

# Importance of microscale interactions for aquatic food web dynamics and matter cycling

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## Summary

Methods in the field of microbial ecology have rapidly developed in the recent past. For example, the use of high-resolution techniques such as FT-ICR-MS (Fourier transform ion cyclotron mass spectroscopy) has uncovered an enormous diversity and complexity of natural organic matter produced or degraded microbially either in dissolved or particulate forms. Further, introduction of high-throughput sequencing methods, such as 454 pyrosequencing allow for studying bacterial diversity in natural samples in-depth. As a consequence, our knowledge on the vast diversity and complexity of bacterial habitats and on the phylogentic diversity and physiological responses of natural bacterial communities to their environment has greatly changed. Studies on intra- and interspecies interactions even with higher organisms demonstrate that bacteria can rapidly adapt to temporal and spatial changes in their environment. Since aquatic bacteria are able to efficiently exploit organic matter point sources such as particles/aggregates and higher organisms, they have greatly expanded their life space. Particles/aggregates and organisms such as phytoplankton provide 'hotspots' for microbial growth and transformation processes. Yet, our sampling strategies often exclude such point sources when using pre-filtration or low sampling volumes. Consequently, aquatic microbial ecologists have largely overlooked the fact that many aquatic bacteria may possess a complex lifestyle and frequently alternate between surface attachment and free-living stages. Studies on interactions of aquatic bacteria with surfaces including living organisms enable better understanding of physiological adaptations and population dynamics, as well as their contribution to biogeochemical cycles.

