



Conference Abstract

Keystone species of coastal ecosystems from the Bay of Biscay

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Abstract

Estuarine and coastal ecosystems play a fundamental role in human activities. Since millions of people depend on the numerous resources they offer (i.e., fisheries, transportation, and recreational activities), these ecosystems are also exposed to a high anthropogenic pressure. In order to better monitor and regulate such pressures, it is critical to improve our understanding of the functioning of these ecosystems. This is especially important for microorganisms, considering, for instance, their important roles in biogeochemical cycles. In this study we investigate estuarine and coastal microbial communities along the coast of the Basque Country using eDNA metabarcoding of bacterioplankton and microbenthos samples along a time series, from locations that present different degrees of disturbance. Metabarcoding of the 16S and 18S rRNA gene was carried out, and the OTU and taxa tables generated were used to reconstruct ecological networks, representing potential biological interactions. These ecological networks were used to identify on one hand the species that play a major role in the maintenance of the whole community structure (keystones), and on the other, complex network modules affected by environmental impacts. Here, we define keystone taxa as those that presented the highest ratio between the degree of connectivity (number of associations they established within the network) and their relative abundance. The underlying aim of this study is to develop novel “bioindicators” based on taxa that are both sensitive to impacts and important for community structure.

Results of two seawater communities, one from offshore waters and the other from the coast, showed similar bacterial composition at family level, dominated by Flavobacteraceae and Rhodobacteraceae. Nevertheless, their ecological network properties differed strongly: for a similar number of taxa that established associations, the connectance was similar in both communities, but the number of associations in the coastal community was twice as high as for the offshore one, resulting in a higher modularity. Identified keystone taxa were taxonomically different between both communities: those from the coastal community belonged to Protobacteria, Bacteroidetes, Firmicutes, and Fusobacteria phyla, while the keystones from the offshore community belonged to Proteobacteria, Actinobacteria, Chloroflexi, Thaumarchaeota, PAUC34f and Verrucomicrobia. Moreover, we identified “connector” taxa that presented the highest values of betweenness centrality. These taxa, without having a high degree of connectivity, may be important for the interaction structure because they connect modules, i.e., highly connected subnetworks within the whole network. Further, hierarchical clustering was performed to identify seasonal trends and to better understand the associations retrieved. Taxa with different seasonal preference often grouped together in the same modules, which indicates that modularity was not caused primarily by seasonality.

Keywords

microbial ecology, marine ecology, biomonitoring, ecosystem functioning

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