

Microbiology in the “-omics” era: a report on the 2nd FEMS Congress (Madrid, 4-8 July 2006)

Summoned by the FEMS (Federation of European Microbiological Societies), about 1500 European microbiologists met in Madrid from July 4–8, 2006, to attend the organization’s 2nd Congress. The comprehensive scientific program covered the wide spectrum of areas influenced by microbial life in the biosphere, including biomedicine and biotechnology. The presentations ranged from the most basic research to highly specialized applications (for instance, the contribution of microbes to nanotechnology). The motto of the official T-shirt of the Congress, “I live in a microbial world”, served as a reminder of the central role of microorganisms in the development and maintenance of life on Earth, and as an invitation to all of society to share with microbiologists the implications of that reality. Actually, given the intense pace of the Congress, it is hard to believe that our thorough exploration of the microscopic world began relatively recently (about 150 years ago). After a welcoming “Fermentation Party,” conceived to acquaint our international guests with the richness and variety of Spanish fermented food, attendants had the

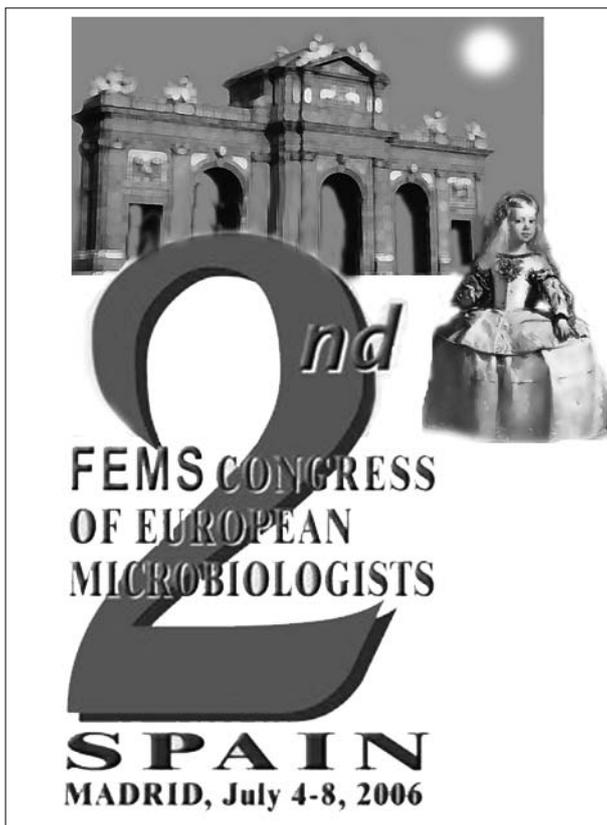
opportunity to partake in the excitement of sharing the progress in microbial knowledge, as presented in five plenary lectures, 22 symposia, and 19 workshops. Researchers from 63 countries presented a wealth of data that confirmed the current good health of microbiology. Most of the research presented in Madrid fit into three broad mainstream categories: health (the study, treatment, and prevention of infectious dis-

eases), environment (microbial ecology, evolution, and adaptation to different habitats), and biotechnology (microbiological knowledge for industrial uses, including food preparation and safety). Apparently, none of these categories has escaped the rush of the current post-genomic revolution. The scientific committee of the Congress, co-chaired by Eliora Ron (current FEMS president) and César Nombela (former FEMS president and head of the Local Organizing Committee on behalf of the Spanish Society for Microbiology, SEM), was far-sighted enough to put the focus on the novel “-omic” perspective, to which microbiology is critically contributing: genomics, proteomics, metabolomics, biomics, etc. This plunge into the future was best appreciated by first examining the past, as Ernst Rietschel did in his fascinating

retrodiagnosis of the infectious diseases that ended the lives of several of the world’s greatest musicians (Rossini, Bizet, and Mahler, among others).

