Joint Retreat 2019

25 – 26 June 2019

Hotel Luna, Kouty

Czech Republic

CEITEC IMG IST AUSTRIA

Book of Abstracts

Joint Retreat 2019

25–26 June 2019

Hotel Luna, Kouty u Ledče nad Sázavou, Czech Republic

Editors:

Erik Képeš
Veronika Kozlová
Cosimo Lobello
Táňa Macháčková
Tarakaramji Moturu
Zdeňka Pavlačková
Barbora Peltanová
Jan Poduška
Igor Turčan
Dragana Vukić

ISBN 978-80-210-9300-3
ISBN 978-80-210-9301-0 (online : pdf)

Contents

Welcome Address

Dear attendees!

During the past four years, the two-day retreats organized by Ph.D. students of CEITEC for other students have become an annual tradition and it is our great pleasure to welcome you to the fourth issue of the retreat, this time called **Joint Retreat 2019**. The name has changed slightly to account for the fact that not only CEITEC Ph.D. students and postdocs are attending this retreat, but also students and researchers from three other institutes are participating – the **Institute of Molecular Genetics (IMG) AS CR**, the **Institute of Science and Technology (IST) Austria** and the **Institute of Organic Chemistry and Biochemistry (IOCB) AS CR**.

Although the name has changed, the original idea behind the event remains the same – to bring together Ph.D. students and young researchers from different scientific fields and give them a chance to present and discuss their research, get mutually inspired and make new contacts. This year, the topics of the conference are **Life Science**, **Material Science and Physics** and **Mathematics and Computer Science**. You can look forward to more than a hundred of student contributions in the form of a talk or a poster and 6 invited lectures.

We sincerely hope that you will enjoy your stay at Hotel Luna and that the Joint Retreat 2019 will be a pleasant and inspiring event for you!

Your organizing committee

Erik Képeš	Zdeňka Pavlačková
Anzer Khan	Barbora Peltanová
Veronika Kozlová	Jan Poduška
Cosimo Lobello	Markéta Šámalová
Táňa Macháčková	Igor Turčan
Tarakaramji Moturu	Dragana Vukić

Sponsors

The organizers of the Joint Retreat 2019 would like to thank the sponsors of the event for their generous contributions. The list of sponsors follows.

Platinum sponsors

Platinum sponsor and a sponsor of the Best Poster Award

Thermo Fisher Scientific is the world leader in serving science. Through a combination of brands – Thermo Scientific, Applied Biosystems, Invitrogen, Fisher Scientific and Unity Lab Services – they offer an unmatched combination of innovative technologies, purchasing convenience and comprehensive services. The Brno-based branch is the world's largest production of electron microscopes.

Platinum sponsor and a sponsor of the Best Talk Award

BD is a global medical technology company providing innovative solutions that help advance medical research and genomics, enhance the diagnosis of infectious disease and cancer, improve medication management, promote infection prevention, equip surgical and interventional procedures and support the management of diabetes.

měřicí technika - morava
messtechnik - moravia
measurement technic - moravia

Platinum sponsor

Measurement Technic - Morava is a Moravian company supplying the Czech and Slovak market with state-of-the-art measuring devices for physical and chemical analyses. It represents world's top manufacturers like Bruker, Specs or Createc, and provides support, training and service.

Gold sponsors

BioVendor®

MERCK

Silver sponsors

Photon Systems Instruments

CZECHINVEST
Investment and Business Development Agency

Bronze sponsors

tataabiocenter

DYNEX

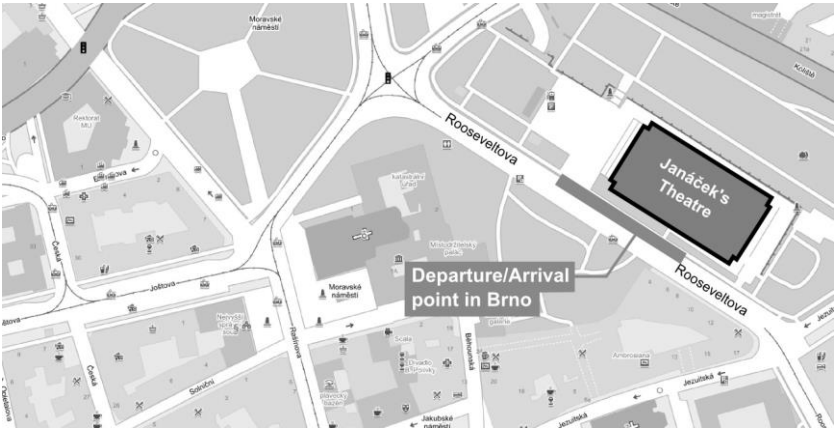
eppendorf

Practical Information

» Transportation

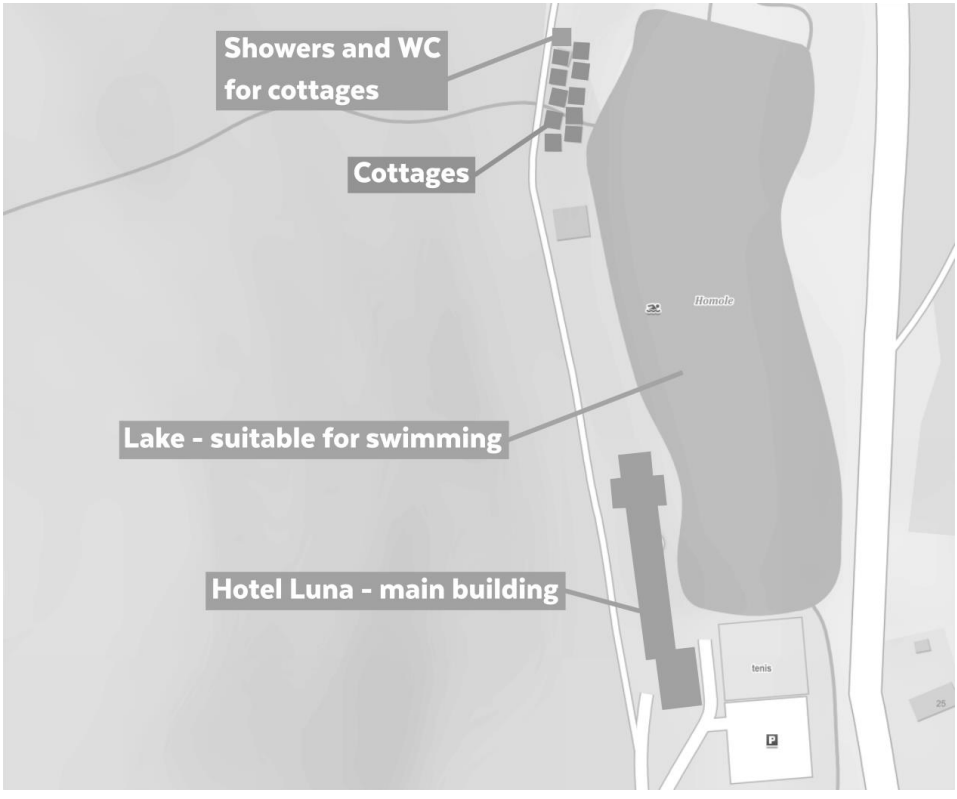
A direct bus connection from Brno to Kouty is provided by the organizers of the conference for all participants. It is free of charge. The time schedule of the transportation is the following:

	25 June – Brno to Kouty	**26 June – Kouty to Brno**
Departure point	Rooseveltova street, Brno (next to Janáček's theatre)	Hotel Luna, Kouty
Departure time	7:30	18:00
Arrival point	Hotel Luna Kouty at 9:00	Rooseveltova street, Brno



» Venue

For this year's retreat, the conference hotel Luna was chosen. Hotel Luna is located near the small village of Kouty in the beautiful nature of Bohemian-Moravian Highlands in the vicinity of Ledeč nad Sázavou. The hotel itself is a fully equipped conference center with several lecture halls. It also features a wellness facility with a pool and a sauna. Next to the hotel, there is a lake suitable for swimming.



» Accommodation

Hotel Luna offers two types of accommodation. The first is a classic double room with two single beds and a bathroom. The second option is a cottage for four people. The simple wooden cottages are located close to the hotel building near the lake, each is equipped with two bunkbeds only. The bathrooms for the cottages are in a separate building.

The participants will check in right after arrival or later during lunch time. The check-out should be done **before 10 am**. A room to safely store luggage will be provided.

» Meals

Breakfast, both lunches and the dinner buffet will be served in the hotel restaurant. The coffee breaks will be served in the lecture hall directly.
The lunch meals are pre-ordered. The participants were asked to choose their preferred meal from the menu upon registration. The options are below.

Tuesday, 25 June	**Wednesday, 26 June**
1. Roast chicken, rice	1. Roast pork in sour cream sauce, dumplings
2. Roast pork, potato dumplings, sauerkraut	2. Smoked roast pork, mashed potatoes, pickles
3. Indian vegetable curry with baby carrots and beans, rice (vegetarian)	3. Sweet quark dumplings (vegetarian)

» Poster Session

The student poster session will take place on **Tuesday, 25 June from 19.30 until 21.00**, social evening will continue after. The participants are encouraged to place their posters either right after registration or during one of the coffee breaks. The recommended format of the posters is A0, but it is also possible to mount smaller posters to the poster stands.
By being selected for a poster, students are automatically enrolled in the **Thermo Fisher Best Poster Award**, in which other students and the invited speakers will vote for the best poster. The winners are in for a valuable prize. The voting will be done via voting tickets. Every student will get 2 poster votes, which can be used to support their two favorite posters (or just one poster). By the end of the poster session, the tickets will be thrown into a ballot box located at the door to the poster room. The results of the poster session will be announced just before the closing of the conference. In case of a draw, the better poster will be chosen by the speakers.

» Talks

The talks will take place in the lecture hall on the first floor of Hotel Luna. The **allocated time for a student talk is 8 minutes with 2 minutes for discussion**. The equipment for the presentation (a PC, microphones and a laser pointer) will be provided.

The **BD Best Talk Award** contest will take place. Every participant will get 1 vote to support their favorite talk of the whole event. The author of the best talk will be also awarded a valuable prize.

» **Video Presentation**

This year, a video presentation option was included for those participants who are freshmen and/or are afraid that their results obtained so far are not enough for a talk or a poster. In a short video presentation, they can introduce their lab and their topic in general. The videos will be projected on a screen in a loop during the poster session. **The videos should not be longer than 5 minutes**.
A contest for the best video presentation will take place together with the **Best Poster Award**.

» Internet Connection

Wi-fi connection in Hotel Luna is free of charge and not protected by password

» Emergency Phone Numbers

The emergency phone number in Czechia is 112.

» Insurance

The organizers of the event do not accept liability for any injury, loss or damage, arising from accidents or other situations during the event. Participants are, therefore, advised to arrange accident and health insurance.

» Program Changes

The organizers cannot assume liability for any changes in the program due to external or unforeseen circumstances.

» Contact Information

Dragana Vukić, e-mail: dragana.vukic@ceitec.muni.cz, phone: +420 778 790 501
Jan Poduška, e-mail: poduska@ipm.cz, phone: +420 723 675 741
Zdeňka Pavlačková, e-mail: zdenka.pavlackova@ceitec.cz, phone: +420 770 110 745

Invited talks

Abstracts and speaker biographies

doc. RNDr. Monika Dolejská, Ph.D.

Senior researcher
CEITEC Veterinary and Pharmaceutical University Brno
Molecular Microbiology Research Group
E-mail: dolejskam@vfu.cz

Biography

The successful scientific career of Monika Dolejská began with obtaining a master's degree in Microbiology at the Faculty of Science of the Masaryk University in Brno in 2006. She continued with her Ph.D. studies at the Faculty of Veterinary Hygiene and Ecology of the Veterinary and Pharmaceutical University in Brno specializing in antimicrobial resistance. She obtained her Ph.D. in 2009. During her Ph.D. studies, she started working as Assistant Professor at the Department of Biology and Wildlife Diseases at the VPU. In 2011, she also became Junior Researcher at CEITEC VPU. Since 2012 she has been leading the Laboratory of Molecular Biology at the Department of biology and Wildlife Diseases, VPU. Since 2014 she has also been working at CEITEC VPU as Senior Researcher in the group lead by prof. Alois Čížek. She received the degree of Associate Professor in 2018. Her habilitation thesis was focused on the antibiotic resistance of enterobacteria. During her career she has been awarded two Research Excellence Awards and in 2018 she was awarded the prestigious L'Oréal-UNESCO Award for Women in Science.

Panel: Life Science

Antibiotic resistance and One Health concept: flow and fate of multi-drug resistant bacteria in the human-influenced environment

Monika Dolejská

An increasing incidence of antimicrobial resistant (AMR) bacteria have been reported globally as a result of the extensive use of antibiotics in human and animal medicine, causing one of the greatest medical challenges of our time. AMR bacteria including those resistant to clinically important antibiotics and drugs of last resort are being reported not only in humans but also in food-producing and companion animals and the environment including wildlife, underlining the scope of this problem. Multi-drug resistant bacteria and AMR genes carried by various mobile genetic elements can be exchanged between different niches (humans, animals, environment), therefore One Health approach is crucial for understanding the genomics, transmission pathways and public health risks of AMR bacteria.

The environment represents an important and generally overlooked component of AMR with many unresolved questions. Current data indicate that multi-drug resistant bacteria can spill over from their anthropogenic sources into natural ecosystems, possibly creating secondary reservoirs in the environment where clinically important resistance can be maintained and from where it can spread further. Insufficiently treated wastewater may play a significant role in the dissemination of AMR bacteria and AMR genes into surface water and wildlife. Moreover, accumulation of human refuse on landfills was suggested the major anthropogenic driver in the transmission of multi-drug resistant bacteria into wildlife, especially to wild bird species such as gulls that are increasingly foraging on waste in urban areas.

In order to understand the extend of the problem of AMR and to fill in the current gaps in our knowledge, our research focus on the impact of human activities and the role of the environment in the transmission of AMR. We apply comparative genomics of bacteria originating from diverse sources that are resistant to critically important group of antibiotics used to treat infections and humans and animals. Our pilot projects indicate that such bacteria are spreading in wild migratory birds in most continents. Moreover, we demonstrated that plasmids carrying AMR genes and high-risk bacterial clones of increased virulence and resistance found in wildlife

resemble those disseminating in animals and humans, highlighting the frequent transmission between these sources.
This presentation will highlight general principles of AMR using One Health concept, focusing on surveillance of clinically relevant antibiotic resistance mechanisms in wildlife and comparative genomics of AMR bacteria and plasmids carrying the resistance genes.

Acknowledgement: This research has been supported by Czech Science Foundation 18-23532S, Czech Health Research Council NV18-09-00605 and the National Sustainability Program II (LQ1601) provided by the Ministry of Education Youth and Sports of the Czech Republic.

RNDr. Dominik Filipp, CSc.

Group Leader
Institute of Molecular Genomics of Czech Academy of Sciences
Laboratory of Immunobiology
E-mail: dominik.filipp@img.cas.cz

Biography

Dominik Fillip obtained his RNDr, degree in the field of molecular biology and genetics at the Comenius University in Bratislava, Slovakia in 1987. After that, he was admitted to the Institute of Molecular Genetics in Moscow as a graduate student. He obtained the CSc. degree there in 1991. He began his rich professional career in Bratislava as a research associate at the Comenius University, Department of Genetics. He stayed in Bratislava until 1994 (with a post-doctoral fellowship in Marseille during 1992-1993). Then he was admitted to the Department of Immunology of the University of Toronto as a post-doctoral fellow. He spent the rest of the 1990s and the beginning of the 2000s in Toronto. In 2001, he became a Senior Lecturer at the University of Toronto. In 2007, he moved to the Czech Republic, where he became the head of the Laboratory of Immunology at the Institute of Molecular Genetics, AS CR Prague. There, he leads a research group focused on immune signaling and autoimmunity, maintaining a close collaboration with many leading laboratories in the Czech Republic and in the world. Dominik Fillip also supervises students and teaches immunology in Charles University in Prague.

Panel: Life Science

How the transcriptional regulator Aire keeps autoimmunity at bay

Dominik Filipp

The thymus is the site of T-cell lineage commitment and the place where highly autoreactive T cells are removed or are converted to T regulatory cells with immune suppressive function. In this presentation, I will focus on critical cellular and molecular components of this process, medullary thymic epithelial cells (mTECs) and the transcription factor, autoimmune regulator (AIRE), respectively, which regulate this process and prevent autoimmunity. Additional aspects of this process which have been the subject of our current studies, including the role of Toll-like receptors which are expressed on mTECs as well as the discovery of a new population of cells that express AIRE in the lymph nodes, will be put into the context of mechanisms that establish immune tolerance.

Mgr. Jan Zouhar, Ph.D.

Group Leader, director of CEITEC Mendel University
CEITEC MENDELU
Plant Stress Responses Research Group
E-mail: jan.zouhar@mendelu.cz

Biography

Mgr. Jan Zouhar, Ph.D., the director of CEITEC Mendel University in Brno, has a broad scientific experience spanning various fields of plant cell biology and biochemistry. He graduated and obtained his Ph.D. in Biochemistry at the Faculty of Science, Masaryk University in Brno. As a trained biochemist, he started his career studying enzymes and their structure-function relationships. Shortly after his studies finished, he moved to the USA to work as a postdoc at a plant research laboratory firstly located at Michigan State University then moving to University of California - Riverside. During his five-year stay, he became familiar with plant genomics and proteomics. His comprehensive description of Arabidopsis vegetative vacuolar proteome became one of the important publications in the field of plant endomembrane research.

After obtaining a number of competitive fellowships, Dr Zouhar moved to National Center for Biotechnology and then Center for Plant Biotechnology and Genomics in Madrid, Spain where he spent next 10 years of his career. His main interest laid in plant cell biology that allowed for a successful characterization of numerous novel genes linked to various functions in plant endomembrane system. He also gained expertise in transcriptomic responses to abiotic stress in Arabidopsis.

In 2017, Dr Zouhar returned to the Czech Republic and a year later, he became the director of CEITEC organizational unit at the Mendel University in Brno and a group leader at the same institution. He is an author or co-author of 23 scientific publications in impacted journals with more than 1200 citations.

Panel: Life Science

Endoplasmic reticulum and cellular stress responses in plants

Jan Zouhar

Plants as sessile organisms are subjected to various environmental stresses. The corresponding cellular stress responses often require a massive transport of newly synthesized proteins through the endomembrane system. Importantly, all these proteins are synthesized at the endoplasmic reticulum and such an increased demand may reduce the protein folding capacity of this organelle. Therefore, eukaryotes contain a sophisticated system of monitoring the correct protein folding, modification and assembly. Under the steady state conditions, the aberrant secretory proteins are recognized and degraded by the Endoplasmic-Reticulum-Associated Degradation (ERAD) pathway, which operates posttranslationally. Under conditions when the ERAD pathway is not sufficient to reestablish ER homeostasis, the accumulation of the unfolded proteins triggers a signaling pathway termed the Unfolded Protein Response (UPR). The UPR pathway includes mainly transcriptional responses to alleviate the cellular stress. Recent data suggests the UPR also regulates expression of the ERAD machinery, indicating that even though the ERAD and UPR pathways are currently mostly studied separately, there is a significant crosstalk between them during the stress responses.
The current knowledge in the field and future research directions will be discussed.

doc. Lucy Vojtová, Ph.D.

Group Leader
CEITEC Brno University of Technology
Advanced Biomaterials
E-mail: lucy.vojtova@ceitec.vutbr.cz

Biography

Doc. Lucy Vojtová, Ph.D. graduated in Macromolecular chemistry at the Brno University of Technology in 2000, where she also habilitated. Since 2006 she has been teaching at the Faculty of Chemistry, BUT. Since 2011 she has been joining CEITEC BUT, where she is currently posted as a group leader of the Advanced Biomaterials. Within a 3-year postdoctoral fellowship at Columbia University in New York City, she began to work on biomaterials and tissue engineering. She has received 8 patents and has published more than 45 articles in reputable journals dealing with polymer synthesis and functionalization, life-time controlled hydrogels, drug delivery systems and nanostructured scaffolds for regenerative medicine of both hard and soft tissues.

Panel: Physical and Material Science

A new approach in the treatment of injured spine using osteoinductive resorbable hybrid polymer/ceramic biomaterials: preclinical study

Lucy Vojtová

Due to the degenerative spinal diseases, comminuted fractures of vertebral body, spine malformations, and bone defects after tumor resection, lumbar intervertebral fusion procedures have rapidly increased over the last decade in the USA and Europe. Recently, we have developed novel biomimetic and bioactive hybrid polymer/composite biodegradable porous implant suitable for bone fusion. Its cytotoxicity tested on human mesenchymal stem cells and induction of new bone formation between vertebrae preclinically evaluated in vivo on Large white pig will be described and discussed. The novel technique utilizing tissue engineering should reduce complications of currently used auto- and allografts or metallic, PEEK or titanium cages.

Acknowledgement: This research was carried out under the project CEITEC 2020 (LQ1601) and grant nr. 17-31276A supported by Czech Health Research Council.

Chris Wojtan, Ph.D.

Professor, Group Leader
Institute of Science and Technology Austria
Visual Computing Group
E-mail: wojtan@ist.ac.at

Biography

Professor Wojtan obtained his bachelor's degree in computer sciences. During his Ph.D. he was working under the supervision of Greg Turk at the Georgia Institute of Technology. In December 2010 he defended his thesis titled "Animating Physical Phenomena with Embedded Surface Meshes". Throughout his Ph.D. he was a visiting researcher at Carnegie Mellon University and ETH Zurich. In February 2011 he became an assistant professor and in January 2016 a professor at IST Austria.
His research interests include physics-based animation (dynamics of fluids, solids, and more exotic materials), numerical algorithms (numerical integration, conservation schemes, efficient data structures, finite element methods, computational fluid dynamics), geometry processing (mesh generation, deformation, discretization, topology changes), and animation control (optimization, animation with constraints). His work was cited over 1400 times.
He has received numerous awards, such as the Outstanding Graduate Research Assistant Awards, the Microsoft Visual Computing Award, and the IST Austria "Golden Chalk" Best Lecturer Award. In 2015 he received a European Research Council (ERC) Starting Grant.
Currently, prof. Wojtan is the head of the Scientific Computing service unit. In addition, he is the chair of the female faculty recruiting committee and mentor to several 1st year Ph.D. students. He was the co-organizer of World Congress on Computational Mechanics (WCCM) minisymposium in 2018 and the Conflict of Interest Coordinator of SIGGRAPH 2019.

Panel: Mathematics and Computer Science

How to Make a Big Splash: Physics Simulation for Computer Animation

Chris Wojtan

Computers are getting more and more powerful, and computer scientists are developing better and better algorithms. Despite this constant progress, it is still extremely difficult to simulate things we see in everyday life, like splashing liquids, fracturing solids, tiny bubbles and foams, and detailed water ripples. Our approach to solving these problems combines numerical algorithms for solving differential equations with geometric algorithms for computing shapes. I will present some of my group's research on the simulation of natural phenomena, including new methods for animating water waves, bubbles, liquids, and fracturing solids. These techniques have potential applications in computational physics, engineering, the motion picture industry, virtual reality, and video games.

Prof. Ing. Martin Fusek, CSc.

Professor, deputy director for strategic development
Institute of Organic Chemistry and Biochemistry of the AS CR
E-mail: fusek@uochb.cas.cz

Biography

Prof. Fusek graduated from the University of Chemistry and Technology in Prague in the field of organic chemistry, he obtained the CSc. title in the field of biochemistry at the Institute of organic chemistry and biochemistry, Academy of Sciences Czechoslovakia, in 1988. During the period of 1989 – 1995, he was working at a postdoc position in the USA and West Germany. He has authored more than 50 original articles in impacted journals and 2 monographs Since 1995 he has been an external lecturer at the Institute of Chemical Technology in Prague, where he was awarded the title of Professor in Biochemistry in 2012. From 1995 to 2007 he worked for Sigma-Aldrich and Merck in the Czech Republic and abroad. Since 2007, he has been dealing with the technology transfer at IOCB ASCR. Since 2009, he has been the Executive Director of IOCB TTO, which provides the technology transfer process for IOCB, AS CR. and since 2012 he is the Deputy Director for Strategic Development at the same institute. He is a member of several supervisory boards of scientific institutions, a member of the CSCH Bureau and other organizations.

Extra Talk: Tech Transfer

Translation of Results of Basic Research for Human Use

Martin Fusek

Nucleoside Triphosphate transporter for labeling of DNA of living cells.

Main author: Dr. *Tomáš Kraus* (IOCB Prague)
Patent in major countries awarded in 2018.
Partner: Merck Millipore.
License signed in 2017, down payment + royalties.
Product on the market in 2019 see: https://www.sigmaaldrich.com/technical-documents/articles/biology/cell

Modified prolactin releasing peptide for treatment of obesity, diabetes type II and neurodegeneration.

Main author: Dr. *Lenka Maletínská* (IOCB Prague)
3 Patents awarded in major countries in 2018/2019
Partner: Novo Nordisk
License signed in 2017, down payment, milestone payments, royalties
Cooperation – 3 years of cooperation of the research supported by Novo Nordisk

Novel compounds for cancer treatment

Main authors: *Dr. Pavel Majer* (IOCB Prague) and Dr. *Barbera Slusher* (Johns Hopkins University, Baltimore)
Multiple patents awarded in 2018/2019 in major countries
Partner: DRACEN Pharmaceuticals – USA incorporated spin-off which received investment of 40 mil USD from Deerfield investment company to develop this compound to clinical use.
License signed 2018, shareholder participation, down payment, royalties

DIANA analytical method.

Main author: *Václav Navrátil* (IOCB Prague)
2 patents pending

Partner: DIANA biotechnologies s.r.o. - an IOCB Prague spin-off company incorporated in 2018. Received investment from VC company BTZ in the amount of 2.5. mil € in 2018. CEO – Václav Navrátil.
License transferring the rights from IOCB Prague to DIANA Biotech signed in 2018. Shareholder participation, minimal down payment, royalties.

Novel method of isolation of ^{177}LU isotope from Ytterbium oxide after irradiation for medical purposes.

Main author: *Miloš Polášek* (IOCB Prague)
Patent pending
Partner: SHINE Medical Technologies, USA
License signed in 2019. Down payment, milestone payments, royalties.

Life Science

Students' Abstracts

T01: The architecture of human SMC5/6 complex: downfall of the guardian

Marek Adamus[1*], Lucie Vondrová[1], Edita Balkóová[1], Lenka Jurčišinová[1], Stephan Gruber[2], Saskia N. van der Crabben[3], Kateřina Zábrady[4], Antony W. Oliver[4], Sharon E. Plon[5], Johanne M. Murray[4], Gijs van Haaften[3], Zbyněk Zdráhal[1], Jan J. Paleček[1]

[1] Central European Institute of Technology and Faculty of Science, Masaryk University, Brno, Czech Republic

[2] Department of Fundamental Microbiology, Faculty of Biology and Medicine, Université de Lausanne, Lausanne, Switzerland;

[3] Wilhelmina Children's Hospital, University Medical Center Utrecht, Utrecht, The Netherlands;

[4] Genome Damage and Stability Centre, School of Life Sciences, University of Sussex, Brighton, United Kingdom;

[5] Human Genome Sequencing Center, Baylor College of Medicine, Houston TX, USA

*marek.adamus@ceitec.muni.cz

One of the many challenges a cell faces is chromosome safekeeping, maintenance, replication, and segregation. Such a task requires a robust chromosome guarding machinery of protein complexes. A family of Structural Maintenance of Chromosome (SMC) complexes is one of the most important guardians. The SMC complexes are involved in nuclei organization, DNA replication, condensation, and segregation. So far, three eukaryotic (cohesin, condensin, and SMC5/6) and three prokaryotic (SMC/ScpAB, MukBEF, MksBEF) SMC complexes have been described. They share common SMC-kleisin circular architecture allowing them to embrace and hold DNA. It was shown that the prokaryotic SMCs and the eukaryotic SMC5/6 complex's NSE subunits share even more structural similarities. They interact with the kleisin subunit and form stable homo- or hetero-dimers through winged-helix (WH) domains, thus they were re-classified into a new protein family called KITE (Kleisin Interacting Tandem winged-helix Elements of SMC complexes). Recently, mutations in human NSE3 KITE subunit were linked to a newly described chromosome breakage syndrome combined with B and T cell immunodeficiency. We found that these mutations destabilized the SMC5/6 complex by disrupting interactions between NSE3 KITE and NSE4 kleisin subunit, therefore suggesting the key role of KITE-kleisin interactions in the complex's guardian function.

Acknowledgement: Czech Science Foundation (GA18-02067S) and Ministry of Education, Youth and Sports of the Czech Republic (LQ1601).

T02: Deciphering the Role of an F-Actin Regulatory Protein MPRIP in Nuclear Architecture

Can Balaban[1*], Martin Sztacho[1], Pavel Hozak[1,2,3]

[1]Institute of Molecular Genetics ASCR v.v.i., Department of Biology of the Cell Nucleus, Vídeňská 1083, 142 20, Prague 4, Czech Republic

[2]Microscopy Centre, Institute of Molecular Genetics ASCR v.v.i., Vídeňská 1083, 142 20, Prague 4, Czech Republic

[3]Institute of Molecular Genetics ASCR v.v.i., Division BIOCEV, Laboratory of Epigenetics of the Cell Nucleus, Průmyslová 595, 252 50, Vestec, Czech Republic

*can-balaban@hotmail.com

Nuclear compartmentalization is crucial for spatiotemporal regulation of key processes such as transcription and splicing. Recently, we have identified an F-actin regulatory protein (MPRIP) in nucleus by using microscopy and biochemistry methods. Having two PH domains, MPRIP has an affinity to Phosphoinositols and as a key regulator of protein phosphatase 1, it is a potential mediator for dephosphorylation of Pol II and splicing machinery [1]. We have first investigated the localization of the endogenous MPRIP by super-resolution microscopy (STED) and visualized that it forms nanoscale foci in the nucleoplasm, which partly coalesce with PIP2 containing structures in nucleus, particularly with nuclear speckles and sub-population of Nuclear Lipid Islets (NLIs) [2]. To study the dynamics of endogenous MPRIP nanoscale foci is extremely challenging, therefore we employ GFP-MPRIP overexpression, in order to address question about the inner dynamics and mobility of MPRIP induced condensates. The transient transfections experiments showed that highly expressing protein undergoes phase separation by accumulating in nucleus where it forms condensates that are up to 5 µm in diameter. We presume that this formation is mediated by the C Terminal- Intrinsically Disordered Region (IDR). The Fluorescence recovery after photobleaching (FRAP) and live-cell imaging experiments uncovered their rapid motion, of which we have quantified the diffusion coefficients as a way to comprehend how the protein might act at endogenous levels. Here, we showed that MPRIP, an actin regulatory protein, is present in mammalian nucleus and partly localize to proximity of PIP2 rich structures. We hypothesize that MPRIP might regulate transcription by recruiting its known interactor, Protein phosphatase 1, to the vicinity of NLIs. Altogether, these data indicate that MPRIP might be an important regulator of Pol II transcription, while the exact pathway remains to be enlightened.

