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PROKARYOTIC MICROBIAL DIVERSITY FROM MARAMBIO AND CLEAR WATER MESA ISLAND, ANTARCTICA

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The Antarctic benthic areas that receive sufficient solar radiation are covered by microbial mats. For thousands of years, these microorganisms have been exposed to extreme conditions, such as low temperatures, freeze-thaw cycles, UV radiation, varying salinities, and nutrient concentrations. In this context, many of them have developed adaptations, and as a result, potential microorganisms from endemic taxa, as well as unidentified organisms, may still be discovered. In the James Ross Archipelago (JRA), terrestrial vegetation is limited to lichens and bryophytes, whereas microbial benthic mats are composed of algae and cyanobacteria. However, only a few studies have investigated microbial diversity using high-throughput sequencing technologies. Studies from our group have described the diversity and community structures of microbial mats from Marambio and Vega Islands; however, a comprehensive overview of JRA is still lacking. To address this gap, our study focuses on the prokaryotic diversity of microbial mats from three lakes on Marambio Island and 15 lakes on Clear Water Mesa Island using 16S rDNA gene amplicon sequencing (Illumina Novaseq). Preliminary results indicate that Proteobacteria is the most abundant phylum, with variations observed in the Cyanobacteria (with Oscillatoriales as the predominant order), Bacteroidetes, and Acidobacteria phyla. These differences in abundance could be related to the physicochemical characteristics of the lakes, such as high pH values, organic matter content versus inorganic carbon content, and trace metal concentrations. As these communities are among the first to colonize the soil following the retreat of ice, our multidisciplinary investigation (geomicrobiology) contributes to a deeper understanding of pristine Antarctic ecosystems. By establishing a foundational dataset on lake systems, our study lays the groundwork for future research examining the impacts of climate change.

Palabras clave: Microbial mats, bacteria, amplicon sequencing, microbial ecology