### Feature From the National Academies

## Metagenomics: A Call for Bringing a New Science into the Classroom (While It's Still New)

Anne Jurkowski,\* Ann H. Reid,<sup>†</sup> and Jay B. Labov<sup>‡</sup>

\*Division on Earth and Life Studies, <sup>†</sup>Board on Life Sciences, and <sup>‡</sup>Center for Education, National Research Council, Washington, DC 20001

#### INTRODUCTION

The pace of research and the development of new areas of focus in biology are increasing at breathtaking speed. Unfortunately, exciting new areas of science typically do not appear in science classrooms and textbooks until many years after their inception. This pattern leaves undergraduate, and especially high school, biology education lagging behind scientific advances. The result is that too many students are never afforded opportunities to learn about the cutting-edge discoveries that make biology so exciting to professional scientists.

For example, under the radar of public attention, or even that of most biologists, microbiology is undergoing a renaissance. New ways of thinking about microbes and new technologies for studying them are turning one of the oldest branches of biology into an area of unexpected discoveries. A National Research Council (NRC) committee has recently concluded in its report, The New Science of Metagenomics: Revealing the Secrets of Our Microbial Planet (NRC, 2007a)<sup>1</sup>, that the emerging field of metagenomics may well revolutionize research in microbiology; moreover, the new paradigm on which metagenomics is based has the potential to transform how research and theory in many other areas of biology are configured (e.g., Dunning Hotopp et al., 2007; Figure 1). Metagenomics will also lead to a plethora of practical applications, from new medical approaches to alternative sources of energy, as scientists from many disciplines learn to harness the power of microbial communities.

The birth of this exciting new field (described more fully below) provides the life sciences research and education communities with a powerful and rare opportunity. Metagenomics is so young, and the microbial world it seeks to characterize is so vast, that there is a real possibility that scientists, teachers, and students in many areas of science can work together to advance this field. By acting now to incorporate metagenomics into biology education and to utilize biology education to inform questions and future research paths for metagenomics, the life sciences community can begin to shift from the current situation, in which scientific advances take decades to reach the classroom, toward a system in which education and research are deliberately and strategically integrated with each other from the very beginning.

This article outlines why the new science of metagenomics is so well suited to serve as a model for such an approach to keeping biology education current. It also serves as a call to the life sciences community to help the NRC and its Board on Life Sciences<sup>2</sup> to think about issues, opportunities, and challenges that could be incorporated into some combination of formal studies and convening activities to facilitate the integration of research and education in metagenomics. To further develop the framework for this proposal, we invite interested readers to post responses to the questions that are posed in the final section of this article by clicking on the Reader Comments link.

#### RELEVANCE AND FUTURE APPLICATIONS OF METAGENOMICS TO THE BIOLOGICAL SCIENCES

When we try to pick out anything by itself, we find it is tied to everything else in the universe.

John Muir (Muir, 1911)

Muir's quote is particularly apt and striking when applied to the microbial world. Existing within, on, and around every living being and in nearly every environment on Earth, microorganisms are by far the most abundant and diverse form of life and serve as the "connective tissue" of the planet. Metagenomics is a potent new tool that vastly expands the ability of scientists to study the myriad capabilities of microbial communities and the as yet unrecognized relationships and interactions of microbes with other forms of life and the environment.

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Address correspondence to: Jay B. Labov (jlabov@nas.edu). <sup>1</sup> Additional information and resources from the National Academies on microbes and metagenomics can be accessed at http:// www.nationalacademies.org/metagenomics.

<sup>&</sup>lt;sup>2</sup> For more information about the Board on Life Sciences, see http:// www.nationalacademies.org/bls.