[1] Mulder, J., Poland, M., Gebbink, M.F.B.G., Calafat, J., Moolenaar, W.H., Kranenburg, O., 2003. p116Rip Is A Novel Filamentous Actin-binding Protein. J. Biol. Chem. 278, 27216–27223.

[2] Sobol, M., et al. 2018. Nuclear phosphatidylinositol 4,5-bisphosphate islets contribute to efficient RNA polymerase II-dependent transcription. Journal of Cell Science 131.

P01: Molecular principles of Cajal body formation

Davide Basello[1,2*], Michaela Efenberková[1], Radek Macháň[2], Nicola Maghelli[3], David Stanek1[1]

[1]Institute of Molecular Genetics, Czech Academy of Sciences, Prague, Czech Republic
[2]Charles University in Prague, Faculty of Science, Prague, Czech Republic
[3]Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany
*Basello@img.cas.cz

The cell nucleus is a highly heterogeneous environment crowded with numerous macro-molecules. Part of the nuclear complexity rises from the presence of a number of different bodies, non-membrane bound structures, which accumulate various proteins and RNAs. One of the "classical" examples of a nuclear body is the Cajal body (CB). CBs are involved in biogenesis, quality control and recycling of spliceosomal snRNPs. Coilin, the essential scaffolding protein of CBs, self-oligomerize and interacts with numerous proteins including snRNPs, and these interactions are important for CB formation. However, the basic information regarding its structure and function are lacking. To uncover molecular principles of CB formation we determined coilin dynamics in the nucleoplasm and CBs and analyzed the snRNP influence on coilin self-oligomerization and CB formation. To eliminate the effect of endogenous coilin, we generated a coilinKO cell line. Then we prepared several different mutated versions of coilin that prevent interaction with snRNPs and express them in coilinKO cells. Our results show that coilin self-interaction does not depend on snRNP binding. However, the mutants that do not associate with snRNPs fail to reconstitute CBs. We also apply different fluorescence microscopy techniques (FRAP, single-point and imaging FCS and 3D-SIM SPT) to determine coilin dynamics in the nucleus and the CB. The data confirm our biochemical results and show that abolishing coilin interaction with snRNPs does not inhibit coilin self-association. Interestingly coilin dynamics inside the CB does not differ from the nucleoplasmic coilin, suggesting that the CB nucleation and maintenance are not based on different coilin mobility inside and outside CBs.

P02: iBodies: exploring the potential of synthetic antibodies

Jana Beranova[1,2], Kristyna Blazkova[1,3], Tomas Etrych[4], Pavel Sacha[1,5], Jan Konvalinka[1,5]

[1]Institute of Organic Chemistry and Biochemistry, The Czech Academy of Sciences, Flemingovo n. 2, Prague 6, 16610, Czech Republic

[2] First Faculty of Medicin, Charles University, Ketrinska 32, 121 08, Prague, Czech Republic

[3]Department of Cell Biology, Faculty of Science, Charles University, Vinicna 7, 128 00 Prague, Czech Republic

[4]Institute of Macromolecular Chemistry, The Czech Academy of Sciences, Heyrovskeho n. 2, Prague 6, 16606, Czech Republic

[5]Department of Biochemistry, Faculty of Science, Charles University, Hlavova 8, 128 43 Prague, Czech Republic

*jana.beranova@uochb.cas.cz

Antibodies represent indispensable tool utilized across various fields of natural sciences. However, there are many factors which significantly limit their application. Low stability inherent to the proteins, difficulty of chemical modification and inconsistency between antibody batches are among the most significant issues which need to be addressed.

Recently described synthetic polymer-based conjugates of N-(2-hydroxypropyl)methacrylamide (HPMA) and low-molecular-weight ligands prove to be a promising alternative to antibodies. So called iBodies [1] consist of highly hydrophilic biocompatible copolymer carrier which can be chemically modified with functional ligands depending on the intended use of the mimetics. Conjugated ligands can serve various purposes, including e.g. detection, identification and immobilization of proteins (or more generally of binding partners) or targeting of biologically active molecules and imaging probes to the desired destination. [2,3]

Within the scope of the project, we aim to explore and develop novel applications of this flexible platform as a chemical biology tool for research as well as diagnostics and therapy.

[1] Sacha, P., et al., iBodies: Modular Synthetic Antibody Mimetics Based on Hydrophilic Polymers Decorated with Functional Moieties. Angew Chem Int Ed Engl, 2016. 55(7): p. 2356-60.

[2] Dvorakova, P., et al., Inhibitor-Decorated Polymer Conjugates Targeting Fibroblast Activation Protein. J Med Chem, 2017. 60(20): p. 8385-8393.

[3] Simon, P., et al., Identification of Protein Targets of Bioactive Small Molecules Using Randomly Photomodified Probes. ACS Chem Biol, 2018

P03: Breaching the wall: Structural studies of phage infection

Ján Bíňovský[1*], Marta Šiborová[1], Jiří Nováček[1], Roman Pantůček[2], Pavel Plevka[1]

[1] CEITEC – Masaryk University, Brno, Czech Republic

[2] Department of Experimental Biology, Masaryk University, Brno, Czech Republic

*jan.binovsky@ceitec.muni.cz

Infection caused by antibiotic-resistant *S. aureus* strains are difficult to treat and can induce life-threatening symptoms. Phage phi812K1/420 from the family *Myoviridae* can infect 95 % of *S. aureus* strains, including those resistant to antibiotics, which makes it a promising agent for phage therapy.

Tail spike protein (TSP) is located at the centre of the phage baseplate. Putative hydrolyse domain of TSP probably degrades *S. aureus* cell wall and detachment of TSP is suggested to trigger structural changes leading to genome release.

We aim to obtain high-resolution structures of TSP from phage phi812K1/420 with combination of cryo-electron microscopy (cryo-EM) and X-ray crystallography. Structures will be evaluated both individually and upon fitting into the structure of the phage baseplate. Analysis of the TSP active site architecture will be complemented with zymography to define key determinants of the phage degradative machinery.

Trimeric organisation of the TSP allowed to collect cryo-EM data for single-particle reconstruction. Preliminary results correspond with the overall TSP arrangement as observed in whole phage baseplate reconstruction.

Achieving TSP characterisation from the structural and functional point of view will shed light to initial steps of the phage infection. Comprehensive description of the phage structure and life cycle is necessary for its approval as pharmaceutical agent, which will be used with, or instead of, antibiotics for treatment of *S. aureus* infections in humans.

V01: Presentation of Ondrej Slaby's Lab

Dominika Brchnelova[1*]

[1] Central European Institute of Technology, Masaryk University, Brno, Czech Republic
*d.brchnelova@gmail.com

Video presentation of Ondrej Slaby's Lab, which focuses on the roles of non-coding RNAs (microRNA, PIWI-interacting RNAs, long non-coding RNAs) in molecular pathology of solid cancers and their potential as innovative diagnostic and novel therapeutic targets in oncology. The video will present members of our research group as well as the range of methods we use daily, such as high-troughput analysis of non-coding RNAs, mainly RNAseq and small RNAseq, *in vitro* analyses of non-coding RNAs as potential therapeutic targets and *in vivo* methods (xenograft models and knock-in/knock-out experiments).

P04: Exploring state-dependent modulation of visual processing in the mouse superior colliculus.

Laura Burnett[1*]

[1] Institute of Science and Technology, Klosterneuburg, Austria

*lburnett@ist.ac.at

For most animals, the ability to see is critical to their survival in the natural world. Many animals rely on vision in order to find food, explore new environments and detect impending threats. In laboratory environments, mice have been shown to initiate stereotyped behavioral responses to ethologically related visual stimuli such as expanding discs or small, moving dots (mimicking an approaching predator/ nearby prey respectively).

Detection of these salient stimuli requires the efficient extraction of the relevant features from the visual scene. Computationally this processing starts already at the level of the retina, with visual information being split into functionally distinct parallel channels related to discrete visual features to the brain. However, how exactly these individual streams are then combined and processed to generate these visually guided innate behaviours is not completely understood. Despite being strongly stimulus-driven, the selection and initiation of these behaviors as well as the intensity with which they are performed also depends upon the current internal state of the animal. Therefore, the underlying neural circuits driving the initiation of these behaviours are necessarily adaptive in order to generate the most appropriate behavioral response.

One brain area in particular, the superior colliculus (SC), appears to have a prominent role in orchestrating these responses. It receives direct input from sensory systems, including almost all retinal ganglion cells in the mouse, dense innervation from numerous brain regions containing modulatory neurotransmitters and has direct efferent projections to premotor areas (in the brainstem?).

Here we aim to understand the role of neuromodulation in early sensory processing. Specifically, we intend to investigate the role of serotonin, a neuromodulator that is strongly implicated in mediating numerous physiological states and appears to reroute direct visual information from the retina to the SC via the visual cortex by direct modulation of retinal ganglion cell axons. Interestingly, it is not known when these inputs are activated during natural behaviour, if they act in a global manner upon all cells within the SC or whether they have a more targeted effect, preferentially targeting cell types with particular properties.

To tackle these questions, I am establishing a system which combines endoscopic imaging with behavioural tracking in freely moving animals to investigate the network behaviour within the SC whilst animals are being presented with a visual stimulation paradigm. Chemo- and optogenetic tools will be used to dissect the specific role of the serotonergic system in modulating SC activity. By furthering our understanding about the specific modulation of visual processing within the SC we expect to shed light on the broader mechanisms by which neuronal networks adapt their activity to context-specific requirements.

P05: ADAPting the mode of migration in dendritic cells

Nikola Čanigová[1*], Martin Loose[1], Michael Sixt[1]

[1] Institute of Science and Technology Austria, Klosterneuburg, Austria
*nikola.canigova@ist.ac.at

Cell migration is a crucial process in development and immunity. Dendritic cells are immune cells that travel large distances over their lifetimes, needing to sense the direction of attractant, polarize to a front and back and propel themselves forward using cytoskeleton. One of the proteins necessary for polarization, cytoskeleton remodeling, protein trafficking and cell migration is a small GTPase ARF6. Its GTPase activating protein (GAP) ADAP1 was also shown to regulate cytoskeleton dynamics, but independently of its GAP activity, posing a question whether it also plays a role in cell migration.

To answer it we generated ARF6 and ADAP1 knock out (KO) dendritic cells using CRISPR-Cas9 system and tested them in 3D collagen migration assays, which mimic their physiological environment. When embedded within the collagen matrix and presented with attractant, the speed of KO cells was indistinguishable from wildtype. However, when forced to invade a dense proteolytically cleavable collagen matrix, the ARF6 KO cells were unable to enter the matrix. This could be due to malfunctioning cell adhesions, since ARF6 is required for integrin recycling. Interestingly, when the cleavable collagen matrix was used in a lower concentration, instead of expected single cell migration mode, the cells switched into a proteolytically active mode, digested the collagen and only started migrating as single cells after several hours. The ADAP1 KO cells seemed to be more effective at the digestion, possibly due to overactivation of ARF6, which was shown to be necessary for delivery of matrix cleaving metalloproteinases to the plasma membrane.

P06: The role of BRAT1 protein in DNA damage response and its links to neurodegeneration

Zuzana Cihlářová[1*], Hana Hanzlíková[1,2], Grace Yoon[3] and Keith W. Caldecott[1,2]

[1] Laboratory of Genome Dynamics, Institute of Molecular Genetics ASCR, Prague, Czech Republic.

[2] Genome Damage and Stability Centre, School of Life Sciences, University of Sussex, Brighton, UK.

[3] Division of Clinical and Metabolic Genetics, and Division of Neurology, The Hospital for Sick Children, University of Toronto, Canada.

*zuzana.cihlarova@img.cas.cz

The human genome is continuously under attack from different agents leading to breakage of one or both strands of DNA. Our cells have developed mechanisms to rapidly repair these lesions, highlighting the importance of genetic integrity. DNA repair defects can lead to a variety of human genetic diseases, with pathologies including growth and developmental defects, immunodeficiency, predisposition to cancer and neurodegeneration.

BRAT1 (BRCA1-associated ATM activator-1) has been recently identified as a sensor of DNA double-strand breaks induced by ionizing radiation. However, the exact mechanism/s by which mutations in BRAT1 gene trigger neurodegeneration and to what extent DNA breaks contribute to this are unknown. In my project, I examine two patients with novel, unpublished, mutations in BRAT1 to address this question. My preliminary data indicate that, contrary to published literature, BRAT1 mutated patients do not exhibit a defect in ATM kinase activation during the DNA damage response. Based on my preliminary findings, I propose that BRAT1 may function during a different DNA damage response, such as DNA single-strand breaks repair for example, which is implicated strongly in neurodegenerative disease.

P07: RNA demethylase FTO influences pre-mRNA processing events

Marek Bartosovic[1,2], Helena Covelo-Molares[1*], Veronika Rajecka[1], Stepanka Vanacova[1]

[1] CEITEC–Central European Institute of Technology, Brno, Czech Republic, Czech Republic
[2] Department of Medical Biochemistry and Biophysics, Karolinska Institutet, Solna, Sweden
*helena.covelo@ceitec.muni.cz

Eukaryotic RNAs can carry more than 100 different types of chemical modifications. Early studies have been focused on modifications of highly abundant RNAs, such as rRNA or tRNAs. However, the development of new detection methods allows nowadays to study also mRNA modifications. Among them, N6-methyladenosine (m6A) is particularly interesting as it can be 'erased' by the RNA demethylases ALKBH5 and FTO.

Our recent study of the RNA demethylase FTO revealed that it preferentially binds to intronic regions of pre-mRNAs, suggesting that RNA demethylation could be a co- or early post-transcriptional process. In addition, we performed transcriptome analysis of HEK293 FTO knockout mammalian cell line and uncovered that depletion of FTO leads to changes in alternative pre-mRNA splicing (AS) and 3' ends of mRNAs. FTO depletion leads mostly to AS exon skipping events and the splicing pattern can be rescued by catalytically active FTO. We were able to reproduce the FTO-dependent AS phenotype by using a reporter mini-gene construct, which we subsequently use to characterize the RNA region(s) and cofactors involved in the AS regulation. Altogether, our data indicate, that FTO and its activity plays a role in determining the mature form of subset of mRNAs via affecting the pre-mRNA processing steps.

T03: Cocaine Place Conditioning Strengthens Location-Specific Hippocampal Coupling to the Nucleus Accumbens

Andrea Cumpelik[1,5*], Lucas L. Sjulson[2], Adrien Peyrache[3], Daniela Cassataro[4], György Buzsáki[5]

[1] Institute of Science and Technology Austria, Klosterneuburg, Austria
[2] Albert Einstein College of Medicine, New York, USA
[3] McGill University, Montreal, Canada
[4] University of California San Diego, California, USA
[5] New York University, New York, USA
*andrea.cumpelik@ist.ac.at

Addiction is characterized by the formation of contextual associations with the place a drug was taken, and subsequent exposure to that place may trigger relapse. To prevent this relapse, it is important to understand the neural circuit which underlies this phenomenon. Conditioned place preference (CPP) is a widely used model of addiction-related behavior that replicates this phenomenon in rodents. We recorded from the brains of freely moving mice to examine interactions between two brain regions, the hippocampus and nucleus accumbens, during the acquisition of cocaine CPP. We found that CPP was associated with recruitment of D2-positive dopamine neurons in the nucleus accumbens to fire in the cocaine-paired location. This recruitment was driven predominantly by selective strengthening of synapses with hippocampal place cells that encode the cocaine-paired location. These findings provide *in vivo* evidence suggesting that the synaptic potentiation in the accumbens caused by repeated cocaine administration preferentially affects inputs that were active at the time of drug exposure. This provides a potential physiological mechanism by which drug use becomes associated with specific environmental contexts.

P08: The effect of plasma-treated polymers rich in amino groups on cytokinetics of cells

Petra Cernochova[1,4*], Jirina Medalova[1,4], Lenka Zajickova[2,4], Lucie Blahova[2], Miroslav Michlicek[2,4], Lucie Bacakova[3], Martin Parizek[3]

[1] Department of experimental biology, MU, Kamenice 5, 62500 Brno, CR

[2] Department of Physical Electronics, MU, Kotlarska 2, 61137 Brno, CR

[3] Department of Biomaterials and tissue engineering, Institute of Physiology of Czech the Academy of Sciences, Videnska 1083, 14220 Prague 4, CR

[4] RG Plasma Technologies, CEITEC, MU, Purkynova 123, 61200 Brno, CR

*petra.eliotek@gmail.com

Synthetic polymers have good properties for tissue engineering except their hydrophobicity. Plasma polymerization improves surface properties of polymers such as hydrophobicity, cell attachment, expansion and proliferation [1]. We studied cell ability to attach and adhere to the surface as it is the prime condition for successful use of the biomaterials, and it affects also cell capacity to proliferate and differentiate in contact with the surface[1].

This work is focused on non-toxic cyclopropylamine (CPA), which can form layers rich in positively charged amine groups when functionalized by plasma. We compared effect of amine-rich dishes on cytokinetic parameters of various types of cells (fibroblasts, keratinocytes, vascular smooth muscle cells and endothelial cells) in order to choose the best condition and cell type for future, more detailed study. We assessed the effect of amine-rich surfaces on the adhesion and cytokinetic parameters of above-mentioned cell and also studied the expression of adhesion molecules by methods like qRT-PCR and Western blotting.

On modified Petri dishes (TPP) we observed that all the amine-rich layers slightly decreased final cell number. However, experiments performed on nanofiber membranes placed in cell crowns showed that functionalization increased the ability of cells to grow compared to the plain PCL membrane. We did not find any significant changes in differentiation, only some interesting trends, which may be better pronounced in long time cultivation. Adhesion was assessed as the ability of cells to resist to the effect of trypsin/EDTA. Plasma modification generally increased adhesion of all cells, but there are cell type specific differences between the types of amine-rich layers. We also studied the expression of main integrines and cadherines, however we have not found any pattern, which would explain the highly increased ability of cells to resist to trypsin/EDTA treatment.

[1] Ryu G. H., Yang W.-S., Roh H.-W., Lee I.-S., Kim J. K., Lee G. H., Lee D. H., Park B. J., Lee M. S., Park J.-Ch., Surf. Coat. Tech., *193*, 60 (2005).

P09: Dissecting hematopoiesis using zebrafish model

Ivana Dobiášovská[1*], Petr Bartůněk[1]

[1] Institute of Molecular Genetics of the ASCR, v.v.i., Prague, Czech Republic
*ivana.dobiasovska@img.cas.cz

Hematopoiesis is a process of formation, development and self-renewal of all blood cellular components, essential for maintaining homeostasis of all vertebrate organisms. Highly specialized cells arise from the common progenitors through the tightly regulated process of cell differentiation driven by specific factors. Elucidating how these factors control the differentiation is necessary to understanding how hematopoietic cells are preserved.

Our research interest aims at the characterization of new genes involved in the regulation of specialized blood cells development with focus on erythrocytes and thrombocytes. Our goal is to utilize the Danio rerio (zebrafish) model due to its less complex hematopoietic system and a higher number of the progeny compared to commonly used mammalian model organisms. This allows simple, fast and quantitative analysis with a possibility of comparison to other model organisms from phylogenetically independent clades (evolution branches) used in our laboratory. In summary, the project has a potential to reveal us novel evolutionary conserved players controlling the hematopoietic development, which will give us insight into the hematopoiesis evolution and underlying information for the studying of human hematopoietic diseases and cancers.

P10: Study of the involvement of light components pathway (PIF4 and PhyB) in high temperature response in inflorescence of Arabidopsis thaliana

Shekoufeh Ebrahimi Naghani[1*,] Helene Robert Boisivon[1]

[1] Mendel Centre for Genomics and Proteomics of Plants Systems, CEITEC MU-Central European Institute of Technology, Masaryk University, 625 00 Brno, Czech Republic
*shekufeh.ebrahimi@gmail.com

Plants must constantly respond to changes in the environment whilst maintaining developmental and growth processes if they are to survive into the next generation. A complex network of signals from temperature and light must correctly converge to achieve successful development, through vegetative to reproductive growth. Temperature can be thought of as an environmental factor that provides both 'inductive' and 'maintenance' signals in development (L. Heggie and KJ, Halliday, 2005). Extremes of temperature represent a significant stress for plants and is a major factor limiting global plant distribution (Mittler, 2006). Many stages of flower development, particularly the late stages of stamen development, are sensitive to heat stress. Many of the temperature-regulated developmental pathways are intimately linked with light signaling. These responses are frequently mediated by manipulating the phytohormone network (L. Heggie and KJ, Halliday, 2005).

The model plant, *Arabidopsis thaliana*, like many higher plants, responds to warmer ambient temperatures by increasing its growth rate and accelerating the floral transition. Arabidopsis is a facultative long day plant, and plants grown under short photoperiods are dramatically delayed in flowering (Halliday and Fankhauser, 2003). Interestingly, late flowering in short days can be overcome by growth at higher temperatures. Therefore, the array of light signals controlling development cannot be separated from temperature responses and hormone mediation. In this study we aim to examine the integration of these pathways in the control of a range of developmental processes including inflorescence and seed development responses in *A. thaliana*.

Acknowledgement: This work was supported from European Regional Development Fund-Project "SINGING PLANT" (No. CZ.02.1.01/0.0/0.0/16_026/0008446).

[1] Fitter, A.H and Fitter, R.S. 2002. Rapid changes in flowering times in British plants. Science 296, 1689-1691.

[2] Halliday, K. J. and Fankhauser, C. 2003. Phytochrome-hormonal signalling networks. Tansley Review, New Phytol. 157: 449-463.

[3] Heggie, L and Halliday, K.J. 2005. The highs and lows of plant life: temperature and light interactions in development. The International Journal of Developmental Biology. DOI: 10.1387/ijdb.041926lh.

[4] Mittler, R. 2006. Abiotic stress, the field environment and stress combination. Trends Plant Sci. 11, 15-19.

T04: Function of phosphatidylinositol 4-phosphate in the cell nucleus

V. Fáberová[1], I. Kalasová[1], P. Hozák[1]

[1] Department of Biology of the Cell Nucleus, Institute of Molecular Genetics, Prague, Czech Republic

*faberova@img.cas.cz

Phosphoinositides are glycerol-based phospholipids. They are composed of hydrophobic fatty acid tail and hydrophilic inositol head. Phosphoinositides are important cytoplasmic signalling molecules. They participate in various processes such as modulation of ion channels and transporters, membrane dynamics and cellular movement. Despite the absence of membranes inside of the nucleus, phosphoinositides are implicated in essential nuclear processes. Through the interaction with their binding partners, they regulate DNA damage response, DNA transcription and RNA processing. Phosphatidylinositol 4-phosphate [PI(4)P] is one of the most abundant phosphoinositides in the cell, however, its nuclear functions are still poorly understood. Our preliminary data show that PI(4)P localises to the nuclear membrane, nuclear speckles and forms small foci in the nucleoplasm. Furthermore, nuclear PI(4)P interacts with many RNA-binding proteins including heterogeneous nuclear ribonucleoproteins (hnRNPs). hnRNPs are associated with RNA polymerase II transcripts and have important roles in mRNA processing. We focus our research on hnRNP U. One portion of hnRNP U is found in the soluble hnRNP particles and another portion is tightly associated with chromatin. hnRNP U also plays a role in the initiation of RNA polymerase II transcription. We would like to investigate the impact of phosphoinositide binding on hnRNP U function in the cell nucleus. Altogether, our study will bring new insights into the nuclear functions of phosphoinositides.

P11: Altered immune responses in mice with LST1 adaptor protein deficiency

Matej Fabisik[1*], Jarmila Kralova[1], Jolana Tureckova[2], Jana Balounova[2], Simon Borna[1], Tereza Skopcova[1], Jan Prochazka[2], Frantisek Spoutil[2], Bernard Malissen[3], Radek Sedlacek[2], Tomas Brdicka[1]

[1] Laboratory of Lukocyte Signalling, Instute of Molecular Genecs ASCR

[2] Czech Centre for Phenogenomics, hosted by the Instute of Molecular Genecs ASCR

[3] Centre d'Immunologie de Marseille-Luminy, Aix Marseille Université, INSERM, CNRS UMR, Marseille, France

*matej.fabisik@img.cas.cz

Transmembrane adaptor protein LST1 is expressed in leukocytes of the myeloid lineage. Previous study has revealed mild effects of LST1 deficiency on the outcome of influenza infection in mice. Except for this specific case, its overall function at the organismal level is still to be determined. At the molecular level, LST1 was shown to interact with cytoskeleton regulating proteins and to promote the formation of tunneling nanotubes. It also contains an ITIM motif in its intracellular tail, which was shown to bind phosphatases SHP-1/2 in monocytes. To study the physiological function of LST1 we have performed a thorough analysis of LST1-deficient mice. At steady state, these mice displayed no apparent phenotype. However, when we challenged LST1-deficient mice with pro-inflammatory stimuli, some aspects of their responses were altered. IP injection of viral mimetic PolyI:C resulted in significant reduction in splenic $CD8^+$ T cell percentages. However, the most striking differences were observed when we induced acute colitis in these mice by dextran sodium sulphate, as a model of disease, where myeloid cells are heavily involved. We found significantly better course of acute colitis in LST1-deficient animals in all observed parameters (body weight, colon length…). This was accompanied by alterations in splenic monocyte populations. Interestingly, we also saw the same significant decrease in CD8+ splenic T cells as after polyI:C injection. Collectively our data suggest, that LST1 is not required for leukocyte development and immune system homeostasis, but it is involved in the regulation of several types of immune responses.

P12: Coarse-grained approach to protein-protein interactions in RNA pol II mediated RNA transcription

Francesco Luca Falginella[1*], Robert Vácha[1]

[1] Central European Institute of Technology, Brno, Czech Republic
*falginella.francesco@gmail.com

Among the plethora of biological processes occurring within eukaryotic cells, transcription has a prominent role being the first step retrieving the information from DNA and the cause of a number of diseases when impaired. As such, many studies have focused on the understanding of its regulation, dynamics, and functional impact. However, the control of the temporal and spatial evolution of the protein complexes recruited to the transcription site, which impacts the RNA polymerase activity, remains unknown. An illustrative case is RNA Polymerase II and its flexible C-terminal domain (CTD), which is responsible for the recruitment of interacting partners via a vast array of post-transcriptional modifications (so-called CTD code). Due to the highly flexible and repetitive nature of CTD, shed light on the fine structural details of such interaction via experimental techniques poses a challenging task, so an alternative approach implies resorting to computational simulations. Here, we introduce a release of FAUNUS model tuned to reproduce CTD-protein interactions and dynamics in the form of experimentally determined binding constants and high resolution all-atom Molecular Dynamics simulations of the known interacting partner SPT6 in solution. Moreover, because of the coarse-grained representation a wide range of CTD modification states and interacting partners combinations could be investigated using a desktop computer. Our model could be useful in a variety of applications including intrinsically disordered proteins and spatial arrangement of large protein domains.

P13: 2D nanomaterials & selectively oxidized cellulose as carriers for platinum anticancer drugs

Michaela Fojtů[1,2*], Jan Balvan[2], Lukáš Münster[3], Jan Vícha[3], Zdeněk Sofer[1], Michal Masařík[2], Martin Pumera[1,4]

[1] Center of Advanced Functional Nanorobots, Department of Inorganic Chemistry, University of Chemistry and Technology Prague, Technická 5, 166 28 Prague 6, CZ

[2] Department of Physiology, Faculty of Medicine, Masaryk University, Brno, CZ

[3] Centre of Polymer Systems, Tomas Bata University in Zlín, tř. Tomáše Bati 5678, 76001 Zlín, CZ

[4] Future Energy and Innovation Lab, Central European Institute of Technology, Brno University of Technology, Purkyňova 656/123, Brno, CZ-616 00, CZ

*fojtum@vscht.cz

Platinum-containing therapeutics are approved worldwide for treating various types of cancer. Among the most widely used ones belong first-generation platinum drug cisplatin (CP) and second-generation drug oxaliplatin (OP). Although widely used because of their extraordinary therapeutic efficiency, their administration is accompanied with serve side effects and risk of cancer cells' drug resistance development [1]. The application of nanotechnology in the area of drug delivery became a blockbuster of the biomedical research. Nanoplatforms loaded with anticancer drugs represent a versatile tool for tissue-specific drug targeting and hold great promise to overcome the problems associated with chemoresistance due to the altered mechanism of drug uptake. We investigated two types of totally distinct nanocarriers: selectively oxidized cellulose (DCC) and 2D nanomaterial black phosphorus (BP). With BP we achieved potentiation of OP anticancer effect, with CP-DCC higher CP tumour accumulation, prolonged mice survival rate and reduction of tumour volume. [2]

[1] T. C. Johnstone, K. Suntharalingam, S. J. Lippard, Chemical Reviews 2016, 116, 3436-3486; T. C. Johnstone, G. Y. Park, S. J. Lippard, Anticancer Research 2014, 34, 471-476.

