



Abstract

The Role of Cyanobacteria in the Aquatic Resistome [†]

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Abstract: The aquatic environment is a reservoir of antibiotics, pathogenic and native microorganisms, and antibiotic resistance genes (ARGs), constituting a key aspect of the One Health approach. Thus, the problem of antibiotic resistance is no longer restricted to bacterial pathogens but is a consequence of the interplay between distinct clinical and environmental drivers. In the project “ExplorAR—Exploring the Aquatic Resistome”, we investigated the putative role of cyanobacteria (CB) in the freshwater resistome, using a multidisciplinary approach based on phenotypic/genotypic/genomic tools. In this presentation, we disclose the main results of the project: (i) the development of a microdilution-based antibiotic susceptibility assay for CB; (ii) the establishment of an antibiotic susceptibility profile of CB genus/species; (iii) the identification of CB strains with reduced susceptibility to multiple antibiotic classes; (iv) the identification of ARGs in CB genomes; (v) the characterization of the antibiotic resistance profile of CB-associated bacteria; (vi) mapping the occurrence of CB and ARGs in surface freshwater reservoirs by high-throughput sequencing approaches. Overall, ExplorAR strongly supports the hypothesis that CB are environmental players in the emergence and dissemination of ARGs in water environments, contributing to the problem, and challenges, of antibiotic resistance.

Keywords: antibiotic pollution; antibiotic resistance; aquatic resistome; cyanobacteria; minimum inhibitory concentration; next-generation sequencing

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