Letters

Minority Microbiologists and ASM

Congratulations on Marion Johnson-Thompson’s excellent article “Contribution of African-American Scientists to ASM” in the February issue of Microbe (p. 82). The emergence of minority microbiologists, from Wilton Taylor and Gerald Stokes to Clifford Houston, the first African-American President of ASM, occurred only during the last 30% of the history of SAB/ASM. As Marion Johnson-Thompson so rightly points out, “Times have changed and environments are more supportive of the presence of blacks in the discipline of microbiology and in ASM.” Minority recognition accompanied ASM’s renewed interest in governmental affairs. This transition is another example where individuals make a difference. Robert Watkins is one such individual. Initially hired in 1975 as Robert Acker’s administrative assistant, Watkins made a substantial impact through effective coordination of the public affairs activities of the Society. He provided a valuable link between the newly formed Public Affairs Committee under the leadership of Don Cox, the Executive Director, and public affairs components of other professional biological societies. In 1975 this title was later changed to Public Affairs Officer.

The ASM Public and Scientific Affairs Board (PSAB) was formed in 1979 to “serve the science of microbiology by promoting adoption of sound policies at local, national, and international levels that affect the discipline of microbiology or which should be influenced by knowledge gained from research in microbiology.” There was considerable discussion as to the breadth of activities that this new Board would undertake. This process took several years. In my opinion the creation of the Committee on the Status of Minority Microbiologists in 1984 would not have been possible without the wise and thoughtful role of Bob Watkins and without the able chairmanship of Gerald Stokes. As the founding Director of the Office of PSAB, Bob Watkins’s sound advice not only guided the scope and functions of this new Board, but also convinced members early on the Board of the importance of minority members to the Society. His contacts with the Black Caucus in Congress and other minority organizations were invaluable in assisting PSAB in promoting ASM’s goals. These contacts were significantly aided by Henry Williams, one of the early ASM Congressional Fellows, who brought his experience and insights to ASM. The Robert D. Watkins Graduate Research Fellowship, created in 1997, is recognition of his many contributions to ASM.

I applaud ASM’s continued efforts to engage underrepresented members in the Society’s activities. We would do well to heed Marion Johnson-Thompson’s summary and advice as well as the recommendations of the ASM Minority Task Force (1998) under the leadership of George W. Counts.

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Risks of Lyme Vaccine


Nobody disputes the attractiveness of a vaccine to counter the epidemic spread of Lyme disease and related tickborne coinfections (R. B. Stricker, ASM News 70: 1–2, 2004). However, the scientific community must first acknowledge the very real problems with “a disastrous episode in the history of public health” related to Lymerix® before it can move on to a safer and more effective vaccine strategy. Blaming the Internet is not enough.

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FDA and the Antibiotic Breakpoint Updating Process

We read with interest the Current Topics article prepared by Jeffrey L. Fox, “FDA reasserts authority over antibiotic breakpoint updating process,” in the May 2007 issue of Microbe (p. 222). We were disappointed that such an important article did not present a more balanced view of all stakeholders, including interviews with additional clinical microbiologists or clinicians including those specializing in infectious diseases. However, Fox accurately points out the key regulatory requirements of the Food and Drug Administration (FDA) and the patient safety benefits of regular updates to breakpoints in the face of emerging bacterial resistance. FDA and Clinical and Laboratory Standards Insti-
tute (CLSI, formerly NCCLS) share common interests in establishing breakpoints for interpretation of antimicrobial susceptibility tests. CLSI convened a special meeting in January, which included representatives from FDA, CDC, large and small pharmaceutical companies, diagnostic devices companies, clinical microbiologists, and infectious diseases clinicians from the United States and abroad, to discuss how CLSI and FDA can best work together on the issue of antibiotic susceptibility test interpretive breakpoints. The group recommended that CLSI publish the initial FDA breakpoints of newly approved antimicrobial agents following a brief presentation to CLSI by the drug’s sponsor. If the CLSI Subcommittee on Antimicrobial Susceptibility Testing (AST) does not agree with the FDA breakpoints, the drug will not be included in the CLSI susceptibility testing publications. Further, CLSI would not propose any alterations of the FDA breakpoints for at least two years following approval of the official drug label. If, after that time, emerging resistance or other issues arise that suggest the need to revise the breakpoints, the subcommittee would review all relevant data to determine if a change would be warranted. These recommendations have been endorsed by CLSI’s AST Subcommittee, Area Committee on Microbiology, and Board of Directors. This new approach should assuage the concerns of pharmaceutical companies that the FDA and CLSI breakpoints might differ for their new drugs. It should also better serve clinical microbiology laboratories and diagnostic device manufacturers because there will not be conflicting breakpoint recommendations for new drugs in the United States.