Good times for pathogenomics. It would be impossible to list and comment here on all the presentations at the Congress, but I would like to draw attention to a few of the highlights. In the field of medical bacteriology, the implications of pathogenomics, a post-genomic approach devoted to mining and functionally interpreting data obtained from sequencing the whole genomes of pathogenic bacteria. Hacker, who is director of the Center for Infectious Diseases at the University of Würzburg, Germany, was awarded the FEMS-Lwoff Award, named after the

distinguished microbiologist André M. Lwoff (1902-1994) [1]. This is the most prestigious honor bestowed by FEMS, and was established to mark the 25th anniversary of the Federation, six years ago [2]. For the occasion, Hacker, held a lecture on the evolution of bacterial pathogens, mostly based on research carried out by his team on *Escherichia coli* (so christened after the eminent Würzburg microbiologist Theodor Escherich, 1857-1911).



Early in the meeting it had already become clear that pathogenomics is one of the landmarks of current research in microbiology. At the "Frontiers in Pathogenomics" workshop, a European network of projects that focus on this productive field was created and is scheduled to become operative in 2007. The primary goal of pathogenomics is to use the overwhelming wealth of information provided by genome sequencing to discover the genes responsible for infectious diseases. Perhaps the most powerful tool for this purpose is comparative genomics. The potential of such an approach is emerging from its infancy, as evidenced by the novel DNA sequencers based on PCR in emulsion and the pyrosequencing-based strategies, both of which were presented by commercial exhibitors during the Congress. These machines can sequence a genome of 2 million bases in a single run of 5½ h, a result that would take months with the current technology. The team led by Hacker has contributed to the post-genomic era by comparing the whole genomes of certain isolates of *E. coli*, namely, the harmless commensal inhabitants of the human body, with aggressive pathogenic strains. Their efforts resulted in the discovery of seven pathogenicity islands in an isolate causing severe infections of the urinary tract. The genetic information contained in these islands is yielding amazing insight into the molecular mechanisms of bacterial virulence. Moreover, the evolution of pathogens and commensals is written in the structure and nature of these genomic islands. Hacker also presented an intriguing hypothesis on the dynamics of bacterial evolution, honoring Darwin's theories but pushing them one step forward: there is a fast-developing "microevolution" that gradually feeds the requirements of natural selection to drive the macroevolution of new, more competent species.

I could not close this brief mention of the contribution of post-genomics to our advances against infectious disease without noting the use of "reverse genetics" in vaccine development. The Italian researcher Guido Grandi reported major advances based on this strategy in the development of vaccines against meningitis and β -hemolytic streptococci.

Avian flu: the threat is in the air. Virology was also broadly represented at the meeting, with discussions of emergent pathogens taking the lead. By chance, on July 7, 2006, the first case in the Iberian peninsula of highly pathogenic H5N1 avian influenza virus was reported and involved a bird found dead in its natural environment near the city of Vitoria (Basque Country). At the same time that the Spanish health authorities made the report public, experts on the field from around the world were attending the "Emerging Infections" symposium in Madrid. H5N1 was inevitably being debated. When authorities on influenza, such as Albert Osterhaus,

Adolfo García Sastre, Alan Hay, and Brian Mahy, were asked by journalists about measures to be taken to avoid spreading of the virus and its threat to human health, they all agreed on a major essential point: There is no real threat unless the virus is transmitted to domestic fowl by infected wild migrating birds, which have acted as reservoirs of the disease, as has massively been the case in some regions of Asia. All measures to be adopted at this stage of the situation in Europe should be directed at avoiding this form of transmission. Infection of poultry would not only have important economic consequences, but might also constitute a serious risk for farm workers and potential consumers. We must remember that every case of human infection is a chance given to the virus to mutate into a form transmissible from human to human. After recovery of the genome of the deadly 1918 pneumonia virus, which killed around 40 million people, researchers hypothesized that a mutational event of this kind was responsible for the historic pandemic episode. A second scenario of risk involves the creation of a human transmissible virus: in this case, a person (or an animal sharing a habitat with humans) would be simultaneously infected with a common flu virus and a highly pathogenic avian flu virus, followed by the reassortment of both viral genomes which could result in a highly pathogenic human flu virus. According to epidemiologists, this was the likely scenario in two other human viral pandemics of the 20th century, i.e., Asian flu (1957) and Hong Kong flu (1968).

