With the kind support of

Faculty of Information Technology, Brno University of Technology

Božetěchova 1, 612 66 Brno

12th June 2012

registration from 11:00

EVALUATION | **2012**

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LECTURES

Part of CEITEC Common Evaluation of Scientific Excellence

PROGRAMME

	Room No. D0206	Room No. D0207
11:30 - 12:30	**Prof. Michael Sattler** Institute of Structural Biology, Helmholtz Centre Munich, Germany Munich Center for Integrated Protein Science and Chair Biomolecular NMR, Department of Chemistry, Munich University of Technology, Germany	**Prof. Herbert Störi** Institute of Applied Physics, Vienna University of Technology, Austria
12:30 - 12:45	Break	
12:45-13:45	**Prof. Ingo Schubert** Department of Cytogenetics and Genome Analysis, Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, Germany	**Prof. Andrew J. Wyrobek** Life Sciences Division, Lawrence Berkeley National Laboratory, University of California, USA
13:45-14:00	Break	
14:00-15:00	**Prof. Wilhelm Gruissem** Department of Biology , ETH Zurich, Switzerland	**Prof. Jürgen Fleig** Institute of Chemical Technologies and Analytics, Vienna University of Technology, Austria

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CEITEC Common Evaluation of Scientific Excellence Lecture

Prof. Michael SATTLER

12th June 2012

11:30 - 12:30

Institute of Structural Biology, Helmholtz Centre Munich, Germany
Munich Center for Integrated Protein Science and Chair Biomolecular NMR, Department of Chemistry, Munich University of Technology, Germany

Evaluator of CEITEC Research Programme 3 - Structural Biology

Molecular recognition and dynamics in splicing regulation

Faculty of Information Technology, Brno University of Technology, Room no. D0206

Božetěchova 1, 612 66 Brno

Lecture abstract:

Molecular recognition of RNA plays a crucial for many essential RNA processing events during gene regulation. Two studies will be presented that highlight the role of conformational dynamics during molecular recognition: i) the recognition of poly-pyrimidine tract RNA by the essential splicing factor U2AF65 during spliceosome assembly and ii) the recognition of dimethyl-arginines by Tudor domains in snRNP maturation.

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CEITEC Common Evaluation of Scientific Excellence Lecture

Prof. Herbert STÖRI

Institute of Applied Physics, Vienna University of Technology, Austria

12th June 2012

11:30 - 12:30

Evaluator of CEITEC Research Programme 1 - Advanced Nanotechnologies and Microtechnologies

A Plasma-Emission-Detector implemented in a Micro Fluidic Device

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Faculty of Information Technology, Brno University of Technology, Room no. D0207

Božetěchova 1, 612 66 Brno

Lecture abstract:

A plasma emission detector implemented with micro-fluidic technology is presented. The discharge volume is in range of several 10 nano-litres, permitting high power density at low total power. Using a d.c. or pulsed d.c. glow discharge in helium at atmospheric pressure the device has a high sensitivity to carbon injected in the form of an organic analyte and is also able to detect hetero-atoms such as fluorine, chlorine, phosphorus or sulfur present in the analyte. The detector permits the construction of portable and battery-operated analytical instruments, e.g. a miniaturized gas chromatograph for environmental monitoring. The limit of detection is in the range of 200 pg for carbon and approximately an order of magnitude higher for the other elements mentioned. Construction and operation of the device and of the gas chromatograph will be discussed.

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CEITEC Common Evaluation of Scientific Excellence Lecture

Prof. Ingo SCHUBERT

12th June 2012

12:45 - 13:45

Department of Cytogenetics and Genome Analysis,
Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, Germany

Evaluator of CEITEC Research Programme 4 - Genomics and Proteomics of Plant Systems

Plant Centromeres

Faculty of Information Technology, Brno University of Technology, Room no. D0206

Božetěchova 1, 612 66 Brno

Lecture abstract:

