

## Microbial activity in aquatic systems from cell to biosphere

E.B. Sherr, B.F. Sherr

College of Oceanic and Atmospheric Sciences, Oregon State University, 104 Ocean Admin Bldg.,  
Corvallis, OR, USA, 97331-5503

---

### ABSTRACT

The field of aquatic microbial ecology is flourishing. At the cell and molecular level, aquatic ecologists are unravelling the taxonomic composition of natural microbial assemblages, and evaluating cell-specific activity *in situ*. At the biosphere level, detection of changes in concentration of atmospheric oxygen has shown a strong seasonal signal of microbial production and respiration in the sea on a hemispheric scale. Future challenges include (but are certainly not limited to): 1) time - understanding temporal variability in microbial activity, particularly with respect to season; 2) temperature - evaluation of how rises in temperature in a warming world will affect microbial activity, and thus system function, in aquatic ecosystems; and 3) taxonomy - extending studies of microbial diversity and of cell-specific activity to additional aquatic habitats and to protists. There is also the exciting possibility that in the not too distant future, microbial life may be discovered on other planetary bodies in our solar system.

---

### Introduction

At the very end of his autobiography, 'Naturalist', Harvard professor Edward O. Wilson wrote, "If I could do it all over again, and relive my vision in the twenty-first century, I would be a microbial ecologist"[51]. This statement, from one of the best regarded scientists in the world, is an indication of the excitement generated by our field. Microbial ecology is still a young science, with important new discoveries to be made. The progress that has already occurred has created general public awareness that there is a lot more to bacteria than 'germs', that microbial activity sustains the healthy functioning of natural systems, and that there is great commercial opportunity in microbes. Here we would like to explore what we perceive to be some of the 'leading edges' of the field of aquatic microbial ecology, in which recent findings are discussed in the context of 'where do we go next?' This is our own perspective of some of the topics on which bright young investigators might be working in the next century.

The field of aquatic microbial ecology is large and complex. It spans studies of microbial organisms in the sea, which occupies over two thirds of the earth's surface; in freshwater – which includes lakes, rivers, hot springs, and groundwater; in aquatic sediments; in hydrothermal vents and methane seeps; and in marine and freshwater ice. While 'microbial ecology' often is thought to imply *bacteria*, in aquatic systems virtually all of the carbon transformations and elemental cycling at the base of food webs are accomplished by *microbes* - algae, heterotrophic protists as well as bacteria. In the classic 'changing paradigm' paper of L.R. Pomeroy [33], one of the major points was the

**Microbial Biosystems: New Frontiers**

*Proceedings of the 8<sup>th</sup> International Symposium on Microbial Ecology*

*Bell CR, Brylinsky M, Johnson-Green P (ed)*

*Atlantic Canada Society for Microbial Ecology, Halifax, Canada, 1999.*

importance of nanophytoplankton in marine production and respiration. The role of microbes, including bacterial as well as algal autotrophs, in primary production constitutes a major difference in the structure of aquatic versus terrestrial food webs.

Many of the advances in aquatic microbial ecology in the last 25 years have involved discoveries of new groups of organisms. Initially, these were of new and expanded functional groups. Discovery of the high abundance of pico-autotrophs: coccoid cyanobacteria and  $< 2 \mu\text{m}$  sized algae in the sea and in oligotrophic lakes [43], and then of pelagic prochlorophytes in the ocean [7], extended downward the size range of primary producers in aquatic systems. Discovery of food webs based on chemosynthetic sulfide-oxidizing bacteria, growing as mats and as internal symbionts, at hydrothermal vents was of enormous scientific and public interest [21]. Such systems now include methane seeps and methane ice communities on the sea floor, in which food webs may depend on growth of methane oxidizing bacteria [30]. During the same period, the importance of phagotrophic protists, as grazers of picoplankton and of phytoplankton of all sizes [37], and as a food resource for larger zooplankton [42], in both marine and freshwater systems, was firmly established. Finally, viruses, including bacteriophages and viruses that infect algae, have been found in high number in aquatic systems, and are thought to be an important source of mortality for bacteria and for phytoplankton blooms [16,44].