Osterhaus (from the Institute of Virology, Rotterdam) emphasized the lessons to be learned from the incidents of the last decade involving transmission to humans of highly pathogenic avian influenza, namely the H5 and H7 types. Regarding H5N1, it is well-known that, over the last two years, around 230 people have acquired the avian virus in Asia after contact with sick birds, and that 130 of them died. However, human to human transmission has not been strictly proven, except perhaps in one case. However, an H7N7 outbreak in the Netherlands in 2003 caused 78 cases of human conjunctivitis and, occasionally, more severe disease (including one fatal case) in farm workers and veterinarians; besides, transmission to familiars was reported. Osterhaus also mentioned that cats fed with infected birds developed fatal systemic disease, so that felines should be controlled in the case of an outbreak of avian influenza. Mahy (Centers for Disease Control, USA) closed the Congress by pointing out that H5N1 is the most important candidate for a potential pandemic threat. He agreed that massive vaccination of poultry would be the best long-term prevention measure. In this sense, the vaccine developed by the García Sastre laboratory (Mount Sinai School of Medicine, New York), by means of engineering the vaccinal form of Newcastle virus, aims to act

as a dual vaccine that with one shot protects birds against both Newcastle disease and the highly virulent H5N1. An important advantage of this vaccine over those developed from attenuated influenza virus is that it would allow vaccinated animals to be distinguished from those that have been naturally infected.

Bioremediation at its best. Environmental microbiology is one of the fields taking advantage of the post-genomic era. A major topic at the Congress was bioremediation, that is, the use of microbial metabolic capabilities to eradicate recalcitrant chemicals released to the biosphere by our obnoxious industrial activity. The Spanish researcher Víctor de Lorenzo reminded us that in our daily life we deal with no less than 40,000 xenobiotics and that microorganisms have not yet had the chance to evolve into efficient and sufficiently avid metabolizers to meet the challenge posed by them. Nevertheless, as official scavengers and recyclers of our planet, they are our only hope if we are to attempt decontaminating it. We already know that microbial consortia are able to feed on truly recalcitrant compounds, opening a door of hope for our future. De Lorenzo proposed that we envision microbial consortia, mostly composed of as-yet-unidentified life forms, as “landscapes” of catalytic activities upon which a given compound flows towards the valleys that will lead it to mineralization. Based on this rationale, his laboratory has worked on the development of bioinformatic tools that integrate all known catalytic abilities, which, in turn, can be applied in a quest for “shortcuts” in a universal enzymatic landscape. By this means, it would even be possible to predict the biodegradability or recalcitrance of putative novel xenobiotics that organic chemistry could at some time generate. One of the achievements of de Lorenzo and his team has been the isolation of genes responsible for enzymatic activities involved in the removal of chlorinated compounds. Metagenomics, also known as biomics, will help microbiologists in the search for these activities regardless of the microorganism of origin. Such efforts are sowing the seeds for systems biology, a frontier science between computation and biology that aims to predict the behavior of living systems. Peer Bork (European Laboratory for Molecular Biol-

ogy, Heidelberg, Germany) introduced the concept of comparative metagenomics, a perspective that will no doubt eventually shed light on the adaptation of microbial consortia to different environments. Bork also predicted that in the future cellular systems will be analyzed in 4D; that is, ordering the networks established by systems biology in the three dimensions of space and adding the parameter time. He supported his prediction with some very interesting preliminary data obtained from the minimum genome of *Mycoplasma*.

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Of the many “take-home” messages of the Congress, perhaps “enroll the -omics wave” should head the list. No one can ignore that microbiology is currently in a new Golden Age, inaugurated by the ability to functionally analyze genomes and metagenomes. There is not the slightest doubt that your favorite research field has already been inundated by the “-omics wave.” Join the trend or be marooned in the 20th century and accused of reductionism! And consider that only 50 years ago you had to isolate your microorganism of interest in pure culture in order to be recognized as a microbiologist. Today, this is no longer necessary; instead, the gates of microbiology will be open to you if you can manage to obtain the microorganism’s genome, print a microarray for its transcriptomic analyses, set up the necessary proteomic tools and, ultimately, use your computer to predict the bacterium’s behavior. It is now time to integrate the wealth of knowledge that has accumulated from these approaches, and to use the “-omics wave” to take advantage of all that microbiology has to offer humanity.

