
Microbes: problems and ways for linking diversity and ecosystem functioning when dealing with planktonic bacteria (RMP 4.6)

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There is a general agreement that the major ecosystem functions (e.g., decomposition, mineralization, nutrient cycling, bioremediation, community respiration etc...) are carried out by microorganisms. These encompass organisms of the two prokaryotic domains *Bacteria* and *Archaea*, but in a variety of ecosystem functions also many protist groups (within the *Eucarya*) are involved. The functions are not only related to heterotrophic metabolisms but include as well autotrophic and mixotrophic modes of growth (e.g., primary production). The facts that many environmental processes impacting the whole biosphere are driven by prokaryotic microbes, that prokaryotes comprise the hugest metabolic diversity, and that their phylogenetic diversity probably far exceeds that of eukaryotic organisms suggests that an analysis of microbial diversity and functions is of crucial importance to advance our understanding of the relation between biodiversity and ecosystem functioning and sustainability.

However, this can not be done at the same level that it is commonly done for large eukaryotic organisms. In the communication we will discuss the arguments that have been put forward to distinguish the peculiarities in the biodiversity study of bacteria as compared to that of other organisms. we will also show several different ways of linking biodiversity with function for pelagic microorganisms, through correlation analyses, through single-cell analysis techniques, through analysis of genomic information or through analysis of cultured microorganism information. For example, I will show how linking the use of specific radiolabeled tracers to specific groups of bacteria allow us to understand the changes in carbon and sulfur cycling that occur during a summer event at a Mediterranean coastal station in Blanes.