# THE NEW SCIENCE OF **METAGENOMICS**

## **Revealing the Secrets of Our Microbial Planet**

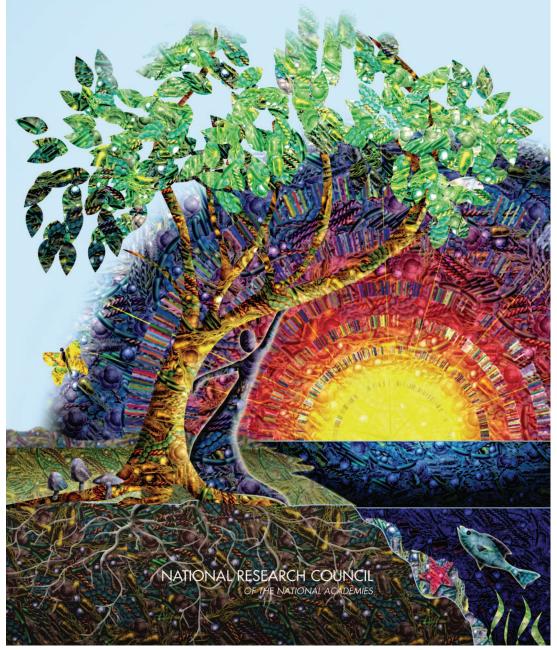


Figure 1. The cover of the NRC report on metagenomics (NRC, 2007a).

#### The Metagenomics Process

A miniscule fraction—most scientists estimate <1%—of the microbial species on Earth can be cultured and studied using classical microbiology and genomics techniques. But by using recently developed metagenomics tools, researchers apply genomic analysis to entire microbial communities at once, bypassing the need to isolate and culture individual species. Metagenomics studies begin by obtaining a sample from a particular environment such as seawater, soil, or the human gut, extracting genetic material from all of the organisms in the sample and then analyzing the DNA in that mixture to gain insights on how members of the community interact, change, and perform complex functions (Figure 2).

Because it does not depend on establishing pure cultures, metagenomics offers access to millions of microbial species that previously could not be studied. It also enables researchers to examine microorganisms in the context of the environments in which they naturally exist, studying entire communities at the same time (e.g., Bohannon, 2007).

#### Applications of Metagenomics

Virtually all biologists, regardless of their field, will find that greater understanding of microbial communities and metagenomics can contribute to their own research. Studying microbial communities through metagenomics can help biologists tackle fundamental scientific questions and address related social, environmental, and economic problems. The following are some of the potential applications of metagenomics:

Advances in the Life Sciences. Deciphering how species within microbial communities function and interact can partially answer fundamental questions about many aspects of microbial, plant, and animal biology and greatly enhance understanding of ecology and evolution. Metagenomics could help address such questions as: What constitutes a genome? What is a species? How diverse is life?

*Earth Sciences.* Exploring how microbial communities in the soil and in the oceans affect atmospheric balances and environmental conditions can help scientists better understand, predict, and potentially address global changes.

*Medicine*. Hundreds of drugs available today were derived from chemicals first found in microbes; access to the ge-

nomes of additional microbial species holds great promise for discovering thousands more. Studying the human "microbiome"—the trillions of bacteria living within and on the human body—may lead to new ways to diagnose, treat, and prevent disease (e.g., Gill *et al.*, 2006).

*Alternative Energy.* New sources of energy could be developed by harnessing the power of microbial communities to produce byproducts including hydrogen, methane, butanol, and even electric current.

*Environmental Remediation.* Understanding the microbes that degrade environmental chemicals can help clean up such pollutants as gasoline leaks, oil spills, sewage, industrial discharges, and nuclear waste.

*Biotechnology.* Identifying and exploiting the versatile and diverse biosynthetic capabilities of microbial communities may lead to the development of beneficial new industrial, food, and health products.

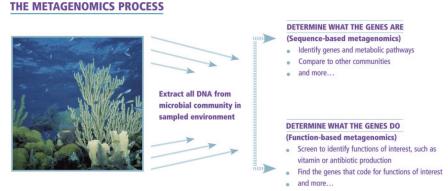
*Agriculture.* Gaining a better understanding of the beneficial microbes living in, on, under, and around domestic plants and animals can contribute to improved methods for detecting disease agents in crops, livestock, and food products and can facilitate the development of farming practices that take advantage of the natural alliances among microbes and plants and animals.

*Biodefense and Microbial Forensics.* Studying the DNA and biochemical fingerprints of microbial communities helps specialists monitor known and potential pathogens, create more effective vaccines and treatments against potential bioterror agents, and reconstruct events in which microbes have played a role.