Centromeres – like telomeres – are as old as eukaryotic chromosomes and are essential for correct segregation of nuclear genetic information from cell to cell and from generation to generation. Although centromeres of related species may share similar sequences, centromeric DNA sequences are neither sufficient nor necessary for centromere formation. The components of the proteinaceous complex, the kinetochore, which makes a centromere functional, are more conserved than centromeric DNA, even between distantly related phyla. The same is true for nuclear division-specific histone modifications. Now it is widely agreed that centromere positions are defined epigenetically. A basic step is the incorporation of the centromeric histone H3 variant CENH3 into (some) centromeric nucleosomes. In contrast to other nucleosomal core histones, CENH3 is not incorporated simultaneously with DNA replication during S-phase of the cell cycle. There mode of maintenance of centromere positions and of establishing kinetochores along mitotic and meiotic cell cycles are enigmatic. We present data and models for centromere maintenance through the cell cycle via CENH3 incorporation and demonstrate some experimental approaches to trace the routes of CENH3 deposition at centromeres.

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Prof. Andrew J. WYROBEK

12th June 2012

12:45 - 13:45

Life Sciences Division, Lawrence Berkeley National Laboratory, University of California, USA

Evaluator of CEITEC Research Programme 7 - Molecular Veterinary Medicine

Genetic differences in transcript responses to low-dose ionizing radiation identify molecular functions associated with breast cancer susceptibility

Faculty of Information Technology, Brno University of Technology, Room no. D0207

Božetěchova 1, 612 66 Brno

Lecture abstract:

Population exposures to low-dose (LD) ionizing radiation are steadily increasing from medical and other sources and genetic variation is expected to be a major determinant of cancer risks after LD exposures. It is well known that the human breast is sensitive to radiation-induced cancer after higher doses, but we know remarkably little of the tissue responses after LD exposures nor how the mechanisms by which genetically different individuals vary in their LD cancer risks. We applied a systems approach that compared LD-induced chromosome damage and transcriptional responses in strains of mice with genetic differences in their sensitivity to radiation-induced mammary cancer (BALB/c and C57BL/6) to identify tissue mechanisms of susceptibility or resistance for LD-induced breast cancer. We identified distinct transcript-level differences in the LD responses between sensitive and resistant mice sampled before radiation exposure and at early and late times after exposure. We discovered major genetic differences in pathways associated with resistance and susceptibility to breast cancer, and used these differences to identify two expression signatures that have promise for predicting an individual's risk to LD induced breast cancer. Our findings demonstrate that the responses of the mammary tissue to LD exposures are strongly non-linear providing molecular evidence against the LNT risk model and new evidence that mammary tissue responses vary dramatically by genetic background. Our findings suggest that the commonly used biological assumptions concerning the mechanisms by which LD radiation is translated into breast cancer risk should be re-examined and suggest a new strategy to identify genetic features that predispose or protect individuals from LD-induced breast cancer.

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CEITEC Common Evaluation of Scientific Excellence Lecture

Prof. Wilhelm GRUISSEM

12th June 2012

14:00 - 15:00

Department of Biology, ETH Zurich, Switzerland

Evaluator of CEITEC Research Programme 4 - Genomics and Proteomics of Plant Systems

Integrating leaf growth and circadian regulation - a systems approach to support genome scale metabolic modelling of plant biomass production

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Faculty of Information Technology, Brno University of Technology, Room no. D0206

Božetěchova 1, 612 66 Brno

Lecture abstract:

Plant leaves originate from meristematic stem cells by cell division and subsequent cell elongation. The continuous ontogeny and morphogenesis of leaves ultimately determines plant biomass production, but the underlying regulatory mechanisms are still poorly understood. While the emerging leaf is a metabolic sink, later in development it becomes a source tissue in which metabolism is regulated during the circadian rhythm. A full understanding of the developmental process and metabolic changes requires quantitative data at various levels. We have acquired large multi-scale datasets of Arabidopsis leaf number 6 at four stages of development and at end-of-day/end-of-night from three leaf growth baseline conditions (optimal water, water deficit and 18 hours light). The data are incorporated into a relational database built with MySQL and linked to external databases for integrated data analysis. Results from the integrated data analysis reveal interesting developmental correlations between DNA ploidy and protein synthesis as well as unexpected dynamics of end-of-day/end-of-night mRNA regulation that is not reflected at protein levels. These and other data provide an important basis for the construction of genome scale metabolic (GSM) models to predict metabolic flux changes in various conditions to improve crop performance. Our current Arabidopsis compartmentalized GSM model, which accurately predicts metabolism in day-night and other conditions, can be used to examine shared pathways between compartments, metabolic fluxes of central carbon metabolism, or production of single metabolites of interest such as vitamins.

