



CONNECTING PEOPLE AND INTEGRATING DATA, RESOURCES AND IDEAS ACROSS LATIN AMERICA: THE MSUDAQUA COLLABORATIVE NETWORK OF AQUATIC MICROBIAL ECOLOGY

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Latin America contains nearly one-third of the world's freshwater resources, encompassing broad environmental gradients and exceptional aquatic diversity distributed across unique biomes. Founded in 2017, the μ SudAqua network connects researchers and students in aquatic microbial ecology across Latin America with the goal of strengthening collaborations and uniting efforts to investigate microbial ecology in diverse aquatic ecosystems throughout the region. Over the years, the network has organized workshops, webinar series, and working groups focused on emerging questions across multiple spatiotemporal scales, promoting integrated regional studies on the functioning of the microbial world along environmental gradients. Among its main activities are the integration and standardization of methodologies, combining multi-omics, flow cytometry, environmental analyses, and comparative ecological studies. The network also contributes to the development of sampling and data-processing protocols, as well as the establishment and maintenance of long-term regional observatories for monitoring aquatic ecosystems. Given that most studies on inland aquatic ecosystems have been conducted in the Northern Hemisphere, important gaps remain in the global understanding of microbial diversity



patterns. Addressing these gaps requires integrating published and unpublished sequencing data from diverse aquatic systems, an effort undertaken by the μ SudAqua network. This work has resulted in the μ SudAqua [db] version 2, a 16S rRNA amplicon database with more than 850 georeferenced samples. One of our ongoing studies aims to identify biogeographic patterns of bacterioplankton through the reanalysis of μ SudAqua [db] integrated with more than 500 samples from eastern Canada data (CarBBAS database - Quebec). Our results reveal novel microbial communities in newly added μ SudAqua [db] samples and clear biogeographic patterns, including high spatial heterogeneity, significant ecoregional differences, and contrasting population distributions. These results highlight the importance of integrating contrasting databases to advance our understanding of microbial diversity at different scales. They also highlight the key role of open, collaborative research at the continental scale in the advancement of microbial ecology and environmental sciences in Latin America.

Palavras-chave: *bacterioplankton; amplicon sequencing; biogeography*