

Bacterial diversity, composition and dynamics in and around recreational coastal areas.

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A comparative study on the composition of bacterial communities in a coastal area in the West Mediterranean receiving the impact of recreation-derived activities (from a marina and a beach) was performed by terminal-restriction fragment length polymorphism (T-RFLP) of 16S rDNA along spatial and temporal scales. Interpolation of concentration of hydrophobic compounds, chlorophyll and bacterial cells in seawater over the geography of the sampling area using geographic information systems techniques (GIS) allowed the delineation of two different habitats: bay and marina (with low and high levels of impact respectively), and a transition zone between them. Accordingly, the 16S rDNA T-RFLP profiles of bacterial communities in the area differed mainly spatially, with gradual changes in community composition and structure when approaching the beach and marina. Bacterial communities in impacted areas had higher diversity and equitability, as well as different composition. The main bacterial populations inferred in bay samples, which were members of the Alphaproteobacteria (mainly SAR11 and Roseobacter groups), were replaced by a different population of the Roseobacter clade, and members of the Gammaproteobacteria and Bacteroidetes in more impacted areas. There were also differences in the dynamics of bacterial communities. While temporal variations in bacterial communities in bay samples were lower and mainly determined by temperature, an important factor for the functioning of this ecosystem, variation in impacted areas was more irregular, not so much temperature-driven, and in the case of the transition zone (beach) reflected the use of the coast during warmer periods.

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