

"Life-style dependent differences are crucial for understanding diversity and function of aquatic microorganisms"

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Studies on intra- and inter-specific interactions even with higher organisms demonstrate that bacteria can rapidly adapt to temporal and spatial changes in their environment. Aquatic bacteria have optimized and dramatically expanded their living space by efficient exploitation of organic matter point sources such as particles/aggregates and higher organisms. Although it is evident that particles/aggregates and organisms such as phytoplankton are “hotspots” for microbial growth and transformation processes, it has not affected sampling strategies of aquatic microbial ecologists, who often focus solely on the free-living bacterial fractions and a priori exclude higher organisms by non-representative water sampling. Therefore, it is not surprising that aquatic microbial ecologists have largely overlooked the fact that many aquatic bacteria may possess a complex life style and frequently alternate between a free-living and a surface-associated stage.

In accordance to this conception, genome analyses of aquatic bacteria –even of free-living ones– have revealed that the majority of cells contain genes associated with motility, chemosensing, and surface attachment. Here, we propose that modern concepts in aquatic microbial ecology should take into account the high chemical diversity and spatio-temporal variability of the bacterial environment. Interactions of aquatic bacteria with surfaces including living organisms are the key to understanding their physiological adaptations and population dynamics, as well as their contribution to biogeochemical cycles.