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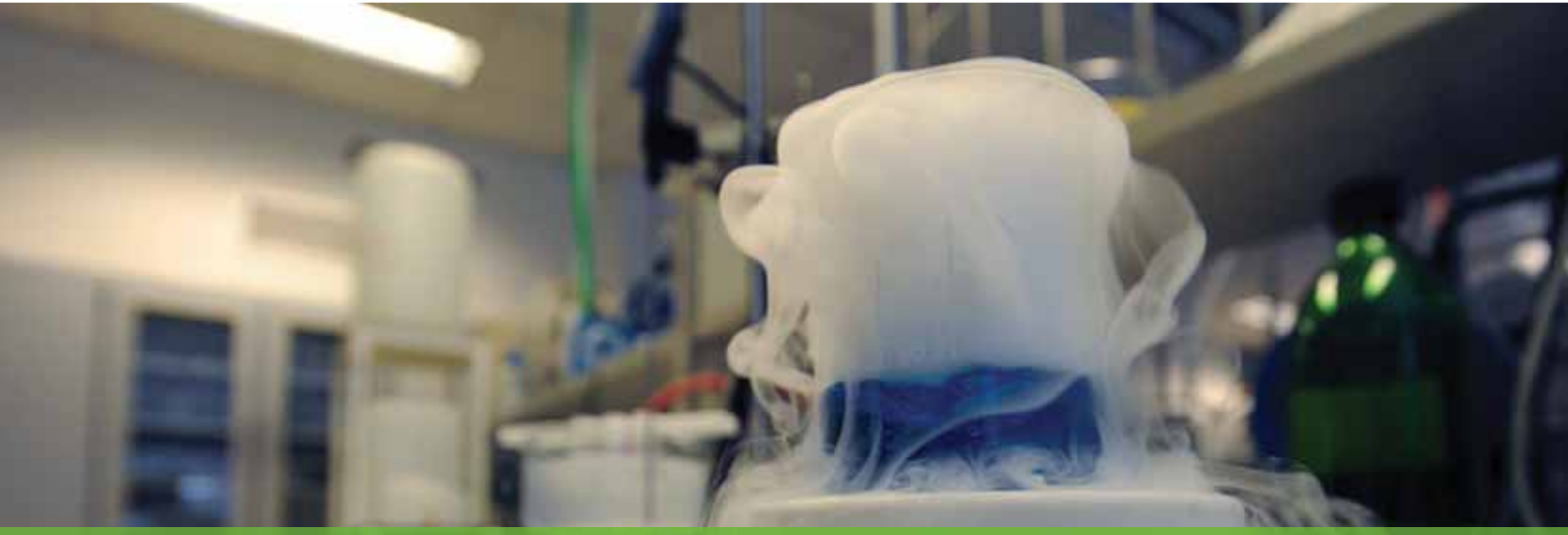

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Prof. Jürgen FLEIG

Institute of Chemical Technologies and Analytics, Vienna University of Technology, Austria

12th June 2012

14:00 - 15:00

Evaluator of CEITEC Research Programme 2 - Advanced Materials

Fundamental science behind solid oxide fuel cells

Faculty of Information Technology, Brno University of Technology, Room no. D0207

Božetěchova 1, 612 66 Brno

Lecture abstract:

Solid oxide fuel cells (SOFCs) are highly efficient and environmentally friendly devices for direct conversion of chemical into electrical energy. Despite being already in the process of commercialization, much improvement is still possible regarding efficiency, stability and economic scalability of SOFCs. At this point fundamental scientific studies come into play. Particularly, the solid state electrochemical processes in such cells have to be understood in detail: The kinetics of electrode reactions as well as of ion transport strongly affects the performance of the cells and deserves scientific investigation. In this talk a brief introduction into the functional principles and applications of SOFCs is given and then it is exemplarily discussed how the basic knowledge "behind SOFCs" can be improved by impedance and tracer studies on model electrodes.

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