#### Value of Metagenomics to Biology Education

Muir's quote also has an important relevance for science education. What separates chemistry, genetics, molecular biology, evolution, ecology, and other disciplines? Where do they intersect, and how do they build from and upon each other?

Metagenomics helps bridge the gap between genetics and ecology, demonstrating that the genes of a single organism are connected to the genes of others and to the entire com-



**Figure 2.** The process of metagenomics. Metagenomics involves obtaining DNA from all microorganisms within a community, without necessarily identifying all of the species involved. After the genes are sequenced and compared with identified sequences, the functions of these genes can be determined.

munity. In fact, the processes of metagenomics demonstrate that it is important to study genes and organisms in context and to appreciate the entire diversity of life, even in a single setting. These messages have important relevance across biology and would be valuable additions to any biology class—perhaps especially those at the introductory level.

Because metagenomics draws from and impacts a wide range of fields, it is a valuable tool for teaching themes and concepts that are woven throughout biology education. Indeed, teaching and learning about metagenomics clearly could incorporate the kinds of changes in K–12 and undergraduate science education that numerous reports have called for over the last decade (e.g., American Association for the Advancement of Science, 1993; Handelsman *et al.*, 2004, 2006; Labov, 2004; NRC, 1996, 1999, 2002, 2003, 2005, 2007b; National Science Foundation, 1996; Rutherford and Ahlgren, 1991).

Some faculty feel that they must use introductory courses to provide students with virtually all the knowledge they will use to understand the basic concepts of a discipline. Some also view introductory courses as a way to help students learn how to interpret news and other information about science so that they can make more informed decisions in the home, at the doctor's office, and in the voting booth. Too often, however, such courses fail to convey the complex beauty of the living world and the innumerable ways that biology impacts "real life." Learning about metagenomics at the introductory level-with an emphasis on its potential real-world applications-could serve to illuminate the basic principles of a wide variety of fields, the connections among them, and the broader relevance of scientific advances to real-world issues. If students can see that there really are interesting unsolved questions that they can play a role in answering, the recruitment of talented young people to science careers may be facilitated. In this way, students will encounter a science that is dynamic rather than static.

## THE BENEFITS OF INTEGRATING EDUCATION AND RESEARCH

The benefits of integrating metagenomics and other new sciences into biology education at an early stage would serve not only biology students but scientists and their research projects, as well. Experience shows that when researchers teach, their own understanding becomes deeper, leading to new and often unexpected questions and avenues for research that are posed by students, as well as contributing to the development of creative approaches to problems (Full, 2007). If the biology community can integrate education about metagenomics with advances in research from the beginning, students could become active participants in developing the field.

Teaching a new or emerging field is an ideal way to deeply engage students in exploring fundamental questions that are at the heart of scientific pursuit and to encourage them to ask their own questions. Indeed, in the case of the emerging field of metagenomics, the most basic questions may be the most profound. Addressing these questions in turn inspires young minds and active researchers alike, and science benefits.

Others have seen the value of integrating emerging science with education. A number of efforts are currently under way to integrate genomics research and education. For example,

- Campbell *et al.* (2006, 2007) have established the Genome Consortium for Active Teaching (GCAT). The goal of this consortium is to facilitate the use of modern genomics methods in undergraduate education with an emphasis on preparing the next generation of life science researchers as recommended in the NRC report *Bio2010: Transforming Undergraduate Education for Future Research Biologists* (NRC, 2003). This effort has initially focused on the use of microarray analysis in undergraduate science laboratories (Campbell *et al.*, 2007).
- The Genomics Education Partnership (GEP),<sup>3</sup> established at Washington University in St. Louis and supported by the Howard Hughes Medical Institute (HHMI), provides opportunities for undergraduates to participate in genomics research. In this program students learn how to take raw genomics data to finished sequence and to annotate genes, with the ultimate goal of student publication (e.g., Slawson *et al.*, 2006). The GEP provides opportunities for faculty and students from primarily undergraduate institutions to collaborate on genomic research projects.
- Also sponsored by HHMI, *Phage-Hunters* enables both undergraduate and high school students to isolate and characterize the genomes of previously unknown bacteriophages. Research findings and a description of this student-oriented program are described in Hatfull *et al.* (2006) and on the website of HHMI.<sup>4</sup>
- Brad Goodner at Hiram College and his colleagues have also worked to incorporate genomics research into undergraduate biology programs. In addition to involving many students in research that is examining the genomics and other aspects of the biology of several species of bacteria (e.g., *Agrobacterium tumefaciens*: Goodner *et al.*, 1999, 2001; *Chromohalobacter salexigen*: Csonka *et al.*, 2005), Goodner and colleagues have been investigating ways to improve biology education more generally through the use of genomics research (e.g., Goodner, 2003; Goodner *et al.*, 2003).

