Spatio-temporal dynamics of microbial communities under river run-off impact along French coastline inferred by co-occurrence network analyses of eDNA long term time series

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Résumé

Microbes and their interactions play an important role in ecosystem functionning, sustaining biogeochemical cycles and contributing to approximately 50% of the primary production on Earth. The composition of microbial communities is subject to spatio-temporal variability in response to biotic and abiotic factors. In estuarine ecosystems, river inputs represent the main driver of this variability, but the extent to which they influence the spatio-temporal dynamics of microbial co-occurrence patterns remains poorly understood. Co-occurrence networks are a powerful tool to depict community structures and can be used to infer putative interactions. However, networks have been rarely constructed by using long term data series thus limiting our comprehension of the evolution of microbial interactions over time. In this study, we aimed to characterize the extent to which network topologies varies across space and time along an estuarine environmental gradient and identify what are the drivers of this variability. Coastline (impacted by riverine inputs) and offshore water samples (non-impacted), sampled twice a week during two years, were collected in 4 ecosystems distributed along metropolitan French coastlines in the frame of the eDNA network ROME (Reseau de Microbiologie Environnementale Integré). We estimated bacterial and eukaryotic microbial community compositions through metabarcoding. Subsequently, we reconstructed sample specific networks and compared their topological properties at local (in a given ecosystem) and regional (among the 4 studied ecosystems) scales. Our results showed that riverine inputs and environmental variables (salinity and temperature) significantly enhance species richness and that this factor mostly influence networks topologies, notably through an increase in network complexity. This complexity can foster ecosystem functioning and buffer microbial communities against environmental variations. Overall, this study highlights strong spatio-temporal variations in microbial community networks providing important insights for a better understanding of microbial community dynamics in estuarine ecosystems.

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Mots-Clés: co, occurrence network, estuaries, time, series, microbial communities