

Wed 18 May 2022

14:00-16:00 Accommodation

14:30-16:00 **Registration**

16:00-16:10 **Opening & Welcome**

16:10-17:10 **Keynote Lecture by Craig S. Pikaard, Indiana University, USA**

RNA-directed DNA methylation and nucleolar dominance: seeking the "how" and "why" of genic and chromosomal silencing (page 8)

Session 1 Abiotic factors in chromatin remodelling (chair Jiří Fajkus)

17:15-17:30 **Célia Baroux**, Super resolution imaging identifies light-inducible transcription superclusters towards the nuclear periphery in *Arabidopsis* (p9)

17:30-17:45 **Vicente Rubio**, Dangerous liaisons: COP1, DET1 and HY5 regulatory loops in controlling chromatin functions and plant development (p10)

17:45-18:00 **Rocío Núñez Vázquez**, Histone H3 variants: new players of the abiotic stress response in *Arabidopsis* (p11)

18:00-18:15 **Léa Faivre**, H3K4me3-H3K27me3 bivalency poises COR genes for induction (p12)

18:15-18:30 **Daniel Schubert**, Genetic and epigenetic control of heat stress memory in *Cyanidioschyzon merolae* (p13)

18:30-20:00 Accommodation / Průhonice park

20:00-23:00 **Dinner & networking**

Thu 19 May 2022

07:00-10:00 Breakfast in hotels

Session 2 DNA methylation, histone variants and modifications (chair Christel Carles)

09:00-09:15 **Mathieu Ingouff**, Insights into the dynamics of core actors of CG methylation maintenance in *Arabidopsis* (p14)

09:15-09:30 **Ioanna Kakoulidou**, Parental pericentromeric methylation status drives methylome remodeling and heterosis in *Arabidopsis* hybrids (p15)

09:30-09:45 **Iris Sammarco**, DNA methylation in the wild: stable environmentally-induced epigenetic signature across clones of the wild strawberry (*Fragaria vesca*) (p16)

09:45-10:00 **Kateryna Fal**, Manipulating Histone methylation in *Arabidopsis* with the dCas9 tool: de-repression of the CUC3 boundary gene as a study case (p17)

10:00-10:05 **Minerva Trejo Arellano**, Leveraging the evolutionary information in genomic and epigenomic databases to reconstruct DNA methylation systems (p18)

10:05-10:10 **Pierre Bourguet**, The H2A.W histone variant contributes to transposon silencing (p19)

10:10-10:15 **Tomáš Kašpar**, The function of SPT6L containing putative AGO-hook in the complex of Pol II (p20)

10:15-10:20 **Vojtěch Čermák**, What governs loci sensitivity to DNA methylation? (p21)

10:20-10:25 **Rodolphe Dombey**, Epigenetic regulation of transposable elements in duckweeds (p22)

10:25-10:30 **Miguel Vega-Palas**, A complex network of interactions governs DNA methylation at telomeric regions (p23)

10:30-11:00 **Coffee break & discussion**

Thu 19 May 2022**Session 3 Chromatin dynamics and plant development** (chair Aleš Pečinka)

- 11:00-11:15 **Leor Eshed Williams**, PRC2 and TrxG interactions required for the acquisition of new cell identity during regeneration in *Arabidopsis* (p24)
- 11:15-11:30 **Sara Farrona**, Novel interactors of the Polycomb Group (PcG) pathway and their role in plant development (p25)
- 11:30-11:45 **Simon Amiard**, *Arabidopsis* TRBs: All the same but all different? (p26)
- 11:45-11:50 **Franziska Turck**, The cis-regulatory code underpinning epigenetic gene regulation (p27)
- 11:50-11:55 **Jordi Moreno-Romero**, Polycomb activity regulates the response of *Arabidopsis* to plant proximity (p28)
- 11:55-12:00 **Claire Jourdain**, The histone-binding protein PDS5C regulates flowering and nuclear morphology in *Arabidopsis* (p29)
- 12:00-12:05 **Naseem Samo**, Polycomb Repressive Complex 2 represses storage reserve metabolism during seedling emergence (p30)
- 12:05-12:10 **Aline V. Probst**, The Histone Chaperone HIRA is a positive regulator of seed germination (p31)
- 12:10-12:25 **Martin Trtílek (PSI)**, High-throughput automated phenotyping as a shortcut to more effective biostimulants: from seeds to crops (p32)
- 12:25-12:30 **Tereza Dobisová (Labdeers)**, Seed-to-plant, plant-to-seed phenotyping (p33)
- 12:30-12:45 **Photographing by Oliver Beneš**
- 12:45-14:00 **Lunch & networking**
- 14:00-15:45 **Poster session & discussion**
For more details see pages 68-101

Thu 19 May 2022**Session 4 Transcribing through chromatin** (chair Valérie Gaudin)