Participation of students at many age levels has contributed to the advancement of numerous international research efforts (e.g., Monarch Watch,<sup>5</sup> Global Challenge,<sup>6</sup> and Council on Undergraduate Research<sup>7</sup>).

<sup>&</sup>lt;sup>3</sup> Additional information is available at http://gep.wustl.edu/.

<sup>&</sup>lt;sup>4</sup> Additional information is available at http://www.hhmi.org/ news/hatfull20060609.html.

<sup>&</sup>lt;sup>5</sup> Monarch Watch is an educational outreach program based at the University of Kansas that engages citizen scientists in large-scale research projects. This program produces real data that relate to a serious conservation issue. Monarch Watch gets children of all ages involved in science. For more information, see http://www.world wildlife.org/monarchs/publications/bbrfactsheet.pdf.

<sup>&</sup>lt;sup>6</sup> Founded by the Arno Group, LLC and the University of Vermont's College of Engineering and Mathematical Sciences, teams of U.S. high school students collaborate with international counterparts to address global climate change. Additional information is available at http://www.globalchallengeaward.org/.

<sup>&</sup>lt;sup>7</sup> The mission of the Council on Undergraduate Research is to support and promote high-quality undergraduate student-faculty

#### METAGENOMICS AS A MODEL FOR EDUCATION-RESEARCH INTEGRATION

There is still so much to know in the field of metagenomics that research by students could advance the field significantly. For example, many metagenomics projects involve collecting and processing huge numbers of samples to compare microbial communities from similar environments in different locations. Imagine an enormous sampling effort involving students from all over the world: a global soil analysis, for example. With a relatively simple infrastructure of sampling kits and established procedures, the body of data available for metagenomic analysis could expand enormously as the result of student efforts. Technical advances, advances in basic microbiology, and the establishment of an efficient data management and bioinformatics framework in the coming years could well make student participation in metagenomic sampling a viable possibility both technically and economically.

A first step is to raise interest in and awareness of these possibilities among both the biology education and research communities. Frameworks will need to be developed for engaging students in learning about microbial communities and their influences on and interactions with other organisms in different environments and the practical applications of metagenomics. From there, the role of metagenomics in biology education can evolve and expand where necessary in response to the needs of students and researchers.

There is also a need to educate new and practicing K–12 and postsecondary faculty about the science underlying metagenomics, its interdisciplinary implications, and the potential for both students and their instructors to participate in both basic and applied research. Such an effort would benefit from engaging all components of the life sciences community in making decisions about how metagenomics can be integrated with the current system of science education.

#### HOW CBE-LSE READERS CAN CONTRIBUTE

The authors of this article, the NRC's Board on Life Sciences, and the senior editors of *CBE-LSE* invite a discussion among the life sciences community to explore how metagenomics might be a viable addition to tomorrow's biology curriculum. Please contribute your thoughts about the following questions by clicking on the Reader Comments link.

- 1. How might you envision metagenomics being incorporated into *your* discipline of biology? What does it have to contribute to your field? For example, are there ways that a better understanding of previously unstudied microbial communities might affect your area of research (e.g., Dunning Hotopp *et al.*, 2007)? Are there ways in which metagenomic sequencing or functional metagenomics could help you to gain insights about your field?
- 2. How might life sciences faculty build metagenomics into current courses for biology majors and especially courses

that might not currently include consideration of microbes and microbial biology?