The second wave of discoveries about microbes in aquatic systems has involved the application of molecular genetics to microbial diversity. New, taxonomically distinct, and previously uncultured species, and groups of species of prokaryotes have been identified in marine [11,12,13,17,19], hot spring [47] and lake [31] ecosystems. One of the more interesting findings is that archaeal genomes appear to be widely distributed in marine bacterioplankton [12, 15]. No longer can we view bacterial assemblages as simply a 'black box' of unknown composition. Taxon-specific genetic probes allow us to track the abundance and relative activities of identified taxonomic components of microbial communities *in situ* [17,24]. The real excitement is in not simply knowing 'who is there', but in combining molecular genetic approaches to determining 'who is active, and just what are they doing?' Examples are identifying the presence and expression of specific genes, such as the *nir* gene for dissimilatory nitrite reductase [46], and determining cell-specific abundance of rRNA of specific taxonomic groups of bacteria [24].

### **Some prospects for future research in aquatic microbial ecology**

#### *TIME - temporal scales of microbial activity*

Investigations of microbes *in situ* have considered spatial scales from ecosystem level down to nanoscale patchiness [23]. Time scales are equally important. Two examples of temporal scales in microbial ecology will illustrate the need to focus on time as well as spatial variability in microbial processes in future studies.

#### *Diel variability in heterotrophic microbial processes*

The idea that if the growth of heterotrophic bacterioplankton in the euphotic zone depends directly on photosynthetic production, then there should be day/night cycles in bacterial activity is not new. However, there have been relatively few investigations of this hypothesis, and past studies have yielded equivocal results. Recently, Gasol et al. [18] reported strong diel cycles in bacterial incorporation of radiolabeled leucine and thymidine

in the oligotrophic Mediterranean Sea, with highest uptake rates during the day, and lowest rates at night. These results are empirical evidence for close coupling between bacterial and phytoplankton production. They also show that for systems with close trophic coupling, the time of day in which samples are collected for bacterioplankton productivity assays does matter. In such systems, short-term (diel) temporal variability is as important a consideration as is small-scale (cm to meters) spatial variability.

*Seasonal variability in heterotrophic microbial processes*

Newly available data on the seasonal variation in atmospheric oxygen content show a strong seasonal signal in oceanic production and respiration at a hemispheric scale [2,22]. The marine component of the seasonal atmospheric oxygen signal indicates net production of oxygen in the upper water column from late winter to mid-summer, and then net diffusion of oxygen from the atmosphere to the sea during the rest of the year [2,22]. The annual increase in atmospheric oxygen during spring is equivalent to a net community production of about 50 gC/m<sup>2</sup>/yr, 5-fold greater than measured rates of export flux via sinking particles, and 1/3 of average annual primary production in the ocean [38]. This is a large amount of organic carbon that does not appear to be immediately respired by heterotrophic microbes. This phenomenon indicates a seasonal offset of weeks to months in the annual cycle of production and consumption of organic carbon in the sea. Such an offset is at odds with studies, like that of Gasol et al. [18], which indicate a tight trophic coupling between phytoplankton production and bacterial activity. Elucidating mechanisms that contribute to the presumptive seasonal offset in production/respiration processes in the sea, and likely also in lakes, can be a goal of future research in aquatic microbial ecology.

*TEMPERATURE - in the context of both seasonal cycles and of potential effects of global warming on aquatic microbial processes*

Temperature has long been recognized as a major controller of microbial activity, and must be an important factor in determining seasonal cycles of microbial heterotrophy at mid to high latitudes. However, there seem to be fewer investigations of this physical control on microbial processes *in situ* than studies of biotic controls, e.g. substrate quantity and quality, grazing, and viral mortality. Present concerns regarding response of natural systems to global warming are renewing interest in temperature effects on aquatic microbial communities. Recent studies have demonstrated striking effects of temperature on bacterial activity in lakes [14] and in marine systems [40,45,49]. Such effects include winter/summer differences in proportional uptake of radiolabeled leucine and thymidine [40,45]. We have found markedly different responses to added substrate by coastal marine bacteria with temperature shifts of 4-8°C up from ambient [6]. Since climate change models predict greater, and earlier, warming in polar environments compared to other regions of the planet [5,26], temperature effect studies in higher latitude aquatic systems would be especially relevant [48].

