

Anthropic impact in estuarine bacterioplankton diversity

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Planktonic communities are widely used as indicators of water pollution level, as they are vulnerable to water quality status. Indeed, it has been proposed that estuaries microbial composition changes during eutrophication period due to the increase of pollutants and hypoxia. In the present study, we characterized the bacterial community structure of two macro-mesotidal estuaries with contrasting pollution levels by sequencing the V4 region of the 16s rRNA gene, as described in the Earth Microbiome Project primers and protocols. While Bilbao estuary crosses a densely populated urban area, the Urdaibai estuary is an UNESCO biosphere reserve. Both estuaries were sampled monthly along a salinity gradient, in water mass (30-33-35‰) and surface (freshwater). In addition, heavy metals and PAHs were analysed together with other environmental variables potentially shaping the microbial community structure (temperature, pH, DO, salinity, ...). Results evidenced that the bacterial species composition and abundance of both estuaries significantly differed between the inner and outer water masses. Moreover, seasonal effects on community structure were detectable in the inner zones of both estuaries, but only minor variation were found in the outer waters, presumably due to a more stable physicochemical environment common in open sea waters. Interestingly, the eutrophication effect is only detectable in the inner zone of Bilbao estuary. In fact, community structure significantly differed in this period, suggesting a low turnover time for inner water mass in this estuary.

Keywords:

metagenomics, estuary, bacterioplankton, pollution

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