Exploring marine bacterial communities with a focus on bacteria attached to particles

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Abstract

Prokaryotes (Bacteria and Archaea) and phytoplankton have been widely investigated in terms of taxonomy, physiology, metabolism and their role in biogeochemical cycles, however, the relationship with one another is still little known. Phytoplankton can interact with free-living (FL) prokaryotes but can also maintain particle- attached (PA) prokaryotes on their surface, facilitating exchanges in the region surrounding their cells, the phycosphere. In this study, prokaryotic community structures of both PA and FL were determined with the hypothesis that the interaction is not casual but based upon processes linked to the physiology and characteristics of the living particles. In order to obtain a detailed morphological and taxonomical identification of FL and PA prokaryotes, High Throughput 16S rRNA gene Sequencing and Scanning Electron Microscopy were used as main tools. In the first part of the thesis, the prokaryotic community composition was analyzed in diatom cultures, based upon growing evidence that many diatom species rely on mutualistic interactions with their microbiota. Skeletonema marinoi, known to produce PUAs (PolyUnsaturated Aldehydes) and the non PUA-producing Skeletonema tropicum were used to understand if the diatom-attached prokaryotic communities present host-specificity also in relation to the presence or absence of secondary metabolites. In the second and third part of the thesis the temporal and spatial scales of FL and PA prokaryotes distribution and diversity were investigated *in situ* to also understand the environmental drivers regulating them. Generally, PA and FL prokaryotes accommodate significantly divergent communities, especially when analyzed at a fine taxonomic level, in relation to the origin and abundance of particles. All the data together provide a clear and comparable assessment of PA and FL prokaryotic diversity, at different sites and under different conditions, making a significant contribution to the field of marine microbial ecology for a better definition of marine microbiome and its potential functional role.