[2] M. Fojtu, X. Y. Chia, Z. Sofer, M. Masarik, M. Pumera, Advanced Functional Materials 2017, 27, 7; L. Munster, M. Fojtu, Z. Capakova, T. Vaculovic, M. Tvrdonova, I. Kuritka, M. Masarik, J. Vicha, Biomacromolecules 2019, 20, 1623-1634.

T05: HERMES – A software tool for prediction and analysis of magnetic field-induced residual dipolar couplings in nucleic acids

Ilektra-Chara Giassa[1], Andrea Vavřinská[2], Jiří Zelinka[3], Jakub Sebera[4], Vladimír Sychrovský[4], Rolf Boelens[2], Radovan Fiala[1], Lukáš Trantírek[1*]

[1] Central European Institute of Technology, Masaryk University, Brno, Czech Republic

[2] Bijvoet Center for Biomolecular Research, Utrecht University, Utrecht, The Netherlands

[3] Faculty of Science, Masaryk University, Brno, Czech Republic

[4] Institute of Organic Chemistry and Biochemistry of the Czech Academy of Sciences, Praha, Czech Republic

[*]lukas.trantirek@ceitec.muni.cz

HERMES is a web application for prediction of fiRDC and analysis of magnetic field induced RDC. fiRDC prediction is based on input 3D model structure(s) of nucleic acid (NA) fragment(s) [1] and built-in library of nucleic acid base specific magnetic susceptibility tensors and reference geometries [2]. When 3D model of NA is provided alongside experimental fiRDC, the program allows validation of the structure against calculated fiRDC data. When multiple models are provided, it allows identification of NA model(s) consistent with experimental fiRDC and/or quick assessment of nucleic acid fragment oligomeric state [3]. Additionally, the program built-in routine for rigid body modeling allows assessment of relative orientation of two domains in the nucleic acid structure. The program is written in MATLAB language and is executed on an Apache server interfaced with HTML, JavaScript and PHP. The web application and the source code in MATLAB are publically accessible at hermes.ceitec.muni.cz.

Acknowledgement: The project was supported by grant from the Czech Science Foundation [16-105045].

[1] van Buuren BN, Schleucher J, Wittmann V, Griesinger C, Schwalbe H, Wijmenga SS (2004) NMR spectroscopic determination of the solution structure of a branched nucleic acid from residual dipolar couplings by using isotopically labeled nucleotides. Angew Chem Int Ed Engl, 43(2):187-92.

[2] Vavřinská A, Zelinka J, Šebera J, Sychrovský V, Fiala R, Boelens R, Sklenář V, and Trantírek L (2016) Impact of nucleic acid self-alignment in a strong magnetic field on the interpretation of indirect spin–spin interactions. J Biomol NMR, 64: 53–62.

[3] Al-Hashimi H, Tolman J, Majumdar A, Gorin A, Patel D (2001) Determining Stoichiometry in Homomultimeric Nucleic Acid Complexes Using Magnetic Field Induced Residual Dipolar Couplings. J Am Chem Soc, 123, 5806-5807.

P14: Chronic inflammation affects hematopoietic stem cells

Srdjan Grusanovic[1,2*], Petr Danek[1,2], Miroslava Kardosova[1], Monika Burocziova[1] and Meritxell Alberich-Jorda[1]

[1] Laboratory of Hemato-oncology, Institute of Molecular Genetics of the Czech Academy of Science, Videnska 14220, Prague, Czech Republic

[2] Department of Molecular and Cellular Biology, Genetics and Virology, Faculty of Science, Charles University

*srdjan.grusanovic@img.cas.cz

Chronic inflammation affects one-third of the human population and it is characterized by increased levels of cytokines and chemokines. Recent evidence shows that, despite their quiescence, hematopoietic stem cells (HSCs) may directly respond to these extracellular factors. In order to understand whether and how chronic inflammation may affect HSC functions we employ a unique mouse model, i.e. CMO mice. These mice suffer from chronic multifocal osteomyelitis (CMO) due to a mutation in the *proline-serine-threonine phosphatase-interacting protein 2* (*Pstpip2*) gene, resulting in a chronic and progressive inflammatory disorder.
Flow cytometry analysis of bone marrow samples demonstrated that CMO mice exhibit increased bone marrow cellularity and elevated numbers of HSCs. We tested whether the bone marrow environment in the CMO mice affects HSC fitness. In vivo bone marrow transplantation assays demonstrated a reduced repopulating ability of WT HSCs exposed to CMO environment compared to WT HSCs exposed to WT environment. Next, we observed increased numbers of HSC in spleens of CMO mice. Upon transplantation, CMO splenocytes demonstrated a remarkable engraftment ability compared to WT controls. Considering that CMO mice have increased levels of IL-1β and that this cytokine signals through the MyD88 adaptor protein, we crossed our mice to MyD88 KO mice. The resulting offspring did not develop inflammation or expansion of HSCs in the bone marrow and spleen. Together, our data indicate that chronic inflammation has an effect on the HSC pool and that IL-1β is one of the key cytokines mediating the inflammatory signals in the CMO mouse model.

T06: Development of synthetic antibody mimetics targeting opioid receptors

Martin Hadzima[1,2*], Aleš Machara[1], Pavel Majer[1], Pavel Šácha[1], Jana Pokorná[1], Libor Kostka[3], Vladimír Šubr[3], Jan Konvalinka[1]

[1] Institute of Organic Chemistry and Biochemistry AS CR, Czech Republic
[2] Dept of Organic Chemistry, Faculty of Science, Charles University, Czech Republic
[3] Institute of Macromolecular Chemistry AS CR, Czech Republic
*martin.hadzima@uochb.cas.cz

Morphine and its congeners are irreplaceable in pain management. Recently, clinical studies on relapse of cancer indicated a possible correlation between administration of opioid agonists, overexpression of opioid receptors and cancer reoccurrence/tumour growth [1]. General lack of reliable tools for study of opioid receptors convinced us that development of alternative methods is desired.

The main goal of my work was to find an appropriate ligand attachment, at an appropriate position using PEG linkers, to enable their use in the innovative iBodies concept [2]. iBodies are biocompatible polymer conjugates based on *N*-(2-hydroxypropyl)methacrylamide copolymers decorated by specific ligands, an affinity anchor and a fluorescent moiety, that can be used as antibody mimetics for specific targeting, visualisation and isolation of proteins. For the modification we chose following ligands: naltrexone (μ-opioid receptor), naltrindole (δ-opioid rec.) and nalfurafine (κ-opioid rec.). Series of fluorescently labeled ligands were prepared. Attachment of the fluorescent tag allowed us to study the affinity and selectivity of these modified ligands. Based on the results, ligands for development of synthetic antibody mimetics were selected.

Acknowledgement: Supported by Czech Science Foundation (GAČR 16-02938S).

[1] Wigmore, T. et al. Curr. Opin. Support. Palliat. Care 2016, 10, 109.
[2] Šácha, P. et al. Angew. Chem. Int. Ed. Engl. 2016, 55, 2356.

T07: Toward structure analysis of a huge algal virus

Miroslav Homola[1*], Carina R. Büttner[1], Tibor Füzik[1] and Pavel Plevka[1]

[1] Structural Virology Group, CEITEC Masaryk University, Brno, Czech Republic
*mirdahomola@gmail.com

The *Emiliania huxleyi* virus 86 (EhV-86) is an important agent in terminating regular population explosions of *Emiliania huxleyi* – the most abundant alga in marine ecosystems. We are attempting to solve the structure of EhV-86 using several cryo-electron microscopy techniques.

The unicellular alga *Emiliania huxleyi* is widely distributed photosynthesizing marine eukaryote, creating regular population explosions called blooms. These algal blooms, visible from space, influence the global climate by absorption of carbon dioxide as *E. huxleyi* uses this molecule for production of calcareous plates, covering its surface. The algal bloom collapses usually one week after infection by coccolithoviruses, in most cases by EhV-86. Among the other large double-stranded DNA viruses that infect green algae, EhV-86 differs in possessing a lipid membrane outside of the capsid shell, which it acquires while exiting the algal cell via budding. The membrane and large dimensions of the EhV-86 virus particle make it quite challenging for purification and subsequent 3-dimensional reconstruction.

To determine the near-atomic resolution structure of the EhV-86 virion, we use cryo-electron microscopy (cryo-EM). The observed heterogeneity of viral particle morphology pushes reconstruction by so-called single particles analysis, i.e. averaging over many particles – toward tomography, i.e. using only few particles, each imaged at many angles. We also investigate the replication machinery of EhV-86 inside the algal host cell using lamellas – thin cell sections produced by focused ion beam milling. The combination of our results obtained from various cryo-EM approaches will provide a comprehensive insight into the EhV-86 life cycle and interactions with the *Emiliania huxleyi* host cell.

P15: Interactive exploration of trends in biomacromolecule structure quality with ValTrends^{DB}

Vladimír Horský[1*], Veronika Bendová[1,2], Dominik Toušek[1], Radka Svobodová[1], Jaroslav Koča[1]

[1] CEITEC - Central European Institute of Technology, Masaryk University, Brno, Czech Republic

[2] Department of Mathematics and Statistics, Faculty of Science, Masaryk University, Brno, Czech Republic

*vladimir.horsky@mail.muni.cz

Improvements of methods for biomacromolecular structure acquisition have in recent decades come hand in hand with the rising importance of biomacromolecular structural data. However, the experimental nature of such methods has led to the occurrence of errors in structure models, which in turn were responsible for retraction of several articles from esteemed journals. Scientific community reacted to the emergence of this phenomenon by developing, utilizing, and propagating various software tools that validated geometric quality and adherence of structure model to the underlying experimental data. The Protein Data Bank (PDB), the largest database of structures of biomacromolecular complexes, deployed their own validation pipeline that checks nearly every structure stored in the database.

With the emergence of tangible focus on quality, we were curious whether it had any impact on newer structures. To provide food for thought for these questions, we have carried out a wide range exploratory analysis of trends between quality and features of structures of biomacromolecular complexes. Results of this analysis are presented using interactive information-rich plots in the ValTrends^{DB} database (ncbr.muni.cz/ValTrendsDB).

Recently, we have added new functionality to the weekly-updated ValTrends^{DB} database that enables users to interactively explore trends from the analysis and compare them to user-defined sets of structures, e.g., structures of a journal, protein family, experimental method, or structures from an author.

T08: Cryo-EM Structure of Phage P68: From Head to Tail

Dominik Hrebík[1], Dana Štveráková[2], Karel Škubník[1], Tibor Füzik[1], Roman Pantůček[2], Pavel Plevka[1]

[1] Central European Institute of Technology, Masaryk University, Kamenice 5, 625 00, Brno, Czech Republic

[2] Department of Experimental Biology, Faculty of Science, Masaryk University, Kamenice 5, 625 00, Brno, Czech Republic

*dominik.hrebik@ceitec.muni.cz

Bacteriophages from the family *Podoviridae* use short non-contractile tails to eject their genomes into bacteria. However, there is limited high-resolution information about structure and mechanism of genome delivery of podoviruses that infect Gram-positive bacteria such as *S. aureus*. Here we used cryo-electron microscopy and X-ray crystallography to determine the structures of *S. aureus* phage P68 in its native form, genome ejection intermediate, and empty particle. The structure of the native phage was solved to 3.3 Å and 3.9 Å for capsid and tail respectively. We show that residues from N-terminus of the major capsid protein enable incorporation of P68 portal complex into phage head by forming a special interface. P68 head contains seventy-two subunits of inner core protein, which are positioned between the portal complex and phage genome. Fifteen of the inner core proteins bind to and alter the structure of adjacent major capsid proteins and thus specify attachment sites for head fibers. Unlike in the previously studied phages, head fibers of P68 enable positioning of its virion at cell surface for genome delivery. P68 genome ejection is triggered by disruption of interaction of one of the portal protein subunits with phage DNA. The inner core proteins are released before the DNA and probably enable translocation of phage DNA across bacterial membrane into cytoplasm. The genome translocation mechanism and the portal assembly mechanism is likely to be conserved among bacteriophages infecting gram-positive bacteria.

P16: Electron Spin Resonance Detection of Human MicroRNA 21-5p in Renal Cell Carcinoma

Jakub Hrubý[1*], Júlia Kováčová[2], Ondřej Slabý[2], Petr Neugebauer[1]

[1]Central European Institute of Technology, Brno University of Technology, Czech Republic
[2] Central European Institute of Technology, Masaryk University, Czech Republic
*jakub.hruby@ceitec.vutbr.cz

MicroRNAs (miRNAs) belong to a family of short non-coding RNA involved in a variety of cellular processes. Their main function is regulation of gene expression, and thus they have been found to be heavily dysregulated in many pathological states including cancer [1].

Our approach aims at applying the electron spin resonance (ESR) spectroscopy to a complex biological system and establishing a semi-invasive method of detection of human microRNA (miRNA) in renal cell carcinoma. Nowadays, detection of miRNAs´ presence in cancer cells is done by performing quantitative polymerase chain reaction (qPCR) which monitors gene amplification of a target sequence by attaching fluorescent chemical compounds. Herein, we are focused on gaining an insight into the physical and chemical environment by using a spin probe, namely a nitroxide spin label (2,2,6,6-Tetramethylpiperidin-1-yl)oxyl (TEMPO) directly attached to anti-hsa-miR-21-5p oligonucleotides.

We started by collecting peripheral blood samples from both healthy subjects and patients with renal cell carcinoma. Simultaneously, we put emphasis on a selection of a suitable spin label conjugation with the anti-hsa-miR-21-5p oligonucleotide and tested its stability. This task was crucial as a lifetime of radicals in samples can be rather short as they have a natural tendency to make bonds. We used a specially designed flat cell for measurements of physiological solutions as they contain water that easily attenuates microwave irradiation used in ESR. We believe that this project will establish foundations of semi-invasive ESR diagnostics of human renal cell carcinoma.

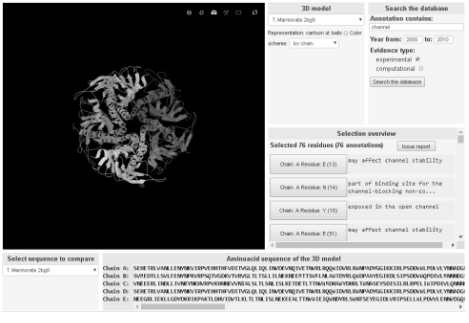
[1] Peng, Y., & Croce, C. M. (2016). The role of MicroRNAs in human cancer. *Signal transduction and targeted therapy*, *1*, 15004.

T09: Structural bioinformatics of nicotinic acetylcholine receptors: NACHRDB

Aliaksei Chareshneu[1*], Ravi José Tristao Ramos[1], Crina-Maria Ionescu[1], Jaroslav Koča[1]

[1] NCBR and CEITEC, Masaryk University, Brno, Czech Republic
*479052@mail.muni.cz

The nicotinic acetylcholine receptor (nAChR) is an evolutionary ancient allosteric membrane protein mediating the synaptic transmission. This prototypic pentameric ligand-gated ion-channel is involved in many physiological processes (from learning to motor control), neurological diseases (Alzheimer's and Parkinson's diseases, schizophrenia, epilepsy), and addictions (alcohol, tobacco). Since its biochemical isolation in 1970, extensive studies generated huge amounts of structural-functional data. However, the cumulative knowledge on nAChRs, spanning ~50 years of research, is not systematically accessible. The wide variety in receptor types, residue numbering schemes, and methods used, together with diverse terminology, the absence of comprehensive structural annotation, and the scattered nature of the existing findings make it harder to summarize the current knowledge and apply it efficiently to promote further discoveries. There is no single resource providing an access to and visualization of such diverse, complex, and extensive information. To fill this gap, we developed NACHRDB (https://crocodile.ncbr.muni.cz/Apps/NAChRDB/) – a web-accessible manually curated database which not only provides intuitive and fast access to relevant structural-functional data on nAChRs, but also facilitates its interpretation by integrating the residue-level annotations with interactive and highly responsive visualization of sequence and 3D structure. We believe that NACHRDB can not only guide further studies in the field of nAChRs, but also serve as a key starting point in unification of the state-of-art knowledge in the broad field of ion channels.



P17: Activation of human RNase L using various phosphonate oligoadenylates

T. Jandušík[1]*, O. Páv[1], O. Šimák[1], J. Snášel[1] and I. Rosenberg[1]

[1] Institute of Organic Chemistry and Biochemistry AS CR, v.v.i., Flemingovo nám. 2, 16610 Prague, Czech Republic

*jandusik@uochb.cas.cz

The short oligoadenylates with unique 2′-5′- (2-5A) linkages play a significant role in interferon-induced antiviral defence mechanism of cells. Interferon induces expression of the dsRNA dependent 2-5A synthetase utilizing ATP as a substrate for the synthesis of 5′-phosphorylated 2-5As, (pp)p5′Ap(Ap)nA2′ (where n is mainly 1 or 2). These 2-5As bind to a latent endoribonuclease RNase L and activate it. Activated form is capable of cleaving pathogenic ssRNA and thus preventing expression of viral proteins.[1]

Since the presence of the 5′-phosphate group in 2-5As is essential for the RNase L activation, several 2-5As were synthesized on solid-phase from the phosphonate monomers (Figure 1) and the ability of these oligoadenylates to stimulate human recombinant RNase L cleavage activity was evaluated. Our preliminary data suggested the substitution of 5′-terminal phosphate for 5′-terminal phosphonate in 2-5A afforded oligoadenylates with excellent activation efficiency and with improved stability against cleavage by phosphomonoesterases.

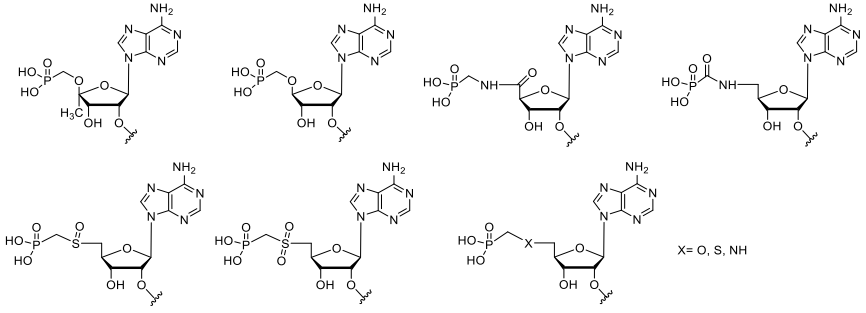


Figure 1. Phosphonate modifications of 5′-end nucleotide incorporated into 2-5A

[1] Player, M.R.; Torrence, P.F. Pharmacol. Ther. 1998, 78, 55-113.

P18: Zebrafish model of human leukemia

Jovana Jovicic[1*], Martina Snegonova[1], Trevor Epp[1], Petr Bartunek[1]

[1] Institute of Molecular Genetics of ASCR, Prague, Czech Republic

*jovana.jovicic@img.cas.cz

The main objective of the project is to develop a zebrafish model for human leukemia in order to identify new oncogenic or tumor suppressor roles of epigenetic regulators.

Epigenetic modifications regulating chromatin state and gene expression include DNA methylation and demethylation and histone modification. Epigenetic regulators are responsible for marking both DNA and histones, in a reversible but heritable manner. Recently, it has been found that epigenetics plays an important role in leukemogenesis, since there are commonly occurring mutations in known epigenetic regulators. As the epigenetic machinery is highly conserved among vertebrates; it is possible to model human diseases in non-mammalian model organisms, such as zebrafish (Danio rerio). There are many advantages of the zebrafish model compared to traditional murine models; high numbers of progeny, rapid, external development, cost-effective maintenance is some of the recognized attributes. Zebrafish has been proven to be valuable in cancer research as it facilitates tumorigenesis monitoring in real time in vivo. There are zebrafish models which mimic well human disease progression and focusing on epigenetic modifiers might complete our understanding of this field. Our aim is to develop new model of human leukemia in zebrafish and to identify new potentially oncogenic or tumor suppressor roles of epigenetic regulators by overexpressing them under the hematopoietic lineage-specific promoters (pu.1, rag2 and gata1). We are focusing on the set of 80 genes selected according to their mode of action and expression pattern. In addition, we will employ a sensitive bioluminescent reporter system, which will enable us to monitor the progression of the disease. We aim to develop a medium-throughput screening platform that would enabling us to test potential leukemia therapeutics.

P19: Dynamic measurements of circulating microRNAs reflect different biological effects of radiofrequency ablation and transarterial chemoembolisation in liver cancer patients

Jaroslav Juracek[1*], Tomas Andrasina[2], Barbora Cechova[1], Jan Zavadil[2], Ondrej Slaby[1]

[1] Masaryk University, Central European Institute of Technology, Brno, Czech Republic

[2] Department of Radiology and Nuclear Medicine, University Hospital Brno and Masaryk University Brno, Brno, Czech Republic

*juracek.jaroslav@gmail.com

The majority of liver tumors are unresectable, therefore other therapeutic modalities as radiofrequency ablation (RFA) and transarterial chemoembolization (TACE) are applied. Both methods cause characteristic changes in liver tissue (inflammation, hypoxia, tissue destruction) accompanied by systemic secretion of microRNA into the bloodstream. Since RFA and TACE differ in the dynamics with which they affect the tumor tissue, we aimed to investigate whether the level of circulating microRNAs could reflect such changes. The concentrations of circulating miRNA were determined in series of blood plasma from 4 time points using miRNA-specific TaqMan assays and qRT-PCR method. In RFA cases we observed significant increase of miRNA concentrations immediately after intervention (miR-122, $P = 0.0002$; miR-200a, $P = 0.015$). In TACE we observed delayed increase in miRNA concentrations at time point 24 hours after intervention (miR-21, $P < 0.0001$; miR-210, $P = 0.03$; miR-122, $P = 0.0004$; miR-200a, $P = 0.0098$; miR-34a, $P = 0.0027$). In both methods, the initial increase was followed by a steady decline of miRNA levels. Dynamic changes in circulating miRNA levels were in accordance with the nature of the RFA and TACE biologic effects. Our preliminary data indicates potential usage of circulating miRNAs for monitoring of the systemic effects of RFA and TACE therapy and their ability to reflect efficacy of intervention procedures.

Acknowledgement: Supported by MHCR- DRO (FNBr, 65269705).

P20: Chromosome aberrations detected by FISH in newly diagnosed cancer patients

D. Kadlčíková[1], P. Musilová[1], H. Hradská[1], M. Petrovová[2], I. Selingerová[3], M. Vozdová[1], M. Svoboda[2], J. Rubeš[1]

[1] Department of Genetics and Reproduction, Central European Institute of Technology - Veterinary Research Institute, Brno, Czech Republic

[2] Clinic of Comprehensive Cancer Care, Masaryk Memorial Cancer Institute, Brno, Czech Republic

[3] Regional Centre for Applied Molecular Oncology, Masaryk Memorial Cancer Institute, Brno, Czech Republic

*kadlcikova@vri.cz

Chromosome aberrations are the robust biomarker as regards predictivity related to cancer risk. Fluorescence in situ hybridization (FISH) technique is able to detect stable aberrations which tend to cumulate during life. We investigated blood lymphocytes of 124 patients with newly diagnosed solid tumors (27 with gastrointestinal cancer and 97 with breast cancer) prior to cancer treatment and 79 healthy control subjects. Metaphase spreads were hybridized with painting probes for chromosomes 1, 2 and 4 and a pancentromeric probe. Aberrant cells were classified according to the Protocol for Aberration Identification and Nomenclature [1]. To control the confounding effect of age (and optionally smoking), binary logistic regression was used and adjusted odds ratios with 95% confidence intervals were calculated. Regarding nonsmokers, untreated gastrointestinal and breast cancer patients had increased frequency of aberrant cells. However, chromosome damage affected different cytogenetic endpoints in these groups. Gastrointestinal cancer is associated with elevated frequency of unstable chromosome aberrations; nevertheless, an acute exposition to diagnostic X-rays might have contributed to the increase of unstable aberrations found here. On the contrary, stable translocations and cells with complex rearrangements contributed to chromosome damage in breast cancer patients. The associations between chromosome damage and cancer observed in nonsmokers were mostly not pronounced in smokers. In healthy controls, chronic exposition to tobacco smoke increased the frequencies of cytogenetic parameters with the exception of dicentric chromosomes. However, this smoking related difference was not observed in groups of cancer patients.

Acknowledgement: Supported by Ministry of Health of the Czech Republic, grant no. 15-33968A and CEITEC 2020 (LQ1601).

[1] Tucker, J.D., Morgan, W.F., Awa, A.A., Bauchinger, M., Blakey, D., Cornforth, M.N., Littlefield, L.G., Natarajan, A.T., and Shasserre, C. (1995). PAINT: a proposed nomenclature for structural aberrations detected by whole chromosome painting. Mutat. Res. Lett. 347, 21–24.

P21: The transcription factor C/EBPγ regulates mast cell development and function

Miroslava Kardosova[1*], Lucie Potuckova[2*], Ivana Halova[2], Petr Danek[1], Polina Zjablovskaja[1], Lubica Draberova[2], Petr Draber[2], Meritxell Alberich-Jorda[1]

[1] Institute of Molecular Genetics, Laboratory of Hematooncology, Academy of Sciences of the Czech Republic, Prague, Czech Republic

[2] Institute of Molecular Genetics, Laboratory of Signal Transduction, Academy of Sciences of the Czech Republic, Prague, Czech Republic

*kari@img.cas.cz

Development of hematopoietic stem cell towards mature mast cell is regulated by networks of interacting transcription factors – expression of GATA1, GATA2, STAT5, and MITF, and downregulation of C/EBPα are already known to be important determinants of mast cell identity. Recently, we described transcription factor C/EBPγ as a C/EBPα target gene, and observed that C/EBPγ is abundantly expressed in mast cells. To study whether C/EBPγ have role in mast cell development and function, we used *Cebpg* conditional knockout mice, which allow excision of *Cebpg* in the hematopoietic system. *Cebpg* $^{flox/flox}$ *Vav-iCre*$^{-}$ and *Cebpg* $^{flox/flox}$ *Vav-iCre*$^{+}$ mice, referred here as WT and *Cebpg* KO respectively, showed similar numbers of peritoneal mast cells in steady state conditions. Nevertheless, mice lacking *Cebpg* presented defective peritoneal mast cell repopulation after intraperitoneal injection of distilled water, which abolishes the presence of mast cells in the peritoneum. To further explore the effects of *Cebpg* ablation in mast cells, we generated bone marrow derived mast cells (BMMCs). We observed that BM from *Cebpg* KO mice produced reduced number of BMMCs compared to WT controls. Functionally, we demonstrated that deletion of *Cebpg* reduced mast cell migration towards antigen, SCF or PGE, and impaired degranulation upon FcεRI-mediated activation. Next, we aimed to investigate the mechanisms by which C/EBPγ is controlling these processes. Our data showed that BMMCs exhibit increased C/EBPα levels in the absence of C/EBPγ, probably contributing to the observed defects. In summary, we revealed C/EBPγ as a new important component of the mast cell transcriptional network which suppresses C/EBPα expression, thereby favoring mast cell function.

T10: A Structural Basis for the Cross-Talk Between Histones and RNA Polymerase II

Aiste Kasiliauskaite[1*], Tomaš Klumpler[1], Jiři Novaček[1], Richard Štefl[1]

[1] CEITEC – Central European Institute of Technology, Masaryk University, Kamenice 753/5, 625 00 Brno, Czech Republic

*aiste.kasiliauskaite@ceitec.muni.cz

Transcription of eukaryotic protein-coding genes requires transfer of RNA polymerase II (Pol II) through nucleosomes. Nucleosomes are inherent barriers of transcription, and Pol II stalls at multiple locations within a nucleosome. Nucleosome core particle (NCP) consists of 145–147 base pairs of DNA wrapped around a histone protein octamer. Transcription elongation factors accompany Pol II to facilitate efficient transcription. They enable polymerase progression through NCPs and ensure re-establishment of chromatin after polymerase passage. The mechanisms underlying these processes, however, remain puzzling and poorly understood.
Our aim is to present molecular details underlying Spt6 (histone chaperone and transcription factor) binding events. In our study we are revealing this long-standing open question by identifying elements of Spt6 that mediates interactions between Pol II and nucleosome. Cryo-electron microscopy, X-ray and Small Angle X-ray Scattering (SAXS) are used to study the macromolecular complex. Our findings provide a fundamental mechanistic insight into the functional specialization of Spt6 and have implications for the understanding of crosstalk between RNAP II and chromosomes.

P22: Next-Generation Sequencing analysis and validation of microRNAs in cerebrospinal fluid of brain tumor patients

Alena Kopkova[1], Jiri Sana[1], Marek Vecera[1], Tana Machackova[1], Pavel Fadrus[2], Ondrej Slaby[1]

[1] Central European Institute of Technology (CEITEC), Masaryk University, Brno, Czech Republic

[2] Department of Neurosurgery, University Hospital Brno, Masaryk University, Brno, Czech Republic

*alena.kopkova@ceitec.muni.cz

Cerebrospinal fluid (CSF) bathes all central nervous system (CNS), and thus is supposed to reflect possible pathological conditions. From this perspective, CSF looks as ideal source of diagnostic biomarkers of brain tumors. MicroRNAs, short non-coding RNAs involved in the pathogenesis of many cancers including brain tumors, might represent group of new biomarkers. Analysis of CSF miRNAs in brain tumor patients promises a new diagnostic approach enabling more accurate diagnosis. Next-generation sequencing was performed for analysis of miRNAs in 75 CSF samples taken from 32 glioblastomas (GBM), 11 meningiomas, 13 brain metastasis patients and 19 non-tumor donors. CleanTag Small RNA Library Prep Kit were used for cDNA library preparation. NextSeq 500 instrument together with Next 500/550 High Output v2 Kit - 75 cycles were used for final sequencing analysis. Subsequently, according to NGS results levels of 10 miRNAs were measured in independent set of CSF samples (41 GBM, 44 meningiomas, 12 metastasis patients and 20 non-tumor donors) using TaqMan Advanced miRNA Assays (ThermoFisher Scientific). NGS analysis revealed 22, 12 and 35 CSF miRNAs with significantly different levels in GBM, meningiomas and patients with brain metastases respectively, in comparison with non-tumor CSF. Subsequent validation of selected CSF miRNAs has confirmed different levels of 7 miRNA in GBM, 2 in meningiomas and 2 in patients with brain metastases compared to non-tumor donors.