- 15:45-16:00 **Klaus Grasser**, Function of elongation factors associated with transcribing RNA polymerase II in *Arabidopsis* (p34)
- 16:00-16:15 **Simon Obermeyer**, Comparative analysis of different types of transcription elongation factors in *A. thaliana* (p35)
- 16:15-16:30 **Rafał Archacki**, BRAHMA-containing SWI/SNF complex prevailing in *Arabidopsis* requires BRD subunits for assembly and stability (p36)
- 16:30-16:45 **Kateřina Adamusová**, Gene repression by the epigenome of transcriptional elongation (p37)
- 16:45-17:00 **Eduardo Mateo-Bonmati**, Linking non-coding transcriptional termination with chromatin silencing (p38)
- 17:00-17:15 **Julia Engelhorn**, Pan-cistrome analysis of genetic and epigenetic variation influencing transcription factor binding sites in maize (p39)
- 17:15-17:20 **Pavla Navrátilová**, Promoter architecture and cis-regulatory landscape in barley (p40)
- 17:20-17:25 **Hana Šimková**, Intricate regulation of ribosomal RNA transcription in cereals (p41)
- 17:25-17:30 **Konstantin Kutashev**, Extensions of single molecule RNA fluorescence in situ hybridization method (p42)
- 17:30-18:00 **Coffee break & discussion**

Thu 19 May 2022**Session 5 Telomeres and centromeres** (chair Inna Lermontova)

- 18:00-18:05 **Jiří Fajkus**, Monophyletic origin of plant telomerase RNAs – how far it reaches? (p43)
- 18:05-18:20 **Fredy Barneche**, Antagonistic role of histone H1 on the H3K27me3 chromatin landscape at genes and telomeric repeats (p44)
- 18:20-18:35 **Michal Závodník**, New insights into telomere maintenance in plants with unusual telomeric sequences (p46)
- 18:35-18:50 **Yi-Tzu Kuo**, An independently evolved satellite DNA-based holocentromere is composed of megabase-scale centromere units in lilioid monocots (p47)
- 18:50-19:05 **Ulkar Ahmadli**, The centromere targeting mechanism of KNL2 and CENP-C proteins (p48)
- 19:05-19:10 **Alžběta Kusová**, Telomere-associated proteins in lower plants (p49)
- 19:10-19:15 **Miloslava Fojtová**, Dynamics of *A. thaliana* telomeres during callus propagation and the toolset for analysis of telomere lengths profiles (p50)
- 19:15-19:20 **Agata Kilar**, The epigenetic landscape of the plant TR gene (p51)
- 19:20-19:25 **Manikandan Kalidass**, The protein-protein interaction network of KNL2 in *A. thaliana* (p52)
- 19:25-19:30 **Ramakrishna Yadala**, CAF as a new centromere and kinetochore assembly factor in plants (p53)
- 19:30-19:35 **Sheng Zuo**, Recurrent duplications of kinetochore assembly factor KNL2 and its conserved function in plants (p54)
- 20:00-23:00 **Dinner & networking & live music „My Tri“**

Fri 20 May 2022

07:00-10:00 Breakfast in hotels

Session 6 Chromatin in plant reproductive development (chair François Roudier)

09:00-09:15 **Yanru Li**, H1 citrullination – an atypical modification regulating germline fate in *Arabidopsis* (p55)

09:15-09:30 **Ruben Gutzat**, Two AGO proteins with transposon-derived sRNA cargo mark the germline in *Arabidopsis* (p56)

09:30-09:45 **Fen Yang**, Defects in meiotic chromosome segregation lead to triploid offspring in *Arabidopsis* SMC5/6 complex mutants (p57)

09:45-10:00 **Hua Jiang**, H3K9 demethylases are required for male meiosis in *Arabidopsis* (p58)

10:00-10:15 **Petra Procházková Schrupfová**, RUVBL proteins are involved in plant gametophyte development (p59)

10:15-10:20 **Amit Kumar**, Histone deacetylases regulate heat stress induced haploid embryogenesis in *Brassica napus* (p60)

10:20-10:25 **Amit Kumar Singh**, Investigation of chromatin remodelling function during meiosis and plant reproduction (p61)

10:25-11:00 **Coffee break & discussion**

Session 7 Chromatin in mitosis and DNA repair (chair Crisanto Gutiérrez)

11:00-11:05 **Aleš Pečinka**, DNA protein crosslink repair – on the interface between chromatin and genome stability (62)

11:05-11:20 **Martina Nešpor Dadejová**, Laser microirradiation as a versatile system for probing protein recruitment and protein-protein interactions at DNA lesions in plants (p63)

11:20-11:35 **Jorge Fung-Uceda**, Intricate relationship between H3K27me1 diurnal deposition and DNA damage response (p64)

11:35-11:50 **Petr Cápál**, Flow-sorted mitotic chromosomes as a tool to uncover their 3D architecture (p65)