*TAXONOMY/SPECIFIC ACTIVITY - extending molecular approaches in aquatic microbial ecology*

Despite the avalanche of publications on molecular diversity of microbes that has appeared in the last decade or so, this area of research is really just beginning to flower. Investigations of prokaryotic taxonomic diversity are being extended to diverse habitats and

associations, for example the deep-sea [13,32], deep aquifers [41], water pockets within ice in Antarctic dry lakes [34], endonuclear symbionts of protists (1), and bioluminescent symbionts of marine fish [20]. Application of molecular techniques to investigate the diversity and distribution of heterotrophic eukaryotes (protists) in aquatic systems is still at a very early stage [25, 36].

The greatest gains will accrue from determining cell-specific activity for selected taxonomic types of microbes. This in turn depends on methods, such as taxon-specific rRNA probes, and probes for specific genes, that are still in development. Studies using general diagnostics for cell-specific activity, e.g. CTC, a fluorogenic indicator of ETS activity, have shown that only a small proportion of bacterial cells in natural aquatic assemblages are highly metabolically active [8,39]. Use of cell-specific stains that detect membrane integrity has shown that variable fractions of suspended bacterial cells have intact cell walls and membranes in both marine and freshwater [9,27,35,50] systems. Bacterioplankton in oligotrophic systems also appear to have very low growth efficiencies, often < 5-10% [3,10]. These results support the idea that in general, most bacterial cells observed in aquatic systems are either dormant (in a state of starvation/survival) or dead [28]. However, we have found that a large fraction (up to 80-90%) of apparently metabolically inactive bacterial cells can be induced to show detectable ETS activity (via the CTC method) within 20 - 30 hours with temperature increase and/or addition of organic substrate [6]. It would be of great interest to determine the relative state of metabolic activity of specific taxonomic components of a bacterial assemblage at any one time, and then to be able to determine what factors control their level of activity, as well as the overall growth efficiencies of the assemblage.

### OTHER TOPICS

A number of other research directions could also have been discussed here, for example: chemical communication between microbes; symbiotic associations; importance of microstructure/microniches to microbial processes in aquatic milieu; biofilms; impact of pollution/eutrophication on aquatic microbial processes. Farther out on the research horizon for microbial ecologists is perhaps the most exciting prospect of all - the search for extraterrestrial life, a discipline that the US National Aeronautics and Space Administration has now formally recognized as 'Astrobiology' [4]. If life is found on other planetary bodies in the solar system, it undoubtedly will be primarily, or exclusively, microbial life. Models for such organisms are microbes living in extreme environments on earth: anoxic waters, deep subsurface aquifers, hot springs, hydrothermal vents, and ice, all habitats of interest to aquatic microbiologists [29]. Among those who attended this ISME-8 symposium may be scientists who will be directly involved in the discovery and description of the first known extraterrestrial life forms.

### References

1. Amann R, Springer N, Ludwig W, Gortz H-D, Schleifer K-H (1991) Identification *in situ* and phylogeny of uncultured bacterial endosymbionts. *Nature* 351:161-164.
2. Bender M, Ellis T, Tans P, Francey R, Lowe D (1996) Variability in the O<sub>2</sub>/N<sub>2</sub> ratio of southern hemisphere air, 1991-1994: implications for the carbon cycle. *Global Biogeochem Cycles* 10:9-21.