Acknowledgement: This work was supported by grant of Czech Grant Agency nr. 17-17636S and by the Ministry of Education, Youth and Sports of the Czech Republic CEITEC 2020 (LQ1601).

P23: miR-376b-3p predicts therapeutic response to sunitinib in metastatic renal cell carcinoma

Julia Kovacova[1*], Ondrej Slaby[1,2]

[1] Masaryk University, Central European Institute of Technology, Brno, Czech Republic
[2] Masaryk Memorial Cancer Institute, Department of Comprehensive Cancer Care, Brno, Czech Republic
*juli.kovacova@gmail.com

Metastatic renal cell carcinoma (mRCC) is routinely treated with sunitinib, a tyrosine kinase inhibitor (TKI) of VEGF signalisation. Although disease eventually progresses in most mRCC patients, length of progression-free survival (PFS) is variable. Patients with initial resistance to sunitinib could be redirected to other therapeutical options, however, there is currently no biomarker for prediction of therapeutical response. MicroRNAs (miRNAs) belong to class of short non-coding RNAs and could serve as biomarkers of therapy response due to their unique. Their biomarker potential has been discussed concerning many diseases including mRCC, but current knowledge is very weak, has several discrepancies and is acquired on relatively small cohorts. In this study, candidate microRNAs have been chosen based on global expression profiling using Affymetrix GeneChip 4.0 in 47 samples of FFPE mRCC tissue of patients treated with sunitinib (good response n=25, PFS longer than 17 months; poor response n=22, PFS shorter than 9 months). Validation was performed using qRT-PCR TaqMan assays on an independent cohort of 132 FFPE samples from mRCC patients treated with. Local ethical committees at all involved centres approved the study protocol and all patients signed an informed consent. Of all tested miRNAs, expression of miR-376b-3p was the most significantly deregulated in non-responding patients with high statistical significance ($p>0,005$) and AUC 0,76. Although other independent validations and functional analyses are necessary, miR-376b-3p presented here seems to be very promising as tools for therapy personalization.

Acknowledgement: This work was supported by Ministry of Health of the Czech Republic, grant nr. NV18-03-00554.

P24: Haematopoiesis in sea lamprey

Martin Kovář[1*], Petr Bartůněk[1]

[1] Institute of Molecular Genetics of the ASCR, Prague, Czech Republic
*martin.kovar@img.cas.cz

Haematopoiesis is the specific process in vertebrates during which terminally differentiated blood cells with a specific function arise from a haematopoietic stem cells (HSC) through different progenitors. Now we have a deep knowledge about the haematopoiesis in the standard vertebrate models, but in field of the haematopoiesis evolution our knowledge is restricted. Main reason is that the process of the haematopoiesis is deeply conserved. In all regular vertebrate models, we detect the same key role geneses involved in the haematopoiesis and as well we observe the same range of blood cell types. Therefore, we need to involve an unconventional animal models and extent our pallet of model animals into the history of vertebrates as far as possible. Because of this reason we are interested in the haematopoiesis in a sea lamprey, which is representative of a jawless taxon. This is the taxon of the most ancestral vertebrates living up to date. The aim of this project is to map haematopoietic process in sea lamprey on cellular and genetic level with special attention to embryonic development.

P25: The role of CD45 phosphatase in murine model of autoinflammatory osteomyelitis

J. Kralova[1*], K. Ilievova[1], J. Prochazka[1], F. Spoutil[1], P. Kasparek[1], P. Angelisova[1], T. Skopcova[1], J. Pokorna[1], A. Drobek[1], R. Sedlacek[1], T. Brdicka[1]

[1] Institute of Molecular Genetics of the ASCR, Prague, Czech Republic
*kralovaj@img.cas.cz

PSTPIP2 is an adaptor protein expressed in the myeloid cells which deficiency leads to the development of auto-inflammatory disease in mice, designated as chronic multifocal osteomyelitis (CMO). The main manifestation is sterile inflammation of the bones and soft tissues. Enhanced production of pro-inflammatory cytokine IL-1β by neutrophils is the main factor driving CMO development and progression. In addition, hyper-activation of various signaling pathways in CMO neutrophils has been observed. The negative regulatory effect of PSTPIP2 protein on signaling pathways and IL-1β production is likely mediated by its interacting partners. These include inhibitory molecules, such as CSK, SHIP1 and PEST family phosphatases. However, the exact mechanism of how PSTPIP2 inhibits signaling is not known. To address this question and thus better understand CMO disease mechanism, mouse strains harboring mutation in either binding site for PEST family phosphatase or for SHIP-1 are being established. As Csk negatively regulates Src family kinases (SFKs) and its binding site on PSTPIP2 is not known and Csk binding is partly dependent on PEST family phosphatases, analysis of the CMO $Ptprc^{-/-}$ mice with inhibited SFKs were performed instead. Detailed analysis of this strain including disease free curves, CT scans and IL-1β production was performed and data will be presented showing partial alleviation of disease symptoms.

P26: Cryo-EM structure of NDH plastoquinone reductase

Vladyslav Kravchuk[1*], Leonid Sazanov[1]

[1] Institute of Science and Technology Austria, Klosterneuburg, Austria
*vkravchu@ist.ac.at

This is abstract is not published on request of the author. It will be presented on site.

P27: Dynamic Recognition at Interfaces of Protein/RNA Complexes: What Can Computations Tell Us?

Miroslav Krepl[1,2*]

[1] Institute of Biophysics of the Czech Academy of Sciences, Královopolská 135, 612 65 Brno, Czech Republic

[2] Regional Centre of Advanced Technologies and Materials, Department of Physical Chemistry, Faculty of Science, Palacký University, tř. 17 listopadu 12, 771 46, Olomouc, Czech Republic

*krepl@ibp.cz

Ribonucleic acid (RNA) molecules are involved in countless key processes in living organisms, including gene expression, cellular defense and catalysis of chemical processes. *In vivo*, RNA molecules always interact with proteins, since they are synthesized to the point of their degradation. Understanding the principles of protein/RNA interaction is therefore a matter of biologically imminent importance. At the same time, structural studies of protein/RNA complexes by the three leading experimental methods for structure determination (e.g. X-ray crystallography, NMR spectroscopy, Cryo-EM) are inherently more complicated than determining the structure of the individual monomers.

In my research, I use molecular dynamics (MD) simulations to study the protein/RNA complexes. Many biomolecular complexes are inherently dynamical, which makes MD an important tool to complement the experimental techniques of structural biology which typically provide only static ensemble-averaged pictures of the molecular complexes.

I have successfully applied MD to study dynamic recognition at protein/RNA interfaces of Fox-1, CUG-BP2, HuR, and HIV-1 reverse transcriptase (RT) proteins. I showed that dynamic recognition is an important and so far under-appreciated element of RNA recognition by proteins. It constitutes unique evolutionary response to situations in which specific protein interactions with RNA are vital, but at the same time the cell needs to rapidly switch between numerous RNA sequences. I predict that dynamic recognition by proteins will be increasingly recognized as important structural and functional element in biology of RNA and DNA molecules. Studies of such systems will require diverse methodologies, ranging from structural biology and computational methods to advanced biochemical approaches.

P28: Dose-dependent regulation of horizontal cell fate by Onecut family of transcription factors

Michaela Kreplova[1*], Andrea Kuzelova[1], Barbora Antosova[1], Herbert Jagle[2], Zbynek Kozmik[1]

[1] Institute of Molecular Genetics of the Academy of Sciences, Prague, Czech Republic.
[2] University Hospital Regensburg, Regensburg, Germany.
*michaela.kreplova@img.cas.cz

Onecut (Oc) transcription factors family are represented by three members in mammals: Onecut1 (Oc1), Onecut 2 (Oc2) and Onecut3 (Oc3). Only Oc1 and Oc2 are expressed at high levels in the mouse retina. Mouse retina is composed of seven retinal cell types that are generated from common pool of retinal progenitor cells. Pax6 is required for their multipotency and plays important role in their differentiation. Oc1 and Oc2 transcription factors were identified as Pax6 downstream-acting factors and are expressed in precursors of HCs, retinal ganglion cells and cone photoreceptors. Ablation of either Oc1 or Oc2 gene in mouse retina results in markedly decreased number of HCs, but no defects in other retinal cell types. Simultaneous deletion of Oc1 and Oc2 leads to complete loss of HCs. Lack of HCs is reflected by absence of outer plexiform layer, which is composed of processes from HCs and bipolar cells and photoreceptor terminals. Here we study how the dose of Onecut transcription factors influences HCs and other retinal cell types, especially retinal ganglion cells and cone photoreceptors. We observed significant decrease of HCs according to dose of Onecut transcription factors. Flash ERG responses were also impaired in accordance with reduced level of Onecut proteins and thus with decreased number of HCs. This study suggests that HCs are exquisitely sensitive to the dose of Onecut transcription factors and are required for proper retinal function.

P29: Beta-lactamase producing *Escherichia coli* and antibiotic resistance genes in municipal and hospital wastewaters

Iva Kutilova[1,2*], Pimlapas Leekitcharoenphon[3], Matej Medvecky[1], Patrick Munk[3], Valeria Bortolaia[3], Sünje J. Pamp[3], Monika Dolejska[1,2]

[1] Central European Institute of Technology, University of Veterinary and Pharmaceutical Sciences Brno, Brno, Czech Republic

[2] Department of Biology and Wildlife Diseases, Faculty of Veterinary Hygiene and Ecology, University of Veterinary and Pharmaceutical Sciences Brno, Brno, Czech Republic

[3] Research Group for Genomic Epidemiology, National Food Institute, Technical University of Denmark, Lyngby, Denmark

*kutilova.iva@gmail.com

Wastewaters represent environment where sewage from different sources is interacting and are considered the hot spots of antimicrobial resistance (AMR).

In this study, level of AMR in municipal (outflow/inflow to/from wastewater treatment plant (WWTP)), hospital (inflow/outflow to/from hospital WWTP and raw sewage from hospital) and river waters in the city of Brno (Czech Republic) was examined. Total vs cefotaxime (CTX)-resistant *E. coli* were enumerated in all samples. Based on phenotypic and genotypic results, representative CTX-resistant isolates and whole-community DNA were subjected to sequencing (Illumina) and bioinformatics analysis.

In total 95.6% (n=158) of CTX-resistant *E. coli* were extended-spectrum beta-lactamase (ESBL) producers and were detected in all samples except the outflow from hospital WWTP. Most isolates were positive for gene $bla_{\text{CTX-M}}$ (98.7%; n=151) encoding ESBL. The metagenomic analysis showed high prevalence of pathogenic bacteria in hospital WWs and majority of non-pathogenic bacteria in municipal WWs, treated and river waters. Genes encoding resistance to aminoglycosides, beta-lactams and macrolides were frequently detected, however $bla_{\text{CTX-M}}$ was not found in this metagenomic dataset.

The study confirmed municipal treated water as source of multi-resistant *E. coli* and AMR genes for the environment. Moreover, the combination of two different approaches brought complex view on AMR in water environment.

Acknowledgement: The study was funded by projects 204/2018/FVHE, LQ1601, ZD189011 and 18-23532S.

V02: Tour through the drug screening in the lab of Functional Genomics

Adriana Ladungová[1*]

[1] Central European Institute of Technology (CEITEC), Masaryk University, Brno, Czech Republic

*ladungova@mail.muni.cz

The Laboratory of Functional Genomics led by Michal Šmída is located at MU part of the Central European Institute of Technology (CEITEC) in Brno. The main area of the research group focuses on improving the therapeutic options and revealing the molecular mechanisms involved in chronic lymphocytic leukemia. That includes investigating the mechanisms of resistance to monoclonal antibody therapy in B-cell malignancies; the targeted gene editing and whole-genome knockout screens using CRISPR/Cas9 technology; and repurposing of approved drugs for personalized therapy.

The video briefly reveals the environment of the laboratory and points out the ongoing drug screen project. For this research project, 900 clinically approved drugs are applied on both primary cells and immortalized cell lines edited by CRISPR/Cas9 system, cultured in an established co-culture model of cultivation mimicking the tumor microenvironment. The application of the drug library and the cell seeding is fully automatized by a liquid handling system as described in the video.

Taking this virtual tour offers the viewer to dip into a daily science routine, making an attempt to acquaint them with the drug screening approach, laboratory equipment, instruments, and the surroundings as well.

Acknowledgement: This research is financially supported by the Ministry of Education, Youth and Sports of the Czech Republic under the project CEITEC 2020 (LQ1601).

T11: The role of terminal transferase PAPD7

Zuzana Loubalová[1#*], Radek Malík[1#] and Petr Svoboda[1]

[1] Institute of Molecular Genetics of the ASCR, Vídeňská 1083, 142 20 Prague 4, Czech Republic

[#]Equal contribution

*zuzana.loubalova@seznam.cz

RNA-specific ribonucleotidyl transferases are polymerases that modify RNA molecules by adding ribonucleotides to their 3´ ends. PAPD7, an enzyme with putative 3´ poly(A) transferase activity, is involved in a post-transcriptional quality control mechanism. Papd7 is ubiquitously expressed with an exceptionally high expression during the oocyte-to-zygote transition, which makes it a great candidate for a factor regulating gene expression during this process. To investigate the function of PAPD7, we used a conditional knock-out ESC line from a gene knock-out consortium EUCOMM and generated a whole mouse knock-out lacking a predicted critical exon from the gene structure. Knock-out mice are viable; females show minimal fertility phenotype; however, we observe impairment of spermatogenesis and male sterility. Notably, we have found that the mutant Papd7 allele lacking the critical exon can still produce truncated PAPD7 containing just one of the two annotated functional domains. The truncated PAPD7 appears to reduce the Papd7 mutant phenotype and provides a model for uncoupling biological roles of the N- and C-terminal parts of the protein.

P30: Fine mapping of *Hstx2* locus modulating the *Prdm9*-dependent hybrid male sterility in mice

Diana Lustyk[1*], Kristian Ullrich[2], Michelle Yancoskie[3], Linda Odenthal-Hesse[2], Yingguang Frank Chan[2], Jiří Forejt[1], and Petr Jansa[1*]

[1] Laboratory of Mouse Molecular Genetics, Division BIOCEV, Institute of Molecular Genetics, Czech Academy of Sciences, 25250 Vestec, Czech Republic

[2] Max-Planck-Institute for Evolutionary Biology, 24306 Plön, Germany

[3] Friedrich Miescher Laboratory of the Max Planck Society, 72076 Tübingen, Germany

*dianaw@img.cas.cz

Hybrid sterility (HS) is a postzygotic reproductive barrier between closely related species. The laboratory model of HS between *Mus musculus musculus* and *Mus musculus domesticus* subspecies was established in our laboratory based on the wild-derived strain PWD/Ph (PWD) and the laboratory strain C57BL/6J (B6). The incompatibilities between two major genetic factors of HS, $Prdm9^{PWD/B6}$ gene on the chromosome 17 and $Hstx2^{PWD}$ locus on the X chromosome, are responsible for male sterility of (PWD x B6)F1 hybrids. So far, *Prdm9* has been the only HS gene identified in vertebrates. Here we analyzed *Hstx2* locus, which harbors 4.7 Mb interval on the X chromosome. To facilitate the positional cloning and to overcome the recombination suppression within 4.7 Mb of *Hstx2* locus we used two approaches, a Spo11/Cas9 transgene and a humanized *Prdm9* allele to introduce meiotic recombination to novel sites inside *Hstx2*. We succeeded to reduce $Hstx2^{PWD}$ interval to 2.70 Mb (X: 66.51-69.21 Mb). We show that shorter *Hstx2* locus still operates as a major X-linked factor for hybrid sterility, and controls homologous chromosome synapsis. Despite intensive further crosses, the 2.70 Mb interval stayed a recombination coldspot. To investigate the lack of recombination we analyzed optical maps of this genomic interval to get insight into structural anomalies as a possible cause. We observed high incidence of subspecies-specific insertions/deletions along the chromosome, with striking copy number polymorphism of the mir465 cluster within *Hstx2* locus.

P31: N-Fluoroalkyl-1,2,3-Triazoles: Easily Available Compounds with High Synthetic Potential

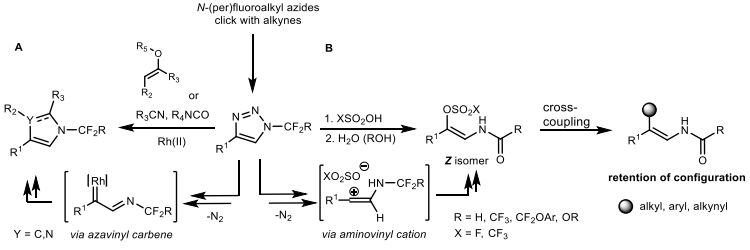
Athanasios Markos[1,2*], Vladimir Motornov[1] and Petr Beier[1*]

[1] Institute of Organic Chemistry and Biochemistry of the Czech Academy of Sciences, Flemingovo nám. 2, CZ-166 10 Prague 6, Czech Republic

[2] Department of Organic Chemistry, Faculty of Science, Charles University, Hlavova 2030/8, CZ-128 43 Prague 2, Czech Republic

*beier@uochb.cas.cz

N-Fluoroalkyl triazoles, easily available heterocycles *via* copper(I)-catalyzed azide-alkyne cycloaddition (CuAAc) of safe and stable *N*-fluoroalkyl azides and alkynes [1,2], are building blocks with a great synthetic potential. Recently, we have reported that *N*-fluoroalkyl triazoles undergo rhodium-catalyzed transannulations to afford previously unreported *N*-fluoroalkyl heterocycles such as pyrroles, pyrrolones, imidazoles and imidazolones (Scheme A) [3]. This year, we have described a stereoselective and metal free transformation of *N*-fluoroalkyl triazoles to (*Z*)-*β*-enamido triflates and fluorosulfonates in presence of trifluoromethanesulfonic or fluorosulfonic acid, respectively. Acid-mediated transformation of *N*-fluoroalkyl triazoles proceeds in comparison to Rh-catalyzed reactions *via* aminovinyl cation. The vinyl triflates are stable solids and undergo cross-coupling reactions to a variety of substituted enamides (Scheme B) [4].



[1] Z. E. Blastik, S. Voltrová, V. Matoušek, B. Jurásek, D. W. Manley, B. Klepetářová, P. Beier, Angew. Chem. Int. Ed. **2017**, *56*, 346–349

[2] S. Voltrová, I. Putovný, V. Matoušek, B. Klepetářová, P. Beier, Eur. J. Org. Chem. **2018**, 5087–5090

[3] V. Motornov, A. Markos, P. Beier, Chem. Commun. **2018**, *54*, 3258–3261

A. Markos, S. Voltrová, V. Motornov, D. Tichý, B. Klepetářová, P. Beier, Chem. Eur. J.

[4] 10.1002/chem.201901632

P32: Analysis of spatiotemporal expression pattern of Arabidopsis dirigent proteins and role of cytokinins in their regulation

Alesia Melnikava[1*], Candelas Paniagua[2], Eliska Spackova[1], Marketa Samalova[1], Jan Hejatko[1]

[1] Central European Institute of Technology (CEITEC MU), Masaryk University, Brno, Czech Republic

[2] School of Biology, University of Leeds, Leeds, UK

*alesiamelnikava@mail.muni.cz

Dirigent proteins were found to impart regio- and stereoselectivity on the phenoxy radical coupling reaction during lignan and lignin biosynthesis. 1st dirigent protein was identified in *Forsythia suspensa*, allowing formation of (+)-pinoresinol from coniferyl alcohol monomers [1].

Arabidopsis dirigent proteins (AtDIRs) represent a large and unexplored gene family, consisting of 26 members. Of these, however, only few were functionally characterized. AtDIR5/AtDIR6 seem to be involved in (-)-pinoresinol biosynthesis [2] and AtDIR10/ESB1, was shown to control Casparian strip formation in the root endodermis [3]. According to the phylogenetic analysis *AtDIR13/AtDIR14* are the closest paralogues of *AtDIR5/AtDIR6*, but they lack the conserved residues necessary for (-)-pinoresinol formation.

We propose that cytokinin can control the cell wall composition and/or properties possibly in a response to (a)biotic stress or as a part of developmental regulations via regulation of *AtDIR13/14*. The suggested mechanism might be important in a stress and/or developmental response like control of vascular tissue development and/or lateral root formation.

Hereby, we present our data showing the expression pattern of *AtDIR13/AtDIR14* and their response to CKs treatment. Using single-copy *Arabidopsis* transgenic lines being homozygous for transcriptional fusions *pAtDIR13::NLS:3XGFP* and *pAtDIR14:GUS*, we found that *AtDIR13/AtDIR14* are active mainly in the vascular tissue of the root and the expression throughout the root appears at the 2nd day of the seedlings development. However, *AtDIR14* seems to be active in the shoot vascular tissue, too. Moreover, both *AtDIR13* and *AtDIR14* are strongly upregulated by cytokinins in the *Arabidopsis* roots, the most noticeable zone is the root tips.

Acknowledgement: Supported by CEITEC 2020 (LQ1601).

[1] Davin L. B., Wang H. B., Crowell A. L., Bedgar D. L., Martin D. M., Sarkanen S., Lewis N. G.: Science *275* (5298), (1997).

[2] Kim K. W., Moinuddin S. G. A., Atwell K. M., Costa M. A., Davin, L. B., Lewis N. G.: J. Biol. Chem. *287*, (2012).

[3] Hosmani, P. S., Kamiya T., Danku J., Naseer S., Geldner N., Guerinot M. L., Saltb D. E.: Proc Natl Acad Sci U S A 110, (2013).

P33: Designer cytokine Hyper IL-6 in erythropoiesis

Tereza Mikulášová[1], Ondřej Svoboda[1,2], Petr Bartůněk[1]

[1] Institute of Molecular Genetics of ASCR, Prague, Czech Republic

[2] University of California, San Diego, CA, USA

*tereza.mikulasova@img.cas.cz

Interleukin 6 (IL-6) is a cytokine responsible for processes such as an acute inflammation, B-cell maturation and hematopoiesis in general. It signals via the receptor complex containing IL-6Rα and the β-receptor gp130. gp130 is a common β-receptor for all cytokines belonging to IL-6 family, therefore it is present in the membrane of most cells. IL-6Rα, however, is expressed only in a subset of cell types such as hepatocytes, monocytes, macrophages, neutrophils and some lymphocytes. Nevertheless, IL-6 can also stimulate cell types lacking IL-6Rα in their membranes (e.g. hematopoietic progenitor cells - HPCs). This trans-signaling is possible due to the naturally occurring soluble form of IL-6R (sIL-6R). Because a high level of sIL-6R is necessary for efficient trans-signaling, a synthetic molecule of covalently linked human IL-6 and sIL-6R, called Hyper IL-6, was already designed. It was shown that Hyper IL-6 expands human and mouse HPCs in vitro. It could be then beneficial for the improvement of HPCs expansion needed in treatment of human diseases where the hematopoiesis is impaired. But because of the broad range of IL-6 signaling effects, it is also important to understand its role in vivo. Nevertheless, in vivo studies of hyper IL-6 function during development would be very challenging or even impossible in mouse or human. Because of the external and fast development, embryo transparency and availability of numerous transgenic lines, we chose zebrafish as a suitable organism for in vivo developmental studies. For these experiments, we designed a single construct from which all the sequences for zebrafish IL-6, sIL-6R and Hyper IL-6 were derived and cloned. In this project, we focus on the effects of IL-6 trans-signaling on HPCs proliferation during embryonic development. Besides the in vivo experiments, we are also studying the effect of IL-6 trans-signaling on ex vivo HPCs cultures by employing recombinant zebrafish IL-6, sIL-6R and Hyper IL-6 proteins. Particularly, we are interested in erythroid progenitor self-renewal and proliferation induced by IL-6 trans-signaling.

P34: New Substrates for Viral NudiX Enzymes in RNA caps

Maria-Bianca Mititelu[1*] and Hana Cahová[1]

[1] Institute of Organic Chemistry and Biochemistry, Flemingovo nam. 2, Prague 6, 16610, Czech Republic

*maria-bianca.mititelu@uochb.cas.cz

NudiX hydrolases belong to a super family of enzymes widely distributed among all classes of organisms including viruses, bacteria, archaea, and eucaryotes. They are involved in cellular metabolism and homeostasis, as well as mRNA processing. As their name suggests they catalyze hydrolysis reactions, more precisely they cleave nucleoside diphosphates linked to moiety-X. The biological functions of many NudiX enzymes are not fully understood given the high diversity in substrate preferences. They can cleave nucleoside triphosphates, dinucleoside polyphosphates, non-nucleoside polyphosphates, capped mRNAs, but also small molecules such as NAD and CoA. Some DNA viruses such as Poxviruses and the African Swine Fever Virus also code for their own NudiX enzymes. The recent discovery of NAD and CoA as new RNA caps leads to the reassessment of RNA structure and to define the real substrates of viral NudiX enzymes as well as their roles in infection.

T12: Lone pair-π and anion-π interactions as stabilization factors of RNA tetraloops

Klaudia Mráziková[1,2*], Holger Kruse[1], Jiří Šponer[1], Pascal Auffinger[3]

[1] Institute of Biophysics of the Czech Academy of Sciences, Brno, Czech Republic,

[2] National Centre for Biomolecular Research, Faculty of Science, Masaryk University, Kamenice 5, 625 00 Brno, Czech Republic

[3] Institute de Biologie Moléculaire et Cellulaire du CNRS, Strasbourg, France

*mrazikova@ibp.cz

UNCG and GNRA tetraloops are RNA hairpin loops with biological role in RNA folding and RNA tertiary interactions. Molecular dynamics (MD) simulation is a computational technique which uses empirical force field (FF) to describe the time evolution of RNA. MD simulations of UNCG and GNRA are often problematic.[1] There are several interactions involved in stabilization of these tetraloops, which may be challenging for FF to reproduce, e.g. lone pair-π interaction in UNCG or anion-π interaction in GNRA. Quantum mechanics (QM) is able to study molecules with high accuracy. Therefore, QM is able to detect inaccuracies in FFs. In addition, it accounts for electronic effects of molecules, which allows us to study molecular interactions in depth.

Here, we used highly accurate QM methods to analyze optimal distances, interaction energies and nature of the lone pair-π and anion-π interactions to estimate their importance in the stabilization of the tetraloops, and to evaluate AMBER FF. We show that although stabilization coming from the lone pair-π and anion-π interactions is significant, AMBER FF is able to describe them sufficiently.

Acknowledgement: This work was supported by grant 16-13721S and by the project SYMBIT reg. number: CZ.02.1.01/0.0/0.0/15_003/0000477 financed by the ERDF.

[1] Banáš P. et al.; JCTC, 2010, 6, p. 3836-3849.

T13: How to learn a rule (through hippocampal-prefrontal interactions)

Michele Nardin[1*], Karola Kaefer[1], Jozsef Csicsvari[1]

[1] Institute of Science and Technology (IST) Austria, Klosterneuburg, Austria
*michele.nardin@ist.ac.at

Successful execution of many types of behaviour relies on the synchronous activity between the medial prefrontal cortex (mPFC) and the hippocampus (HC), but the nature of the information that is being communicated is still unclear. Here we analyse tetrode spiking data recorded simultaneously in the HC and mPFC while rats execute a rule switch task on a plus maze. We show that the decoding of spatial information from mPFC cells can become as precise as hippocampal cells' when the linearized position between start and goal is decoded. We report that a subpopulation of cells in the two areas shares an above than chance noise correlation which is independent of the task rule. Among the paired cells, each PFC cell couples with more than one HC cell. These pairs have a cofiring similarity higher than chance and PFC cells that are coupled to HC cells show a better decoding precision than non-coupled ones, suggesting an exchange of spatial information between the two areas. Moreover, the activity of PFC encodes highly non-local positions when the animal is at decision and goal areas. This non-local activity is non-random and highly structured and can predict future actions (if forward) or past actions (if backward). This suggests that mPFC trajectory-like reactivation may offer a mechanistic explanation of how a new rule is acquired.

P35: Plasmid-mediated resistance to colistin in healthy chicken in Paraguay

Kristina Nesporova[1,2*], Adam Valcek[1,2], Ivana Jamborova[1,2], Matej Medvecky[2], Ivan Literak[1,2], Monika Dolejska[1,2]

[1] Department of Biology and Wildlife Diseases, FVHE, UVPS Brno, Brno, Czech Republic
[2] CEITEC VFU Brno, UVPS Brno, Brno, Czech Republic, Czech Republic
*krisnesporova@gmail.com

According to WHO, the antibiotic resistance is one of the major problems to deal with in our millennium. High occurrence of multi-drug resistant Gram-negative bacteria led to reintroducing less user-friendly antibiotics such as colistin to human medicine. Until the discovery of *mcr-1* gene in 2016, only chromosomally-encoded resistance to colistin was observed. This type of resistance can be transferred only to other generations of bacteria. However, *mcr* (mobile colistin resistance) genes are plasmid-mediated and can be transferred very easily even within different Enterobacterales and cause problems in treatment of bacterial infections.

We observed high prevalence (24%; 16/66) of *mcr-5* gene in our samples from finisher broiler chicken from 12 different farms in Paraguay. We obtained 28 *mcr-5*-carrying *Escherichia coli* isolates and characterize them using diverse microbiological and molecular methods including whole-genome sequencing and conjugation experiments.

We were the first to detect *mcr-5* gene within conjugative plasmids of various types. This indicates it can be transfered more easily than it was originally thought as it was detected only within small non-conjugative plasmids before. Moreover, we observed frequent association of *mcr-5* and genes encoding resistance to extended-spectrum beta-lactams in the same plasmid – IncI1/ST113-*mcr-5*-$bla_{\text{CTX-M-8}}$ and IncI1/ST12-*mcr-5*-$bla_{\text{CMY-2}}$. IncI1/ST113 and IncI1/ST12 are epidemic plasmid lineages disseminating the beta-lactamase genes worldwide. Their association with *mcr-5* represents a big threat for public health.

