

Predictions for the Future of Microbial Oceanography

BY DAVID L. KIRCHMAN AND CARLOS PEDRÓS-ALIÓ

It has been said that making predictions is difficult, especially about the future, and clearly it is especially challenging for fast-moving fields like marine microbial ecology and microbial oceanography. The pace of discovery and the vitality of these fields are evident in the preceding articles of this special issue and to anyone reading *Science* and *Nature* (not to mention the plethora of specialized journals) or attending the countless meetings relevant to the study of marine microbes. So, at first, discussing the future seemed daunting to us, and we thought that no reader would like any of our predictions, except the self-evident one: that the future of marine microbial science is bright. But then, seven other predictions became obvious to us. We are confident that all readers will like these predictions and will agree that all of them will be 100% fulfilled ten years from now.

PREDICTION 1.

All Marine Microbes Will Be Cultivated by 2017.

One way to tell microbial ecologists apart is whether they say marine microbes are *unculturable* or are just *uncultured*. The terms refer to one of the most important observations in microbial oceanography: the number of bacteria retrieved by cultivation-dependent methods is much less than the total number of bacteria that

can be counted by microscopy. Some would argue that these bacteria cannot be cultured because of intrinsic properties of marine microbes (*unculturable*), whereas others opine that all marine bacteria can, in fact, be cultivated if only

we knew the proper growth conditions and the right technique (*uncultured*). This culturability question applies to virtually all microbes found in the ocean, but microbial scientists examining chemotrophic bacteria (those that use organic or inorganic compounds for energy) get exercised about this issue more so than those working on phototrophic microbes (those that use light energy). Some argue that the inability to isolate a microbe from the ocean and grow it in the lab is the biggest barrier preventing future progress in marine microbial ecology (see Giovannoni et al., this issue).

By the year 2017, we predict that microbial ecologists will no longer argue

about suffixes or prefixes, and the gaps between the worlds of cultured and uncultured/unculturable bacteria will disappear. Isolation techniques will continue to improve, and more and more important microbes will be tamed and

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brought into the lab for detailed experiments (see Giovannoni et al., this issue). But even without these advances, the distinctions among cultured, uncultured, and unculturable bacteria will become less important with the continued application of cultivation-independent techniques to examine microbes in the oceans, regardless of whether they

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are culturable or not. The cultivation-independent techniques started off with the cloning of 16S rRNA genes and continue with the explosion of genomic-based approaches now underway (more on this below).

Another view was expressed by Selman Waksman (1888–1973), who probably knew a thing or two about the culture debate: “It is not merely sufficient to isolate an organism, cultivate it and determine what it does in pure culture; it is far more important to determine what it does in its natural substrate and how these activities dovetail with the activities of other bacteria, as well as the whole complex mass of higher plants and animals” (Waksman, 1934). Waksman won a Nobel Prize in 1952 for his pure-culture studies, but he was also a pioneer in microbial oceanography with his work on microbes and processes in the nitrogen cycle, among other topics.

PREDICTION 2.

Every Microbial “Species” in the Ocean Will Be Sequenced by 2017.

Microbiologists will immediately see that the real problem with this prediction is not the sequencing part, but the word “species.” Jim Tiedje predicted back in 1998 that microbiologists would continue to argue about the definition of species for the next 20 years (Tiedje, 2000), a prediction that still looks safe today. As we continue to move into the Age of Genomics (See Moran and Armbrust, this issue), it may be easier for microbial ecologists to sequence the oceans (that is, sequence genes in seawater without isolating the microbes carrying them) than to agree on what a species is.

