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Relatório Final de Pós-doutorado

Título: The influence of micropollutants from domestic wastewater on bacteria-microalgae consortia in an microalgae-based sewage treatment system.

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1. Introduction

Despite numerous advances in the treatment of sanitary sewage, the conventional treatment processes have ongoing issues, such as high loads of nutrients, pollutants and micropollutants, which result in the release of a contaminated effluent into water bodies, representing a potential risk to the environment and to the population (Wang and Wang, 2016; Grandclément et al., 2017).

Among the various technologies constantly evaluated, algae-based systems for sewage treatment have been gaining visibility and recognition as a real potential for applications around the world. The use of algae in the treatment of sanitary sewage is promising due to its ability to assimilate macronutrients and micronutrients in its biomass (Fernandes et al. (2017), De Wilt et al. (2016) and Boelee et al. (2011), and their potential to remove micropollutants and other contaminants such as pathogens (Ruas et al., 2023; Pompei et al., 2023; Pompei et al., 2024).

Sewage treatment systems that employ microalgae-bacteria consortia have the potential to increase nutrient removal efficiency through mutual interaction and synergistic effects (Fallahi et al., 2021). Knowledge and control of the mechanisms involved in microalgae-bacteria interaction can improve the system's ability to transform and recover nutrients (Fallahi et al., 2021). Furthermore, they present numerous advantages related to the economy, energy saving, and a more safe environment, due to cooperative interactions between microalgae and bacteria (Zhang et al., 2020).

Several studies cited in reviews on microalgae-bacteria interactions suggest that they are species-specific, sophisticated and determined by high biological diversity in consortia (Ramanan et al., 2016; Fallahi et al., 2021), highlighting the importance of greater exploitation of native species.

It is known that the microorganisms present in these systems are responsible for removing nutrients, organic matter and other compounds harmful to human health present in the effluent (Pompei et al., 2023a, b). These microorganisms, including microalgae, establish a variety of interactions ranging from mutualistic, facultative, parasitic and species-specific associations (Bagatini et al., 2014; Eiler and Bertilsson, 2007). In addition to these interactions, microorganisms also respond to the conditions of the environment in which they are located. Thus, the nutrient recovery potential and biocompound production profile by microalgae are closely related both to biotic interactions and to abiotic growth conditions.

In association with bacteria, algae generally are benefited by remineralized nutrients (Paerl et al., 2001), growth promoters (Croft et al., 2005), vitamins or vitamin precursors (Grant et al., 2014) and even antibiotics production provided by the associated bacteria against other bacteria and viruses (Mayali and Azam, 2004). The bacteria, in turn, feed on the organic matter, mainly polysaccharides, and nutrients produced and released by the algal cells in the phycosphere (Bell and Mitchell, 1972). Some bacteria live immersed in the polysaccharide matrix, being protected against predators (Seymour et al., 2017). It is in the phycosphere that the exchange of compounds between algae and bacteria occurs (Seymour et al., 2017).

While the diversity within microalgae-bacteria microbial communities has been well documented (Astafyeva et al., 2022; Fuentes Cordero et al., 2016; Paddock et al., 2020) none at tropical environment, as Brazil. Also, little is known about the key organisms affected by the presence of micropollutants present into the wastewater. This is the first study showing that the presence of domestic sewage micropollutants can change the microbial communities (mainly microalgae and bacteria) composition during sewage treatment in microalgae-based system.

4. Conclusions

The metabarcoding of 16S rDNA and 18S rDNA genes revealed the dynamics of both eukaryotic and prokaryotic communities in a flat panel closed PBR for sanitary sewage treatment. There was a statistically difference in terms of composition both, for eukaryotic and prokaryotic communities, considering the initial and the final time of each batch operation, revealing changes in the composition of the communities, and consequently in their function in the system. However, there were no statistical difference in composition for both eukaryotic and prokaryotic communities, considering the presence of the 13 selected micropollutants added. Although, it is noted a slight difference not statistically proved in changes in terms of composition of bacteria. Furthermore, Patescibacteria seems to be an indicator of the micropollutants presence in the samples.

Into the bacteria group the Firmicutes (%) and Proteobacteria (%) were the most abundant bacterial phyla; in archaea group the XX and XX were the most abundant phyla, being majority at the beginning of the treatment (funcao metabolica exercida pela maioria %). The cyanobacteria was observed in low diversity in the community (%), como descrito por outro auto rem trabalho similar. The dominant microalgae during the treatment was *Tetradesmus obliquus* (<90%).

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