1. Soyer-Gobillard MO (2002) Scientific research at the Laboratoire Arago (Banyuls, France) in the twentieth Century: Edouard Chatton, the “master”, and André Lwoff, the “pupil”. *Int Microbiol* 5:37-42
2. Trüper HG (2000) Twenty-five years of FEMS. *Int Microbiol* 3:135-137

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Taking the pulse of Latin American microbiology: the 18th ALAM Congress (Pucón, 23-26 October 2006)

Over 600 scientists from sixteen countries (Argentina, Brazil, Chile, Colombia, Cuba, Mexico, Uruguay, Venezuela, Canada, France, Germany, Japan, Spain, Sweden, UK and USA), met in Pucón (23-26 October, 2006), in the beautiful Chilean Lake District, for the 18th Latin American Congress of Microbiology, organized by the Latin American Association for Microbiology (ALAM). The congress was held in conjunction with the 28th Chilean Congress of Microbiology, and the 3rd Chilean Congress of Food Microbiology and Hygiene. Prof. Michael Seeger, president of the Chilean Society for Microbiology, chaired the meeting, which was a great success.

What emerged from the ALAM Meeting in Pucón was a synthesis of the microbiological opportunities and challenges for Latin America and the Caribbean region for the coming decades. The growth of the Internet, e-science, and wiki interactive sites and software have provided unprecedented opportunities for collaborative research in many areas of fundamental and applied microbiology, to which Latin American scientists are clearly responding. Also, the global nature of the threats posed by new and re-emerging infectious diseases requires cooperation that transcends borders. Because the Congress involved so many issues of international concern, we believe that an overview of the proceedings of the meeting could be of interest to our colleagues outside Latin America. The participation of the Spanish microbiologists was significant, and Prof. Ricardo Guerrero, current president of the Spanish Society

for Microbiology (SEM), was invited to attend the ALAM Assembly. There, several initiatives to establish permanent cooperative relationships between ALAM and SEM were discussed.

New and re-emerging diseases. As defined by the US Centers for Disease Control and Prevention, new and re-emerging diseases are "diseases of infectious origin whose incidence in humans has increased within the past two decades or threatens to increase in the near future". They include human and bovine tuberculosis, cholera, and hantavirus infections. Four two-hour symposia and a lecture were devoted to discussing human and bovine tuberculosis (TB). TB is the leading cause of death due to a single infectious agent among adults in the world. *Mycobacterium tuberculosis* is the most common cause of human TB, but an unknown proportion of cases are due to *M. bovis*.

About 645,000 cases of human TB were reported in Latin America and the Caribbean region in 2000 (up from 570,000 in 1990) but the actual number is likely to be much higher. In fact, many countries, especially those with few resources, are unable to report all TB cases due to difficulties in identifying suspected cases, establishing a diagnosis, and recording cases. The incidence of TB is especially high in Peru (191 per 100,000 people) and Bolivia (130 per 100,000) compared to about 20-50 per 100,000 for many of the other Latin American countries. Industrialized countries typically report less than 20 cases per 100,000. There is concern that Peru and Bolivia represent significant reservoirs of the

disease that can be spread by global activities. There is also major concern that TB may be reemerging due to an increase in the multidrug resistance of *M. tuberculosis* (topic covered by P. Silva, Brazil), to the fact that it is increasing in HIV compromised patients, and to the possibility that zoonotic TB may emerge as a serious public health threat particularly in countries such as Argentina, Paraguay and Uruguay, where *M. bovis* infections are present in animals and the conditions favor zoonotic transmission. Improved surveillance and the



need to improve techniques for rapid diagnosis of TB were pinpointed as critical issues. Many of the deaths caused by TB in the developing world are due to wrong or late diagnosis. The technology needed to create more accurate and less expensive tests already exists, however, and new tests could easily be developed with funding. Above all, there is a great need for tests that can detect latent TB and identify people at high risk of developing the active disease. These topics were discussed by many participants including E. Montoro (Cuba), M-A. Telles (Brazil), A. Cataldi (Argentina), N. Morcillo (Argentina) and C. Martín (Spain). How the genome information of *M. bovis* is being exploited for disease control was presented by S. Gordon (UK). A Latin American-European collaborative project concerning latency in *M. tuberculosis* was described by M-J. García (Spain).