Regardless, it is clear that many

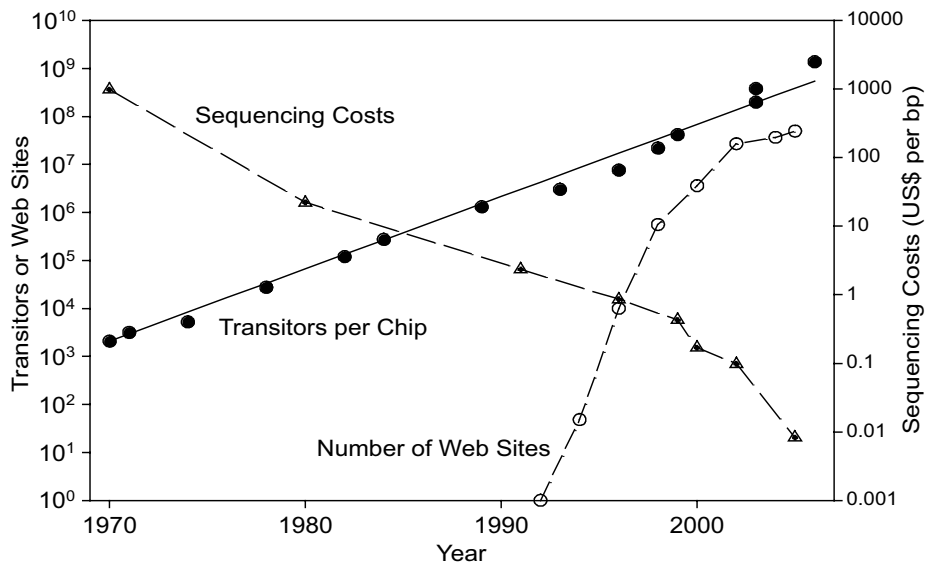


Figure 1. Power of computers (number of transistors per chip), number of Web sites, and sequencing costs over the last 30 years. The increase in computer power number has been following Moore’s Law (the regression line), which predicts the doubling in the number of transistors per chip every two years. Data from Shendure et al. (2004) and <http://www.intel.com/technology/mooreslaw/>

microbes will be sequenced by 2017. This explosion in sequencing has been aided by advances in sequencing speed and ease, which were originally driven by biomedical applications, most notably the Human Genome Project. As sequencing speed has increased, costs have decreased (Figure 1) and will do so even more dramatically in the near future. Just as marine microbial ecology has benefited from the Human Genome Project, which cost nearly \$3 billion all told, so too will it benefit from the race for the \$1000 genome predicted for the near future (Service, 2006) and other developments spurred on by more lucrative fields using genomic data. These developments lead to the prediction that the barriers between the genomic haves and have-nots will diminish, if not disappear completely by 2017. But, not everyone need be a sequencer.

Already, genomic and metagenomic data generated by one research group are being used by other groups around the world, a collective effort that we predict will become more formally organized by 2017. Analogous to physicists gathering together to analyze data from particle accelerators or eagerly awaiting pictures from Mars, microbial scientists of various stripes will come together (if only virtually) to analyze the data avalanche from megasequencing efforts. Already, microbiologists and bioinformaticians meet at annotation jamborees to pore over sequences, but integrating genomic and environmental data into a cohesive story will require even larger and more diverse teams than is now the case. It will take a village, or at least a multidisciplinary team, to properly digest the terabytes of sequence and environmental data already accumulating and then

to experimentally explore what these sequences mean.

As in other areas of science (and indeed everyday life), computers figure prominently in marine genomics today and will continue to do so in the next decade. Marine and terrestrial genomics have contributed their share to the explosion of Web sites around the world (Figure 1), and the Web, perhaps even more so than decreasing sequencing costs, has allowed many marine scientists to play in the genomics arena or at least watch closely from the sidelines. Another key to this participation is the continual improvements in computers. Fortunately, “Moore’s Law,” which predicts a doubling of computing power every two years, seems to be holding true so far (Figure 1). Moore, of the eponymous law, is Gordon Moore, the cofounder of Intel and of the Gordon and Betty Moore Foundation, which has generously supported marine microbial ecology in the genomics arena (www.moore.org). In addition to raw computer power, marine microbial ecologists will continue to need innovative approaches to analyze genomic data and to combine these data with the more traditional numbers provided by oceanographers.

We probably will need a good part of the next 10 years to digest the genomic data from ongoing sequencing efforts, but the next decade will undoubtedly also see more use of proteomic and other “omic” approaches in the oceans. After all, unexpressed genes and unsynthesized proteins do a biogeochemical cycle no good, and understanding the role of microbes in the oceans requires us to know about microbial activity, not just

genomic potential. Genomic studies of cultivated and uncultivated microbes have already generated many hypotheses that would fundamentally change our views of how the ocean works—if shown to be true. A radical thought is that these hypotheses may be tested with traditional, nongenomic techniques in oceanography and microbial ecology.

PREDICTION 3.

Marine Microbial Ecology Will Take Over Mainstream Microbial Science by 2017.

In their book *The Microbe’s Contribution to Biology*, A.J. Kluyver and C.B. Van Niel outline how microbiology led to the formulation and testing of many basic principles in biology, as much as they were known in the mid-1950s (Kluyver and Van Niel, 1956). We predict that what microbiology did for biology over a half century ago, marine microbial ecology will do for mainstream microbial sciences over the next ten years.

