

Final Report - SMM Grants in Aid of Research 2022

Genomic investigation of offshore *Tursiops truncatus* populations in archipelagos of the Atlantic and Pacific Oceans

Awardee: Brenda Godoy Alexandre (Msc, PhD student)

Laboratory of Cytogenetics and Animal Evolution, Department of Genetics, Federal University of Rio Grande do Sul (UFRGS), Porto Alegre, Brazil.

brendagalex@gmail.com

The common bottlenose dolphin (*Tursiops truncatus*) has worldwide distribution in temperate and tropical waters; differences in morphology and genetics reveal two distinct ecotypes, inshore and offshore. Offshore populations are more challenging to study and, thus, have not been investigated deeply. Oceanic ecotype has been found to show large population sizes, high genetic diversity and low population structure. Using genomic techniques, we aim to improve the knowledge about the population structure and connectivity patterns of offshore populations of *T. truncatus* in the Atlantic Ocean. Here, we used 70 samples from individuals across the São Pedro São Paulo Archipelago (SPSPA, Brazil); Azores, Madeira and Canary Islands (Macaronesia Region, Portugal and Spain respectively); the Revillagigedo Islands (Mexico), and individuals sampled in the Brazilian middle and outer continental shelf and in the shelf break. We used double-digest restriction site-associated DNA sequencing (ddRAD-seq), resulting in 22,413 single-nucleotide polymorphisms (SNPs) across all individuals. Population structure analyses, such as Principal Component Analysis (PCA) and clustering algorithms (FastStructure) revealed three major clusters: (1) SPSPA, (2) the other samples from Brazilian waters, and (3) populations from Macaronesia and Mexico. Our results indicate that the samples with the highest genetic diversity are the Azores, while the lowest values were from the SPSPA sample. Additionally, inbreeding levels were investigated by detection of runs of homozygosity that showed that SPSPA had higher levels of individual homozygosity than other populations. This study suggests a level of genetic isolation of SPSPA from other offshore populations, which should be considered and carefully discussed. In order to evaluate how environmental variables shaped genetic structure found in our dataset a seascape genomic approach will be used. These are preliminary results, other analyzes are being carried out to finalize this scientific article for subsequent publication in a scientific journal. Our work contributes to advancements in the population genetics field of the offshore ecotype, and these findings will support the conservation actions needed to protect the small and resident SPSPA population. I intend to present the final results of this research in 2024 at the 25th biennial of the Society of Marine Mammalogy.