- 3. How might life sciences faculty include metagenomics in courses for nonbiology or nonscience majors?
- 4. What aspects of metagenomics might best be incorporated into interdisciplinary science courses?
- 5. How might your students begin to actively participate in the development of the field? What resources would you need to engage your students in this type of research? Can you envision projects involving all students in a course as well as research by individual or small groups of students?
- 6. What additional advice would you give the NRC about the kinds of studies and convening activities that are needed to help the scientific community integrate research and education about metagenomics?

#### REFERENCES

American Association for the Advancement of Science (1993). Benchmarks for Science Literacy. Washington, DC. http://www. project2061.org/publications/bsl/online/bolintro.htm (accessed 31 August 2007).

Bohannon, J. (2007). Ocean study yields a tidal wave of microbial DNA. Science 315, 1486–1487. http://www.sciencemag.org/cgi/content/full/315/5818/1486 (accessed 31 August 2007).

Campbell, A. M., Eckdahl, T. T., Fowlks, E., Heyer, L. J., Hoopes, L.L.M., Ledbetter, M. L., and Rosenwald, A. G. (2006). Collaborative programs. Genome Consortium for Active Teaching (GCAT). Science 311, 1103–1104. http://www.sciencemag.org/cgi/content/summary/311/5764/1103?ijkey=2150492ecc52bf6784dd7 ce340006a495cbd8904&keytype2=tf\_ipsecsha (accessed 31 August 2007).

Campbell, A. M., Ledbetter, M.L.S., Hoopes, L.L.M., Eckdahl, T. T., Heyer, L. J., Rosenwald, A., Fowlks, E., Tonidandel, S., Bucholtz, B., and Gottfried, G. (2007). Genome Consortium for Active Teaching: Meeting the Goals of BIO2010. Cell Biol. Educ. 6, 109–118. http:// www.lifescied.org/cgi/content/full/6/2/109?maxtoshow=&HITS= 10&hits = 10&RESULTFORMAT = &author1 = campbell&and orexactfulltext = and & searchid = 1&FIRSTINDEX = 0&sortspec = relevance&resourcetype=HWCIT (accessed 31 August 2007).

Csonka, L. N., Connor, K. O., Larimer, F., Richardson, P., Lapidus, A., Ewing, A. D., Goodner, B. W., and Oren, A. (2005). What we can deduce about metabolism in the moderate halophile *Chromohalobacter salexigens* from its genomic sequence. In: Adaptation to Life at High Salt Concentrations in Archaea, Bacteria, and Eukarya, ed. N. Gunde-Cimerman, A. Oren, and A. Plemenitas, Dordrecht: Springer, Chapter 18, 267–287.

Dunning Hotopp, J. C. *et al.* (2007). Widespread lateral gene transfer from intracellular bacteria to multicellular eukaryotes. Published online 30 August 2007 [DOI: 10.1126/science. 1142490] (in *Science* Express Reports). Abstract available at http://www.sciencemag.org/ cgi/content/abstract/1142490v1?maxtoshow=&HITS=10&hits=10& RESULTFORMAT = & fulltext = Dunning + Hotopp & searchid = 1 & FIRSTINDEX=0&resourcetype=HWCIT (accessed 31 August 2007).

Full, R. J. (2007). Remarks from plenary session at the Summer Institute of Science Education for New Civic Engagements and Responsibilities (SENCER). Portland, ME, August 4, 2007. http:// sencer.net/Institutes/pdfs/SSI\_2007/Presentations/Plenary\_Full. pdf (accessed 31 August 2007).

Gill, S. R., Pop, M., DeBoy, R. T., Eckburg, P. B., Turnbaugh, P. J., Samuel, B. S., Gordon, J. I., Relman, D. A., Fraser-Liggett, C. M., and Nelson, K. E. (2006). Metagenomic analysis of the human distal gut microbiome. Science *312*, 1355–1359.

collaborative research and scholarship. Additional information is available at http://cur.org.

