Letters

Coordinating Efforts to Understand Microbes in the Environment

I am writing in regard to a Current Topics article by Jeffrey L. Fox in the January 2005 issue of *ASM News* (p. 6). The article discussed the increasing number of 16S rRNA sequences and their continued utility in studies of environmental microbiology. In addition, the article quoted some pioneers in the field lamenting the lack of concerted efforts to characterize all the microbial players in the environment. I completely agree with these sentiments. The article also suggested that there are no concerted efforts in the genome sequencing arena to capture this diversity. I agree that there are few such efforts but I would like to point out one that we are doing at TIGR. We have been sequencing genomes of representatives of phyla of bacteria for which there are no available complete genome sequences as part of the national Science Foundation "assembling the Tree of Life" program (more information on our project can be found at http://www.tigr.org/tol). Unquestionably there is a need for a much more globally organized approach to characterizing the genomes of organisms from across the tree as well as those that might be of relevance in the environment. ASM might be the ideal group to organize such an effort across all types of microbes.

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Origin of AIDS Revisited

The origin of the AIDS pandemic remains a mystery (*ASM News*, January 2005, p. 15). One theory holds that human immunodeficiency virus type 1 (HIV-1) evolved from a chimpanzee retrovirus, SIVcpz, that crossed the species barrier in an unknown manner (F. Gao, E. Bailes, D. L. Robertson, et al., Nature **397:**436–441, 1999). This theory is based primarily on the discovery of a chimp named Marilyn who was found to be infected with a retrovirus that closely resembled HIV-1 (R. V. Gilden, L. O. Arthur, W. G. Robey, et al., Lancet **i:**678–679, 1986). Extensive testing in other chimps has so far failed to reveal similar infection in more than a handful of animals, and the origin of SIVcpz itself remains a mystery.

We have examined new information about chimps such as Marilyn who were used in animal experiments or followed in the wild in the 1960s (W. D. Hillis , Am. J. Hyg. **73:**316–328, 1961; B. W. Allmond, Jr., J. E. Froeschle, and N. B. Guilloud, Am. J. Epidemiol.**85:**229–239, 1967; J. Goodall, *The Chimpanzees of Gombe: Patterns of Behaviour*, Harvard University Press, Cambridge, 1986; J. van Lawick-Goodall, *In the Shadow of Man*, Houghton Mifflin Company, Boston, 1971). Chimps from African vendors were sometimes inoculated intraperitoneally with pooled human whole blood in order to "protect them from human diseases." This practice was thought to be the cause of an infectious hepatitis outbreak among chimp handlers in 1960 at Holloman Air Force Base in New Mexico, the same location where Marilyn was housed. Thus inoculation with human blood in Africa could have been the source of Marilyn's retroviral infection. Furthermore, chimps in Africa and the United States suffered from outbreaks of poliomyelitis, and these animals received an oral polio vaccine derived from human diploid cell strains on at least one occasion in 1967. Thus, chimps were exposed to blood products and vaccines that could have transmitted an HIV-1 precursor virus that evolved into SIVcpz (S. Corbet, M. C. Muller-Trutwin, P. Versmisse, et al., J. Virol. **74:**529–534, 2000). This virus would have been difficult to transmit among chimps, as HIV-1 is not readily transmitted from infected to uninfected animals (P. N. Fultz, C. Greene, W. Switzer, B. Swenson, et al., J. Med. Primatol. **16:**341–347, 1987). Hence the small number of SIVcpz cases.

Sporadic exposure of chimps to human blood products and vaccines in the 1960s suggests that SIVcpz evolved in parallel with HIV-1, rather than being its evolutionary parent. The common source of the human and chimp retrovirus that spawned the AIDS pandemic remains to be elucidated (B. Goldberg and R. B. Stricker, J. Theor. Biol. **204:**497–503, 2000).

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Single-Cell Microbiology Needs Visions

In a review published recently in *Microbiology and Molecular Biology Reviews* (**68:**538–559, 2004), Brehm-Stecher and Johnson pointed out the need for single-cell microbiology to address the heterogeneity issues compounding the population approach of studying microbiology and summarized recent advances in technologies that have enabled unprecedented efforts of studying microorganisms as single cells. I am glad to see that, after years of appealing for mainstream microbiologists to pay due attention to the importance of individual approaches of studying microorganisms (*ASM News* **65:**185, 1999 and **66:**123, 2000; *Logical Biology* 1:5–16 and 25–31, 2000), this field finally got its appropriate attention. However, I am very disappointed to say that, besides introducing tools and technologies and compiling some application data, this review provided little insight in understanding individual microbial lives.

In my opinion, a lack of suitable tech-

nologies is only a minor obstacle for applying the single-cell approach to study microbial life. A "mind constraint" is in fact the greatest cause for ignoring the necessity of studying microbial life on the individual basis. This mind constraint started with some dogmatic views which were based on indirect observations and subjective reasoning but have been reinforced into some "law-like" principles through casual or even irresponsible citations (Logical Biol. **1**:5–16 and 25–31, 2000). To promote logical reasoning and judgment in biological research, I launched an Internet-based journal called *Logical Biology* (http://logibio.com). I published most of my unique observations on single bacteria and novel hypotheses of microbial life there, along with some critical reviews and logical and historical analyses on microbiology. The journal has also published original papers on observations of bacterial aging and disclosed the application of a true cell age synchronization methodology. These novel observations and reasoning shed lights into the current debate on cell synchronization methodologies (Trends Biotechnol. **23**:9–10, 2005).

I believe that there has been too much emphasis on the role of technologies for the delay or advancement of single-cell microbiology. In my opinion, a lack of insightful vision is the paramount problem in advancing single-cell microbiology, especially when plenty of technologies are available. I also believe that the holy grail of single-cell microbiology is not revealing the differences and identifying the scope of heterogeneity in parameters measured by the population approaches. In fact, the quick and easy process of using population/culture approaches to obtain the average values of some biotic parameters is and should continue to be the strong point of microbiology as compared with macrobiology. The soul and spirit of single-cell microbiology should be reflected in its power to reveal the true causes underlying the variations within a population. I compare most current single-cell studies as the "cross-sectional" type where multiple individual microorganisms are separately measured at the same time. This kind of study may play only a minor role in extending our knowledge of microorganisms because it mainly adds some "standard deviation" type data to the existing knowledge of "averages." In contrast, the "longitudinal" single-cell studies where individual microorganisms are followed for their life time—a time period that should be at least longer than one "cell cycle" (cell reproduction cycle)—would be much more important for reaching a true understanding of microbial lives as single cells (Sci. China **42**:644–654, 1999).

Woese recently made a very truthful and pertinent remark about the relationship between technology and vision on the science development. He said that "Science is impelled by two main factors, technological advance and a guiding vision (overview) . . . without the proper technological advances the road ahead is blocked. Without a guiding vision there is no road ahead." (Microbiol. Mol. Biol. Rev. **68**: 173–186, 2004). Now we have many much advanced technologies for performing research on single cells/ microbial individuals. However, what visions do we have for guiding research in single-cell microbiology?

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