


ORIGINAL ARTICLE

Seasonal rather than spatial variability drives planktonic and benthic bacterial diversity in a microtidal lagoon and the adjacent open sea

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Abstract

Coastal lagoons are highly productive ecosystems, which are experiencing a variety of human disturbances at increasing frequency. Bacteria are key ecological players within lagoons, yet little is known about the magnitude, patterns and drivers of diversity in these transitional environments. We carried out a seasonal study in the Venice Lagoon (Italy) and the adjacent sea, to simultaneously explore diversity patterns in different domains (pelagic, benthic) and their spatio-temporal variability, and test the role of environmental gradients in structuring assemblages. Community composition differed between lagoon and open sea, and between domains. The dominant phyla varied temporally, with varying trends for the two domains, suggesting different environmental constraints on the assemblages. The percentage of freshwater taxa within the lagoon increased during higher river run-off, pointing at the lagoon as a dynamic mosaic of microbial taxa that generate the metacommunity across the whole hydrological continuum. Seasonality was more important than spatial variability in shaping assemblages. Network analyses indicated more interactions between several genera and environmental variables in the open sea than the lagoon. Our study provides evidences for a temporally dynamic nature of bacterial assemblages in lagoons and suggests that an interplay of seasonally influenced environmental drivers shape assemblages in these vulnerable ecosystems.

KEYWORDS

bacterial diversity, benthic, lagoon, planktonic, seasonality

1 | INTRODUCTION

Prokaryotes are key components within lagoons, due to their roles as primary producers (e.g., photoautotrophic bacteria) and agents of organic matter remineralization and particles degradation, cycling of biogeochemically relevant elements, pollutants degradation, and transfer of matter and energy to higher trophic levels. A number of studies investigated the relevance of functional prokaryotic processes in lagoons (Abreu, Biddanda, & Odebrecht, 1992; Manini et al., 2003; Pugnetti et al., 2010) while, surprisingly, their

biodiversity has been less studied, with the majority of studies published after the advent of ribosomal gene sequencing (Mohit, Archambault, & Lovejoy, 2015; Mohit, Archambault, Toupoint, & Lovejoy, 2014). Pioneer studies, carried out by cloning and sequencing of rRNA genes, revealed a high diversity (Benlloch, Rodríguez-Valera, & Martínez-Murcia, 1995). Other studies addressed the temporal and spatial patterns of lagoon planktonic prokaryotes (Celussi, Pugnetti, & Del Negro, 2009; LaMontagne & Holden, 2003; Piccini et al., 2006; Simonato, Gómez-Pereira, Fuchs, & Amann, 2010), while less studies addressed diversity in lagoon sediments (Mohit et al.,