T14: Structural insight into the transcriptional machinery of bacteria using X-ray crystallography

Markéta Nováková[*1], Jana Škerlová[1], Irena Sieglová[1,2], Milan Fábry[2], Pavlína Řezáčová[1]

[1] Institute of Organic Chemistry and Biochemistry, AS CR, Prague, Czech Republic
[2] Institute of Molecular Genetics, AS CR, Prague, Czech Republic
*marketa.novakova@uochb.cas.cz

In this basic science project, we study 3D structures of protein transcriptional repressors of the carbon catabolism from *Bacillus subtilis*.

Adaptability of bacterial responses to environmental changes is unbelievable. Bacteria can survive many inhospitable conditions such as (a potential) starvation. One of their weapons for survival is the ability to utilize more nutrition sources. For a high efficiency of a nutrient usage the strict control is highly needed. This regulation is usually controlled at the level of gene transcription via proteins, transcriptional factors (TF), which specifically bind DNA depending on a presence or absence of a nutrient molecule. TF can work either as activators or repressors. For understanding this regulation machinery on molecular level, it is necessary to know 3D structures of those proteins.

In view of the enormous number of bacterial species it is advantageous to have some model organisms for generalization of our knowledge to related species. One of those is *Bacillus subtilis*, which is the model organism for the huge group of Gram-positive bacteria. We focus on transcription repressors of carbon catabolism in *B. subtilis*. The work-flow of our investigation is as follows: firstly, we produce the recombinant protein in *Escherichia coli*, then we purify it using chromatography techniques and then crystallize in special solutions. Harvested protein crystals are then used for X-ray diffraction experiment. Using special software, we are able to determine the structure of the protein from obtained diffraction data.

P36: A missense DDX38 mutation linked with retinitis pigmentosa

Mina Obuca[1*] and David Stanek[1]

[1] Institute of Molecular Genetics of the ASCR, v. v. i., Prague
*mina.obuca@img.cas.cz

During splicing, snRNPs and pre-mRNA undergo a series of association-dissociation steps and eight RNA helicases play essential roles in controlling these conformational rearrangements. A large number of human diseases are consequence of splicing errors. Surprisingly, most mutations in ubiquitously expressed spliceosome components exhibit a tissue specific phenotype. For example, mutations in several snRNP-specific proteins cause retinitis pigmentosa (RP), a major cause of blindness. A missense mutation in the RNA splicing helicase DDX38, which results in the Gly332Asp substitution was associated with early-onset autosomal recessive RP. Our aim is to determine how RP mutation affect DDX38 function. We provide evidence that the DDX38 helicase interacts with several components of the active spliceosome and that the RP mutation does not inhibit these interactions. We further show that the knockdown of DDX38 as well as the expression of RP-related mutant protein affect splicing efficiency of several ubiquitously expressed and retina specific genes. Moreover, we showed that the knockdown of DDX38 and expression of the mutant variant enhance usage of cryptic splice sites. We hypothesize that DDX38 has role in RNA splicing quality control and that RP-related mutation affects this function.

P37: Plasmids in pathogenic multiresistant *Escherichia coli*

Jana Palkovicova[1,2*], Iva Kutilova[1,2], Monika Dolejska[1,2]

[1] Central European Institute of Technology, University of Veterinary and Pharmaceutical Sciences Brno, Brno, Czech Republic

[2] Department of Biology and Wildlife Diseases, Faculty of Veterinary Hygiene and Ecology, University of Veterinary and Pharmaceutical Sciences Brno, Brno, Czech Republic

*palkovicova.jane@gmail.com

Even though *Escherichia coli* is a gastrointestinal tract commensal, ExPEC strains (extraintestinal pathogenic *E. coli*) represent a serious issue to public health. Plasmids contribute to the successful dissemination of the ExPEC strains thanks to many virulence and antibiotic resistance genes they carry. In our recent study [1] we showed that some sublineages of *E. coli* ST131 obtained from diverse sources including humans, animals and waste water contained specific plasmids from incompatibility group F (IncF). These plasmids have mosaic structure, they contain often more than one IncF plasmid replicon, and encode $bla_{CTX\text{-}M}$ genes that allows extended-spectrum beta-lactamases production. The focus of this study is to better understand the impact of plasmids on the host fitness and on a worldwide spread of these clinically important strains.

To study the bacterial fitness in the presence and absence of plasmid we need to eliminate IncF plasmids from wild-type isolates. Plasmid-free cells will be obtained using plasmid constructs. These constructed plasmids carry IncF plasmid replicons which interfere with the replicons of wild-type IncF plasmids. We will use commercial plasmid pCURE2 [2] and a new plasmid construct pCURE-F we designed to specifically target IncF replicons which are carried by the strains from our collection. The pCURE plasmids are then eliminated thanks to their instability in a non-selective medium. After we successfully eliminate the plasmids, further analyses, such as whole genome sequencing, growth curves and competition assays, will be done aiming to understand the impact of IncF plasmids on the host cell.

Acknowledgement: This study is funded by project GA18-23532S.

[1] Jamborova, I. et al. 2018, *Antimicrob Agents Chemother*, 62: e00519-18.

[2] Hale, L. et al. 2010, *Biotechniques*, 48:223-8.

P38: Immunosensing of the honeybee bacterial pathogen *Melissococcus plutonius*

Matěj Pastucha[1,2*], Zdeněk Farka[1], Veronika Poláchová[1,2], Zuzana Mikušová[1,2], Radka Obořilová[2], Petr Skládal[1,2]

[1] CEITEC MU and [2] Department of Biochemistry, Faculty of Science, Masaryk University, Brno, Czech Republic

*matej.pastucha@ceitec.muni.cz

Western honeybee is an invaluable pollinator of many agricultural crops. European Foulbrood caused by the bacterium *Melissococcus plutonius* is one of the most serious honeybee diseases. In case of an outbreak, an effective method for the diagnosis is necessary, preferably sensitive enough to detect the pathogen before clinical symptoms manifest.

In this work, we have exploited the antibody-based approach to develop new methods for the detection of the germ. No commercial antibodies were available; therefore, a new polyclonal antibody was prepared. This allowed us to develop an enzyme-linked immunosorbent assay (ELISA) for bacteria confirmation in laboratory with the limit of detection (LOD) of 7.1×10^4 CFU·mL^{-1}. We further improved the sensitivity 400× by utilizing click-conjugated photon-upconversion nanoparticles (UCNPs) as a label for luminescence readout. [1]

In the next part of the research aiming for a portable detection system, we have developed an electrochemical immunosensor utilizing horseradish peroxidase as a label. [2] With the LOD of 6.6×10^4 CFU·mL^{-1} and analysis time of 2 h, this allows sensitive in-field detection to prevent infection spreading and subsequent losses of honeybee colonies.

[1] Poláchová V, Pastucha M, Mikušová Z, Mickert M J, Hlaváček A, Gorris H H, Skládal P, Farka Z. Click-conjugated photon-upconversion nanoparticles in an immunoassay for honeybee pathogen Melissococcus plutonius. Nanoscale 2019, 11(17), 8343–8351.

[2] Mikušová Z, Farka Z, Pastucha M, Poláchová V, Obořilová R, Skládal P. Amperometric Immunosensor for Rapid Detection of Honeybee Pathogen Melissococcus plutonius. Electroanalysis 2019, submitted.

P39: CRISPR/Cas9 gene editing and functional screening in chronic lymphocytic leukemia

Helena Peschelová[1*], Veronika Kozlová[1], Václav Hejret[1] and Michal Šmída[1,2]

[1] Central European Institute of Technology (CEITEC), Masaryk University, Brno

[2] Department of Internal Medicine – Hematology and Oncology, Medical Faculty of Masaryk University and University Hospital Brno

*helenapeschelova@mail.muni.cz

Chronic lymphocytic leukemia (CLL) patients carry a variety of somatic mutations, whose thorough exploration could shed light on the etiology of the disease, or even lead to the discovery of potential novel drug targets. However, as primary CLL cells do not proliferate *in vitro*, there is a lack of suitable models mimicking the genetic heterogeneity observed in patients. Our aim is to establish isogenic cell lines harboring the most frequent CLL mutations and to investigate unique vulnerabilities specific to these mutations.

We made use of HG3 cells, a well-established CLL cell line, and using CRISPR/Cas9 technology we generated stable isogenic knockout cell lines in *ATM* and *TP53* genes, two prominent CLL drivers. We are also working on establishing cell lines with knock-in mutations of *MYD88*, *NOTCH1* and *SF3B1*.

The *ATM* knockout cell line was then used for CRISPR/Cas9 functional genetic screening to reveal genes synthetic lethal to *ATM* by comparing the abundance of gene knockouts in the beginning of the experiment vs. after 3-week incubation. Gene knockouts that were depleted in the *ATM* knockout cells but not in wildtype control should have a synthetic lethal relationship with the *ATM* gene. Altogether we obtained 11 candidate ATM-synthetic lethal genes, which are now being validated.

In conclusion, we have established three stable *ATM* knockout CLL cell lines and subsequently performed a CRISPR/Cas9 functional genetic screening, which yielded 11 candidate synthetically lethal genes. After thorough validation, some of the most interesting genes might serve as potential therapeutic targets for patients with ATM mutations.

Acknowledgement: This research has been financially supported by the Ministry of Education, Youth and Sports of the Czech Republic under the project CEITEC 2020 (LQ1601).

P40: Twin-arginine translocase experimental plan

Gergely Pinke[1*], Leonid Sazanov[1]

[1] Institute of Science and Technology Austria, Klosterneuburg, Austria
*gpinke@ist.ac.at

Twin-arginine translocase system is present in Archaea, bacteria and plant chloroplasts. The peculiarity of this transport system compared to other systems (such as the general secretory or Sec pathway) is its ability to transport fully folded proteins across membranes utilizing the proton motive force only. In this poster I'm presenting the current purification results and future electron cryo-microscopy imaging experimental plan to elucidate the novel mechanism it operates with.

T15: Atomic details on protein-protein recognition - role of side chain dynamics in binding between HP1 and H3 proteins.

Pavlína Pokorná[1,2,3*], Jiří Šponer[1,2], Miroslav Krepl[2], Eva Bártová[2]

[1] Central European Institute of Technology, Masaryk University, Brno, Czech Republic
[2] Institute of Biophysics of the Czech Academy of Sciences, Brno, Czech Republic
[3] National Centre for Biomolecular Research, Faculty of Science, Masaryk University, Kamenice 5, 625 00 Brno, Czech Republic
*pokorna.pavlina@ibp.cz

Human heterochromatin protein 1 (HP1) is the main factor responsible for heterochromatin formation and maintenance. Its chromo-shadow domain (CSD) is responsible for homodimerization; the dimer then acts as a hub at chromatin, transiently interacting with variety of binding partner proteins (BPs) [1,2]. In this work, we focus on interactions of HP1(CSD) dimer with one of its BPs, histone H3 N-terminal tail, using molecular dynamics (MD) simulations [3]. Our goal has been to complement the available X-ray crystallography data [4] and to unravel potential dynamical effects in the molecular recognition.

Our data suggest an active role of HP1 Trp174 sidechain dynamics in distinguishing residues bound in conserved HP1 CSD hydrophobic pockets. MD simulations also reveal an intricate competition between negatively charged groups of HP1 C-terminal residues and solvent anion binding near the conserved hydrophobic pockets, which depends on BP sequence. Moreover, post-translationally modified H3 phosphoTyr41 can bind to the same site.

Overall, simulations suggest that the HP1(CSD)-BP recognition involves structural dynamics of both partners and that structural communication between the adjacent binding pockets may contribute to fine-tuning of the sequence recognition. Further, our study gives insights into the ability of several contemporary pair-additive force fields to describe similar protein-protein interfaces and can thus be used as MD simulation benchmark for protein force fields.

[1] Cheutin T. et al.: Science 299, 5607 (2003).
[2] Eissenberg J. C. & Elgin S. C. R.: Trends Genet. 30, 3 (2014).
[3] Šponer J. et al.: Chem. Rev. 118, 8 (2018).
[4] Liu Y. L. et al.: J. Biol. Chem. 292, 14 (2017).

P41: Mapping neural circuit activity to behavioral output in flies

Victoria Pokusaeva[1*]
[1] Institute of Science and Technology, Klosterneuburg, Austria
*victoria.pokusaeva@ist.ac.at

Nowadays there exist multiple techniques that allow manipulation of neuronal activity *in vivo*. Using these techniques allows filling the gap between neuronal activity and animal behavior. However, in the real environmental conditions neural circuits often have very complex patterns of activity. Mimicking these pasterns artificially is technically very challenging. We developed a method that enables modulation of activity of individual cells within a neural circuit in flies using optogenetics in combination with genetic mosaic technique. With this method each of the cells can be optogenetically activated or inhibited independently of its neighbors. We believe that this technique will help answer the question how behavior of animals are instructed by neural networks.

To test the newly developed method we used the network of ~40 Lobula Plate Tangential Cells (LPTCs) in *Drosophila melanogaster*. This neural circuit in flies is responsible for the processing of the wide-field visual motion, or optic flow. This way flies can read the changes in the environment during the flight, and adjust their behavior accordingly. All LPTCs are unique: each cell in the network samples visual information about different motion directions from different location within the panorama. Moreover, in order to perform their task well LPTCs have to communicate with each other. This complicated dynamics within the LPTCs neural circuit makes it challenging to study the behavioral output of this network. We overcame this problem by developing a new genetic tool that allows differential optogenetic modulation of neuronal activity in combination with principled behavioral assay. This approach helped us to understand how behavior is instructed by the network of LPTCs.

P42: LYNX: LYmphoid NGS panel analysis tool

Tomáš Reigl[1*], Karol Pál[1], Veronika Navrkalová[1,2], Jakub Hynšt[1], Tomáš Hron[3], Karla Plevová[1,2], Nikos Darzentas[1,4], Zbyněk Halbhuber[3], Šárka Pospíšilová[1,2]

[1] CEITEC Masaryk University, Brno, Czech Republic

[2] University Hospital Brno, Czech Republic

[3] HPST, s.r.o., Prague, Czech Republic

[4] University Hospital Schleswig-Holstein, Kiel, Germany

*tomas.reigl@gmail.com

Introduction: Next-generation sequencing (NGS) is currently one of the fastest developing technologies in medicine and other biological fields. NGS sample preparation by hybridization (so-called "capture-based" NGS) is technically simple approach and has more universal usage than amplicon-based methods. Nevertheless, for many diagnosticians, analysis of NGS data is still a challenge. Therefore, in cooperation with a private company HPST, s.r.o., we aim to create an easy-to-use web-based bioinformatics tool for analysis and visualization of data from NGS panel currently under our implementation for mutation screening in lymphoid malignancies.

Methods: Based on data from a custom capture-based NGS panel developed in cooperation between University Hospital Brno, CEITEC MU and HPST, s.r.o., we develop a bioinformatics pipeline focused on analysis of gene mutations, copy number variants (CNVs), and antigen receptor rearrangements. The pipeline will be wrapped in a modern web-based user interface, making the tool available to all users.

Results: LYNX bioinformatics tool is currently under development, but our cornerstones for single types of analyses (gene mutations, CNVs and immunoglobulin rearrangements) are already in testing phase on a pilot set of samples. Thanks to the cooperation with HPST, s.r.o., we are going to share knowledge not only in data analysis and software development, but also in creating relationships with and satisfying customers/users.

Acknowledgement: Supported by TACR ZETA TJ02000133.

P43: A novel behavioural task for testing memory generalization

Heloisa S. C. Chiossi[1*], Jozsef Csicsvari[1]

[1] Institute of Science and Technology Austria, Klosterneuburg, Austria
*hchiossi@ist.ac.at

Learning and memory are some of the processes that support the adaptation of an organism to its environment and ultimately lead to survival. One of the brain areas that seems to be involved in associating information and memory consolidation is the retrosplenial cortex, in coordination with the hippocampus. In this step of the Ph.D. project, I am studying the phenomena of generalization of information during consolidation happening between those brain areas. Standard behavioural paradigms such as the Morris Water Maze and the Cheeseboard Maze can allow for some types of spatial memory testing but not all. In order to test for generalization of memory contents, we developed a context discrimination task in a novel maze. The maze fixes the trajectory to a linear track, which facilitates spatial comparison between different contexts. Sandwells for hiding food are placed at regular spacing, imposing a cost on randomly searching for reward (digging), prompting the animal to target only the remembered reward locations. The behaviour paradigm we propose on this maze consists of two pairs of rewards that must be remembered on the same day, each identifiable by a set of contextual cues. One of the reward locations is the same for both contexts, whilst the second reward is context-dependent. Cortical encoding of memories might be capable of generalizing information that does not depend on context, reducing their storage cost. The next step of this project will be to study the differences between hippocampal and cortical representations of these contextual memories.

P44: Thermomorphogenesis during seed development

Juan Francisco Sánchez Lopéz[1*]

[1] CEITEC Masaryk University, Brno, Czech Republic
*sanchez.lopez@ceitec.muni.cz

In the past decades the average annual temperatures have arisen due to global warming. High ambient temperatures shorten the life cycle of many crops, reducing the grain yield. Periods of extreme weather also have a negative effect on crop production, affecting the development and viability of both female and male gametes, causing heat-induced sterility, and reducing the receptivity of stigma to pollen, pollen tube growth in the stigma and style and ovule penetration Even in the case of successful fertilisation there are more chances of abortion and the quality of resilient seeds are altered. The morphological changes in plant development due to high temperatures is called thermomorphogenesis. The plant reproductive development has been suggested to be the most sensitive stage to heat stress. Auxin and cytokinin are two plant hormones closely involved in the regulation of plant development, including the correct development of seedpod, ovule, seed and embryo. The aim os this project to identify the relevant genes involved in the developmental adaptation of the flowering plant to increase of its growth temperatures, and to develop genetic tools and methodologies to study the mechanisms of this acclimation.

Acknowledgement: This work is supported by Czech Science Foundation, project 19-05200S and by The South Moravian Center for International Mobility (JCMM).

P45: Exploring the Neuronal Principles of Attention in *Drosophila* Visual Processing

Roshan Kumar Satapathy[1*]

[1] Institute of Science and Technology, Klosterneuburg, Austria
*rsatapat@ist.ac.at

Animals encounter a multitude of stimulus in their natural environment. However, at any moment, behaviour is usually guided by a small subset of these stimuli, depending on the internal state and the immediate needs of the animal. This is usually achieved through selective attention, where neural processing is restricted to a relevant subset of incoming stimuli while ignoring non-essential stimuli. Despite multiple studies in humans, non-human primates and rodents, the neuronal mechanisms underlying selective attention remain unclear.
I aim to uncover the computational principles and neuronal mechanisms involved in attention-like processes in *Drosophila melanogaster*, a model organism that enables unmatched specificity in circuit manipulations thanks to powerful genetic tools. I will investigate the variability in the response of individual flies to the same stimulus over several trials to infer the impact of the internal state of the animal on its behaviour. Importantly, I will generate visual competition between two stimuli that evoke separate responses, and study the role of attention in determining the resulting behaviour of the animal. Specifically, I will study the modulation of and interaction between optomotor response and male courtship tracking, two innate and highly stereotypic visual behaviors. Both of these behaviours have been studied in the fruit fly in depth and the circuits involved in each are known in great detail. I will take advantage of this fact to pinpoint the neural circuitry involved in the modulation of sensory processing by carefully combining behavioural analysis and *in vivo* physiology in *Drosophila*.

P46: ADAR2 variants associated with microcephaly, intellectual disability, and seizure

Jiří Sedmík[1*], Mark P. Fitzgerald[2], Rivka Sukenik-Halevy[3,4], Tiong Y. Tan[5,6,7], and Mary A. O'Connell[1]

[1] CEITEC, Masaryk University, Kamenice 735/5, A35, Brno, CZ 62500, Czech Republic
[2] Children's Hospital of Philadelphia, Philadelphia, USA
[3] Sackler School of Medicine, Tel Aviv University, Tel Aviv, Israel
[4] Genetics Institute, Meir Medical Center, Kfar Saba, Israel
[5] Murdoch Children's Research Institute, Melbourne, Australia
[6] Victorian Clinical Genetics Sevices, Melbourne, Australia
[7] Department of Paediatrics, University of Melbourne, Melbourne, Australia
*jura7ik@gmail.com

Double-stranded RNA-specific adenosine deaminases (ADARs) are a family of enzymes that catalyse the hydrolytic deamination of adenosine to inosine in dsRNA. The editing and RNA-binding activities of ADARs affect RNA processing, stability, and can even lead to RNA re-coding. The enzyme ADAR2 was previously reported to be essential for recoding of transcripts found predominantly in the brain. Impaired ADAR2 editing causes early-onset epilepsy and eventual death in mouse models.

Human ADAR2 variants were found in three patients suffering from microcephaly, severe intellectual disability, and seizures. In the first patient, a homozygous mutation in one of the double-stranded RNA-binding domains was identified, whereas, in the second patient, biallelic mutations located in or around the deaminase domain were identified. The third patient carries a homozygous mutation in the deaminase domain. To evaluate the effects of these mutations on ADAR2 activity, we used fibroblasts derived from one of the patients, as well as vectors expressing wild type and mutant ADAR2 proteins.

Here we will present the results of *in vitro* assays that show reduced editing activity of ADAR2 mutants. We did observe the proper localisation of the mutant proteins. We detected changes in ADAR2 mRNA splicing induced by one of the mutations. Lastly, we observed normal ADAR2 mRNA and protein levels in patient fibroblasts. Together, these results provide evidence that the mutations have a small but significant effect on ADAR2 activity that may lead to the observed phenotype. Proper neuronal model is needed to characterise the effects of these mutations on brain development.

Acknowledgement: Funded under the FP7 project ‚The ERA Chair Culture as a Catalyst to Maximize the Potential of CEITEC' (ID 621368) of the European Union.

[1] NISHIKURA, Kazuko. *Annual review of biochemistry*, 2010, 79: 321-349.
[2] BRUSA, Rossella, et al. *Science*, 1995. 270: 1677-1680.

P47: Using the gold standard LC-MS/MS to quantify ribosomal RNA in mRNA samples preparation

Ketty Sinigaglia[1*], Stanislav Stejskal[1], Helena Covelo[1], Štěpánka Vaňáčová[1], Liam Keegan[1], Mary O'Connell[1]

[1] Central European institute of Technology, Brno, Czech Republic
*ketty.sinigaglia@ceitec.muni.eu

RNA base modifications gave birth to the epitranscriptome field They can affect RNAs metabolism and are essential for properly expressing the repertoire of RNA. One of the most common and best studied type of RNA editing in higher eukaryotes is the hydrolytic deamination of adenosine to inosine within double-stranded RNAs (dsRNAs), by the enzyme family adenosine deaminases acting on RNA (ADAR). A to I editing is one of the easiest RNA modifications to detect [1].
Identifications of modified bases in mRNAs mainly relies on mass spectrometry or antibodies that are specific for the modified base. Reverse-transcription based methods take advantage of the inability of the reverse transcriptase to extend the cDNA chain upon encountering chemical blocks in the RNA template. Interpreting the results of reverse transcription from purified RNA can be difficult, as the enzyme is sensitive to RNA secondary structures and fragmentation by nucleases, which can lead to pausing of the transcriptase. Mass spectrometry-based methods have recently emerged as powerful tools for identifying and quantifying RNA modifications. Detecting low-abundance mRNA modifications with LC-MS/MS is challenging because poly(A) RNA preparations are frequently contaminated with tRNA or rRNA. Poly(A) selection uses high salt concentrations to promote binding of the poly(A) tails to oligo(dT) immobilized on beads. However, these high-salt buffers promote hybridization of semi-complementary RNA sequences to mRNA leading to the risk of having false positive results. We investigated how salts can negatively affect peak detection. Furthermore we focused on determining a reliable measurement of rRNA still remaining in the mRNA samples after the different steps of purification.

[1] B.L. Bass, K. Nishikura, W. Keller, P.H. Seeburg, R.B. Emeson, M.A. O'Connell, C.E. Samuel, A. Herbert, A standardized nomenclature for adenosine deaminases that act on RNA, RNA 3 (1997)

T16: Higly active Dicer improves antiviral immune response in mice

Eliska Svobodova[1*], Radek Malik[1], Brigita Benkoova[2], Irena Jenickova[1], Maria Borsanyiova[2], Sona Sarmirova[2], Shubhada Bopegamage[2], Petr Svoboda[1]

[1] Institute of Molecular Genetics, Academy of Sciences of the Czech Republic

[2] Slovak Medical University in Bratislava

*eliska1svobodova@gmail.com

RNA interference (RNAi) serves as an antiviral immune response in plants and invertebrates but vertebrates including mammals evolved an independent interferon-based immune response while proteins which could mediate RNAi serve in the gene-regulatory microRNA pathway. As an exception, mouse oocytes have highly active RNAi because of a truncated Dicer isoform - Dicer^{O}, which lacks N-terminal DExD helicase domain. Dicer^{O} is efficiently converting long double-stranded RNA (dsRNA) into small RNAs and initiates effective RNAi. Here we tested whether Dicer^{O} expression could also enhance RNAi in the soma of mice and whether it could improve antiviral immune response. We thus generated mice where one endogenous Dicer allele was engineered to ubiquitously express Dicer^{O}-like isoform - denoted Dicer^{X}. While heterozygous mice are viable and fertile, homozygotes die perinatally, demonstrating importance of the N-terminal DExD domain and suggesting why Dicer^{O} expression remained restricted to the oocyte during evolution. We infected Dicer^{X} mice with CVB3 virus and our initial data show that Dicer^{X} allele mediates clearance of the virus from infected tissues and prevents systemic infection observed in wild type mice. The molecular mechanism of the effect and relationship with normal mammalian innate immunity response is under investigation.

P48: Novel methodology for seeding leukemic B cells into porous scaffolds and for their DNA isolation

Hana Svozilova[1,2*], Lucy Vojtova[3], Daniel Horak[4], Jiri Baloun[1,2], Radana Studena[2], Zdenek Plichta[4], Vladimir Proks[4], Yvona Brychtova[2], Anna Panovska[2], Michael Doubek[1,2], Jiri Mayer[2], Sarka Pospisilova[1,2*]

[1] Center of Molecular Medicine, CEITEC MU, Brno, Czech Republic

[2] Department of Internal Medicine - Hematology and Oncology, University Hospital Brno and Medical Faculty MU, Czech Republic

[3] Advanced Polymers and Composites, CEITEC BUT, Czech Republic

[4] Institute of Macromolecular Chemistry AS CR, v.v.i, Prague, Czech Republic

*svozilova.hana@gmail.com

Chronic lymphocytic leukemia (CLL) is a malignancy of mature B cells. These cells have been found to shortly undergo apoptosis outside of the patient's body. Development of a suitable 3D *in vitro* culture platform which also enables direct DNA isolation from the 3D-cultured cells has, therefore, represented an important goal in CLL research.

Patients' cells were seeded on porous collagen or hydrogel scaffolds in different concentrations ranging from 1 to 50 million cells/ml. Cell distribution and viability were quantified by confocal microscopy or/and resazurin reduction. DNA isolation was performed with DNAzol, G2 buffer, and FastDNA spin kit for soil.

The optimal cell distribution and viability were achieved when the scaffolds were placed into tubes with a suspension of 50 million cells/ml and rotated. The highest DNA concentration was obtained with FastDNA spin kit for soil. By this, we have shown synthetic materials are suitable for accommodation of leukemic B cells. Furthermore, their porosity enables to perform direct lysis and DNA isolation of 3D-cultured cells. These results represent an important step toward developing a 3D CLL drug-testing platform.

Acknowledgement: This research has been financially supported by the MEYS CR under the projects CEITEC 2020 (LQ1601), Czech-Bioimaging large RI project LM2015062 and MUNI/A/1105/2018; and by the Ministry of Health of the Czech Republic under the research grants AZV-MZ-CR 15-31834A and DRO (FNBr, 65269705). The first author is a Brno Ph.D. Talent Scholarship Holder funded by the Brno City Municipality.

P49: The role of Zinc Finger Protein 644 in mouse metabolism

Katarzyna Szczerkowska[#1*], Nicole Chambers[#1], Karel Chalupsky[1], Frantisek Spoutil[1], Jan Prochazka[1], Radislav Sedlacek[1]

[#]authors contributed equally to this work

[1] Laboratory of transgenic models of diseases; Institute of Molecular Genetics, Biocev, Prumyslova 595, 252 50 Vestec

*katarzyna.szczerkowska@img.cas.cz

ZNF644 is a C2H2 zinc finger gene encoding a putative transcription regulator, of which a point mutation (S672G) is associated with inherited high myopia in humans. Mouse with truncated form of the protein not only mimics human myopia disease phenotype but also shows sever drop in weight from weaning at 4 weeks of age and decreased body size. To investigate the role of Zfp644 in mice metabolism, we perform essential examinations such as hormonal concentration in blood, full body scanning, including bone mineral density, tissue mineral density, lean mass and fat percentage in organism; weight measurements and calorimetry. All experiments were repeated multiple times in a period of 30 weeks. Results of this examinations suggest higher basal metabolic rate and oxygen consumption in Zfp644$^{\Delta}$8 males. Interestingly, males challenged with HFD showed even higher differences in metabolic rate between transgenic and control animals. Additionally, our preliminary transcriptomic data show difference in expression of many genes related to metabolism, hormonal homeostasis as well as growth factors and growth hormone; between homozygous and control animals. Here we present our most recent data on influence of Zfp644 on a mouse metabolism. Reveling the mechanism behind it would extend our knowledge of metabolism and potential new factor(s) driving it.

