through collaboration, but for several reasons, it was not possible.

These tissue samples were used in two different approaches after DNA extraction: 1) I amplified a portion of 650 bp of the mitochondrial control region (CR mtDNA) through the primers t-Pro-whale M13Dlp1.5 (5' TGTAACACGACAGCCAGTTCACCCAAAGCTGRARTTCTA-3') and Dlp8 (5'-CCATCGWGATGTCTTATTTAAGRGGAA-3') following the protocol by Tezanos-Pinto et al., (2008); and, 2) I selected just those samples with high quality and high DNA concentrations (<400 ng of DNA) and I followed a well-established protocol of Double digest restriction-site associated DNA (ddRADseq) (Peterson et al. 2012) in order to build a genomic library of Atlantic Spotted dolphin. This library was built in the Ecology & Evolutionary Biology Department of the University of Michigan.

The CR mtDNA data were analyzed with other sequences of *S. frontalis* gathered from GenBank. In total, I compiled 545 sequences of CR mtDNA, being 80 sequences resulting of my PCR amplification that included individuals that were never analyzed before (for example, those samples from Canary Islands and Uruguay). I had geographic information for all these sequences, therefore this dataset was analyzed on the basis of seascape genetics. I investigated population differentiation of Atlantic spotted dolphin along Atlantic Ocean and its relationship with the marine environment. In relation to genetic structure, our results were in agreement with those already proposed for different populations in Western North Atlantic and Gulf of Mexico. We also confirmed that individuals that occupied oceanic islands in the Eastern Atlantic form one population connected with those from oceanic waters of Western North Atlantic. Individuals recorded in the Atlantic waters of South America deserve further studies to completely understand the genetic structure and its relationships with others populations, but we suggested so far that individuals from southeastern Brazil represent one distinct population and exhibit low levels of genetic diversity based on CR mtDNA marker. We had detected some level of Isolation-by-distance and Isolation-by-Resistance. We attributed the low levels of correlation between genetic and geography/environment due to such large-scale analyzed here and we also hypothesized that different process could play a role to explain the genetic patterns recovered such as social structure and some level of philopatry within populations. Currently, the manuscript presenting these results is under review and it will be part of my thesis.

Genomic data of *S. frontalis* is still under analyses. Specifically, I obtained genomic data from Southwestern Atlantic Ocean (Brazil and Uruguay), Caribbean (Colombia and Guadeloupe Island) and Eastern Atlantic (Canary Islands). My preliminary results are very interesting and suggest some

level of differentiation among these regions. However, the differentiation level seems to be not related to geographic distances. I believe that these results are very important to understand how the species is structured in the South Atlantic. At this point, I'm working to finish the analyses of this dataset and I'm writing the manuscript. This manuscript will be part of my thesis too.

Some preliminary results, I presented as a poster at the SMM Biennial Conference at Halifax, Canada.

I am very grateful to the Society for Marine Mammalogy for supporting part of my project. I believe that this kind of support is very important for us students be able to perform high-quality studies and to promote conservation of marine mammals.