Emerging or re-emerging problems associated with hantavirus infections, dengue fever, shigellosis, malaria and cholera were covered in several posters. Recent advances in understanding infections by *Helicobacter* were presented in a session coordinated by A. Venegas (Chile). New strains of influenza with pandemic potential (e.g., bird flu) and plans to counteract a possible pandemic if they reach South America were discussed in a session coordinated by L-F. Avendaño (Chile).

The number of people living with HIV has risen to an estimated 1.8 million [www.unaids.org/en/HIV_data/] in Latin America, where the frequency is about 7 per 1000 adults. In Haiti, the frequency is even higher, it nearly doubling that in Latin America, with an estimated 13 per 1000 people infected. In the Caribbean, the AIDS epidemic claimed an estimated 24,000 lives in 2005, making it the leading cause of death among adults aged 15–44 years in that region of the world. Fundamental aspects of the molecular biology of HIV that help in understanding its life cycle and in the design of vaccines were covered by M. López-Lastra (Chile), J-F Mouscadet (France) and V. Parissi (France). J-L Darlix (France) discussed how HIV can hide in intracellular assembly particles avoiding immune surveillance and making vaccine design particularly challenging.

Increasing antifungal drug resistance, antibiotic and antiviral resistance. Twelve Latin American and Caribbean countries have taken concrete steps to curtail the growth of antibiotic resistance, mainly through the creation of surveillance systems. However, so far only Chile and Cuba have implemented truly nationwide programs to curb antibiotic resistance. Beginning in 1999, Chilean public health authorities began enforcing local drug-dispensing laws, complementing their efforts with a public information campaign.

Sessions were devoted to an analysis of the increasing incidence of *Candida* infections (coordinator V. Silva, Chile), and M. Valvano (Canada) gave a lecture regarding the mechanisms used by the *Burkholderia cepacia* group of organisms to escape immune detection and to become resistant to multiple drugs. A session convened by R. Lagos (Chile) explored the mechanisms exploited by microcins—small microbial peptides—to kill susceptible competing bacteria. E. Calva (Mexico) and G. Mora (Chile) discussed molecular aspects of *Salmonella enterica*. There were also talks on horizontal transfer of genes in nature via mobile genetic elements such as phage and plasmids (S. Maloy, USA) and integrons (D. Centrón, Argentina).

Microbial biotechnology, genome biology and bioinformatics. Issues related to biotechnological applications of microbiology were covered in sessions related to salmon culture (convenor X. Fuentes, Chile), algal blooms (convenor A. Cembella, Germany), decontamination of pollutants (convenor M. Seeger, Chile), wine (convenor E. Reyes, Chile) and biomining (convenor D.S. Holmes, Chile). The microbiology of food was discussed in a number of sessions and included an overview of residual antimicrobial agents in food (B. San Martín, Chile). R. Conrad (Germany) gave a lecture on methanogens and the production of the greenhouse gas methane.

A course was given on phylogenetic approaches involving infectious microorganisms (F-M. de Campos Fernández) and workshops were presented on annotating and interpreting complete microbial genomes (D.S. Holmes and J. Valdés, Chile) and on microbiology, biotechnology and sustainable development (coordinators, M. Seeger and M. Espinoza, Chile). A talk was presented by B. Wanner (USA) that described new efforts to provide a comprehensive and coordinated bioinformatics resource for *Escherichia coli*.

