Terceira Sessão: Conservação e áreas afins – Comunicações orais

Unveiling exotic and invasive species in marine protected areas using environmental DNA (eDNA)

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Marine biological invasions are a significant threat to global biodiversity, triggering negative impacts on native ecosystems. Managing non-native species is increasingly challenging as organisms progress through different stages of invasion. Thus, early detection is a critical tool to establish procedures to prevent their spread. Recent methodologies, such as the metabarcoding of environmental DNA (eDNA), has proven to be an efficient tool for detecting non-native species, overcoming limitations of visual methods. In Brazil, the southeastern region harbors the largest port of Latin America and also the highest number of recorded exotic and invasive species. More specifically, 73 exotic species are recorded along the São Paulo coast, including 10 that are known to occur in the Tupinambás Ecological Station and the Wildlife Refuge of the Alcatrazes Archipelago. Here we used eDNA samples to identify non-native species within the Archipelago. Water and sediment samples were collected from 25 sites and two gene regions targeting a wide diversity of marine metazoans, a fragment of cytochrome oxidase I (COI) and the hypervariable region V4 of the minor subunit of nuclear ribosomal DNA (18S), were amplified and sequenced. The study focused on high reliability of taxonomic assignments, with only assignments having 100% percent identity and a minimum score of 400 being retained. Among the non-native species identified there are four (i.e., Temora turbinata, Megabalanus coccopoma, Carijoa riisei, and Ophiactis savignyi) of which all but C. riisei were not previously known for Alcatrazes and might be the first record in the archipelago. It is important to highlight that for the 150 non-native species cataloged in Brazil, only 90 and 62 species had available data at the NCBI database for the COI and 18S, respectively. Such limitations highlight the need to expand and improve genetic databases to strengthen the potential of eDNA as an early detection tool.

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