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Abstract

Assessing the Reason Why Heterotrophic Bacteria Present in Aquatic Environments Are Not Affected by Microcystins and Unraveling Alternative Genes for Microcystin Degradation †

Joana Andrade [1], Catarina Silva [2], Luis Vieira [2], Miguel Pinto [3], João Paulo Gomes [3] and Elisabete Valério [1,4,*,‡]

[1] Departamento de Saúde Ambiental, Instituto Nacional de Saúde Doutor Ricardo Jorge, Avenida Padre Cruz, 1649-016 Lisboa, Portugal; joana.andrade.8a@gmail.com
[2] Departamento de Genética Humana, Instituto Nacional de Saúde Doutor Ricardo Jorge, Avenida Padre Cruz, 1649-016 Lisboa, Portugal; catarina.silva@insa.min-saude.pt (C.S.); luis.vieira@insa.min-saude.pt (L.V.)
[3] Departamento de Doenças Infecciosas, Instituto Nacional de Saúde Doutor Ricardo Jorge, Avenida Padre Cruz, 1649-016 Lisboa, Portugal; miguel.pinto@insa.min-saude.pt (M.P.); j.paulo.gomes@insa.min-saude.pt (J.P.G.)
[4] Blue Biotechnology and Ecotoxicology (BBE), CIIMAR—Interdisciplinary Centre of Marine and Environmental Research, University of Porto, Terminal de Cruzeiros do Porto de Leixões, Av. General Norton de Matos, s/n, 4450-208 Porto, Portugal
* Correspondence: elisabete.valerio@insa.min-saude.pt
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‡ Presenting author (oral communication).

Abstract: Cyanobacteria are a ubiquitous and diverse group of phototrophic prokaryotes, which mainly inhabit aquatic ecosystems. In certain optimal environmental conditions, there may be a rapid increase in cyanobacteria populations, leading to the formation of blooms, which are frequently associated with the presence of cyanotoxins. Microcystins (MCs) are the most frequent hepatotoxin produced by cyanobacteria. Scarce previous studies have shown that the growth of aquatic heterotrophic bacteria, which co-occur with cyanobacteria, may not be affected by the presence of MCs, or may present a reduction, never being totally inhibited by their presence. In this study, we examined the effects of three microcystin variants (MCLR, MCRR and MCYR) on a set of heterotrophic aquatic bacteria living in the same ecosystem as cyanobacteria. In particular, the impact of microcystins on the growth of heterotrophic bacteria was tested, and a PCR screening for the presence of microcystin-degrading genes (*mlr*) was performed. The growth assays supported the hypothesis from previous studies, where most heterotrophic bacteria were only slightly or not at all affected by exposure to MCs. Moreover, it seems that the behavior of the isolates when exposed to these cyanotoxins was strain specific. A new bacteria, *mlr*+, was identified, belonging to *Flectobacillus* sp. Furthermore, we decided to perform a genomic study of 14 isolates from a set of potentially interesting bacteria, including *Flavobacterium* spp. and *Aeromonas* spp., to search for xenobiotic-related genes that could be involved in MC degradation. The whole-genome sequencing analysis of these 14 isolates revealed that no COG genes (COG0625; COG0841; COG1566) were present; however, genes similar to CAAX genes were present in the *Aeromonas* spp. isolates analyzed. These results shed new light into alternative molecular mechanisms for microcystin degradation.

Keywords: microcystins; biodegradation; heterotrophic bacteria; *mlr* genes; CAAX genes

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