

Year's comments for 2004

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With this issue, INTERNATIONAL MICROBIOLOGY has completed its seventh year of publication. Traditionally, the Editorial of the December issue reviewed news events from the world of microbiology that had taken place over the year, and provided a brief update concerning the journal itself, e.g. number of articles received and published, types of articles published, and geographical origin of the articles. However, in 2002 and 2003 we were forced to abandon that custom because our publisher during those years demanded—due to the several month's necessary to produce the journal—that the articles for the December issue were submitted during the summer. Now, with our move to another publisher, Viguera Editores, we can again devote this Editorial to the year's comments. For this and several other reasons, we are convinced that the decision to switch from an international publisher to a local one was a sound one, especially now, in the era of electronic publishing. Viguera Editores [www.viguera.com], located in Barcelona, has many years of experience in scientific publishing—both printed and electronic media—, particularly in the fields of medicine and life sciences. Moreover, the company considers the publication of scientific journals as providing an important service to science by facilitating the diffusion of knowledge.

Since its very beginning, INTERNATIONAL MICROBIOLOGY has been a staunch proponent of the Open Access Initiative [2]. Our journal can be accessed directly at its website [www.im.microbios.org], as well as through the PubMed database (National Institutes of Health, USA) and through the services of SciELO-Spain [http://scielo.isciii.es], an electronic virtual library supported by the Instituto de Salud Carlos III (Madrid) that provides a selection of Spanish medical and life science journals on-line at no cost.

An analysis of the number of visits to our website revealed that, from January 1 until November 30, 2004, the number of “hits” increased more than 150% compared to

2003, with an increasing trend. Of the journal's viewers, 39.4% were from Spain, followed by those from North America (USA 12.1%, Mexico 4.7%). Those that have reached the INTERNATIONAL MICROBIOLOGY website through a search engine have done so mostly via Google.

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Fifty years ago, in April 1954, the famous bacteriologists Albert Jan Kluver (1886-1965) and Cornelis Bernardus van Niel (1897-1985) were in charge of that year's “John M. Prather Lectures” at Harvard University. Under the title “The Microbe's Contribution to Biology”, Kluver and van Niel offered a new vision of microbiology. Those six lectures changed the approach to modern microbiology research and teaching and were published two years later by Harvard University Press in a book of the same title [3]. Kluver, considered to be the father of comparative biochemistry, disseminated the idea of the unity of life and promulgated the use of microorganisms to understand biochemical pathways and energy transformation. He proposed that all life is connected by the cycling of matter, and all organisms are connected through a web of ecosystems [1]. As far back as 1962, Roger Y. Stanier (1916-1982) and van Niel had already stated that, despite incredible progress in bacteriology, a clear concept of a bacterium had not yet been achieved [10]. Even now, when we know almost every detail of the molecular biology of *Escherichia coli* and of several other bacteria, and have sequenced large portions of the genome of many microorganisms, we continue to ignore the essential mechanisms that permit a cell to live and evolve in an environment that is usually hostile, as well as those mechanisms that allow us to differentiate a living being, i.e. a cell, from replicative molecules. This is because molecular studies tend to overlook the organism as a whole.

Articles reporting the genomic sequence of a bacterium often lack in their Introduction a brief but necessary description of the microorganism's main morphobiochemical and ecological features, upon which—whether one agrees or not—its classification in *Bergey's Manual* is based. In the case of a well-known bacterium, a short description may not be necessary, but detailed analyses of the genomes of uncommon organisms would be improved if they were preceded by a short comment on the bacterium's size, morphology, Gram stain, metabolism, habitat, etc. As Paul Nurse has recently pointed out, we must learn "...the importance of spending more time trying to understand the real biological significance of observations made on cells and organisms before undertaking detailed investigations of the molecular mechanisms involved. Understanding the biology properly is as important as the subsequent mechanistic insight." [5].

Nowadays, studying the microbial world is not only a matter of searching a genomic database, but also realizing that microorganisms can make use of similar capabilities for diverse purposes [9]. In this regard, genomics has revealed many previously unknown aspects of microbial capabilities and has contributed to placing microorganisms in their proper location in the tree of life. Despite the availability of this powerful tool, two major issues have impeded the development of microbiology into an independent scientific discipline. First, difficulties remain in establishing an evolutionary framework for drawing a microbial evolutionary tree. In fact, until recently, there were many biologists who argued that all prokaryotes constitute a monophyletic taxon. Second, the study of microbial diversity is limited due to the impossibility of culturing many bacteria. It has therefore been necessary to search for other approaches, ones that differ from those used by botanists and zoologists to study plant and animal diversity.

According to the Genomes OnLine Database (GOLD), which monitors genome projects worldwide, in October 2004 more than 230 genomes—most of them prokaryotic—had been completely sequenced. Currently, there are more than 500 ongoing prokaryotic genome projects. During 2004, two bacterial genomes—those of *Wolbachia pipientis* and *Methylococcus capsulatus*—were published in *PLoS Biology*, the first journal to be published by the Public Library of Science, which is one of the leading participants in open-access publishing [2,11,12]. The publication of two complete genomes in *PLoS Biology* shows that this journal has consolidated its place in the scientific literature and that authors are confident that their articles will reach a large readership. *W. pipientis* is an obligate intracellular bacterium of *Drosophila melanogaster*. Now that the complete genomes of the two species—host and parasite—are known,

the system *W. pipientis*–*D. melanogaster* is an ideal model in which to study the biology and evolution of bacterial infections.

Methylococcus capsulatus is the first obligate methanotroph whose genome has been sequenced completely. Sequence analysis has confirmed the previously known metabolic versatility of this bacterium, including its ability to grow on sugars, oxidize chemolithotrophic hydrogen and sulfur, and live under reduced oxygen tension.