Biodiversity. Latin America is considered a major reservoir of biodiversity and is host to many extreme microbial habitats. An overview of microbial diversity was presented by R. Guerrero, Spain, and talks were given on unculturable microorganisms (K-H. Schleifer, Germany), halophiles (R. Rosselló-Mora, Spain) and extreme acid environments (J. Banfield, USA). Efforts to preserve regional microbial diversity in curated culture collections were described in a session coordinated by M. Floccari (Argentina) and included an overview of the accomplishments and objectives of the Latin American Federation of Culture Collections (FELACC).

Lacunae. Given the proportion of the Congress dedicated to the important issue of new and emerging diseases, it was

perhaps surprising to find no participants representing international public health organizations such as the World Health Organization (WHO), the Pan-American Health Organization (PAHO) or the US Centers for Disease Control (CDC), who could have discussed the regional plans adopted by Latin America for controlling emerging infections. Nor was there discussion regarding the efforts put in place by the Health authorities from Central American countries to control the epidemics of dengue fever and dengue hemorrhagic fever that recently swept through Central and South America. If we are to protect ourselves against emerging diseases, the essential first step is effective global disease surveillance to give early warning of emerging infections. This must be tied to incentives such as national development, and eventually be backed by a system for an appropriate rapid response. World surveillance capabilities are critically deficient, and experts from these agencies were absent from the ALAM Congress. This lack of dialog meant that the important messages presented at the Congress did not reach the ears of national or international policy makers and vice versa.

Cuba was the only Caribbean country represented at the Congress, despite the critical microbiologically-related issues of the region. Having said that, it was clear that the meeting was a resounding success, not only for the excellence and breadth of topics covered but in that it created new networking opportunities and strengthened existing ones both between Latin American countries and between Latin America and the rest of the world.

Highlight. A particular highlight of the four days was the enthusiasm and quality of the many students who participated, many of them as first authors of most of the more than 350 posters. Many were able to attend thanks to the generous support of the Chilean National Commission for Scientific and Technological Research (Conicyt) and the American Society for Microbiology (ASM). There is clearly a bright future for Latin American microbiology with these young people chomping at the bit.

We apologize to all our colleagues whose important contributions we could not cover due to space limitations. Further information regarding the proceedings of the ALAM Congress is provided by [www.alam2006.cl/] and additional information about Latin American microbiology issues can be found at the following resources online:

Some Latin American microbiology resources online:

- SciDev.net (Science and Development Network for developing countries): [www.scidev.net]
- Ciencia hoy (Argentina): [www.cienciahoy.org.ar]
- Interciencia (Venezuela): [www.interciencia.org]
- Jornal da Ciência (Brazil): [www.jornaldaciencia.org.br/index2.jsp]
- Latíndex (Mexico): [www.latindex.unam.mx]
- SciELO (Scientific Electronic Library Online): [www.scielo.org]
- Universia (Consortium of Latin American Universities): [www.universia.net]
- RIB (Latin American-Iberian Bioinformatics Network): [rib.cecalc.ula.ve]

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Appendix. Articles on microbiology or scientific journals in Latin America appeared in the SEM journals:

- Schaechter M, Orrego C (1996) *Microbiol SEM* 12(1):7-8
- Ayala FJ (1996) *Microbiol SEM* 12(2):163-166
- Halvorson HO (1996) *Microbiol SEM* 12(3):343-346
- Colwell RR (1996) *Microbiol SEM* 12(4):519-522
- Cetto AM (1996) *Microbiol SEM* 12(4):647-650
- Lazcano A (1997) *Microbiol SEM* 13(1):7-10
- Allende JE (1997) *Microbiol SEM* 13(2):127-130
- González Cappa SM (1997) *Microbiol SEM* 13(3):267-270
- Toranzos GA (1997) *Microbiol SEM* 13(4):399-402
- Allende JE (1997) *Microbiol SEM* 13(4):529-532
- San-Blas G (1998) *Int Microbiol* 1(1):7-9
- Patarroyo MF (1998) *Int Microbiol* 1(2):89-91
- Cetto AM (1998) *Int Microbiol* 1(3):181-182
- Law C, Piqueras M (2000) *Int Microbiol* 3(4):253-258