

First-ever described Virome of the Amazonian Lake Bolonha: contributions to the understanding of water-related public health concerns

Bruna Verônica Azevedo Gois, Kenny da Costa Pinheiro, Andressa de Oliveira Aragão, Ana Lidia Queiroz Cavalcante, adriana ribeiro carneiro folador, Rommel Thiago Jucá Ramos, Wylerson Guimarães Nogueira

*UFPA - UNIVERSIDADE FEDERAL DO PARÁ/GEAM, Universidade Federal do Pará
-UFPA, UNIVERSIDADE FEDERAL DE MINAS GERAIS, UNIVERSIDADE
ESTADUAL DA PARAÍBA, UNIVERSIDADE FEDERAL DO PARÁ,
UNIVERSIDADE DO ESTADO DO PARÁ*

Abstract

The availability of safe water supplies and adequate sanitation is vital to protect populational health and is one of the basic human rights, according to the World Health Organization. Despite the importance of water supplies, the understanding of the ecology of freshwater viruses still lacks an in-depth description of its diversity, as well as the microbiological interactions that occur in these environments. The Amazonian Lake Bologna, from Belém, capital of the Brazilian State of Pará, is a key source of water that supplies the city and all of its metropolitan region, yet it remains unexplored regarding the contents of its virome and viral diversity composition. Therefore, this work's main aim is to clarify in terms of taxonomic diversity the species of DNA viruses that are present in this lake, especially bacteriophages and cyanophages, since they can act both as transducers of resistance genes and reporters of water quality for human consumption. For this work, we used the metagenomic sequencing data generated by Alves et al. (2020), and we analyzed it at the taxonomic level using the tools Kraken2, Bracken, and Pavian. Later, the data was assembled using Genome Detective, which performs the assembly of viruses. The results observed in this work suggest the existence of a widely diverse viral community and an established microbial phage regulated dynamics in the Lake Bolonha. This work is the first-ever to describe the virome of Lake Bolonha using a metagenomic approach based on high-throughput sequencing, as it contributes to the understanding of water-related public health concerns regarding the spreading of antibiotic resistance genes and population control of native bacteria and cyanobacteria.

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Link to Video: