



Conference Abstract

Structure, diversity and potential metabolic activity of prokaryotic communities of Ebro Delta wetlands (Spain) as revealed by 16S rRNA gene amplicon sequencing

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Abstract

The monitoring of the structure and potential function of the prokaryotic assemblages of aquatic ecosystems can be used for the assessment of ecosystem health. In this work, we analysed by 16S rRNA gene amplicon massive sequencing the aquatic and sediment prokaryotic communities inhabiting three wetlands located in Ebro river Delta (Spain), which differ in their salinity and trophic status. We extracted the DNA from both matrices and sequenced the V4 region of the prokaryotic 16S rRNA gene by Illumina sequencing. The raw sequences obtained were processed and clustered in ZOTUs, which are sequences at 100% identity that were the basis for the structural and statistical analyses. Our results showed that water communities have less diversity and evenness than sediment communities. Moreover, statistical analyses showed that salinity is the main environmental factor that affects the structuration of sediment prokaryotic communities, while seasonality is also a very additional important environmental driver for aquatic communities. We also studied the relationship between the environmental factors and the potential metabolism of the aquatic and sediment prokaryotic communities, specifically for the main metabolic processes of the C-cycle. Focusing on sediment, we observed that methanogenic archaea are present not only in freshwater environments but also in the

saline wetlands, though the observed methane emissions decreased with salinity. To explain this, we studied the potential activity of sulfate-reducing bacteria (SRB) and methanogenic archaea inferring the expression of genes *dsrB* and *mcrA*, which are gene markers for dissimilatory sulfate reduction and methanogenesis, respectively. We observed that, in saline wetlands, the potential activity of methanogens decreases because SRB bacteria outcompete them due to the higher sulfate availability enhancing sulfate-reduction. In the sediment communities of low salinity wetlands the relevance of methanogens is lower in terms of relative abundance, but the methane emissions are higher due to the lower sulfate availability. On the other hand, aquatic methanotrophic bacteria are very important in the net balance of methane emissions in Ebro Delta wetlands, as their relative abundance in the water column influences the amount of methane that is finally released to the atmosphere. In conclusion, our study deepens in the relationship between prokaryotic community structure and function in deltaic wetlands, giving a comprehensive overview of factors influencing the ecological health and certain processes, such as methane emissions, in deltaic systems.

Keywords

Next-generation sequencing, delta river, carbon metabolisms, methane emissions, microbial interactions

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