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Monitoring biofouling on hard substrata through DNA based approaches

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Biofouling formation starts with a first phase in which microscopic organisms (bacteria and microbial eukaryotes) adhere to a submerged surface making it suitable for macroscopic organisms to attach. This initial biological settlement, which occurs during the first hours or days (depending on location and environmental variables) is crucial for the incrustation of other macroorganisms such as invertebrates and algae. Hence, understanding the first stages in biofouling formation is central to investigations on new biofouling prevention strategies, contributing to attenuate consequences of biofilm formation such as economic losses and introduction of non-indigenous species. Yet, identification of microscopic organisms and of macroscopic ones at early developmental stages (e.g. larvae) is a time and resource consuming task that can only be performed by expert taxonomists. We have studied the first stages of biofouling formation via metabarcoding, a potentially more cost-effective and accurate alternative to visual taxonomy for species identification. Metabarcoding consists on sequencing a fragment of the genomic DNA extracted from an environmental sample and comparing it to a reference database for taxonomic assignment. We have applied this technique to 5 x 5 cm polyethylene plates submerged for different time periods at 4 and 20 m depth. By amplification of the bacteria and eukaryotic specific small subunit ribosomal RNA genes (16S and 18S rRNA respectively), we have characterized the sequence of microorganisms responsible of biofouling formation under different conditions. Our results prove metabarcoding as a promising approach to monitor biofouling on hard substrata.

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