

Report on the conference:

## **2nd Czech proteomic conference**

17th – 20th October 2005

Lednice, Czech Republic

2nd Czech proteomic conference was held in a beautiful place in Czech republic, Lednice. Lectures were divided into 5 sessions, which gave the whole overview of proteomic research. I have chosen to write report about bacterial proteomics.

First lecture in this session was by J. Weiser and was called: Proteomic analysis of adaptive gene expression profiles in antibiotic resistant bacteria during cultivation in chemostat. This lecture was about adaptive gene expression profiles in macrolide susceptible strains and antibiotic resistant mutants of *E. coli*. It was interesting, since during the last decade there has been an alarming increase in the appearance of antibiotic-resistant bacteria as a result of an increased use of antibiotics. It was observed quite often that when the antibiotic is removed from the environment the resistant population does not tend to revert back to sensitivity and thus better fitness. But, instead, after growth for many generations it starts to accumulate secondary adaptive mutations and change expression profiles of some genes, which improves the fitness of the organisms and sometimes also restores lost virulence, and the most important, the antibiotic resistance stays. Dr. Weiser showed that bacterial population grown under antibiotic selective pressure practically died off after 76 hours and then recovered during period of 50 hours to a full size again. They analysed changes in protein patterns of *E. coli* cells resistant to streptomycin or erythromycin grown in chemostat in the presence or absence of the antibiotic using high-resolution 2D-electrophoresis. Samples of the cell population were analysed for antibiotic resistance, growth rate and translation accuracy. Their results show difference in protein profiles as in growth rate characteristics of the strains grown in presence and absence of antibiotics.

Second lecture was by Š. Nezbedová called: Two-dimensional gel electrophoresis - a method for studying the effect of *ppk* gene inactivation/overexpression in *Streptomyces lividans*. Her talk was about the examination of the effect of *Streptomyces lividans*' polyphosphate kinase gene (*ppk*) inactivation/overexpression on the other gene(s)' expression during colony morphological differentiation. The main function of PPK is to

convert the  $\gamma$  phosphate of ATP to polyphosphates and in reverse reaction the regeneration of ATP from polyphosphates when an excess of ADP is present. The PPK and the polyphosphates could either directly repress the expression of some proteins required for antibiotic biosynthesis or the polyphosphates can be hydrolysed and thus cause increase of the intracellular phosphate level. It was shown that the inactivation of the polyphosphate kinase gene resulting in low polyphosphate levels caused enhanced antibiotic production. Its overexpression, on the other hand, caused slight decrease in antibiotic production. She compared 2D-gel profiles of total proteins isolated from *Streptomyces lividans* wild type and two *ppk* mutant strains overproducing PPK protein during colony development.

In the next part of this session, which was the next day, L. Hernychová had a lecture called: Identification of bacterial protein biomarkers using LC-MALDI and LC-ESI MS/MS. It was about the identification of protein biomarkers in *Francisella tularensis* and *Coxiella burnetii* by mass spectrometry analysis.

Next two lectures were about iron regulation. M. Basler's lecture was called: The iron-regulated proteome and transcriptome of *Neisseria meningitidis*. *N. meningitidis* is a human bacterium colonizing the nasopharynx of about 10 % of healthy people. Occasionally some invasive clones spread in population and cause the disease. Since production of iron-chelating proteins into mucosal secretions and body fluids constitutes an important mechanism of innate immunity, essentially all human pathogens developed virulence gene regulones responding to concentration of available free ferric ions. He analysed the iron regulated proteome and transcriptome and identified the number of new iron-regulated meningococcal genes of unknown function, which were expressed under iron-limited growth conditions.

Last lecture from J. Lenčo was called: Analysis of alteration in protein patterns in *Francisella tularensis* LVS induced by iron-restriction. She also found many proteins expressed in iron-restricted medium by 2D-electrophoresis and some of them identified by mass spectrometry.