3. Biddanda B, Benner R (1997) Major contribution of mesopelagic plankton to heterotrophic metabolism in the upper ocean. *Deep-Sea Res* 44:2069-2085.
4. Bunk S (1998) Astrobiology makes debut under NASA. *The Scientist* 12 (13):1&14.
5. Cattle H, Crossley J (1996) Modelling Arctic climate change. In: Wadhams P, Dowdeswell JA, Schofield AN (eds) *The Arctic and environmental change*, Gordon and Breach Publ., Amsterdam, pp 1-13.
6. Choi JW, Sherr BF, Sherr EB (1999) Dead or alive? A large fraction of ETS-inactive marine bacterioplankton cells, as assessed by reduction of CTC, can become ETS-active with incubation and substrate addition. *Aquat Microb Ecol* in press.
7. Chisholm SW, Olson RJ, Zettler ER, Waterbury J, Goericke R, Welschmeyer N (1988) A novel free-living prochlorophyte abundant in the oceanic euphotic zone. *Nature* 334:340-343.
8. Del Giorgio PA, Scarborough G (1995) Increase in the proportion of metabolically active bacteria along gradients of enrichment in freshwater and marine plankton: implications for estimates of bacterial growth and production. *J Plankton Res* 17:1905-1924.
9. Del Giorgio PA, Bird DF, Maranger R, Prairie YT (1998) Use of the exclusion nucleic-acid stain TOPRO-1 to assess cell stress or damage in natural bacterioplankton assemblages. *Aquat Microb Ecol* in press.
10. Del Giorgio PA, Cole JJ (1998) Bacterial growth efficiency in natural aquatic systems. *Ann Rev Ecol Syst* 29:503-541.
11. DeLong EF, Franks DG, Alldredge AL (1993) Phylogenetic diversity of aggregate-attached vs free-living marine bacterial assemblages. *Limnol Oceanogr* 38:924-934.
12. DeLong EF, Wu KY, Prezelin BB, Jovine, RVM (1994) High abundance of Archaea in Antarctic marine picoplankton. *Nature* 371:695-697.
13. DeLong EF, Franks DG, Yayanos AA (1997) Evolutionary relationships of cultivated psychrophilic and barophilic deep-sea bacteria. *Appl Environ Microbiol* 63:2105-2108.
14. Felip M, Pace ML, Cole JJ (1996) Regulation of planktonic bacterial growth rates: the effect of temperature and resources. *Microb Ecol* 31:15-28.
15. Fuhrman JA, McCallum K, Davis AA (1992) Novel major archaeobacterial group from marine phytoplankton. *Nature* 356:148-149.
16. Fuhrman JA, Suttle CA (1993) Viruses in marine planktonic systems. *Oceanography* 6:51-63.
17. Fuhrman JA, Lee SH, Masuchi Y, Davis AA, Wilcox RM (1994) Characterization of marine prokaryotic communities via DNA and RNA. *Microb Ecol* 28:133-145.
18. Gasol JM, Doval MD, Pinhassi J, Calderon-Paz JI, Guixa-Boixareu N, Vaque D, Pedros-Alio C (1998) Diel variations in bacterial heterotrophic activity and growth in the northwestern Mediterranean Sea. *Mar Ecol Prog Ser* 164:107-124.
19. Giovannoni SJ, Britschgi TB, Moyer CL, Field KG (1990) Genetic diversity in Sargasso Sea bacterioplankton. *Nature* 345:60-63.
20. Haygood MG, Distel DL (1993) Bioluminescent symbionts of flashlight fishes and deep-sea anglerfishes form unique lineages related to the genus *Vibrio*. *Nature* 363:154-156.
21. Karl DM (1995) Ecology of free-living, hydrothermal vent microbial communities. In: Karl DM (ed) *The microbiology of deep-sea hydrothermal vents*. CRC Press, Boca Raton, pp 35-124.