Already, there is much common ground between marine microbial ecology and other microbial sciences, if only because more marine microbes have been brought into culture and can be studied by the same approaches as used for other microbes. Most importantly, genome-sequence data are used by all scientists regardless of the microbe’s salinity range. The incredibly small genomes of the marine bacterium *Candidatus Pelagibacter ubique* and of the marine green alga *Ostreococcus tauri* are helping to identify essential genes in microbes, marine or otherwise. Genomic and other studies on *Prochlorococcus*, the most abundant photoautotroph (aka. plant) on the planet, are revolu-

tionizing ideas about the species concept, genomic organizations in photoautotrophs, and the regulation of plant growth in nutrient-poor environments. Marine microbes will continue to teach landlubber microbiologists new microbial tricks as genomic and other data from the ocean pours in.

More radically, even uncultivated microbes and approaches are already having an impact on traditional microbiology. Koch’s postulates, which are based on cultivation of presumptive disease-causing microbes, have been axiomatic in medical microbiology since they were handed down in 1875 (Brock, 1999). But now, microbiologists apply cultivation-independent approaches, long routine for microbial oceanographers, to examine bacteria and other microbes in humans where once culture-dependent approaches ruled (Gill et al., 2006). Current discussions about the metagenomic sequencing of the human microbiome (our bodies have more microbial cells than human cells) will sound familiar to marine microbial ecologists doing environmental genomic studies of the ocean. In addition to using the general approach, data from marine metagenomic studies such as the Sargasso Sea project (Venter et al., 2004) are used by biologists far from the ocean and microbial oceanography (Table 1), a point also made by Edwards and Dinsdale (this issue). New data from the Global Ocean Sampling (GOS) expedition (Rusch et al., 2007) undoubtedly will be mined even more extensively by landlocked scientists. Microbial ecology often takes concepts and techniques from mainstream sciences, but the flow will reverse directions by 2017.

	Journal	Citations
<p>Table 1. Some of the journals publishing articles that cited the metagenomic study of the Sargasso Sea (Venter et al., 2004). As of May 8, 2007, 486 papers had cited Venter et al. (2004) according to ISI Web of Science. The diversity of journals in this list is one indication of the impact of marine microbial ecology on sciences far from the oceans and ecology.</p>	<i>Annual Review of Genetics</i>	3
	Biochemical Journals ^a	7
	<i>Journal of Bacteriology</i>	10
	<i>Journal of Biological Chemistry</i>	6
	<i>Journal of Molecular Biology</i>	5
	<i>Genome Research, Genome Biology</i>	12
	Nature Journals ^b	53
	<i>Nucleic Acids Research</i>	9
	PNAS	20
	<i>Science</i>	22
	Trends Series ^c	22
	<i>Virus Research</i>	3

^a Includes: *Biochemistry, Biochemical and Biophysical Research Communications, and Biochimica et Biophysica Acta-Bioenergetics.*

^b Includes: *Nature, Nature Biotechnology, Nature Medicine, Nature Reviews Genetics, and Nature Reviews Microbiology.*

^c Includes: *Trends in Biotechnology, Trends in Ecology and Evolution, Trends in Genetics, and Trends in Microbiology.*

PREDICTION 4.

Pyrococcus furiosus Will Be as Popular Among Kids by 2017 as *Tyrannosaurus rex* Is Today.

As challenging as it is to assimilate metagenomic data or to define a species, try explaining microbes to a seven-year-old kid. But, some marine microbial ecologists and microbial oceanographers already are doing just that. These efforts are taking the forms of podcasts, blogs, and videos that offer glimpses into the unseen world of microbes (e.g., <http://www.microbeworld.org/look>). Other microbial ecologists will soon be drawn to the buzz and will see the value of explaining the beauty and the usefulness of their science not only to kids but to their parents and grandparents as well. We predict that the popularization of microbes will be so successful that in a decade's time, children of all ages will

have more models of microbes than of a certain large dinosaur.

