

**TITLE:** SPATIAL AND TEMPORAL DISTRIBUTION OF FRESHWATER BACTERIAL COMMUNITIES FROM RIVERS IMPACTED BY THE DAM COLLAPSE OF SAMARCO MINING.

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**ABSTRACT:**

Studies on the bacterial community might bring important information about the dynamics and recovery of the impacted areas, since it is recognized as a driving factor of ecosystem maintenance and functioning. One of the main environmental disasters in freshwater occurred on November 5<sup>th</sup> 2015, in Brazil, due to the collapse of a dam (Bento Rodrigues, Minas Gerais state), which is a property of Samarco mining. The collapse discharged about 40 billion liters of tailings into the Doce river, with severe consequences for aquatic and terrestrial biodiversity as well as human health. In order to evaluate the effect of this sudden discharge on freshwater we assessed the bacterial communities at spatial and temporal scales and compared them to a reference river on similar hydrological regimes. For this, we extracted total DNA from water and sediment samples collected from two impacted rivers (Casca and do Carmo), and one non impacted river (Água Fria). Then the V4 variable region of the 16S rRNA gene was amplified and sequenced on the MiSeq platform. Bioinformatical and statistical analyses were performed to identify possible indicator taxa of water quality as well as to provide insights on microbial response facing a situation of sudden environmental stress. Soon after the disaster (7 days), richness and diversity measures from impacted rivers were different from Água Fria river. However, after 150 days, the impacted bacterial communities were as diverse as the reference river. Inverse Simpson's index showed a dominance of a few taxa in all water and sediment communities from seven days after the disaster, in contrast to the remaining sediment communities. These results indicated that impacted communities became more similar to the reference one in so far as the time passed after the disaster, suggesting a possible recovery of the original community composition. Moreover, it was observed specific taxa in both water and sediment samples from impacted rivers, mainly soon after the disaster, such as Rhodocyclaceae, Methylophilaceae, Sporichthyaceae, *Bdellovibrio*, *Erysipelothrix*, *Cloacibacterium* and *Bacteriovorax*. Importantly, it was observed a significant decrease of the majority of these taxa above over time, in contrast with an increase of Gallionellaceae, which highlighted the potential role of them as possible bioindicators of the Rio Doce basin quality.

**Keywords:** bacterial communities, 16S rRNA gene, dam collapse, impacted rivers.

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