



Assessing spatial and temporal patterns of benthic bacterial communities in response to different sediment conditions

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ABSTRACT

Benthic bacterial communities are sensitive to habitat condition and present a fast response to environmental stressors, which makes them powerful ecological indicators of estuarine environments. The aim of this work is to study the spatial-temporal patterns of benthic bacterial communities in response to contrasting environmental conditions and assess their potential as ecological indicators of estuarine sediments. We characterized the diversity of bacterial communities in three contrasting sites on Sado Estuary (SW Coast, Portugal) and 4 sampling occasions, using 16S metagenomic approach. Based on previous studies, we hypothesized that diversity patterns of bacterial communities will be distinct between sites and across sampling occasions. Bacterial communities were more influenced by each site conditions than by temporal variations in the sediments. The main drivers of bacterial distribution were sediments' composition, organic contents, and hydrodynamic activity. This work provided an important baseline dataset from Sado estuary to explore bacterial networks concerning benthic ecosystem functioning.

1. Introduction

Estuaries are complex ecological systems, where the transition from fresh water to sea water occurs (Bonaglia et al., 2014; Schratzberger et al., 2020). The water mixture results on high levels of nutrients in the water column and sediments, making estuaries one of the most productive ecosystems in the world (Elliott and Quintino, 2007). Estuaries present a great diversity of natural habitats, and many supports human activities (Elliott and Quintino, 2007; Schratzberger and Ingels, 2018; Schratzberger et al., 2020; Ridall and Ingels, 2021). However, the intensification of the anthropogenic activities has resulted on an overload of nutrients, organic matter, and contaminants (e.g. metals, pesticides, pharmaceuticals) from terrestrial sources on these habitats, modulating nutrient cycling, stability of communities and food-web structures (Elliott and Quintino, 2007; Grill et al., 2019).

Important processes, such as recycling of nutrients and the degradation of pollutants, occur in soft-sediment intertidal and subtidal habitats. Benthic microorganisms from these sediments are considered mediators of biogeochemical processes that sustain the biosphere (Ridall

and Ingels, 2021), being the first to be affected by environmental disturbances (Schratzberger and Ingels, 2018). As result, the rapid response to biotic/abiotic stressors makes benthic microbial communities powerful bioindicators to evaluate the sediment quality status (Giere, 2009; Patrício et al., 2012; Branco et al., 2018; Schratzberger and Somerfield, 2020; Sagova-Mareckova et al., 2021). Despite of being recognized for their importance in environmental processes, they are rarely used as bioindicators in routine assessments. The environmental monitoring strategies rely on benthic indexes, which are mostly related with the analysis of benthic macroinvertebrates communities (Borja et al., 2015). In case of disturbances in these ecosystems, the need of representative samples and the time-consuming processes in taxonomic identification may represent obstacles to obtain a rapid and reliable evaluation (Rumohr, 2009; Goodwin et al., 2017; Pawlowski et al., 2018). However, recent advances in environmental genomics have improved our knowledge on biodiversity, providing a holistic view of the ecosystems and predicting shifts of biological communities as a response to natural and anthropogenic disturbances (Jessen et al., 2017; Nigel, 2012). The rRNA gene amplicon-based metagenomic has been

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