T17: Electrostimulation of murine embryonic stem cells enhanced cardiomyogenesis

Eva Šafaříková[1,2*], Stanislav Stříteský[3], Jiří Ehlich[3], Lukáš Omasta[3], Ota Salyk[3], Martin Vala[3], Martin Weiter[3], Lukáš Kubala[1,4], Jan Víteček[1,4]

[1] Institute of Biophysics AS CR, Královopolská 135, Brno, CZ

[2] Department of Experimental Biology, Faculty of Science, Masaryk University, University Campus Bohunice, Kamenice 5, Brno, CZ

[3] Faculty of Chemistry, Brno University of Technology, Purkyňova 118, Brno, CZ

[4] International Clinical Research Center - Center of Biomolecular and Cell Engineering, St. Anne's University Hospital Brno, Pekařská 53, 656 91 Brno, CZ

*Safarikova.eva@ibp.cz

Heart diseases are of serious socioeconomic impact. Potentially, the heart damages could be treated by using cardiomyocytes differentiated out of embryonic stem cells (ES). For stem cells application it is necessary to understand principles of their differentiation into cardiac cells [1]. Recent studies have indicated that ES differentiation can be manipulated by exogenous electric field.

To apply exogenous electric field a unique platform based on organic electronics developed in cooperation with Brno University of Technology was used [2]. Embryonic bodies prepared out of murine ES were subjected to electric pulses from 65 to 200mV/mm at frequency of 1Hz [3].

It was found, that electric stimulation induced cell membrane depolarization and increase of cytosolic calcium level. Both events were positively dependent on the total stimulation time. Further, the longer electrostimulation enhanced cardiomyocyte beating during maturation. In order to provide support for the above-mentioned the data analysis of gene expression of two marker genes (Nkx2.5 – cardiomyogenesis marker, Oct4 – pluripotency marker) was estimated.

The work was supported by Czech Science Foundation grant No. 17-24707S

[1] Sachinidis, A. et al., 2003. *Cardiovascular research*, 58,.278–291.

[2] Safarikova, E. et al., 2018. *Sensors and Actuators B: Chemical*, 260, 418–425.

[3] Hernández, D. et al., 2015. *Stem cells international*, 2016.

P50: Novel ligands for Fibroblast Activation Protein

Adéla Šimková[1,2*], Petr Šimon[1], Pavel Šácha[1], Jana Beranová[3], Jan Konvalinka[1,2]

[1] Institute of Organic Chemistry and Biochemistry, Flemingovo n. 2, 166 10 Prague 6

[2] Faculty of Sciences, Charles University, Hlavova 8, 128 43 Prague 2

[3] First Faculty of Medicine, Charles University, Kateřinská 32, 121 08, Prague 2

*adela.simkova@uochb.cas.cz

Fibroblast activation protein (FAP) is a serine protease expressed in more than 90 % epithelial tumors. Because of its minimal or absent expression in healthy adult tissues, FAP can be a perfect platform for selective targeting of diagnostic and therapeutic tools [1,2]. Despite previous broad structure-activity relationship (SAR) studies [3–6] resulted in low-nanomolar FAP binder, its affinity is still not sufficient for its usage in FAP-targeting technologies.

Thus we proposed a novel class of peptidomimetic FAP inhibitors bearing a α-ketoamide warhead. This substitutable functional group allows us to extend the interactions between the inhibitor and its binding site, which could improve the ligand affinity. Since the structure of *N*-terminal part has already been widely optimized [3–6], we conserved the 4-quinolinoyl moiety together with glycyl-pyrrolidyl pattern.

A series of α-ketoamide compounds was synthesized *via* PADAM approach (Passerini reaction – Amine Deprotection – Acyl Migration) followed by peptide coupling chemistry and subsequent oxidation. A fluorescent substrate competition assay was used to determine the IC_{50} values. Resulting SAR study showed an excellent inhibition potency of several α-ketoamide compounds (IC_{50} up to 0.15 nM) that are supposed to be used for FAP targeting in diagnostic applications.

[1] Gorrell, M. D. & Park, J. E. Fibroblast Activation Protein α. In Handbook of Proteolytic Enzymes, Elsevier 2013, p 3395

[2] Liu et al. Cancer Biol. Ther. 2012, 13, 123

[3] Jansen, K. et al. ACS Med. Chem. Lett. 2013, 4, 491

[4] Ryabtsova, O. et al. Bioorg. Med. Chem. Lett 2012, 22, 3412

[5] Poplawski, S. E. et al. J. Med. Chem. 2013, 56, 3467

[6] Jansen, K. et al. J. Med. Chem. 2014, 57, 3053

T18: First Report of plasmid mediated colistin resistance from wildlife in Russia

Hassan Tarabai[1*], Adam Valcek[1,2], Ivana Jamborova[1,2], Rainer Raab[3], Hynek Matusik[4], Sergey V. Vazhov[5], Igor V. Karyakin[6], Ivan Literak[1,2], Monika Dolejska[1,2]

[1] Department of Biology and Wildlife Diseases, Faculty of Veterinary Hygiene and Ecology, University of Veterinary and Pharmaceutical Sciences Brno, Brno, Czech Republic

[2] Central European Institute of Technology, University of Veterinary and Pharmaceutical Sciences Brno, Brno, Czech Republic

[3] Technisches Büro für Biologie, Deutsch-Wagram, Austria

[4] Březolupy, Czech Republic

[5] Shukshin Altai State University for Humanities and Pedagogy, Biysk, Russia

[6] LLC Sibecocenter, Novosibirsk, Russia

*tarabaih@vfu.cz

The aim of this study was to select Enterobacteriaceae isolates with plasmid-mediated colistin resistance genes from cloacal swabs of Eurasian Black and Red Kites. Isolates (13.8%, n=168) that showed reduced susceptibility to colistin (3.5mg/L) were identified using MALDI-TOF MS and tested for mobile colistin resistance encoded by *mcr* genes using PCR. One *mcr-1*-positive *E. coli* isolate was detected and selected for further testing. The isolate was resistant to colistin (MIC > 4mg/L) and susceptible to 18 antibiotics by broth dilution and disk diffusion methods, respectively. WGS using MiSeq (Illumina) revealed the *mcr-1*-positive *E. coli* sample belonged to ST2280. The *mcr-1* gene was located on conjugative IncI2 plasmid pDR164 (59891 bp, GenBank number MK542639). Plasmid pDR164 showed similarity to other *mcr-1*-carrying IncI2 plasmids found in *E. coli* isolates from swine, poultry, human and sewage in USA, Vietnam, Argentina and China. Comparison of pDR164 with other plasmids revealed high similarity in the plasmid backbone and the region carrying *mcr*. In this study, we report the first *mcr-1*-positive isolate in wildlife in Russia.

Acknowledgement: Funded by NV18-09-00605.

T19: Identification of novel chronic lymphocytic leukemia subtypes using pathway mutation scores and machine learning

P. Taus[1*], N. Darzentas[1], K. Plevova[1,2]

[1] Central European Institute of Technology, Masaryk University, Brno, Czech Republic

[2] Department of Internal Medicine – Hematology and Oncology, University Hospital Brno and Faculty of Medicine, Masaryk University, Brno, Czech Republic

*petr.taus@ceitec.muni.cz

Introduction: Chronic lymphocytic leukemia (CLL) is the most common form of adult leukemia with variable clinical course underlain by striking genetic heterogeneity. CLL features a handful of putative driver genes and, more interestingly, a large number of non-recurrently mutated genes with elusive clinical implications. The aim of this study was to unravel the prognostic impact of pathway somatic mutation patterns in CLL.

Materials and Methods: We collected somatic mutation data of 506 CLL patients with available clinical data and 376 CLL patients without clinical data from the International Cancer Genome Consortium and from (Landau et al., 2015) respectively. We analyzed the dataset with clinical data and used the second dataset for the evaluation. We performed gene set enrichment analysis to identify affected biological pathways, calculated pathway mutation scores for each patient, performed consensus clustering and built a classification model. Then, we evaluated the difference in time to therapy (TTT) and overall survival (OS) between the identified CLL clusters. Finally, in order to interpret our results, we implemented network analysis on affected genes in recurrently mutated pathways.

Results: We identified five clusters differing in TTT ($p<0.0001$) in patient subgroup defined with mutated IGHV and five clusters differing in TTT ($p=0.005$) and OS ($p=0.038$) in patient subgroup defined with unmutated IGHV. For example, in the subgroup with mutated IGHV four of these clusters were characterized by distinct affected biological processes, namely cell adhesion, calcium-dependent signaling, synapse organization and ABC-family proteins mediated transport.

Conclusion: Among the CLL patients we identified distinct subgroups with non-recurrently mutated genes involved in a limited number of biological pathways. Our findings have far-reaching implications for CLL diagnostics.

T20: Application of industrial X-ray computed tomography for muscle-skeletal imaging at vertebrates

Markéta Tesařová[1*], Tomáš Zikmund[1], Glenda Comai[2], Eglantine Heude[2], Markéta Kaucká[3,4], Shahragim Tajbakhsh[2], Igor Adameyko[3,4], Jozef Kaiser[1]

[1] Central European Institute of Technology, Brno University of Technology, Brno, Czech Republic

[2] Institute Pasteur, Paris, France

[3] Department of Physiology and Pharmacology, Karolinska Institutet, Stockholm, Sweden

[4] Department of Molecular Neurosciences, Medical University Vienna, Vienna, Austria

*marketa.tesarova@ceitec.vutbr.cz

The development of muscle-skeletal structures at vertebrates is still not fully understood [1]. To understand this complex process, the advanced technical level is required. By using X-ray computed tomography (CT), non-destructive 3D imaging can be exploited with high resolution. The laboratory of X-ray computed micro and nanotomography at CEITEC BUT is predominantly focused on non-destructive testing in the industry and dimensional metrology. However, it has resulted that this approach can also be applied in various scientific fields including biology [2-5]. Modern developmental biology requires a comprehensive approach to compare shapes, volumes and sizes. In this work, we present 3D *ex-vivo* imaging conducted on mouse embryos and salamanders in order to explain the outgrowth and regeneration of skeletal and non-skeletal tissues. This project aims to build a bridge between material and life sciences in the scope of imaging and 3D characterisation of biological tissues.

Acknowledgement: This research was carried out under the project CEITEC VUT-J-19-5764. M.T. was financially supported by the Brno City Municipality as a Brno Ph.D. Talent Scholarship Holder.

[1] ADAMEYKO I. & FRIED K. Front. Physiol. 7, 49 (2016).
[2] KAUCKÁ M. et al. eLife. 7 e34465 (2018).
[3] HEUDE E. et al. eLife. 7 e40179 (2018).
[4] KAUCKÁ M. et al. Sci. Adv. 8 e1600060 (2016).
[5] TESAŘOVÁ M. et al. Sci Rep. 8, 14145 (2018).

P51: Comprehensive splice-site analysis of marine Diplonemids using comparative genomics approach

Prasoon Kumar Thakur [1*], Lukeš Julius[2] , David Stanek[1]

[1] Institute of molecular genetics, Prague, Czechia

[2] Institute of Parasitology, Biology Centre, Czech Academy of Sciences,Budejovice, 37005, Czechia

*prasoont@img.cas.cz

RNA splicing plays a critical role in regulating gene expression and transcriptome diversity in a variety of eukaryotes. Recent genetic 'barcoding' and single-cell genomics studies by Tara oceans expeditions have revealed that marine Diplonema are amongst the most abundant of marine species. Surprisingly, they have unusual splice site and lack canonical intron (GU-AG) which suggests that marine Diplonema could have evolved an alternative mechanism of intron removal. This implies that they can be an excellent model for the intron evolutionary study. In the present study, we have obtained sequenced genome and transcriptome of several marine Diplonema through our collaborators from the Biological center of the Czech Academy of Sciences in Ceske Budejovice. In this project, we carried out comprehensive splice-site analysis of these species. This project may extend our understanding about genomes and transcriptomes of these recently discovered Diplonema and also has the potential to shed a light on evolutionary and functional aspects of splicing.

P52: Identification of blood plasma microRNA by Next-generation sequencing: a comparative methodical study

Karolína Trachtová[1*], Táňa Macháčková[1], Ondřej Slabý[1,2*]

[1] Central European Institute of Technology, Masaryk University, Brno, CZ

[2] Department of Comprehensive Cancer Care, Masaryk Memorial Cancer Institute, Faculty of Medicine, Masaryk University, Brno, CZ

*trachtova@mail.muni.cz

Recently, microRNAs (miRNAs) circulating in body fluids such as plasma have emerged as potential biomarkers for various types of cancer. Next-generation sequencing is a cost-effective and sensitive approach for miRNA profiling and several library preparation kits are available that declare to work with as little as 1ng of input material. However, the impact of library preparation on sequencing efficacy or technical reproducibility is still insufficiently described, making miRNA detection from biofluids an intricate task.

Here, we examined the performance of two commercially available small RNA sequencing kits (QIAseq miRNA Library Kit (Qiagen), CleanTaq Small RNA Library Prep Kit (Trilink)) on 32 plasma samples from patients with rectal carcinoma. RNA was isolated using the miRNeasy Serum/Plasma Kit (Qiagen).

We focused on accessing the sensitivity, specificity, and precision of selected library preparation methods on miRNA quantification for clinical purposes. QIAseq and Trilink identified varying number of miRNAs (240-413 and 128-325 with >10 CPM, respectively), which reflects the differences in sensitivity and library complexity. Although QIAseq had in average better mapping rates, both kits performed highly ununiformly. Examining technical duplicates, QIAseq showed better reproducibility considering a number of detected miRNAs and composition of top 20 abundant miRNAs. Altogether, our findings suggest that Trilink libraries have a certain technique-specific bias and that miRNA quantification results from plasma sequencing may differ substantially between different library preparation methods.

Acknowledgement: This work was supported by grants of the Czech Ministry of Health nr. 16-31765A, 16-31314A, NV18-03-00554.

T21: IncI1 ESBL-producing plasmids from *Escherichia coli* obtained from patients are closely related to plasmids from *E. coli* of animal origin

Adam Valček[1,2,3*], Louise Roer[3], Søren Overballe-Petersen[3], Frank Hansen[3], Valeria Bortolaia[4], Pimlapas Leekitcharoenphon[4], Helle B. Korsgaard[5], Anne Mette Seyfarth[6], Rene S. Hendriksen[4], Henrik Hasman[3], Anette M. Hammerum[3], Monika Dolejská[1,2]

[1] Department of Biology and Wildlife Diseases, Faculty of Veterinary Hygiene, University of Veterinary and Pharmaceutical Sciences Brno, Brno, Czech Republic

[2] CEITEC VFU, University of Veterinary and Pharmaceutical Sciences Brno, Brno, Czech Republic

[3] Department of Bacteria, Parasites and Fungi, Statens Serum Institut, Copenhagen, Denmark

[4] Research Group for Genomic Epidemiology, National Food Institute, Technical University of Denmark, Kongens Lyngby, Denmark

[5] Division for Risk Assessment and Nutrition, National Food Institute, Technical University of Denmark, Kongens Lyngby, Denmark

[6] Danish Veterinary and Food Administration, Laboratories Division, Ringsted, Denmark

*valceka@vfu.cz

Twelve *E. coli* isolates sharing identical ESBL genes and pMLST were sequenced on Illumina and MinION platforms. The IncI1/ST3 plasmids were obtained from ten *E. coli* isolates (two from patients with bloodstream infections, six from food and two from animals). The IncI1/ST7 plasmids originated from *E. coli* isolates from a patient with bloodstream infection and from a pig. Sequences of IncI1/ST3 and IncI1/ST7 plasmids harbouring $bla_{\text{CTX-M-1}}$ retrieved from GenBank were used for comparison within the respective group. The ten IncI1/ST3 and two IncI1/ST7 plasmids carrying $bla_{\text{CTX-M-1}}$ were highly similar in structure and organization with only minor rearrangements and differences in the variable region. The high level of similarity was also observed in plasmids from *E. coli* of animal origin from Australia, Switzerland, the Netherlands and France. This study revealed high level of similarity in organization, structure and accessory regions of IncI1/ST3 and IncI1/ST7 plasmids, respectively. These findings suggest broad dissemination of a very successful $bla_{\text{CTX-M-1}}$-carrying plasmid lineages among *E. coli* of both human and animal origin.

P53: Examining factors mediating oligo uridylation and degradation of Eukaryotic aberrant RNAs

Nandan Varadarajan[1]* Stepanka Vanacova[1]

[1] CEITEC- Central European Institute of Technology, Masaryk University, Kamenice 5, 625 00, Brno, Czech Republic

*nandan@mail.muni.cz

The 3`-end RNA uridylation has pivotal role in regulating the global gene expression in Eukaryotes. Terminal uridyltransferase catalyzes the additions of oligo uridine (U) addition to the precursors of different species of RNAs entering TUT-DIS3L2 pathway. DIS3L2 has a diverse RNA species substrate. Our lab identified DIS3L2 RNA substrates using CLIP-seq. TUT-DIS3L2 degradation pathway is not very clearly understood. To identify the co factors/ RNA binding proteins which might be involved in this pathway, we have used proteomics-based pull down approach using RNA as a bait to map and characterize the interactome of TUT-DIS3L2 pathway factors. This RNA bait was chosen based on candidates having large number of reads from our CLIP-seq data. A complimentary biotinylated oligo to the bait was used to perform the experiments. This will help us to identify proteins which are involved in degrading the RNA species identified by DIS3L2 CLIP. Some preliminary proteins candidates have been identified which will be functionally validated.

P54: Searching for transposable elements in hematological malignancies.

Anastasiya Volakhava[1]*, Karla Plevova[1,2], Sarka Pavlova[1,2], Karol Pal[1], Nikos Darzentas[1], Ilgar Mamedov[1], Sarka Pospisilova[1,2]

[1] CEITEC – Masaryk University, Brno, Czech Republic

[2] University Hospital Brno, Brno, Czech Republic

*anastasiya.volakhava@mail.muni.cz

Transposable elements, or transposons, are DNA units present in eukaryotic organisms in a broad diversity of their structures. They have played an important role in evolution of many genomes. In the human genome, the vast majority of transposons is represented by retroelements (REs) that can integrate new copies through RNA-mediated mechanisms. The long interspersed nucleic elements (LINE-1 or L1) utilize a "copy-and-paste" mechanism to retrotranspose copies into new genomic loci. Active L1 retrotransposons also drive retrotransposition of other mobile DNAs, namely, Alu, short interspersed elements (SINEs), and SVA transposons.

Recent findings imply that genomic instability of cancer is associated with transposon reactivation.

The main goal of our research is to explore RE activity in different types of hematological malignancies. To identify tumor-specific RE insertions, we adopted a protocol based on high-throughput sequencing of amplicons containing a part of AluYa5, Alu-Ya8 or L1-HS insertions, and their adjacent genomic regions. By using unique molecular identifiers, we aim to estimate the percentage of cancer cells bearing each particular insertion. We performed a pilot experiment on 42 tumor-normal sample pairs from patients with chronic lymphocytic leukemia, acute lymphoblastic leukemia, and myelodysplastic syndrome. The libraries were sequenced on Illumina NextSeq and obtained sequences are currently subjected to an in-house bioinformatics pipeline for identification of somatic RE insertions.

Acknowledgement: Supported by GACR 19-11299S.

P55: Harnessing the Power of iPSC to unravel the role of splicing factors in the development of retinitis pigmentosa

Felix Zimmann[1*], Zuzana Cvačková[1], David Staněk[1]

[1] Institute of Molecular Genetics of the ASCR, v. v. i., Prague, Czech Republic
*felix.zimmann@img.cas.cz

Retinitis pigmentosa (RP) is a hereditary disease characterized by the progressive degeneration of retina cells eventually leading to total blindness of the patients. Currently more than 90 genes are known to be involved in the pathogenesis of RP. The majority of these genes is expressed in the retina and associated with retinal function. Surprisingly, the second largest group of mutations causing RP affects proteins involved in splicing. However, it remains elusive why mutations affecting RNA splicing, a ubiquitous and essential process for almost every cell, give rise to such a tissue-specific phenotype. To unravel the pathogenic mechanism underlying RP we plan to establish a disease-relevant model. Therefore, we want to create RP-associated mutations in splicing factors through CRISPR/Cas9 genome-editing in human induced pluripotent stem cells (hiPSC)-derived retina cells such as retinal pigment epithelium (RPE) or photoreceptor cells. Here, we present and compare preliminary results of differentiation approaches of hiPSC to a pro-retinal phenotype. We will then analyze splicing efficiency, alternative splicing and alterations in interactions between RNA binding proteins and RNA using RNA-seq and iCLIP methods. The knowledge gained from our analysis will provide new insights into how splicing factor mutations are involved in the pathology of RP.

Physical and Material Science

Students' Abstracts

P56: Transition to turbulence in multi-phase flows

Nishchal Agrawal[1], George H. Choueiri[1], Bjorn Hof[1]

[1] Institute of Science and Technology, Klosterneuburg, Austria

*nishchal.agrawal@ist.ac.at

Many natural and technological important flows involves complex interaction between a carrier fluid phase and a dispersed solid phase. Even though such flows are commonly occurring, little is known about the effect of the presence of a solid phase on the fluid phase, especially when it comes to laminar to turbulent transition. For the transition process, the dependence of critical Reynolds number on the size and concentration of the particles (the solid phase) is known to a certain extent, however the nature of transition is poorly understood. In this study, we experimentally investigated the effect of solid inertial particles on the nature of laminar-turbulence transition in a pipe flow. We used spherical, density matched and mono-dispersed particles. We found out that the nature of transition depends heavily on the concentration of particles. At low particle concentrations, transition occur abruptly via intermittent localized structures called 'puffs', similar to that for a single phase flow i.e., a sub-critical transition, and the critical Reynolds number above which turbulence can be sustained decreases with particle concentration. At higher concentrations, the sub-critical transition is first delayed and eventually completely suppressed and at the same time a different kind of instability appears in the flow (see figure 1). This instability leads to turbulent fluctuations that are not associated with intermittent turbulent structures, rather sets in globally throughout the pipe. This type of instability has never been associated before with particle laden flows. This suggests a mechanism of transition significantly different from that for a single phase Newtonian flow. We infer that at high particle concentration the sub-critical transition is replaced by a super-critical transition.

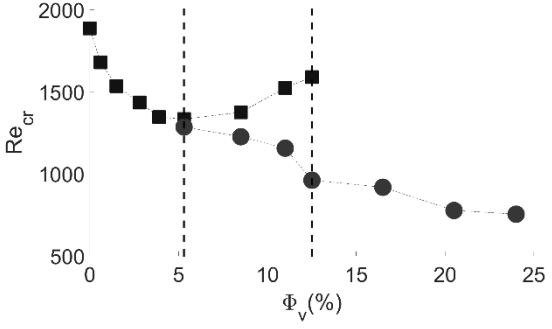


Figure 1 Transition scenario as a function of particle concentration. sub-critical transition (blue squares), supercritical transition (red circles).

P57: Interaction of Stacking Faults in Zincblende GaN Stabilized by Epitaxial Strain

Zdeněk Antoš[1,2*], Petr Vacek[1,2], Roman Gröger[2]

[1] CEITEC BUT, Brno, Czech Republic

[2] Institute of Physics of Materials & CEITEC IPM, Brno, Czech Republic

*zdenek.antos@ceitec.vutbr.cz

III-nitrides have great potential in optoelectronic devices such as LEDs, lasers, in water purification systems, and in high power microelectronics. A comparable stability of GaN in the wurtzite and sphalerite (zincblende) structures opens the possibility to stabilizing the metastable zincblende structure, which may solve the green gap problem in III-nitrides. Controlling stacking faults (SFs) in zincblende GaN is critical to ensure the efficiency of these devices. Similarly as in the diamond crystal structure, it contains two families of {111} planes on which planar stacking faults can be created - glide and shuffle set. However, the SF can only be stable when created in the glide set, where it facilitates a local transformation into the stable wurtzite structure. No stable stacking faults are present in the shuffle set. In this work, we have first utilized the Tersoff potential for GaN to map the energies of generalized stacking faults in the (111) plane, where all atoms were relaxed in the direction perpendicular to this plane. The perfect zincblende structure and the single-layer intrinsic stacking fault (ISF) corresponding to the 1/6[-211] fault vector have the same energy but these states are separated by the energy barrier. Because all {111} planes are identical by crystal symmetry, we have further investigated the interactions between two non-coplanar stacking faults. Starting with a relaxed 1/6[-211] intrinsic stacking fault on the {111} plane, we have introduced step-by-step all possible planar stacking faults on the (1-11) plane. Due to the presence of the former fault, only a half of this latter fault was made on the glide set, but the second half was in the shuffle set. Similarly, we have calculated also the γ surface, where the cut was made in the shuffle set across the entire width of the block. No minima were observed as in the case of a single stacking fault.

V03: Theoretical Investigations of Functional Waveguide Materials for MIR Sensors

Valeria Butera[1*], Hermann Detz[2]

[1] CEITEC Brno University of Technology, Brno, Czech Republic
*valeria.butera@ceitec.vutbr.cz

Mid-infrared (MIR) based, monolithically integrated optical sensors are a recent and rapidly emerging research field. Combining bi-functional quantum cascade lasers and detectors with optical interconnects allows to transform formerly lab-sized spectroscopic setups into compact optoelectronic devices. Our research project supports the development of the next sensor generation by focusing on the adsorption and related reactions of analyte molecules on the waveguide surface in the interaction zone. The experimental counterpart will realize plasmonic, dielectric and hybrid waveguide structures, which allow the realization of highly integrated MIR sensors. Cluster-based density functional theory will be applied to determine the chemical bonding behavior including possible charge transfer and resulting shifts in the absorption spectra of analyte substances. Our studies will be also complemented by periodic boundary condition (PBC) calculations that will allow us to consider larger surfaces and bulk structures. Findings obtained from the surface chemistry model will enable directed optimization of the sensing surface e.g. through engineered roughness or by exploiting field enhancement due to plasmonic near-field antennas. All components will be combined into advanced, fully-integrated prototype sensors, which open new opportunities for further application-oriented research.

T22: Slip Activity in High-purity Chromium Single Crystals Compressed at 77 K

Jakub Holzer[1,2*], Zdeněk Chlup[1], Tereza Kuběnová[1,2], Roman Gröger[1,2]

[1] Institute of Physics of Materials and CEITEC IPM, Czech Academy of Sciences, Žižkova 22, 616 00 Brno, Czech Republic

[2] Central European Institute of Technology (CEITEC), Brno University of Technology, Purkyňova 123, 612 00 Brno, Czech Republic

*holzer@ipm.cz

The plastic deformation of body-centered cubic (bcc) metals at low homological temperatures is controlled by the mobility of $1/2\langle 111\rangle$ screw dislocations. This is strongly affected by non-planar core spreading into three {110} planes in the zone of the Burgers vector [1], which leads generally to the breakdown of the Schmid law. In materials with internal magnetic order, such as α-Fe and Cr, the dislocation glide is further affected by the local state of magnetic order. Recently, Mrovec et al. [2] have shown that the ferromagnetic order in α-Fe can change at $1/2\langle 111\rangle$ screw dislocations, but similar studies on antiferromagnetic Cr are not yet available. Moreover, very little is known about the fundamental mechanisms governing the plastic deformation of Cr below the spin-flip temperature of 123 K, where magnetic spins align into $\langle 100\rangle$ longitudinal spin density waves [3]. The purpose of this work is to investigate the low-temperature behavior of high-purity Cr single crystals deformed under uniaxial compression in three directions across the stereographic triangle. Observation of plasticity at low homological temperatures was compared with the predictions of slip activity studied atomistically using the Bond Order Potential for chromium.

[1] V. Vitek: Philos. Mag. 84 (2004) 415–428.

[2] M. Mrovec, D. Nguyen-Manh, C. Elsässer, P. Gumbsch. Phys. Rev. Lett. 106 (2011) 246402.

[3] S. B. Palmer and E. W. Lee. Philos. Mag. 24 (1971) 311–318.

P58: Babinet's principle for solid and hollow plasmonic antennas

Michal Horák[1*], Vlastimil Křápek[1], Martin Hrtoň[1], Andrea Konečná[2], Filip Ligmajer[1], Michael Stöger-Pollach[3], Tomáš Šikola[1]

[1] CEITEC Brno University of Technology, Brno, Czech Republic
[2] Materials Physics Center CSIC-UPV/EHU, San Sebastian, Spain
[3] USTEM TU Wien, Vienna, Austria
*michal.horak2@ceitec.vutbr.cz

We present an experimental study of Babinet's principle of complementarity in plasmonics which relates the properties of solid plasmonic antennas and complementary apertures of the same size and shape. It allows, for example, studying the magnetic near field by measuring the electric near field by EELS in the complementary structure. We focused on elementary disc-shaped plasmonic antennas [1] and on plasmonic antennas with electric and magnetic hot spots based on Babinet's principle [2].

A set of gold plasmonic antennas was fabricated by focused ion beam lithography as it is a suitable technique for fabrication of small series of plasmonic antennas allowing to fabricate easily both particle and aperture antennas on the same sample [3]. We found differences originating both from the limited theoretical validity of the Babinet's principle and from different operational conditions for elementary disc-shaped plasmonic antennas [1]. Further, we show that combined EELS imaging of a plasmonic antenna and its Babinet-complementary counterpart allows to reconstruct the distribution of both electric and magnetic out of plane near fields of localized surface plasmon resonances supported by the antenna as well as charge and current antinodes of related charge oscillations [2].

Acknowledgement: Supported by Czech Science Foundation (17-25799S), EU Horizon 2020 program (SINNCE, 810626) MEYS CR (CEITEC Nano RI, LM2015041, 2016-2019; CEITEC 2020, LQ1601), and Brno University of Technology (FSI/STI-J-17-4623, FSI/STI-J-18-5225, and CEITEC VUT-J-19-5945).

[1] M. Horák et al, Sci. Rep. 9 (2019) p. 4004.
[2] V. Křápek et al, in preparation.
[3] M. Horák et al, Sci. Rep. 8 (2018) p. 9640.

