

4th CONGRESS OF EUROPEAN MICROBIOLOGISTS FEMS 2011 JUNE 26–30, 2011, GENEVA, SWITZERLAND

The Federation of European microbiological societies (FEMS) nowadays connects 43 national societies within Europe with 30,000 microbiologists from individual societies. This biggest event in microbiology in Europe was hosted by Geneva, Switzerland, where nearly 2,400 participants from 81 countries found the scientific programme interesting and enriching. 2,700 published abstracts and 1,800 posters were accompanied by eight simultaneously running scientific sessions. The conference covered the whole diversity of research in microbiology, ranging from individual cells to complex microbial biofilms, interactions with other elements in the environment, relations between microorganisms and humans, and manipulation of microbes for the benefit of humankind, such as progress in discoveries of anti-cancer metabolites.

Several keynote lectures were organised during the congress, but the biggest interest was expressed among scientists and media representatives for the lecture of Helge Karch who presented the latest results of the outbreak of infections with *Escherichia coli* in Germany. For the latest outbreak is responsible the very rare strain *E. coli* O104:H4 which causes deadly haemolytic-uraemic syndrome and neurological complications. Till 29 June 2011 in Germany were reported 3,801 cases, 834 patients expressed haemolytic uremic syndrome and 46 patients died. The most probable reservoir of this strain are humans. Studies show that “old enemies” of humanity are not defeated at all. There are indications that recent emerges of leprosy in the US is connected with the introduction of armadillos in Texas from Central America in 19th century which can act as a host for this pathogen. Molecular tools helped us to understand spreading of leprosy even in the ancient world, for example it was proven that Romans introduced leprosy in the territories of today France, Greece and Spain. Basic research offers new possibilities in attenuation of pathogenic microbes, for example by codon pair deoptimization of *Streptococcus pneumoniae*. On the other hand more and more evidence is pointing to reservoirs of certain pathogens, for example bats act as reservoirs for some viruses like Ebola, Marburg, and SARS coronavirus. Although public opinion in some European countries does not support vaccination, it is still the best way to protect individuals and populations against infectious diseases.

Studies of interactions between microorganisms and environmental elements give interesting conclusions. For example, it was until recently believed that the bacterial pathogen *Listeria monocytogenes* survives in-

side the free-living amoebae *Acanthamoeba* and in this way is transported to another places, but in fact this bacterium uses amoeba only as a hitchhiker for “free” transport. Among bacterial interactions is worth mentioning the finding of extracellular transfer of electrons by nanowires, such as bacterial pilli type IV. This indicates that each disturbance of sediments influence also such inter-bacterial networks. More and more evidence shows that different layers in rocks are of microbial origin, such as formation of FeS precipitates.

Progress in microbial genetic in the last years is enormous and is trying to answer the question, how little genetic information is enough to sustain life of microbes and if there is “junk DNA” in microbial genomes or we simply don't know its role yet? Novel pathways of exchange of DNA in bacteria are studied, for example by L-forms (cell-wall deficient cells) when heterokaryons are produced. L-forms are reported in most bacterial lineages. With present day technology only one week is enough to complete the mapping of genome of one organism. The role of viruses in the environment is sometimes underestimated, for example in natural environment the ratio of bacteria to viruses is one to ten. New metabolic pathways are discovered under different environmental conditions. For example, environment polluted with arsenic can be successfully remediated with microbes. Today we know that 50% of biomass on the Earth is of prokaryotic origin (Bacteria and Archaea) and most of our oil reserves have been already biodegraded in the subsurface. On the other hand there is still an open question how to improve the yield of nitrogen for human consumption, namely in a year 100 Tg of nitrogen is introduced in agriculture and only 17 Tg ends up in the human food chain. In the wastewater treatment technology use of phages to kill pathogens seems to be an eligible option. Good collaboration between microbiology specialists and engineers is often crucial, for example in assessing the biosafety of drinking water. Namely, water before purification usually contains on average 10⁴ bacteria per ml.

Progress in techniques and methodologies such as metagenomics, transcriptomics, proteomics, pyrosequencing, spectroscopy applications, and single cell analyses is supplemented with achievements of other technical solutions from other branches of nanotechnologies. Nowadays hundreds of genomes per species are available in various databases. Approximately 30 new genes are discovered for each new sequenced genome of a certain species. And here is the question how many