

JMMB: A New Journal With a New Outlook for a New Era

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Basic molecular microbiology and applied biotechnology have traditionally been distinct disciplines relegated to academic and industrial concerns respectively. However, we are entering a new and exciting era of microbiological study and application – one which is revolutionizing our approaches to science and expanding the horizons of biotechnology. This era is dramatically expanding with the advent of genome sequencing. Over twenty fully sequenced microbial genomes are now available for analysis, and many dozens more are being sequenced. Hundreds of sequenced genomes will be at our disposal within the first decade of the 21st century. Extraction of the wealth of information concealed within these genomes will require the development of novel procedures for data processing and will yield reams of data that will allow molecular biologists to be far more productive than ever before. However, their current repertoire of techniques will soon be obsolete, and a new battery of approaches will have to be mastered.

Our understanding of microorganisms, the metabolic processes they catalyze, the genetic apparatuses encoding their proteinaceous constituents and the pathological conditions they cause, has already expanded as a result of the availability of complete microbial genomic sequences. Many research institutes and industrial concerns around the world now devote their efforts primarily to genome sequencing and analysis of the data produced. Dozens of international conferences have been held with the primary purpose of keeping the scientific community abreast of these new developments.

Recent advances in the new disciplines of genomics, proteomics and bioinformatics were inconceivable only a few years ago, and extensive cooperation and collaboration between academic and industrial concerns is proving highly beneficial. Basic and applied microbiology are becoming integrated as never before. Basic discoveries provide ammunition for practical applications, and technological advances often prove to be more important to the progression of basic science than is the individual discovery. The development of novel chip technologies, for example, are revolutionizing our entire approach to molecular biology.

While a vast majority of the thousands of genes identified in newly sequenced genomes are currently without established function, there is not even a clue as to the functions of between 20 and 30% of these genes. This

fact alone is sufficient to cause us to recognize the need for entirely new investigative approaches. Refined software for improved structure-function predictions will be required. Methodologies must be developed for large-scale generation of gene knockouts for the conclusive identification of physiological functions. And reporter gene fusions and DNA probes for the analysis of absolute and differential rates of gene expression for entire genomes must be developed and perfected. Most of these efforts are currently being conducted in biotech companies, and it is the availability of their newly developed research products that will render the standard repertoire of the molecular biologist obsolete. The commercial availability of these new technologies will force the molecular biologist to take new approaches that will greatly enhance productivity.

There are currently no systematic large scale efforts aimed at identifying the biochemical functions of the products of the thousands of recently discovered genes. In cases where sequence analyses provide clues as to these functions, the development of micro methods for over expression of the encoding genes, for purification and characterization of their products, and for the study of their biochemical activities will be required. Such studies are likely to depend upon collaborative efforts transcending national borders and organizational structures. Thus, biomedical and other pharmaceutical companies as well as industrial and academic laboratories are likely to cooperatively participate in these endeavours to an ever-increasing degree.

For “orphan” proteins lacking characterized homologues and for which no clue as to function is available, straightforward biochemical approaches are not likely to prove productive. In these cases, one might, for example, generate relevant information by examining interrelated patterns of gene expression using newly developed chip technologies, or by examining the physiological properties of isogenic knock-out mutants. Nevertheless, entirely new approaches will be needed before systematic solutions to this problem will be available. This need provides major challenges for the next generation of molecular biologists.

The *Journal of Molecular Microbiology and Biotechnology* (JMMB) was born out of the realization that entirely new microbiological disciplines are emerging. Related scientific disciplines that have developed in parallel include microbial genomics, proteomics and bioinformatics. The journal will cater to papers concerned with both theoretical and practical aspects of these new fields. A principal goal of JMMB is to provide a platform for the expression of new ideas that will shape these converging fields. In realizing this goal, we hope to facilitate the merger of basic molecular microbiology with biotechnology. JMMB will thus serve as a partner to help usher in a new era of cooperation and collaboration between disciplines.

The drastic switch in experimental approach made possible by genome sequencing is likely to lead to changes

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in publication approaches. Already, many investigators are finding it preferable to publish the details of their studies on the Internet and to only summarize their findings in hard-copy journals. Virtually all of the major genome sequencing efforts and many additional genome analysis efforts have utilized this approach. Hard-copy journals thus may come to provide summary articles and guides to detailed electronic manuscripts. The latter will be of interest primarily to investigators interested in pursuing detailed studies in a specific field.

In considering how JMMB might best serve the scientific and technological communities, deficiencies of the existing media were evaluated. Most other journals focus on a single field of scientific endeavour rather than trying to appeal to audiences with interests in both the applied and basic fields. No preexisting journal has emphasized the need for amalgamation of microbiology with biotechnology, with equal footing given to each discipline. Further, a platform for the expression of ideas encompassing these two converging fields has been lacking. JMMB hopes to correct these deficiencies.

In creating a format that caters to and serves the broad needs of the basic and applied scientific communities, the editors of JMMB hope to incorporate the best elements of preexisting journals while emphasizing the basic and applied aspects of any problem. We plan to address many far reaching problems in microbiology including (1) microbial and human population control, (2) global climactic and environmental concerns, (3) basic and applied aspects of unculturable microbes, (4) problems in microbial, plant, animal and human pathogenicity, (5) mechanisms and consequences of intercellular communication, (6) industrial applications of genetically modified microbes, (7) genetic engineering for the production of man-made macromolecules, (8) gene, protein and ligand delivery systems, (9) evolutionary studies of microbes and biological macromolecules, and (10) the development of new microbiological technologies. In order to emphasize these and other important topics, we anticipate that at least initially, each issue of the journal will include a written symposium that considers the various ramifications of a particular subdiscipline of microbiology. Each symposium will consist of a collection of articles prepared by prominent experts in the field. Many of these symposia will be solicited, but scientists recognizing a particular need are encouraged to contact the Editor-in-Chief with suggestions. Additionally, original research articles, short correspondences, and self-sustaining reviews will be welcome. We will emphasize a policy of flexibility with a focus on basic microbiology and microbial biotechnology. Theoretical approaches and descriptions of novel, microbiologically-relevant software will also be topical. As *in silico* approaches become increasingly important for macromolecular structure-function predictions, JMMB will provide a medium for the publication of relevant studies. Suggestions from all segments of the scientific community regarding all aspects of journal format will be welcome. With everyone's help, JMMB should evolve into a significant force serving a major segment of the scientific community.