P59: Magnetic phase transition of FeRh/MnRh superstructures

M. Horký[1,2,3]*, S. K. K. Patel[3], J. A. Arregi[1], M. Staňo[1], R. Medapalli[3], V. Uhlíř[1,2] and E. E. Fullerton[3]

[1] Central European Institute of Technology, Brno University of Technology, Purkyňova 123, 612 00 Brno, Czech Republic

[2] Institute of Physical Engineering, Brno University of Technology, Technická 2, 616 69 Brno, Czech Republic

[3] Center for Memory and Recording Research, University of California, San Diego, La Jolla, California 92093-0401, USA

*michal.horky@ceitec.vutbr.cz

Magnetic materials featuring first-order phase transitions between multiple order parameters are outstanding candidates for exploiting new functionalities and emergent phenomena on the nanoscale. A prime example is represented by a class of binary alloys such as MnRh and FeRh. Such compounds undergo the magnetic phase transition from a low temperature antiferromagnetic phase (AF) to a high temperature ferromagnetic phase (FM) at 275 K [1] and 360 K [2] upon heating, respectively. We focus on the epitaxially-ordered superstructure comprising thin film multilayers of FeRh and MnRh prepared by magnetron sputtering. We study the control of magnetic properties of metamagnetic system based on variable thickness of individual layers. Combining of X-ray diffractometry (XRD), vibrating sample magnetometry (VSM) and electrical transport measurements we investigate a mutual interaction between individual layers. Then we detect changes of magnetic properties through the coupled order parameters: crystalline structure, magnetization and electrical resistivity.

[1] A. Chaturvedi and T. Suzuki, AIP Advances. 2016, 6(5).

[2] J. S. Kouvel and C. C. Hartelius, J. Appl. Phys. 1962, 33(3).

P60: Atomic Layer Deposition of Titanium Dioxide on Multi-Walled Carbon Nanotubes for Ammonia Gas Sensing

Preeti Kaushik[1,2], Marek Eliáš[3], Jan Michalička[3], Dirk Hegemann[4], Zdeněk Pytlíček[3], David Nečas[1], Lenka Zajíčková[1,2*]

[1] RG Plasma Technologies, Central European Institute of Technology, Masaryk University, Kamenice 5, Brno 625 00, Czech Republic

[2] Department of Physical Electronics, Faculty of Science, Masaryk University, Kotlářská 2, Brno 611 37, Czech Republic

[3] Central European Institute of Technology, Brno University of Technology, Purkyňova 123, Brno 61200, Czech Republic

[4] Empa, Swiss Federal Laboratories for Materials Science and Technology, Lerchenfeldstrasse 5, St. Gallen 9014, Switzerland

*lenkaz@physics.muni.cz

Carbon nanotube (CNTs)-metal oxide semiconductor (MOS) hybrid nanostructures can provide a new pathway for room temperature chemiresistive gas sensors due to combined properties of both the materials and the creation of heterojunctions between CNTs and MOS. Multi-walled carbon nanotubes (MWCNTs) were grown on Si substrates coated with SiO_2 layer by catalytic chemical vapor deposition (CCVD) and coated by TiO_2 films of different nominal thicknesses, 5, 10 and 20nm, using atomic layer deposition (ALD). The CNT surface is quite inert and therefore, a modification of MWCNTs by carboxyl plasma polymer (PP) film was applied prior to ALD of TiO_2. The carboxyl PPs improved film uniformity, even though the thinnest TiO_2 film still formed an island-like structure. Raman spectroscopy revealed that coating by TiO_2 or carboxyl PP increased structural disorder of sp_2 carbon in the MWCNTs and the thinnest TiO_2 coatings induced the lowest disorder. The thinnest coatings also resulted in the highest sensor response to NH_3. Nevertheless, for all thicknesses the sensors coated with carboxyl PP/TiO_2 double layer showed higher response as compared to the pristine CNTs and those without the carboxyl PP film.

P61: Indirect B-N Interactions in Boronic Acid-Aminoferrocene System: Point of View of Electrochemistry

Martin Konhefr[1*], Karel Lacina[2], Monika Skrutková Langmajerová[1], Zdeněk Glatz[1], Petr Skládal[1,2], Ctibor Mazal[3]

[1] Department of Biochemistry, Faculty of Science, Masaryk University, Brno, Czech Rep.
[2] CEITEC, Masaryk University, Brno, Czech Rep.
[3] Department of Chemistry, Faculty of Science, Masaryk University, Brno, Czech Rep.
*379848@mail.muni.cz

We have broadened the current knowledge about nature of the B-N interactions of iminoboronates mostly in protic solvents using electrochemical methods. This approach is novel in the probing of these intramolecular interactions in imines made from aminoferrocene.

The qualitative conditions and prerequisites for boronate-imine interaction were investigated within electroactive ((ferrocenylimino)methyl)-phenylboronic acids [1]. The role of this interaction throughout the reaction "primary amine-hemiaminal-imine" was assessed. The behaviour of all three ((ferrocenylimino)methyl)-phenylboronic acids is influenced by the character of solvent, the oxidation state of the ferrocenyl moiety and the space separation of the boronic acid moiety from nitrogen atom.

Exceptional redox behaviour of *ortho*-((ferrocenylimino)-methyl)-phenylboronic acid, in comparison with *meta* and *para* isomers has been observed [2]. The interaction between the boron and nitrogen atoms within the structure of the *ortho* isomer is indirectly mediated by a molecule of methanol. Furthermore, another molecule of the primary alcohol can add to imine bond depending on the redox state of the ferrocenyl unit. This *in situ* formation of a hemiaminal ether is facilitated/triggered by oxidation of the ferrocene moiety only in cooperation with the proximate *ortho*-boronic acid moiety. The transition between these two states – the imine and the hemiaminal forms – are thus controllable electrochemically.

The obtained results also provide the possibility to realize molecular switching events and to design improved molecular devices.

[1] Konhefr, M. *et al.*; *Monatshefte für Chemie*, 2017, 148(11), p. 1953
[2] Konhefr, M. *et al.*; *Chemistry Select*, 2018, 3(33), p. 9641

T23: Synthesis and Characterization of Magnetic Iron Oxide Nanoparticles for Bio-applications

Tereza Kuběnová[1,3*], Vít Vykoukal[2], Naděžda Pizúrová[3] and Roman Gröger[3]

[1] Central European Institute of Technology, CEITEC BUT, Brno University of Technology, Purkyňova 123, 612 00 Brno, Czech Republic

[2] Central European Institute of Technology, CEITEC MU, Masaryk University, Kamenice 5, 625 00 Brno, Czech Republic

[3] Institute of Physics of Materials, Academy of Sciences of the Czech Republic, v.v.i., Žižkova 22, 616 62 Brno, Czech Republic

*tkubenova@ipm.cz

Magnetic nanoparticles (NPs) have a potential in bio-applications such as drug delivery or magnetic hyperthermia (MH) for cancer treatment. It is generally known that cancer cells are more sensitive to elevated temperatures than healthy cells. Cancer treatment by hyperthermia relies on that fact. Application of the AC magnetic field with frequencies between tens of kHz to units of MHz causes dissipation of energy from the nanoparticle into the surrounding tissue. This causes a local heating to 43-46°C followed by irreversible structural changes of tumor cells and requires complex optimization of the shape, size and surface coating of these particles in a range of viscous environments mimicking those of a human body.

Here we report synthesis and characterization of NPs of iron oxide. These NPs were prepared by precipitation method. The impact of reaction conditions (temperature, reaction time and type of precursors) on the properties of resulting NPs (size and structure) was investigated. The size, size distribution, and morphology of NPs were studied by dynamic light scattering (DLS), transmission electron microscopy (TEM) and ultraviolet-visible spectrometry (UV-Vis). The composition of NPs was characterised by powder X-ray diffraction (XRD) and Mössbauer spectroscopy. Also, for the reported NPs the hysteresis loops in viscous environment were measured at frequencies relevant to biological applications.

Acknowledgement: This work was supported by the CEITEC Specific research program (Project No. CEITEC VUT J-19-5904).

P62: A hole spin qubit in a Ge hut-wire double quantum dot

J. Kukučka[1*], H. Watzinger[1], L. Vukušić[1] and G. Katsaros[1]

[1] Institute of Science and Technology Austria, Am Campus 1, 3400 Klosterneuburg, Austria
*josip.kukucka@ist.ac.at

Constant transistor miniaturization pushed classical nano-electronics to the limit settled by detrimental quantum effects. A *quantum computer* which would, on the contrary, take advantage of such effects, could offer a different pathway to satisfy growing information needs. Its constitutional unit is a *qubit* which can be implemented in different physical systems. However, the challenge is to find a system which will provide fast manipulation, long coherence time, fast readout and allow scalability, qualities needed to perform quantum algorithms.
The possibility for a high-density qubit packing and interfacing with standard control electronics makes *spin qubits*, hosted in semiconductor quantum dots [1], a promising platform. In the past few years the interest in hole spins has been continuously raising due to their intrinsically large spin-orbit coupling, which can lead to fast and fully electrically controlled spin qubits. Indeed in 2016, the first fully electrically controlled *hole spin qubit* was demonstrated in natural Si [2].
Here we will present a hole spin qubit created in a *Ge hut wire* [3] double quantum dot [4]. Rabi-frequencies of *140 MHz* were reached and dephasing times T_2^* exceeding *130 ns* were measured. More complex measurement protocols were, however, not possible due to the limitations imposed by the current readout. A solution to this problem can come from dispersive readout [5]. First results from gate reflectometry measurements of Ge hut-wire double dots will be presented.

[1] D. Loss and D. P. DiVincenzo, Phys. Rev. A 57, 120 (1998).
[2] R. Maurand et al, Nature Communications 7, 13575 (2016).
[3] J. J. Zhang et al, Phys. Rev. Lett. 109, 085502 (2012).
[4] H. Watzinger, J. Kukučka et al, Nature Communications 9, 3902 (2018).
[5] I. Ahmed et al, Phys. Rev. A 10, 014018 (2018).

P63: Thermally- and electron-induced self-assembly of biphenyl-4,4′-dicarboxilyc acid on Ag(111)

Anton Makoveev[1*], Pavel Procházka[1,2], Lukáš Kormoš[1], Jan Čechal[1,2]

[1] CEITEC BUT, Brno, Czech Republic

[2] IPE BUT, Brno, Czech Republic

*Anton.Makoveev@ceitec.vutbr.cz

Self-assembly of organic and metal-organic species is an exciting field using principles of supramolecular chemistry to construct complex molecular objects [1]. Recently, this approach has been implemented at surfaces [2], where numerous two-dimensional structures with various functional properties can be created. At the moment, there is copious information on resulting thermodynamically stable molecular architectures on diverse substrates, but knowledge of how intermediate kinetically trapped states form and how in general, self-assembly processes develop in time is still scarce. Even less is known about an impact of external stimuli other than thermal heating (e.g. low-energy electrons, photons) on self-assembly of surface-confined molecular networks. The use of modern low-energy electron microscopy (LEEM) set-ups may shed some light on those yet unanswered questions. In this work we present an investigation of 4,4′-biphenyldicarboxylic acid (BDA) self-assembly on an Ag(111) single crystal. Using LEEM we aim to reveal kinetics of how transitional and final BDA structures form at different temperatures and electron beam energies. In addition, an influence of each external stimulus (thermal annealing and electron-beam irradiation) on the kinetics and structural transformations is discussed. Our preliminary results demonstrate significantly different self-assembly patterns when the process is dominated by one of the stimuli, which raises intriguing questions regarding the mechanism of low-energy electrons interaction with the on-surface molecular networks.

[1] Whitesides, G. M., Mathias, J. P. and Seto, C. T. Science, 1991, 254(5036), 1312-1319;

[2] Kühnle, A. Current Opinion in Colloid & Interface Science, 2009, 14(2), 157-168;

T24: Two-dimensional GaN grown on Si(111)7x7 with assisted hyperthermal nitrogen N_2^+ ions at low temperature

J. Manis[1]*, J. Mach[1,2], V. Calkovsky[2], D. Nezval[2], M. Bartosik[1,2], M. Konecny[1,2], L. Kachtik[1], T. Samoril[2] and T. Sikola[1,2]

[1] Central European Institute of Technology, Brno University of Technology, Czech Republic
[2] Institute of Physical Engineering, Brno University of Technology, Czech Republic
*jaroslav.manis@ceitec.vutbr.cz

As the characteristic dimensions of modern top-down devices are getting smaller, such devices reach their operational limits given by quantum mechanics. In addition, functional structures at nanoscale generally have completely different electrical, optical and mechanical properties by comparison with their microscale counterparts. Therefore, there is a great effort to fabricate bottom-up nanostructures of defined properties and integrate them into functional devices. Two-dimensional (2D) materials appear as one of the best solutions to meet these challenges. The representatives of III-V semiconductors, such as aluminium nitride (AlN) and gallium nitride (GaN), are great candidates for UV and high-power optoelectronic applications. While both 2D GaN and AlN have been fabricated by migration enhanced encapsulation growth, only GaN has been fabricated as a 2D material with capabilities of its transferring to other substrates and creating functional devices. We propose a new way of fabrication of 2D GaN on the Si(111)7x7 surface using post-nitridation of Ga droplets by hyperthermal (E < 50eV) nitrogen ions at low substrate temperatures (T < 220°C). Such an approach brings well defined conditions of the growth of high purity GaN nanostructures. A well-defined interface between the GaN nanostructure and the silicon substrate together with nanostructure elemental composition was observed by TEM. In addition, SEM, XPS, AFM, Auger microanalysis and measurement of photoluminescence response help to elucidate unique characteristics of the fabricated nanostructures.

T25: Development of the FTIR spectroscopy in high magnetic fields

Jana Midlíková[1*], Antonín Sojka[1], Adam Dubroka[2], Petr Neugebauer[1]

[1] CEITEC BUT (Brno University of Technology), Brno, Czech Republic

[2] CEITEC MUNI (Masaryk University), Brno, Czech Republic

*jana.midlikova@ceitec.vutbr.cz

With dimensions close to a nanometer and the ability to store one bit of information, molecules called Single-Molecule Magnets (SMMs) give a possibility to move the data storage technology forward. For the investigation of SMMs, spectroscopic techniques, such as Electron Paramagnetic Resonance (EPR), are essential due to their ability to probe molecular and electronic properties directly. However, because of systems with large zero-field splitting, Fourier Transform Infrared (FTIR) spectroscopy in high magnetic field is needed in order to access fundamental transitions in SMMs. We propose FTIR spectroscopy in high magnetic fields as a very important tool in the characterization of SMMs. This method allows studying EPR of SMMs with very large zero-field splitting, mainly based on transition metal complexes [1] or lanthanides [2] that cannot be studied by common EPR systems since they do not provide experimental access to the magnetic resonance transitions. It also presents an ideal experimental technique that can probe band structure and elucidate electronic properties of novel 2D materials, such as graphene [3]. The method of FTIR spectroscopy in high magnetic fields will be mediated by compact FTIR magneto-optical setup built at CEITEC, which is basically FTIR spectrometer connected to 16 Tesla cryogen-free superconductive magnet.

[1] Rechkemmer, Y., et al. A four-coordinate cobalt(II) single-ion magnet with coercivity and a very high energy barrier. Nature communications, 2016.

[2] LIDDLE, S. T. and VAN SLAGEREN, J. Improving f-element single molecule magnets. Chemical Society Reviews, 2015.

[3] ORLITA, M., et al. Approaching the Dirac Point in High- Mobility Multilayer Epitaxial Graphene. Physical Review Letters, 2008.

T26: Plasma Polymerization on Non-planar and Porous Substrates: Sticking Probability and Deposition Penetration Depth

Miroslav Michlíček[1,2*], Lenka Zajíčková[1,2], Lucie Bláhová[1]

[1] Plasma Technologies, CEITEC, Masaryk University, Brno, Czech Republic

[2] DPE, Faculty of Science, Masaryk University, Brno, Czech Republic

*michlicekm@mail.muni.cz

In this contribution, we highlight some aspects which need to be considered for successful optimization of a low-pressure plasma polymer deposition process on non-planar substrates such as biological tissue cultivation wells, porous scaffold, mats, etc. It is clearly shown on example of cyclopropylamine/argon mixture that geometry different from the simple planar (e.g. piece of silicon placed on the electrode) changes the film deposition rate and chemistry through altered ion bombardment, gas flow pattern and diffusion geometry and boundary conditions. We report unexpectedly high penetration of deposition into porous materials [1,2]. We conclude that the effective sticking probability of film forming species must be, therefore, relatively low to allow for multiple collisions with surface in the Knudsen regime. Finally, we estimate the effective sticking probability by evaluating measurements of step coverage in a microtrench. [3]

[1] E. Kedroňová, Plasma Process. Polym., 12, 1231 (2015).

[2] M. Michlíček, Appl. Surf. Sci., 471, 835 (2019).

[3] H. Komiyama, Chem. Eng. Sci., 54, 1941, (1999).

T27: Enhancement of polypropylene–epoxy glue adhesion by thin plasma polymer films deposited in gliding arc discharge with cross flow gas inlets

Kateřina Polášková[1,2*], Petr Jelínek[1,2], Filip Jeník[3], Zdenka Jeníková[3], Jiří Cerman[4], Lenka Zajíčková[1,2]

[1] CEITEC Masaryk University, Brno, Czech Republic
[2] Faculty of Science, Masaryk University, Brno, Czech Republic
[3] Faculty of Mechanical Engineering, ČVUT, Prague, Czech Republic
[4] Surface Treat a.s., České Budějovice, Czech Republic
*polaskova.katerina@mail.muni.cz

Polypropylene (PP) is a cheap, fully recyclable synthetic polymer with many applications ranging from the automobile industry to food packaging. However, due to its low free surface energy, 27 mJ m^{-2} and chemical inertness a surface modification is required before many of its applications. Nowadays, non-thermal atmospheric pressure plasma discharges are studied as one of the most promising technologies for a low-cost environmentally friendly modification of polymer surfaces. Compared to the plasma treatment (i.e. plasma activation of a polymer surface) deposition of thin plasma polymer films might offer a solution to one of its most pressing problem, its fast degradation.

In this work, n-hexane, cyclohexane, and hexamethyldisiloxane (HMDSO) plasma polymer films were deposited on PP strips by an industrial gliding arc discharge running in dry air. The injection of the vapor monomers was carried out utilizing cross flow gas inlets which geometry was designed with a help of gas dynamic simulations and further studied by fast camera measurements. The influence of the filamentary character of the discharge on the homogeneity of treatment was visualized by the Quicktest measurements. HMDSO plasma polymers had inorganic SiO_x character due to high fragmentation of the monomer molecule. Both n-hexane and cyclohexane films were highly oxidized, which was reflected by a significant increase of the free surface energies. Tensile strength measurements of PP determined the improvement of PP–epoxy–Al bonds with maximum tensile strength being 6.6 times higher than the initial value for untreated polypropylene.

P65: Polymer nanosphere-assembled surface for biosensing based on electrochemical impedance spectroscopy

Jakub Sopoušek[1*], Karel Lacina[1]

[1] Central European Institute of Technology, Masaryk University, Brno, Czech Republic
*423048@mail.muni.cz

Electrochemical impedance spectroscopy (EIS) emerges as the promising method for biosensing thanks to its timesaving and label-free detection capabilities together with the high sensitivity. But despite all the praise, EIS cannot differentiate various (bio)chemical processes as the measurement yields spectrum of surface behavior in a bulk. Thus, it is highly challenging to design a concept of reproducible and reliable impedimetric biosensing system that records only targeted analytical signal. We develop a sensitive surface that provides highly dominant output signal change upon interaction with analyte. The modification layer on the surface employs spherical polystyrene nanoparticles, homopolymer poly-L-lysine, and protein human serum albumin (HSA). The protein acts as an antigen with respect to the corresponding anti-HSA antibody – analyte in a liquid sample. The assembly of nanoparticles, coated by the proteins, forms nanopores which can be blocked by the protein-specific antibody. This effect results in radical changes of impedance as the response comes from differentiation between permeable and isolated state of the modification layer. Furthermore, the developed surface exhibits thin film interference whose effect we turned into the naked-eye control for the successful fabrication. Results of this approach can be applied for testing of blood sera to detect immunological response of a patient's pathologic state.

Acknowledgement: This research has been financially supported by the Ministry of Education, Youth and Sports of the Czech Republic under the project CEITEC 2020 (LQ1601).

P66: Synthesis and Characterization of Photoactive Anatase-Brookite TiO_2 Nanoparticles in presence of MCAA

L. K. Tinoco Navarro[1*], J. Michalička [1], J. Kaštyl[1], J. Cihlař[1,2], K. Částková[1,2], M. Veselý[2], P. Dzik[2]

[1] Central European Institute of Technology, Brno, Czech Republic
[2] Brno University of Technology, (FCH) Brno, Czech Republic
*Katherine.tinoco@ceitec.vut.br.cz

TiO_2 as catalyst still present some limitations regarding its photocatalytic activity. Three different crystal forms exist from it. Anatase, Rutile, and Brookite. However, reports from brookite phase are still scarce. The Anatase-Brookite Nanoparticles represents a great perspective in water quality splitting technologies at visible light. Significant progress has been made in research of TiO_2 nanoparticles based on modification of their crystal structure and particle size. The presence of brookite helps to retarded recombination of holes and accumulation of electrons in the conductive band leading to increasing the oxidation of organic substances and benefits the hydrogen production. So that, structuring a cooperative behavior between the anatase and brookite phases is an important characteristic of TiO_2 catalyst when is applied in "green" technologies. The synthesis of TiO_2 biphasic nanoparticles (BNPs) was performed by sol-gel Hydrolysis/condensation method using Titanium Isopropoxide (TTIP) as a precursor and Monochloracetic acid (MCAA) as a chelating solution. Different analytical methods were used for characterization of crystallography, microstructure and chemical composition of the synthetized TiO_2 BNPs powder. X-ray diffraction (XRD), Transmission Electron Microscopy (TEM), Scanning Electron Microscopy (SEM) revealed the presence of both phases with a content of Brookite between 10 – 30 %. The characterization demonstrate that the non-conventional synthesis under presence of MCCA as chelating solution is possible to obtain TiO_2 Anatase-Brookite BNPs. Finally, by UV photospectroscopy was proof the photoactivity of the BNPs.

P67: Multimode Fiber-Based Endoscope for High Resolution Fluorescence Imaging of Bulk Tissue

T. Tuckova[1], P. Jakl[1], M. Siler[1], J. Trägårdh[1], M. Hons[1], T. Pikalek[1], E. Drazanova[1], L. Kratka[1], S. Simpson[1], T. Tyc[1], H. Uhlirova[1], T. Cizmar[1]

[1] Institute of Scientific Instruments of the AS CR, v. v. i., Brno, Czech Republic
*tereza.chmelik@gmail.com

Imaging of bulk intact biological tissue is one of the main prerequisites to understanding physiological cellular processes. Limited light penetration due to scattering and absorption is one of the major obstacles when it comes to imaging deep in turbid tissues. Optical fibers present a means to deliver and collect light beyond the reach of light focused by microscope objectives with minimal tissue damage. This imaging method however generally suffers from low resolution and low imaging speed. We have built a multimode fiber-based scanning setup for imaging of fluorescently-labeled specimens with high resolution. We will review our latest fundamental and technological progression and present the imaging capability on fluorescently-labeled brain tissue.

P68: Correlation of Structure and EBIC Contrast from Threading Dislocations in AlN/Si films

Petr Vacek[1,2*], Petr Kostelník[3], Roman Gröger[2]

[1] Central European Institute of Technology (CEITEC), Brno University of Technology, Purkyňova 123, Brno 612 00, Czech Republic

[2] Institute of Physics of Materials & CEITEC IPM, Czech Academy of Sciences, Žižkova 22, 616 00 Brno, Czech Republic

[3] ON Semiconductor, 1. Máje 2230, 756 61 Rožnov pod Radhoštěm, Czech Republic

*Petr.Vacek@ceitec.vutbr.cz

Gallium nitride is an important material for optoelectronics and high electron mobility transistors. Epitaxial growth of wurtzite GaN is frequently made on AlN/Si substrates that contain a large density of threading dislocations induced by the mismatch of their lattice parameters and thermal expansion coefficients. We characterize the structural and electrical properties of surface and extended defects found in 220 nm {0001} AlN films grown epitaxially on {111} oriented Si substrate by metalorganic chemical vapor deposition (MOCVD). Three types of surface depressions are recognized by atomic force microscopy (AFM) that correspond to V-defects and their clusters and individual threading dislocations. Transmission electron microscopy studies prove that all V-defects are attached to threading screw or mixed dislocations. The electrical activity of the defects in the AlN film is assessed by measuring the electron beam induced current (EBIC) across a thin layer of Au/Ni/AlN Schottky barrier. The largest drop of EBIC compared to defect-free regions is observed at clusters of V-defects, which have a low density of $(2.4\pm0.4)\times10^{7}$ cm^{-2}. Only a very weak drop of EBIC is found at isolated threading dislocations, which have much higher density compared to clusters of V-defects. Consequently, the electrical properties of AlN films are primarily affected by threading dislocations, despite the relatively weak recombination efficiency of individual dislocations.

P69: Interplay of redox potential and pK_a in aminoferrocene

Jakub Věžník[1,2*], Libuše Trnková[1], Karel Lacina[2]

[1] Department of Chemistry, Faculty of Science, Masaryk University, Brno, Czech Republic
[2] CEITEC, Masaryk University, Brno, Czech Republic
*jveznik@mail.muni.cz

Ferrocenes are quite popular in electrochemistry, due to the simplicity of redox reactions of $Fe^{2+/3+}$ ions. While ferrocene is nonpolar and thus of limited use, its cyclopentadienyl ring opens way for many interesting modifications. One of which is aminoferrocene, the -NH_2 group increases solubility in polar solvents and introduces pH sensitivity to the complex.

The exploration of basic relationship of redox potential and pH revealed many interesting properties of aminoferrocene, just one of which is its sensitivity on the presence of buffer as shown in figure. The connection between the amino group and Fe ion allows us to manipulate the acidity of the compound through electrochemistry and thus change pH in the surroundings of electrode. As this connection runs both ways, the electrochemistry can reveal some interesting properties about surroundings of aminoferrocene.

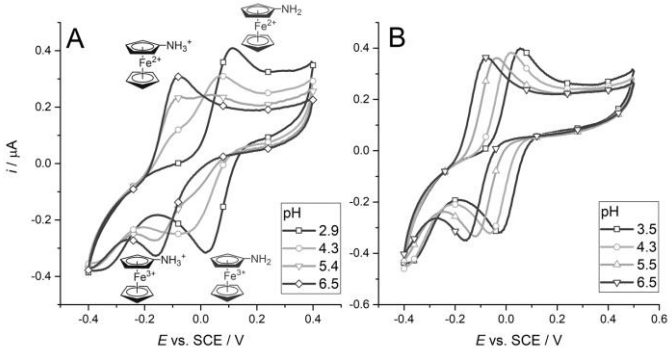


Figure: Cyclic voltammetry of aminoferrocene in A) unbuffered (0.1 M KCl) and B) buffered solution (0.1 M acetate).

Acknowledgement: This research has been financially supported by the project CEITEC 2020 (LQ1601), MUNI/A/1359/2018 and by the Czech Science Foundation, grant nr. 19-16273Y.

T28: The Growth, Phase Transition and Terahertz Properties of $MoTe_2$ crystals

Xixia Zhang[1*], Petr Neugebauer[1], Shanpeng Wang[2], Xutang Tao[2]

[1] Central European Institute of Technology, Brno, Czech Republic

[2] State Key Laboratory of Crystal Materials, Shandong University, Jinan, China

*xixia.zhang@ceitec.vutbr.cz

Two-dimensional layered transition metal dichalcogenides (TMDCs), MX_2 (M = Mo, W, Ta and so on, and X = Se, S or Te), have attracted a lot of interest because of their potential use as two-dimensional components in next-generation devices [1-3]. Very recently, $MoTe_2$ has got particular attention potential because of its exhibition of Weyl fermions, quantum spin Hall effect, superconductivity, extremely large magnetoresistance and structural phase transitions between semiconductor and semimetals [4,5]. However, the efforts are still not enough on $MoTe_2$ to investigate the underlying numerous physical phenomena. Here, we grew the large-sized and high-quality $MoTe_2$ bulk crystals both in 2H and 1T´phase by flux method. The structural transitions among 2H-$MoTe_2$, 1T´-$MoTe_2$ and Td-$MoTe_2$ were systematically investigated by annealing, laser irradiation and cooling in high vacuum in order to get reasonable phase transition temperatures. More importantly, the terahertz properties of the crystals were studied using magneto-optical setup to investigate the electronic structure. The observation of cyclotron resonance and calculations are expected to give an insight into the structure of Fermi surface.

[1] B. Radisavljevic, et al. Nature nanotechnology, 2011, 6(3): 147-150.
[2] A. Splendiani, et al. Nano letters, 2010, 10(4): 1271-1275.
[3] Z Lin, et al. Nature, 2018, 562(7726): 254.
[4] Y Ma, Physical Review B, 2015, 92(8): 085427
[5] K Deng, et al. Nature Physics, 2016, 12(12): 1105.

Mathematics and Computer Science

Students' Abstracts

P70: Ray tracing method for Geodesic Tractography

Temesgen Bihonegn[1*], Jan Slovak[1], Sumit Kaushik[1], Avinash Bansal[1]

[1] Faculty of Science, Masaryk University, Department of Mathematics and Statistics
*temesgent275@gmail.com

In brain, imaging anatomy of white matter has importance in diagnosis and observing neuro diseases over period of time. Fiber tractography is one of the methods to track the white matter fibers which connects different regions of the brain. Earlier methods are based upon principal eigenvectors. They are sensitive to noise and fails in case of crossings and merging regions. Also, they deflect from actual underlying fiber directions. Methods based upon full tensor information are promising known as geodesic tractography. The existing methods like ray tracing are not sensitive to the choice of objective function like in Hamilton-Jacobi method. Introduction of methods like adjugate diffusion tensor as metric proved effective as they sharpen the tensors but their inherent artificial sharpening can also lead to enhanced already present noise, We are looking to use method which could preserve anisotropy while tracking and robust to noise. We have some success in the direction.