The sequencing of three pathogenic spirochetes (*Treponema denticola*, *Leptospira interrogans* serovar Copenhageni and *Borrelia garinii*) and subsequent analyses of their genomes, as well of those of previously sequenced spirochetes, have helped to further our understanding of the differences in their ecophysiology and modes of infection. *Treponema denticola*, an oral spirochete associated with periodontal disease, has a genome three times larger than syphilis-causing *T. pallidum*. A comparison between the *L. interrogans* serovar Copenhageni genome and that of *L. interrogans* serovar Lai, whose sequence was published in 2003, revealed significant structural differences, mainly in the complex polysaccharide surface antigens. The hundreds of genes that code for surface lipoproteins and transmembrane outer-membrane proteins of *Leptospira* might be candidates for the development of vaccines, for example, against leptospirosis, which is one of the most widespread zoonotic disease. Whereas in the United States *Borrelia burgdorferi* sensu stricto is the only causal agent of multisystemic Lyme borreliosis, in Europe, *B. garinii* and *B. afzelli* are the main causative agents. The genomes of *B. burgdorferi* and *B. garinii* share 92.7% of their DNA. Phenotypic differences between the two species seem to depend mainly on the presence or absence of two plasmids and perhaps also on the activity of positively selected genes.

A recently study published in the *International Journal of Systematic and Evolutionary Microbiology* examined the dynamics of microbial genomes, especially the evolutionary forces that drive genome reduction. The completely sequenced genomes of five bacteria that are obligate human pathogens (*Chlamydia trachomatis*, *C. pneumoniae*, *Mycobacterium leprae*, *Rickettsia prowazekii* and *R. conorii*) were compared to each other and to the genome of *Escherichia coli* [8]. The obligate intracellular parasites had smaller genomes, which suggested a continual selective pressure for minimal genome size. In addition, the patterns of protein length and frequency distribution were very similar in all five pathogens, with substantial sharing of the backbone genome. The reduction in the number of genes/proteins was greater for proteins with lengths from 200 to 600 amino acids, which is the size range of many metabolic enzymes. In addition, the

number of genes coding for secondary-metabolite biosynthesis, transport and catabolism, cell motility, and defense mechanisms was substantially reduced.

Thus, it appears that, throughout evolution, genes that once played major roles were eventually discarded because they were no longer under selective pressure. Genome stability is therefore achieved by the loss of selected groups of proteins involved in genome dynamics and gene mobility. The sequencing of an increasing number of genomes in the coming years should bring to light the underlying mechanisms of selection.

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In relation to INTERNATIONAL MICROBIOLOGY, in 2004, 82 manuscripts were submitted. The four issues published during the year consisted of a total of 30 Articles (Reviews, Research Articles and Research Notes), 9 Complements (Editorials and Perspectives), and 13 Book reviews, adding up to 302 pages. The geographical origin of the Articles was as follows: 17 from Spain (of which, one with coauthors from Portugal and another with coauthors from Argentina); 3 from Germany; 2 from Brazil; and 1 from Canada, Colombia, Denmark, Ecuador, Mexico, Norway, Russia (this one with coauthors from Japan), and UK. One of the Perspectives was from Croatia, and another from the USA. A change that we introduced this year was the inclusion of Spanish and Portuguese Abstracts. This was necessary in order for the journal to be included in several Spanish and Latin American databases. We hope that 2005 will also be a fruitful year for the journal, and that we can maintain and even increase the interest of our readers and authors.

Unfortunately, 2004 was also a sad year for us, as three great scientists who were directly or indirectly active in the field of microbiology passed away: Ramon Margalef (1919-2004), David A.A. Mossel (1918-2004) and Joan (John in English) Oró (1923-2004). Margalef (see obituary by J.D. Ros in this journal [7]) has been the greatest Catalan and Spanish limnologist, marine biologist and ecologist of the twentieth century. Although he never called himself a "microbial" ecologist, he had a holistic, integrative vision of ecosystems that included microorganisms, and he stimulated other scientists, including myself, to fathom the role of microorganisms in nature, since he—in his own words—"considered himself too old to start again". Margalef viewed the biosphere as a multi-shaped cover over some heterogeneous spaces that also served as the matrix for evolution, and that was influenced by evolution itself through a system of feedback [7]. Dutch microbiologist David A.A. Mossel (see obituary by B. Moreno on pp. 283-284 of this issue [4]) had been a member of the Editorial Board of the journal *Microbiología SEM*, which later became INTERNATIONAL MICRO-

BIOLOGY, since 1990. He was an expert in food microbiology and remained active in research and teaching even after his official retirement. Biochemist Joan Oró, was born in Lleida, Catalonia, Spain; he studied chemistry in Barcelona from 1942 to 1947, but carried out his whole research, on the biochemistry of the origin of life, in the United States—he moved to Houston in August 1952 as a doctoral student, and retired as Professor Emeritus of the University of Houston in 1994. On Christmas eve in 1959, he achieved the synthesis of adenine from cyanide in his laboratory at the University of Houston. Oró's experiment together with that of Stanley Miller (abiotic synthesis of amino acids) laid the foundations for studying prebiotic chemistry. Oró was very interested in the role of microorganisms in the early evolution of life and, besides his numerous articles and reviews, he co-edited—with Antonio Lazcano—a monographic issue of *Microbiología SEM* [6] devoted to the 7th International Symposium of the International Society for the Study of the Origin of Life (ISSOL), held in Barcelona in 1993. These three great scientists carried out prolific careers in different branches of science and contributed to training several generations of researchers that now can consider fulfilled Virgil's verse: "*Carpent tua poma nepotes*"* [*Eclogues IX*, l. 50].

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*"Your descendants shall gather the fruits."