The popularity of microbes will continue to grow as people realize that we live in the Age of Microbes, which began 3.8 billion years ago, while the Age of Dinosaurs is long past and that the still extant lifestyles of microbes match the exoticism of extinct dinosaurs. *Pyrococcus furiosus* is able to grow in boiling water, *Acidithiobacillus ferrooxidans* can live off of rocks and extract useful copper and iron as a result, and *Polaribacter irgensii* can happily live in the brine channels of sea ice several degrees below freezing. We would not be surprised to see an author take advantage of microbial weirdness and pen a book entitled "Microbial Park" that appears on the bestseller list before 2017. (Frank Schatzing's recent novel, *The Swarm*, has methane-eating

microbes and a *Tyrannosaurus rex*, and was a best seller as *Der Schwarm* in Germany, but it is not flying off bookstore shelves elsewhere [perhaps because of its 881 pages?]) After becoming immensely rich from worldwide royalties, the author will create a foundation that will fund more marine microbial research to solve environmental problems, discover new biotechnological processes, cure human diseases, and entertain kids with feats of their favorite microbes.

PREDICTION 5.

Traditional Methods in Microbial Ecology Will No Longer Be Used by 2017.

There are two reasons why this prediction will be fulfilled by the year 2017. One is that everyone will be doing genomics and other omics (see Age of Genomics above) over the next decade, spending their time in the lab or peering at computer screens rather than on ships filtering water. Students won't bother trying to learn the traditional methods because the original papers are not available electronically. Already, citations to papers about some traditional methods (direct microscopic counts and bacterial production) are showing signs of decline, while reports using molecular or cultivation-independent approaches keep churning out (Figure 2). Perhaps the decline is an artifact of the citation analysis; as methods mature, the original papers, now over 20 years old, are not cited. Still, what is surprising about Figure 2 is that the decline is not even greater, given the excitement for genomics and other molecular approaches for examining marine microbes.

Another reason for the demise of

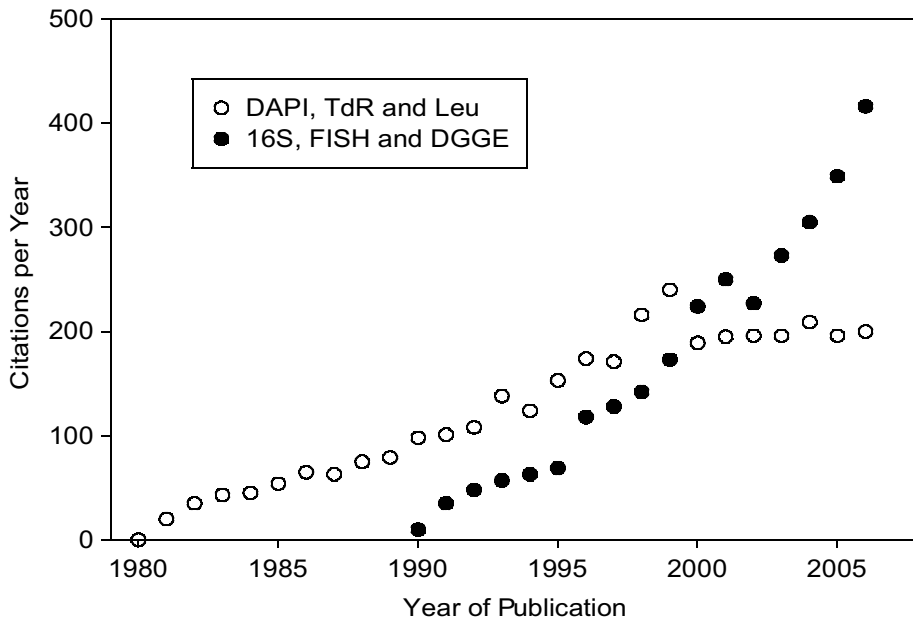


Figure 2. Number of papers citing classics in traditional and molecular microbial ecology. The traditional side of microbial ecology was represented by summing all papers citing Fuhrman and Azam (1980) for the thymidine (TdR) method (666 citations), Porter and Feig (1980) for a direct count method (“DAPI”) (2443 citations), and Kirchman et al. (1985) (370 citations) and Simon and Azam (1989) (792 citations) for the leucine (Leu) method for a total of 3457 unique citations (no duplicates). Molecular microbial ecology was represented by summing all papers citing Amann et al. (1990) for the fluorescence in situ hybridization method (FISH) (934 citations), Giovannoni et al. (1990), who constructed some of the first 16S rRNA clone libraries from the oceans (711 citations), and Muyzer et al. (1993) for denaturing gradient gel electrophoresis (DGGE) (1993 citations) for a total of 3048 unique citations. The analysis was done on May 12, 2007, using ISI Web of Science.

traditional methods is that the questions they targeted will be answered (or we’ll realize they weren’t the right questions), or they will be replaced by better methods. Certainly, there is much room for improvement in these methods. Old approaches already have been freshened up with the addition of molecular facets. For example, the combination of uptake of radiolabeled organic compounds, which was first used in marine microbial ecology 40 years ago (Williams and Askew, 1968), was updated with methods that track ribosomal RNA genes. Unicellular N_2 -fixing microbes were discovered in the ocean by molecular methods, but their contribution to total N_2 fixation and the N cycle was estimated

with old-fashioned size fractionation and ^{15}N experiments.