This approach to publication of FDA breakpoints for new agents allows CLSI to focus on older, often generic antibiotics that may have outdated or unhelpful drug labels regarding susceptibility testing. Some drug labels do not even include minimal inhibitory concentration (MIC) breakpoint criteria (e.g., ampicillin, oxacillin, gentamicin, amikacin). Emerging resistance that has occurred may dictate the need to update the breakpoints included in drug labels. CLSI has filed a citizen’s petition (an open process requiring an FDA response) to FDA to lower the breakpoints for vancomycin when testing Staphylococcus aureus, due to concerns of emerging resistance and reports of increased treatment failures. CLSI breakpoints are used in FDA-cleared susceptibility testing devices with several older drugs that lack useful susceptibility testing criteria in the drug label. CLSI is well positioned to review and revise as needed the susceptibility breakpoints for older agents. FDA does not at present systematically review the susceptibility criteria in older drug labels to determine if updates are needed because of emerging resistance. CLSI intends to adhere to the request of the FDA Deputy Commissioner by filing several additional citizens’ petitions that highlight the need to adopt revised susceptibility breakpoints for some drugs in the spirit of patient safety and improved therapeutic outcomes. This will also allow CLSI to serve its other non-U.S. stakeholders by providing clinically relevant susceptibility testing criteria. CLSI has been and continues to be a global leader in the standardization of antimicrobial susceptibility testing methodology, in quality assurance measures, and in establishing interpretive breakpoints. These tasks are accomplished by a committee of international volunteer experts that produce annual updates to antimicrobial agent breakpoints and quality control ranges. This process has been ongoing for the past 30 years, and will continue indefinitely with collaboration and contributions from all interested stakeholders.

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ERIC–Comprehensive Bioinformatics Resources for Enteropathogens

As part of the nation’s biodefense program, the National Institute of Allergy and Infectious Diseases (NIAID) created a Genomics Initiative. As one component, in 2004 NIAID awarded eight contracts for Bioinformatics Resource Centers (BRCs) for Biodefense and Emerging/Re-emerging Infectious Diseases (the full list of awardees can be viewed at www.niaid.nih.gov/dmid/genomes/brc/). These Centers were set up to promote basic research into the NIAID Category A-C pathogens, with a mission to facilitate discovery of diagnostics, vaccines, and therapeutics.

The Enteropathogen Resource Integration Center (ERIC) (funded by NIAID contract HMSN266200400040C) focuses on integrating genomics information on pathogenic Escherichia, Shigella, Salmonella, and Yersinia of relevance to biodefense, but also includes information on related bacteria for comparative genomics, such as model organism E. coli K-12. All ERIC resources are available through the Web portal at www.ericbrc.org.

ERIC is a bioinformatics resource jointly developed by SRA International, Inc., a Government systems integration contractor, and researchers at the Genome Center of Wisconsin. Its basic mission is to help enteropathogen researchers manage the transformation of the tremendous volume of available data into information useful for their research. This includes ongoing annotation of its genomes, integration and development of bioinformatics tools, and both in-person and virtual online training sessions. ERIC strives to assist the scientific community through its own research as well as through worldwide collaborations.

Full-time scientists are employed to annotate and curate ERIC genomes, including pseudogenes, insertion sequences, and tRNA genes in addition to protein-coding genes. The annotations are continuously updated and publicly available. Moreover, ERIC welcomes and encourages community participation in the annotation process—ERIC’s online annotation system was derived from ASAP(A System for community Annotation of Pathogens).

In addition to its online annotations, ERIC also has an array of tools to assist with scientific research. These tools include MAUVE, a powerful, freely available multiple genome aligner and visualization tool unique in its ability to compare more than a pair of genomes at a time, with an excellent ability to visualize genome rearrangements. ERIC also incor-
porates the Generic Genome Browser (GBrowse) developed by Lincoln Stein to view individual sequence features, allowing users to visually “drill down” to feature annotations of interest. Online searches of annotations by keyword and by sequence are also available. ERIC also offers a wide variety of online tools for microarray analysis and comparison.

A key goal of ERIC’s development is to insure user-friendly and comprehensive integration the data. For example, the results of a BLAST search have Web links back to the genome annotation stored in ASAP, which contains curated literature references and other evidence codes to support the annotations, as well as links to GenBank and other relevant Web resources. Wherever appropriate, updates will be leveraged across all existing and upcoming genomes in ERIC through the use of orthologs. It is important to note again that the annotations available from the main ERIC portal are continuously updated and include supporting evidence. This means that regardless of frequency of deposition elsewhere, ERIC’s records reflect our most up-to-date and complete annotations and curation.

ERIC also presents information such as Standard Operating Protocols (SOPs) for annotation, a summary of the annotated genomes available on or through ERIC (currently numbering 42 genomes), and links to additional NIAID and other useful resources, including links to our seven sister BRCs.

What is most important for ERIC’s development and success is input and usage from the worldwide community of enteropathogen researchers—the ERIC staff is most willing to assist scientists in using and expanding this resource.

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Certify your worth.
Don’t make people guess how valuable you are.