11:50-11:55 **Kateřina Kaduchová**, Analysis of in vivo chromatin dynamics during mitotic division in barley (*Hordeum vulgare*) (p66)

11:55-12:00 **Alžběta Doležalová**, Oligo-FISH reveals spatial organization of rice chromosomes in interphase nuclei (p67)

12:00-12:15 **Concluding remarks & awards**

12:15 **Departure**

Thu 19 May 202214:00-15:45 **Poster session & discussion**

For more details see pages 68-101

P01 **Vangeli Geshkovski**, Chromatin switches in plants: Molecular mechanisms of the ULTRAPETALA1 protein (p70)

P02 **Jean-Baptiste Izquierdo**, Structural and biochemical study of the plant-specific Polycomb antagonist ULTRAPETALA1 (p71)

P03 **Martina Dvořáčková**, The impact of H3 histone variants on chromatin organisation in *Arabidopsis* (p72)

P04 **Adéla Machelová**, The impact of histone H3 chaperones on telomere stability (p73)

P05 **Denisa Tomkova**, Histone H3.3 Lysine 27 to Alanine mutation strongly reduces tri-methylation at H3K27 without affecting the global nuclear organization (p74)

P06 **Kinga Rutowicz**, Do linker histone (H1) variants facilitate transcriptome reprogramming during diurnal rhythm? (p75)

P07 **Laura Ávila Robledillo**, Nuclear 3D architecture of meta-polycentric centromeres of *Pisum sativum* (p76)

P08 **Ludmila Oliveira**, Kinetochore organization in *Cuscuta* species (p77)

P09 **Tereza Dobisová (Labdeers)**, Seed-to-plant, plant-to-seed phenotyping (p78)

P10 **Nicolas Dalle**, Polycomb Repressive Complex 2 regulation of stem cell identity and functions in the moss *Physcomitrium patens* (p79)

P11 **Ahamed Khan**, Evolution of plant PWWP-DOMAIN INTERACTOR OF POLYCOMBSs (PWOs) and its molecular functions in plant development (p80)

P12 **Naseem Samo**, Polycomb repressive complex 2 represses storage reserve metabolism during seedling emergence (p81)

P13 **Mingxi Zhou**, The role of Polycomb Repressive Complex 2 (PRC2) in plant response to light acclimation (p82)

P14 **Iva Mozgová**, Modulation of light responses by PRC2 during seed and seedling development (p83)

P15 **Anna Korytářová**, RNA-centric approach to study RNA-protein interactions of plant telomerase RNA (p84)

- P16 **Klára Přikrylová Konečná**, ARM protein modulates the strength of the response to DNA damage in *Arabidopsis* (p85)
- P17 **Ailbhe Brazel**, Histone demethylases control Hypoxia Response Genes in *Arabidopsis thaliana* (p86)
- P18 **María Sol Gomez**, Efficient deposition of the heterochromatic H3K27me1 histone mark requires ORC1a, a member of the pre-replication complex (p87)
- P19 **Fatimah Abdulhakim**, Understanding the Role of G3BP1 in Plant Stresses (p88)
- P20 **Arsheed Sheikh**, Linker histone H1 regulates immune priming in plants (p89)
- P21 **Marcel Hubinský**, Cytosine oxidative modifications as evolutive architects of *Silene latifolia* sex chromosomes (p90)
- P22 **Linhao Xu**, Mutation of histone H3 serine 28 to alanine influences H3K27me3-mediated gene silencing in *Arabidopsis thaliana* (p91)
- P23 **Robert Piecyk**, Parental pericentromeric methylation status acts as a major quantitative trait locus in the remodelling of hybrid methylomes (p92)
- P24 **Heinrich Bente**, Profiling of transcription factors in *Arabidopsis* endosperm nuclei using CUT&RUN (p93)
- P25 **Zuzana Tulpová**, Dynamic activity of ribosomal RNA loci in cereals (p94)
- P26 **Maike Stam**, RdDM mutants preventing b1 paramutation have opposing chromatin structure effects at the maize b1 gene (p95)
- P27 **María Vaquero-Sedas**, A complex network of interactions governs DNA methylation at telomeric regions (p96)
- P28 **Chaira Longo**, New strategies to study plant epigenetic plasticity: A chemical-based approach (p97)
- P29 **Michael Möbes**, Investigation of transcriptional regulation of genes coding for centromeric proteins KNL2, NDC80 and BUB3.1 by natural antisense transcripts in *Arabidopsis thaliana* (p98)
- P30 **Jothipriya Ramakrishnan Chandra**, Centromeric transcripts and their role in the formation of centromeric chromatin and kinetochore assembly (p99)
- P31 **Daniel Buendía Avila**, How does *Wolffia* (Lemnaceae) silence Transposable Elements? (p100)
- P32 **Marieke Trasser**, Chromatin determinants of de novo transposon silencing in *Arabidopsis thaliana* (p101)