

**Applying biochemical and molecular tools to assess metabolic characteristics in wild marine *Tursiops truncatus* from different subspecies**

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This study aims to investigate if offshore (OF) and coastal (CO) *Tursiops truncatus*, the latter recently defined as the subspecies *Tursiops truncatus gephyreus*, present distinct profiles regarding lipid metabolism, xenobiotic detoxification and antioxidant status, further elucidating the extent of habitat overlap between the subspecies and their exposure to anthropogenic pollutants. The funds made available by this grant were used for acquiring primers and chemical reagents for the quantification of molecular biomarkers. Among the target genes, only *MHCII* transcript levels did not vary between the subspecies ( $p > 0.05$ ). The transcript levels of *MT2A* were significantly higher in coastal *T. truncatus* ( $p < 0.01$ ), suggesting higher metal exposure in the coastal areas. Higher *ILa* transcripts of coastal dolphins ( $p < 0.05$ ) indicates higher immune activity, probably associated to their usage of areas impacted by domestic sewage, a source of pathogenic microorganisms. Regarding genes involved in lipid metabolism, *FASN1* transcript levels were higher in offshore dolphins ( $p < 0.01$ ), while *CERS3B* and *ELOVL4* transcript levels were higher in coastal animals (*CERS3B*:  $p < 0.05$ ; *ELOVL4*:  $p < 0.01$ ). Such results suggest differences in the lipid composition of skin/blubber from coastal and offshore dolphins with a more prominent synthesis of ceramides and very long chain fatty acids in coastal dolphins. The next steps for this study include quantifying the activity of the enzymes SOD, GPx, GR, G6PDH and AchE, which has not yet been accomplished due to the working restrictions imposed in light of the COVID-19 pandemic.