Keywords: DTI (Diffusion tensor imaging), Tractography, Ray tracing Adjugate tensor, White matter

P71: High Angular Resolution Diffusion Imaging Segmentation using Riemann symmetric space

Sumit Kaushik[1*], Aviansh Bansal[1]

[1] Masaryk University, Department of Mathematics and Statistics, Czech Republic
*Sumitkaushik24@gmail.com

This work addresses the problem of segmentation of white matter fiber structures e.g corpus callossum, cingulum etc. Anatomy of these structures has clinical importance in diagnosing and controlling progression of neuro diseases. Diffusion tensor imaging (DTI) gained importance for its better precision than conventional MRI (magnetic resonance imaging). Diffusion of water molecules in complex microstructures is described by Gaussian distribution. This approach is known for its inability to model heterogeneous regions where two or more fibers cross, merge or touch. Other factors which affects segmentation and tractography are noise and low resolution dMRI (diffusion MRI). Gaussian modeling produces second order tensors. These tensors are estimated to have positive semi-definite property. These tensors lie in a Riemann Symmetric geometric space. This geometry is well known. The key idea in this work is to use geometry of 2nd order tensors to process/segment higher order tensors. Higher order tensors give better model for the underlying complex structures. Fourth order tensors are used in this work but the method is extendable to higher orders. This flattening of tensor comes naturally from generalization of scalar and vector as a tensor. Moreover, this isomorphic mapping is an isometry. The contribution is to exploit the observation that diagonal components of the flattened tensor unfolds geometry of the higher order tensor (HOT).

T29: The Polaron Model and the Pekar Functional on Balls

Dario Feliciangeli[1], Robert Seiringer[1]

[1] Institute of Science and Technology Austria, Klosterneuburg, Austria
*dario.feliciangeli@ist.ac.at

The Polaron model [2] is a quantum mechanical model used to describe a negatively charged particle moving through a sea of neutrally charged particles (e.g. an electron moving through a crystal). The resulting system is highly non-trivial. Indeed, the neutral particles will be polarized, generating a potential affecting the negative particle, and displaced from their equilibrium, starting to oscillate.
We are interested in studying the Pekar functional, a single-particle effective potential which turns out to capture the essence of the Polaron model in a particular regime [1,5], called strong-coupling regime. Classically, this functional is studied on the full space [3,4], but we are concerned with the case of confinement to a ball. We investigate existence and uniqueness, up to phase, of minimizers, as well as coercivity properties of the functional around its minimum.

[1] M. D. Donsker and S. S. Varadhan, Asymptotics for the polaron, Communications on Pure and Applied Mathematics, 36 (1983), pp. 505–528.
[2] H. Fröhlich, Electrons in lattice fields, Advances in Physics, 3 (1954), pp. 325–361.
[3] E. Lenzmann, Uniqueness of ground states for pseudorelativistic hartree equations, Analysis & PDE, 2 (2009), pp. 1–27.
[4] E. H. Lieb, Existence and uniqueness of the minimizing solution of choquard's nonlinear equation, Studies in Applied Mathematics, 57 (1977), pp. 93–105.
[5] E. H. Lieb and L. E. Thomas, Exact ground state energy of the strong-coupling polaron, Commun. Math. Phys, 183 (1997), p. 519.

T30: Waves in Computer Graphics

Tomáš Skřivan[1*]

[1] IST Austria, Vienna, Austria
*tskrivan@ist.ac.at

Waves are fascinating and beautiful to watch. We encounter them every day in the form of sound or light, but the most visually amusing are waves on water. We can observe them on many scales, from tiny capillary waves to huge tsunamis. These vastly different scales present a challenge for a computer simulation of water waves. We exploit the fact that at a certain level of description, waves move and bounce around just like particles. Using this we were able to develop fast and scalable algorithms for computer simulation of water waves which can be used in video games or for visual effects in movies. In particular, we will show how to simulate huge ocean with many boats [1] or how to simulate tiny capillary waves on an already existing large water simulation [2].

[1] Jeschke S., Skřivan T., Müller-Fischer M., Chentanez N., Macklin M., and Wojtan C. 2018. Water surface wavelets. ACM Trans. Graph. 37, 4, Article 94 (July 2018), 13 pages. DOI: https://doi.org/10.1145/3197517.3201336

[2] Skrivan T., Soderstrom A., Johansson J., Sprenger C., Museth K. and Wojtan C. Wave-curves: Simulating linear waves on non-planner water surfaces. *Unpublished - work in progress.*

Organizers' Abstracts

Abstracts of the organizers of the Joint Retreat 2019 will not be presented on site but can be discussed.

O01: LIBS analysis methodology for suspensions – classification of algae and cyanobacteria

Erik Képeš[1*], Pavel Pořízka[1,2,] Pavlína Modlitbová[1], Ondrej Adamovsky[3], Jozef Kaiser[1,2]

[1] Central European Institute of Technology, Brno University of Technology, Purkyňova 656/123, CZ-61200 Brno, Czech Republic

[2] AtomTrace a.s., Kolejní 9, CZ-61200 Brno, Czech Republic

[3] Research Centre for Toxic Compounds in the Environment (RECETOX), Kamenice 753/5, CZ-625 00 Brno, Czech Republic

*erik.kepes@ceitec.vutbr.cz

The present work expands on the ability of laser-induced breakdown spectroscopy (LIBS) to analyze suspensions. Namely, it demonstrates a novel methodology for the analysis of biological microorganisms suspended in water. The work was motivated by the possible high impact of algae and cyanobacteria on the quality of water supplies, which urges the development of simple methodologies for the accurate identification of said microorganisms. Considering that the standard procedures of the analysis of microorganisms are expensive and require high expertise, the current work proposes a significantly simpler method based on LIBS combined with chemometrics.

The drops of 19 laboratory-grown algal and cyanobacterial suspensions are deposited on silicon wafers and mapped at a high repetition rate with relatively high lateral resolution. The elemental maps are filtered by applying PCA. The microorganism spectra are averaged to create a highly consistent dataset. Lastly, classification of the treated data is carried out by soft independent modelling of class analogy (SIMCA), achieving over 99 % accuracy and high reproductivity. Furthermore, the positive impact of the application of deep learning is demonstrated by comparing the classification results obtained by a simple convolutional neural network to the results obtained by SIMCA.

O02: Increased endosomal microautophagy suppresses CNS defects caused by loss of ADAR RNA editing in *Drosophila*

Anzer Khan[#2*], Simona Paro[#1], Leeanne McGurk[#1], Nagraj Sambrani[2], Marion C. Hogg[1], James Brindle[1], Giuseppa Pennetta[3], Liam P. Keegan[1,2*] and Mary A. O'Connell[1,2]

[1] CEITEC at Masaryk University, Kamenice 753/5, A35/143, 625 00 Brno, Czech Republic, *anzer.khan@ceitec.muni.cz

Inosine generated by hydrolytic deamination of adenosine catalysed by members of the ADAR family of RNA editing enzymes (Adenosine deaminases acting on RNA), is one of the most abundant modified bases in mammalian transcripts. Editing occurs site-specifically within coding sequences at intron-exon hairpins as well as promiscuously within longer RNA duplexes formed by Alu and other repetitive elements in introns, in mature mRNA 3' UTR regions and in noncoding RNAs. Mutations in human *ADAR1* cause Aicardi-Goutieres Syndrome, a rare childhood genetic autoimmune encephalopathy that mimics congenital virus infection with increased levels of Type1 interferon (IFN). *Adar1* mutant phenotypes reveal an evolutionarily conserved role for inosine, in self versus non-self discrimination between host RNAs and those of viruses and other parasites. On the other hand, ADAR RNA editing of adenosine to inosine likely also mark as self very many host dsRNAs containing repetitive sequences, helping the innate immune system to tolerate these. *Drosophila* has a single *Adar* gene encoding the orthologue of vertebrate ADAR2 which edits nervous system transcripts; hundreds of CNS transcripts are edited site-specifically in *Drosophila*. *Adar* mutant flies show reduced viability, uncoordinated locomotion and age-dependent neurodegeneration. We observe aberrant autophagy with enlarged vacuoles, insufficient canonical autophagy suppressible by reduced *Tor* gene dosage and aberrant induction of innate immune transcripts in *Drosophila Adar* mutant heads. *Adar* mutant phenotypes are suppressed by overexpression of the Hsc70-4 chaperone protein that targets proteins containing the KFERQ pentapeptide sequence for endosomal microautophagy (eMI); eMI is particularly important at synapses. Since vertebrate ADAR2 regulates synaptic plasticity by editing glutamate receptors, we believe *Drosophila Adar* also regulates synaptic plasticity, perhaps especially during sleep. A role for ADAR RNA editing in synaptic plasticity and in learning may explain the independent dramatic evolutionary increases in site-specific editing events in advanced insects and molluscs.

O03: Epigenetic drug screen of CD20-low expressing cell line revealed possible treatment target

Veronika Kozlová[1*], Aneta Ledererová[1], Michael Doubek[1,2], Jiří Mayer[1,2], Šárka Pospíšilová[1,2] and Michal Šmída[1,2]

[1] Central European Institute of Technology (CEITEC), Masaryk University, Brno; Czech Republic

[2] Department of Internal Medicine - Hematology and Oncology, Medical Faculty of Masaryk University and University Hospital Brno, Czech Republic

*kozlovaveronica@gmail.com

Standard of care for B-lymphoid malignancies nowadays relies on the administration of monoclonal antibodies targeted to CD20 antigen. However, repeated cycles of anti-CD20 treatment (e.g. Rituximab) often result in the loss of CD20 from the surface of malignant B cells and in therapy resistance.

We mimicked the situation in patients through chronic exposure of B-lymphoid cell lines to gradually increasing doses of anti-CD20 antibody Rituximab. In this way, we have generated cell lines that are resistant to additional treatment with anti-CD20 antibodies. We could confirm that these resistant cells have downregulated CD20 protein from the cell surface.

Since epigenetic changes were predicted to play a role in CD20 regulation, we aimed to uncover which epigenetic modifiers could be able to enhance the expression levels of CD20 antigen and recover its presence on the cell surface. Therefore, we screened our resistant CD20-low cells against a library consisting of 182 small-molecule compounds targeting various epigenetic modifying enzymes (histone deacetylases, methyltransferases, etc.) to determine surface CD20 expression changes by flow cytometry. Multiple diverse targets were identified, among them also Aurora kinases. The targets with the most significant differences were validated in follow-up experiments.

Our results indicate the role of Aurora kinases in CD20 regulation. Further analysis of mechanisms regulating CD20 expression is needed in order to confirm the involvement of detected targets. These proteins may serve as novel therapy targets to enhance the clinical potential of CD20 monoclonal antibodies.

Acknowledgement: This research has been financially supported by the MEYS of the Czech Republic under the project CEITEC 2020 (LQ1601) and grant MUNI/A/1105/2018.

O04: T Cell Receptor Repertoire in Systemic Anaplastic Large Cell Lymphoma

C. Lobello [1*], K. Pal[1], A. Janikova[2], S. Pospisilova[1,2], V. Bikos[1].

[1] Central European Institute of Technology (CEITEC), Masaryk University, Brno, Czech Republic

[2] Department of Internal Medicine—Hematology and Oncology, University Hospital Brno, Brno, Czech Republic

*cosimo.lobello@ceitec.muni.cz

Systemic Anaplastic Large Cell Lymphoma (sALCL) is a genetically heterogenous disease and it encompasses two different clinical entities of T-cell lymphomas: ALK-positive ALCL characterized by ALK-translocation, and ALK-negative ALCL, delineated by lack of the latter. Although sALCL is a T cell lymphoma it is characterized by lack of T cell receptor (TcR) expression on the cell surface. Since T cells are largely dependent on signals that they receive from their TcR for their development and maturation, this signaling pathway appears to play a key role in lymphomagenesis. Previous works showed that a considerable percentage of ALK-positive ALCL have fully a rearranged TcR loci and that TcR expression is suppressed during the transformation. Contradictory to this, in ALK-negative ALCL the role of TcR is not fully investigated and its involvement in the lymphoma pathogenesis is completely unknown. To better understand the potential contribution of the TcR in sALCL lymphomagenesis, we perform TcR gene repertoire profiling utilizing targeted, amplicon based, high-throughput re-sequencing methodologies. The deep antigen receptor immunogenetic analysis will allow us to investigate the immunogenetic features distinctive among the two sALCL entities that could delineate differences in their pathogenic mechanisms or within the same entity, where their matching with a distinct clinical behavior may render clinical and therapeutic relevance in this analysis.

Acknowledgement: The project was supported by received funding from Czech Science Foundation (GA ČR), project no. 19-23424Y.

We acknowledge the CF Genomics CEITEC MU supported by the NCMG research infrastructure (LM2015091 funded by MEYS CR)

O05: Functional Study of MiR-215 as Tumor Suppressor in Colorectal Cancer

Táňa Macháčková[1*], Kamila Součková[1], Petra Vychytilová[1], Dominika Brchnelová[1], Tomáš Loja[1], Ondřej Slabý[1]

[1] CEITEC - Central European Institute of Technology, Masaryk University, Brno, Czech Republic

*tana.machackova@ceitec.muni.cz

Introduction: MiR-215 is involved in the regulation of the Epidermal Growth Factor Receptor (EGFR) signaling pathway crucial for the development of colorectal cancer (CRC). MiR-215 targets EGFR ligand Epiregulin (EREG) and its transcriptional inducer Homeobox B9 protein (HOXB9) which play role in the pathogenesis of CRC. In this study, we focused on *in vitro* and *in vivo* evaluation of tumor-suppressor effects of miR-215 in CRC cells.

Methods: HCT116+/+, HCT-15, and RKO cell lines were stably transfected with miR-215 and used for *in vitro* functional studies of miR-215. Methods used for in vitro functional studies of miR-215 included clonogenicity assay, MTT test, cell cycle and apoptosis analysis. To evaluate how miR-215 over-expression affects tumor growth *in vivo*, subcutaneous tumors were generated in NSG mice using cells stably transfected with miR-215 and appropriate control cells. In order to compare the metastatic potential of CRC cells expressing miR-215 and control cell lines, we used the intrasplenic metastatic model.

Results: Clones of CRC cells transfected with miR-215 showed increased expression of miR-215 and decreased expression of miR-215-targets EREG and HOXB9 in comparison to control cells. Clonogenicity assay showed that HCT116+/+ and RKO cells transfected with miR-215 have significantly lower clonogenic potential in comparison to control cells. However, transfected cells showed no significant difference in metabolic activity. RKO cells transfected with miR-215 showed significant cell cycle arrest in G2/M phase in comparison to control cells. *In vivo* experiments confirmed that control cells tumors grow significantly faster than the miR-215-tumors. Intrasplenic injections of cells resulted in rapid and extensive liver metastases of control cells compared to just a few or no metastases in cases of miR-215 transfected cells.

This work was supported by a grant of Czech Ministry of Health nr. 16-31765A.

O06: Strigolactone based transcriptome study reveals their role in photosynthesis and cold stress tolerance

Taraka Ramji Moturu[1*], Sravankumar Thula[1], Tomasz Nodzyński[1], Jiří Friml[2], Sibu Simon[1]

[1] CEITEC - Central European Institute of Technology, Masaryk University Brno, Kamenice 5, 625 00 Brno, Czech Republic.

[2] Institute of Science and Technology (IST) Austria, 3400 Klosterneuburg, Austria.

*tarakaramji.moturu@ceitec.muni.cz

Strigolactones (SLs) are a relatively recent addition to the class of plant hormones. They regulate various above and below ground developmental events in plants. Apart from their developmental role, recent studies showed that SLs can act as a responsive molecule during various plant biotic and abiotic stress conditions. To gain further insight into their versatile functions in plants, we have conducted a transcriptome study using synthetic SL specific isomer GR24 5DS. In general, the differentially expressed transcripts mainly have their assigned roles in cell division, cell organization, vesicle trafficking, transcription regulation and RNA processing. A significantly high number of differentially expressed transcripts already reported to have their role in biotic-abiotic stress responses, hormonal pathways and plant development. Interestingly, forty-three differentially regulated transcripts are photosynthesis related. Additionally, we also found transcripts that are involved in cold stress tolerance. We further explored the direct role of SLs in regulating photosynthesis and also their possible role in cold stress tolerance. Our data suggest that SLs has a direct role in enhancing photosynthesis and cold stress tolerance in Arabidopsis.

O07: Elucidation of ADAR1 functions in the Immune Response by using interactome data

Dragana Vukic[1*], Leena Yadav[2], Markku Varjosalo[2], Liam Keegan[1] and Mary O'Connell[1]

[1] CEITEC, Masaryk University, Kamenice 753/5, Brno, Czech Republic

[2] Institute of Biotechnology, University of Helsinki, Biocenter 3, Viikinkaari 1, Helsinki, Finland

*dragana.vukic@ceitec.muni.cz

Adenosine deaminases acting on dsRNA (ADARs) are essential for a normal embryonic development and have a role in preventing innate immune response to endogenous dsRNA. ADARs deaminate adenosine to inosine by hydrolytic deamination, known as A-to-I editing. Our group was the first to demonstrate that this editing event in endogenous dsRNA prevents the interferon (IFN) signaling cascades from dsRNA sensors in the cytoplasm. In accordance, mice lacking Adar1 die at the embryonal stage with heightened levels of type-I IFN and widespread apoptosis. In humans, mutations in ADAR1 cause the autoimmune disorder.

To address the role of ADAR in immune response, we looked at the ADAR1 interactome. For this goal we have prepared a tetracycline-inducible HE239T stable cell line, expressing both isoforms of ADAR1. These proteins were tagged with Strep-tag or BirA at either N- or C-terminus. To further elucidate biological functions of ADAR1, cells were treated with type I IFN. Taken together, until now we have a comprehensive data set of ADAR1 protein complexes with or without induction of immune response. Our data are consistent between all sets and in agreement with all published interacting proteins of ADARs. In addition to the different protein complexes found to interact with ADAR1 upon immune response, we have discovered that tags at the different terminus influences protein stability and interactions.

List of participants with contact information

Life Science

Adamus, Marek	CEITEC MU	marek.adamus@ceitec.muni.cz	**T01**
Balaban, Can	IMG Prague	can-balaban@hotmail.com	**T02**
Basello, Davide A.	IMG Prague	basello@img.cas.cz	**P01**
Beranová, Jana	IOCB Prague	jana.beranova@ymail.com	**P02**
Binovsky, Jan	CEITEC MU	janbinovsky@gmail.com	**P03**
Brchnelova, Dominika	CEITEC MU	d.brchnelova@gmail.com	**V01**
Burnett, Laura	IST Austria	lburnett@ist.ac.at	**P04**
Canigova, Nikola	IST Austria	nikola.canigova@ist.ac.at	**P05**
Cihlářová, Zuzana	IMG Prague	zuzana.cihlarova@img.cas.cz	**P06**
Covelo Molares, Helena	CEITEC MU	helena.covelo@ceitec.muni.cz	**P07**
Cumpelik, Andrea	IST Austria	andrea.cumpelik@ist.ac.at	**T03**
Černochová, Petra	CEITEC MU	petra.eliotek@gmail.com	**P08**
Dobiášovská, Ivana	IMG Prague	ivana.dobiasovska@img.cas.cz	**P09**
Ebrahimi Naghani, S.	CEITEC MU	shekufeh.ebrahimi@gmail.com	**P10**
Fáberová, Veronika	IMG Prague	faberova@img.cas.cz	**T04**
Fabišik, Matej	IMG Prague	matej.fabisik@img.cas.cz	**P11**
Falginella, Francesco L.	CEITEC MU	falginella.francesco@gmail.com	**P12**
Fojtů, Michaela	CEITEC MU	michaelafojtu@gmail.com	**P13**
Giassa, Ilektra-Chara	CEITEC MU	238751@mail.muni.cz	**T05**
Grusanovic, Srdjan	IMG Prague	srdjan.grusanovic@img.cas.cz	**P14**
Hadzima, Martin	IOCB Prague	hadzima@uochb.cas.cz	**T06**
Homola, Miroslav	CEITEC MU	mirdahomola@gmail.com	**T07**
Horský, Vladimír	CEITEC MU	vladimir.horsky@mail.muni.cz	**P15**
Hrebik, Dominik	CEITEC MU	dominik.hrebik@ceitec.muni.cz	**T08**

Hrubý, Jakub	CEITEC BUT	jakub.hruby@ceitec.vutbr.cz	**P16**
Chareshneu, Aliaksei	CEITEC MU	479052@mail.muni.cz	**T09**
Jandušík, Tomáš	IOCB Prague	jandusik@uochb.cas.cz	**P17**
Jovicic, Jovana	IMG Prague	jovana.jovicic@img.cas.cz	**P18**
Juráček, Jaroslav	CEITEC MU	juracekjaroslav@gmail.com	**P19**
Kadlčíková, Dita	CEITEC VRI	kadlcikova@vri.cz	**P20**
Kardosova, Miroslava	IMG Prague	kari@img.cas.cz	**P21**
Kasiliauskaite, Aiste	CEITEC MU	a.kasiliauskaite@gmail.com	**T10**
Kopkova, Alena	CEITEC MU	kopkova.alena@gmail.com	**P22**
Kováčovvá, Júlia	CEITEC MU	juli.kovacova@gmail.com	**P23**
Kovář, Martin	IMG Prague	martin.kovar@img.cas.cz	**P24**
Králová, Jarmila	IMG Prague	kralovaj@img.cas.cz	**P25**
Kravchuk, Vladyslav	IST Austria	vkravchu@ist.ac.at	**P26**
Krepl, Miroslav	IBP Brno	krepl@seznam.cz	**P27**
Kreplová, Michaela	IMG Prague	michaela.kreplova@img.cas.cz	**P28**
Kutilova, Iva	CEITEC VPU	kutilova.iva@gmail.com	**P29**
Ladungová, Adriana	CEITEC MU	ladungova.adriana@gmail.com	**V02**
Loubalova, Zuzana	IMG Prague	zuzana.loubalova@seznam.cz	**T11**
Lustyk, Diana	IMG Prague	diana.lustyk@img.cas.cz	**P30**
Markos, Athanasios	IOCB Prague	athanasios.markos@uochb.cas.cz	**P31**
Melnikava, Alesia	CEITEC MU	alesiamelnikava@mail.muni.cz	**P32**
Mikulasova, Tereza	IMG Prague	tereza.mikulasova@img.cas.cz	**P33**
Mititelu, Maria B.	IOCB Prague	maria-bianca.mititelu@uochb.cas.cz	**P34**
Mráziková, Klaudia	CEITEC MU	laudyklaudy@gmail.com	**T12**
Nardin, Michele	IST Austria	michele.nardin@ist.ac.at	**T13**
Nešporová, Kristína	CEITEC VPU	krisnesporova@gmail.com	**P35**

Nováková, Markéta	IOCB Prague	mnovakova@uochb.cas.cz	**T14**
Obuca, Mina	IMG Prague	mina.obuca@img.cas.cz	**P36**
Palkovicova, Jana	CEITEC VPU	palkovicova.jane@gmail.com	**P37**
Pastucha, Matěj	CEITEC MU	matej.pastucha@ceitec.muni.cz	**P38**
Peschelová, Helena	CEITEC MU	helenapeschelova@gmail.com	**P39**
Pinke, Gergely	IST Austria	gpinke@ist.ac.at	**P40**
Pokorná, Pavlína	CEITEC MU	424122@mail.muni.cz	**T15**
Pokusaeva, Victoria	IST Austria	victoria.pokusaeva@ist.ac.at	**P41**
Reigl, Tomas	CEITEC MU	tomas.reigl@gmail.com	**P42**
S. C. Chiossi, Heloisa	IST Austria	hchiossi@ist.ac.at	**P43**
Sánchez López, Juan F.	CEITEC MU	sanchez.lopez@ceitec.muni.cz	**P44**
Satapathy, Roshan K.	IST Austria	rsatapat@ist.ac.at	**P45**
Sedmík, Jiří	CEITEC MU	jura7ik@gmail.com	**P46**
Sinigaglia, Ketty	CEITEC MU	ketty.sinigaglia@ceitec.muni.cz	**P47**
Svobodová, Eliška	IMG Prague	eliska1svobodova@gmail.com	**T16**
Svozilová, Hana	CEITEC MU	svozilova.hana@gmail.com	**P48**
Szczerkowska, Katarzyna	IMG Prague	katarzyna.szczerkowska@img.cas.cz	**P49**
Šafaříková, Eva	MU	safarikova.eva@ibp.cz	**T17**
Šimková, Adéla	IOCB Prague	adela.simkova@uochb.cas.cz	**P50**
Tarabai, Hassan	CEITEC VPU	hassantarabai@gmail.com	**T18**
Taus, Petr	CEITEC MU	petr.taus@ceitec.muni.cz	**T19**
Tesařová, Markéta	CEITEC BUT	Marketa.Tesarova@ceitec.vutbr.cz	**T20**
Thakur, Prasoon K.	IMG Prague	prasoont@img.cas.cz	**P51**
Trachtová, Karolína	CEITEC MU	trachtova@mail.muni.cz	**P52**
Valček, Adam	CEITEC VPU	valcekam@gmail.com	**T21**
Varadarajan, Nandan	CEITEC MU	nandan@mail.muni.cz	**P53**

Volakhava, Anastasiya	CEITEC MU	volokhova_nastia@mail.ru	**P54**
Zimmann, Felix	IMG Prague	felix.zimmann@img.cas.cz	**P55**

Physical and Material Science

Agrawal, Nishchal	IST Austria	nishchal.agrawal@ist.ac.at	**P56**
Antoš, Zdeněk	CEITEC IPM	antos@ipm.cz	**P57**
Butera, Valeria	CEITEC BUT	Valeria.Butera@ceitec.vutbr.cz	**V03**
Holzer, Jakub	CEITEC IPM	holzer@ipm.cz	**T22**
Horák, Michal	CEITEC BUT	michal.horak2@ceitec.vutbr.cz	**P58**
Horký, Michal	CEITEC BUT	michal.horky@ceitec.vutbr.cz	**P59**
Kaushik, Preeti	CEITEC MU	piscian.preeti@gmail.com	**P60**
Konhefr, Martin	CEITEC MU	martin.konhefr@ceitec.muni.cz	**P61**
Kuběnová, Tereza	CEITEC IPM	tkubenova@ipm.cz	**T23**
Kukučka, Josip	IST Austria	josip2510@hotmail.com	**P62**
Makoveev, Anton	CEITEC BUT	Anton.Makoveev@ceitec.vutbr.cz	**P63**
Maniš, Jaroslav	CEITEC BUT	jaroslav.manis@ceitec.vutbr.cz	**T24**
Midlíková, Jana	CEITEC BUT	jana.midlikova@ceitec.vutbr.cz	**T25**
Michlíček, Miroslav	CEITEC MU	michlicekm@mail.muni.cz	**T26**
Polášková, Kateřina	CEITEC MU	polaskova.katerina@mail.muni.cz	**T27**
Sopoušek, Jakub	CEITEC MU	423048@mail.muni.cz	**P65**
Tinoco Navarro, Lizeth K.	CEITEC BUT	katerinet890911@gmail.com	**P66**
Tuckova, Tereza	CEITEC BUT	tereza.chmelik@gmail.com	**P67**
Vacek, Petr	CEITEC IPM	Petr.Vacek@ceitec.vutbr.cz	**P68**
Věžník, Jakub	CEITEC MU	jveznik@mail.muni.cz	**P69**
Zhang, Xixia	CEITEC BUT	xixia.zhang@ceitec.vutbr.cz	**T28**

Mathematics and Computer Science

Bansal, Avinash	MU	avinashbansal26@gmail.com	**P71**
Bihonegn, Temesgen	MU	temesgent275@gmail.com	**P70**
Feliciangeli, Dario	IST Austria	dario.feliciangeli@ist.ac.at	**T29**
Kaushik, Sumit	MU	sumitkaushik24@gmail.com	**P71**
Skrivan, Tomas	IST Austria	tskrivan@ist.ac.at	**T30**

Organizer's Abstracts

Kepes, Erik	Organiser	erik.kepes@ceitec.vutbr.cz	**O01**
Khan, Anzer	Organiser	anzer.khan@ceitec.muni	**O02**
Kozlová, Veronika	Organiser	kozlovaveronica@gmail.com	**O03**
Lobello, Cosimo	Organiser	cosimo.lobello@ceitec.muni.cz	**O04**
Machackova, Tana	Organiser	tana.machackova@ceitec.muni.cz	**O05**
Moturu, Taraka Ramji	Organiser	tarakaramji.moturu@ceitec.muni.cz	**O06**
Vukic, Dragana	Organiser	dragana.vukic@ceitec.muni.cz	**O07**

Place for notes

Place for notes

Place for notes

Place for notes

Joint Retreat 2019
25–26 June 2019, Hotel Luna, Kouty

Book of Abstracts

Editors:
Erik Képeš, Veronika Kozlová, Cosimo Lobello, Táňa Macháčková, Tarakaramji Moturu, Zdeňka Pavlačková, Barbora Peltanová, Jan Poduška, Igor Turčan, Dragana Vukić

Published by Masaryk University, Žerotínovo nám. 617/9, 601 77 Brno, Czech Republic
First edition, Brno 2019

160 copies
Printed by Litera Brno, Tábor 43a, 612 00 Brno

ISBN 978-80-210-9300-3
ISBN 978-80-210-9301-0 (online : pdf)

Gold sponsors of the Joint Retreat 2019

BioVendor®

MERCK

Silver sponsors of the Joint Retreat 2019

Photon Systems Instruments

CZECHINVEST
Investment and Business Development Agency

Bronze sponsors of the Joint Retreat 2019

tataabiocenter

DYNEX

eppendorf

Platinum sponsors of the Joint Retreat 2019

ThermoFisher
SCIENTIFIC

mt.eu
měřicí technika - morava
messtechnik - moravia
measurement technic - moravia

MUNI
PRESS

ISBN 978-80-210-9300-3