Goodner, B. (2003). Other benefits of genomics. Letter to the editor. ASM News January issue. http://www.asm.org/microbe/index. asp?bid=11774 (accessed 31 August 2007).

Goodner, B. *et al.* (2001). Genome sequence of the plant pathogen and biotechnology agent *Agrobacterium tumefaciens* C58. Science 294, 2323–2328.

Goodner, B. W., Markelz, B. P., Flanagan, M. C., Crowell, C. B., Jr., Racette, J. L., Schilling, B. A., Halfon, L. M., Mellors, J. S., and Grabowski, G. (1999). Combined genetic and physical map of the complex genome of *Agrobacterium tumefaciens*. J. Bacteriol. 181, 5160–5166.

Goodner, B. W., Wheeler, C. A., Hall, P. J., and Slater, S. C. (2003). Massively parallel undergraduates for bacterial genome finishing. ASM News 69, 584–585. http://www.asm.org/microbe/index.asp? bid=23486 (accessed 31 August 2007).

Handelsman, J. *et al.* (2004). Scientific teaching. Science 304, 521–522. http://www.sciencemag.org/cgi/content/full/304/5670/521 (accessed 31 August 2007).

Handelsman, J., Miller, S., and Pfund, C. (2006). Scientific Teaching, New York: Freeman.

Hatfull, G. F. *et al.* (2006). Exploring the mycobacteriophage metaproteome: phage genomics as an educational platform. PLoS Genet. 2(6): e92. http://www.pubmedcentral.nih.gov/articlerender.fcgi? artid=1475703 (accessed 31 August 2007).

Labov, J. B. (2004). From the National Academies: The challenges and opportunities for improving undergraduate science education through introductory courses. Cell Biol. Educ. *3*, 212–214. http://www.lifescied.org/cgi/content/full/3/4/212 (accessed 31 August 2007).

Muir, J. (1911). My First Summer in the Sierra, Boston: Houghton Mifflin.

National Research Council (NRC) (1996). National Science Education Standards, Washington, DC: National Academies Press. http:// www.nap.edu/catalog.php?record\_id=4962 (accessed 31 August 2007). NRC (1999). Transforming Undergraduate Education in Science, Mathematics, Engineering, and Technology, Washington, DC: National Academies Press. http://books.nap.edu/catalog.php? record\_id=6453 (accessed 31 August 2007).

NRC (2002). Learning and Understanding: Improving Advanced Study of Mathematics and Science in U.S. High Schools, Washington, DC: National Academies Press. http://books.nap.edu/catalog. php?record\_id=10129 (accessed 31 August 2007).

NRC (2003). Bio 2010, Transforming Undergraduate Education for Future Research Biologists, Washington, DC: National Academies Press. http://books.nap.edu/catalog.php?record\_id=10497 (accessed 31 August 2007).

NRC (2005). America's Lab Report: Investigations in High School Science, Washington, DC: National Academies Press. http://books. nap.edu/catalog.php?record\_id=11311 (accessed 31 August 2007).

NRC (2007a). The New Science of Metagenomics: Revealing the Secrets of Our Microbial Planet, Washington, DC: National Academies Press. http://books.nap.edu/catalog.php?record\_id=11902 (accessed 31 August 2007).

NRC (2007b). Taking Science to School: Learning and Teaching Science in Grades K-8, Washington, DC: National Academies Press. http://www.nap.edu/catalog.php?record\_id=11625 (accessed 31 August 2007).

National Science Foundation (NSF) (1996). Shaping the Future: Strategies for Revitalizing Undergraduate Science Education, Arlington, VA: NSF. http://www.nsf.gov/pubs/1998/nsf9873/ nsf9873.doc (accessed 31 August 2007).

Rutherford, F. J., and Ahlgren, A. (1991). Science for All Americans, New York: Oxford University Press. http://www.us.oup.com/us/ catalog/general/subject/Education/?view=usa&ci=9780195067712 (accessed 31 August 2007).

Slawson, E. E. *et al.* (2006). Comparison of dot chromosome sequences from *D. melanogaster* and *D. virilis* reveals an enrichment of DNA transposon sequences in heterochromatic domains. Genome Biol. 7, R15.