PREDICTION 6. Remote Sensing of Marine Microbes Will Produce as Much Data as Genomics by 2017.

The GOS expedition released a tsunami of sequence data (Rusch et al., 2007). Yet, those data came from a thin ribbon of only 41 surface stations that stretched along the east coast of North America, through the Gulf of Mexico, and into the eastern end of the equatorial Pacific. Compare this sampling density with that of the international Argo project, which has launched over 3000 drifting buoys to measure tempera-

ture and salinity in the upper 2000 m of the world’s ocean (<http://wo.jcommops.org/cgi-bin/WebObjects/Argo>). Even when *Sorcerer II* completes her round-the-world cruise and the last sequencing run has ended, the area sampled by GOS will be tiny compared to the vastness of the ocean. This sampling problem is not a new one. Biological oceanographers have long suffered from physics envy and have coveted the sample number and density that are routine in physical oceanographic studies.

We predict that microbial oceanographers will soon solve the sampling problem. By the year 2017, genomic-enabled technology will go where traditional microbial methods have not gone before—on moorings and buoys, remotely operated vehicles, and other mobile platforms. We may not have a Star Trek Tricorder for the oceans by 2017, but microarrays, miniature mass spectrometers, and other microfluidic devices will be as common as filtration rigs are today. The lab-on-a chip in the year 2017 will enable microbial oceanographers to finally collect data on scales relevant for understanding the factors controlling microbial communities and those communities’ role in biogeochemical cycles in the oceans.

PREDICTION 7. Models of the Global Carbon Cycle Will Have More Compartments and Links for Microbes than for Physics by 2017.

Today’s biogeochemical models usually try to capture the relevant physical processes while microbes are relegated to a few boxes (“phytoplankton” and “bacteria”), if they are explicitly modeled at

all. We predict that the situation will be the reverse by the year 2017. Microbial oceanographers and biogeochemists already have been pushing modelers to include more microbes and microbial processes explicitly in models rather than just hiding them in an obscure parameter or conglomerating them in a black box. But the oncoming tsunami of genomic data cannot be ignored. Old and new data will surely push out physics in models by 2017.

Unfortunately, we will need microbes in models more than ever over the next decade, as greenhouse gases continue to build up and our planet warms due to gas-guzzling SUVs, dirty coal-fueled power plants, and denuded forests. Information about microbes is essential for predicting how the ocean fares in the Anthropocene, and in turn the ocean is essential for predicting the global climate in 2017 and beyond. Marine microbes produce or consume nearly all greenhouse gases, ranging from carbon dioxide to nitrous oxide, and the ocean dominates nearly all stocks and fluxes of these gases on the planet.


Society needs microbial ecology because of its importance, but microbial ecologists do the work because of its intellectual challenges and rewards. E.O. Wilson said it well near the end of his autobiography (Wilson, 1994):

If I could do it all over again, and relive my vision in the twenty-first century, I would be a microbial ecologist... Into that world I would go with the aid of modern microscopy and molecular analysis. I would cut my way through clonal forests sprawled across grains of sand, travel in an imagined submarine through drops of water proportionately

the size of lakes, and track predators and prey in order to discover new life ways and alien food webs.

The ocean will still harbor virgin clonal forests and undiscovered microbial aliens by the year 2017, leaving much for marine microbial ecologists to do over the next ten years. Surely, all can agree with this prediction.

ACKNOWLEDGEMENTS

We thank Penny Chisholm for her contributions to this paper, several young microbial oceanographers, too numerous to mention here, who shared their visions of the future, and Dave Karl for his comments and input. Writing of this paper was supported by NSF grant MCB -043993 awarded to D.L.K. and by grant GEN μ MAR (CTM2004-02586/MAR) from the Spanish Ministerio de Educación y Ciencia to C.P.-A. 

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