22. Keeling RF, Shertz SR (1992) Seasonal and interannual variations in atmospheric oxygen and implications for the global carbon cycle. *Nature* 358:723-727.
23. Krembs C, Juhl AR, Long RA, Azam F (1998) Nanoscale patchiness of bacteria in lake water studied with the spatial information preservation method. *Limnol Oceanogr* 43:307-314.
24. Lee S, Kemp PF (1994) Single-cell RNA content of natural marine planktonic bacteria measured by hybridization with multiple 16S rRNA-targeted fluorescent probes. *Limnol Oceanogr* 39:869-879.
25. Lim EL, Dennett MR, Caron DA (1998) The ecology of *Paraphysomonas imperforata* based on studies employing oligonucleotide probe identification in coastal water samples and enrichment cultures. *Limnol Oceanogr* 44:37-51.
26. Manabe S, Stouffer RJ, Spelman MJ (1994) Response of a coupled ocean-atmosphere model to increasing atmospheric carbon dioxide. *Ambio* 23:44-49.
27. McFeters GA, Yu FP, Pyle BH, Steward PS (1995) Physiological assessment of bacteria using fluorochromes. *J Microbiol Meth* 21:1-13.
28. Morita RY (1997) Bacteria in oligotrophic environments. Chapman and Hall, NY.
29. Nealson KH (1997) The limits of life on Earth and searching for life on Mars. *J Geophys Res* 102:23,675-23,686.
30. Nelson DC, Fisher CR (1995) Chemoautotrophic and methanotrophic endosymbiotic bacteria at deep-sea vents and seeps. In: Karl DM (ed) *The microbiology of deep-sea hydrothermal vents*. CRC Press, Boca Raton, pp 125-168.
31. Ovreas L, Forney L, Daae FL, Torsvik V (1997) Distribution of bacterioplankton in meromictic Lake Saelenvannet, as determined by denaturing gradient gel electrophoresis of PCR-amplified gene fragments coding for 16S rRNA. *Appl Environ Microbiol* 63:3367-3373.
32. Parkes RJ, Cragg BA, Bale SJ, Getliff JM, Goodman K, Rochell PA, Fry JC, Weightman AJ, Harvey SM (1994) Deep bacterial biosphere in Pacific Ocean sediments. *Nature* 371:410-413.
33. Pomeroy LR (1974) The ocean's food web: a changing paradigm. *BioScience* 24:409-504.
34. Priscu JC, Fritsen CH, Adams EE, Giovannoni SJ, Paerl HW, McKay CP, Doron PT, Gordon DA, Lanoil BD, Pinckney JL (1998) Perennial Antarctic lake ice: an oasis for life in a polar desert. *Science* 280:2095-2098.
35. Porter J, Diaper J, Edwards C, Pickup R (1995) Direct measurements of natural planktonic bacterial community viability by flow cytometry. *Appl Environ Microbiol* 61:2783-2786.
36. Rice J, Sleight MA, Burkill PH, Tarran GA, O'Connor CD, Zubkov MV (1997) Flow cytometric analysis of characteristics of hybridization of species-specific fluorescent oligonucleotide probes to rRNA of marine nanoflagellates. *Appl Environ Microbiol* 63:938-944.
37. Sherr EB, Sherr BF (1994) Bacterivory and herbivory: key roles of phagotrophic protists in pelagic food webs. *Microb Ecol* 28:223-235.
38. Sherr EB, Sherr BF (1996) Temporal offset in oceanic production and respiration processes implied by seasonal changes in atmospheric oxygen: the role of heterotrophic microbes. *Aquat Microb Ecol* 11:91-100.

39. Sherr BF, del Giorgio PA, Sherr EB (1999) Estimating abundance and single-cell characteristics of actively respiring bacteria via the redox dye CTC. *Aquat Microb Ecol* in press.
40. Shiah F-K, Ducklow HW (1997) Bacterioplankton growth responses to temperature and chlorophyll variations in estuaries measured by thymidine:leucine incorporation ratio. *Aquat Microb Ecol* 13:151-159.
41. Stevens TO, McKinley JP (1995) Lithotrophic microbial ecosystems in deep basalt aquifers. *Science* 270:450-454.
42. Stoecker DK, Capuzzo JMcD (1990) Predation on protozoa: its importance to zooplankton. *J Plankton Res* 12:891-908.
43. Stockner JG, Antia NJ (1986) Algal picoplankton from marine and freshwater ecosystems: a multidisciplinary perspective. *Can J Fish Aquat Sci* 43:2472-2503.
44. Suttle CA (1994) The significance of viruses to mortality in aquatic microbial communities. *Microb Ecol* 28:237-243
45. Tibbles BJ (1996) Effects of temperature on the incorporation of leucine and thymidine by bacterioplankton and bacterial isolates. *Aquat Microb Ecol* 11:239-250.
46. Ward BB (1996) Nitrification and denitrification: probing the nitrogen cycle in aquatic environments. *Microb Ecol* 32:247-261
47. Ward DM, Bateson MM, Weller R, Ruff-Roberts AL (1992) Ribosomal RNA analysis of microorganisms as they occur in nature. *Adv Microb Ecol* 12:219-286.
48. Wiebe WJ, Pomeroy LR. (1991) Possible effects of global warming on marine foodwebs at low temperature. pp. 179-183. In: Dudley EC (ed) *The Unity of Evolutionary Biology*, Vol 1, Dioscorides Press, Portland, OR.
49. Wiebe WJ, Sheldon WM, Pomeroy LR. (1993) Evidence for an enhanced substrate requirement by marine mesophilic bacterial isolates at minimal growth temperatures. *Microb Ecol* 151-160.
50. Williams SC, Hong Y, Danavall DCA, Howard-Jones MH, Gibson D, Frischer ME, Verity PG (1998) Distinguishing between living and nonliving bacteria: evaluation of the vital stain propidium iodide and the combined use with molecular probes in aquatic samples. *J Microbiol Meth* 32:225-236.
51. Wilson EO (1994) *Naturalist*. Island Press, Washington DC.