

INDEPTH Prague Meeting



Prague, Czech Republic
February 25th-27th 2019



Welcome to Praha

On behalf of the COST-Action CA16212 “Impact of Nuclear Domains in Gene Expression and Plant Traits” (INDEPTH), we are very pleased to welcome all meeting participants to Praha.

Plant Sciences and INDEPTH in the Czech Republic

By Ales Pecinka

Plant sciences have a long tradition in the Czech Republic and the biology of nucleus is one of the classical themes of plant research in the country. The key plant research institutions are concentrated in the major cities of Praha, Brno, Olomouc and České Budejovice.

The Czech INDEPTH partners include several groups from the Institute of Experimental Botany of the Czech Academy of Science (IEB) in Praha and Olomouc (Doležel, Pecinka, Šimková, Honys), Central European Institute of Technology (CEITEC) in Brno (Dvorácková, Fajkus, Lysak), Palacký University in Olomouc (Šebela, Bitomský) and Biology Centre of the Czech Academy of Science in České Budeeovice (Mozgová).

These groups focus on the analysis of plant nuclear organization, chromatin and chromosome structure, genome stability and gene regulation in the model and crop plants. The Czech INDEPTH partners have unique expertise in flow cytometry and nuclei sorting, proteomics, microscopy, (epi)genomics and genome stability, which they are happy to share with all INDEPTH members.



COST is an EU-funded programme that enables researchers to set up their interdisciplinary research networks in Europe and beyond. We provide funds for organising conferences, meetings, training schools, short scientific exchanges or other networking activities in a wide range of scientific topics. By creating open spaces where people and ideas can grow, we unlock the full potential of science.

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Meeting Schedule

Monday February 25th 2019

9:00-12:00: Meeting for members of INDEPTH Management Committee

12:30-13.15: Arrival/Registration and Poster setup

13:15-13:35 Welcome Speech

13:35-14:15 Opening Keynote: **Eric J. Richards** (Boyce Thompson Institute, USA)

14:15-16:30 **WG1: Quantitative imaging and analysis of the plant nucleus in 3D.**
Chair: **Dimiter Prodanov** and **Ana Paula Santos**

14:15-14.30 **Dimiter Prodanov** (IMEC, Belgium): Summary of WG1 activities

Christophe Tatout (Université Clermont Auvergne, France): Overview of Florence WG1, Workshop, Training school 3D-FISH and OMERO repository at Florida State University

14:30-15:05 Invited speaker: **Andrew French** (Nottingham University, UK): Deep machine learning for plant image analysis

15:05-15:30 Coffee Break

15:30-15.50 **Gwénaëlle Détourné** (Université Clermont Auvergne, France): Characterisation of a novel family of plant nuclear envelope associated proteins (NEAP) in *Arabidopsis thaliana*

15.50-16.10 **Anis Meschichi** (Swedish University of Agricultural Sciences, Sweden): Characterization of chromatin mobility during DNA damage responses in *Arabidopsis thaliana*

16.10-16.30 **Valya Vassileva** (Institute of Plant Physiology and Genetics, Bulgaria): Zebularine-induced DNA demethylation impairs auxin signalling in *Arabidopsis* roots

16.30-16.45 **WG5 Session. Introduce dissemination activities, published papers and future opportunities**

16:45- 17.45 Pecha Kucha Talks (see page 22 for speaker list)

17:45- 19.30 Poster session

20.15- late Gala Dinner



Tuesday 26th February

09:00-11:05 **WG2: Transcriptional regulation through association of chromatin domains with nuclear compartments**
Chair: **Stefanie Rosa** and **Sara Farrona**

09.00- 09.10 Summary of WG2 activities: **Stefanie Rosa** (Swedish University of Agricultural Sciences, Sweden) and **Sara Farrona** (National University of Ireland-Galway, Ireland)

09.10- 09.45 Invited Speaker **Andreas Houben** (Gatersleben IPK, Germany): CRISPR/Cas9-mediated labelling of genomic sequences in living and fixed cells

09.45- 10.05 **Martina Dvorackova** (CEITEC, Czech Republic): Impact of histone chaperone genes and DNA repair pathways on rDNA stability

10.05-10.25 **Francesca Lopez** (National University of Ireland-Galway, Ireland): CRISPR-Cas9 mutagenesis unravels the role of 45s rDNA genes in *A.thaliana* development

10.25-10.45 **Aline Probst** (Université Clermont Auvergne, France): Histone H3.3 deposition pathways in *Arabidopsis thaliana*

10.45-11.05 **Iva Mozgova** (Institute of Microbiology CAS, Czech Republic): Novel roles of PRC2 in photomorphogenesis and seedling establishment

11.05-11.30 Coffee Break

11.30- 12.00 Introduction to plant science from ITC countries:
- Turkey: **Ahmet Tek** (Nigde Omer Halisdemir University)
- Russia: **Elena Salina** (Institute Cytology and Genetics SB RAS)
- Tunisia: **Moez Hanin** (University of Sfax)

12.00- 13.00 Parallel sessions for WG meeting /round table discussion

13:00-14:00 Lunch

14:00-16:25 **WG3: Structure of nuclear domains and the functional output for plant traits**
Chair: **Ales Pecinka** and **Monica Pradillo**

14.00- 14.10 Summary of WG3 activities: **Ales Pecinka** (Institute of Experimental Botany, Czech Republic) and **Monica Pradillo** (Complutense University of Madrid, Spain)

14.10- 14.45 Invited speaker: **Julio Salinas** (Centro de Investigaciones Biológicas, Madrid, Spain): To be or not to be (for plants under adverse environmental conditions). The answer is in the spliceosome

14.45- 15.05 **Moez Hanin** (University of Sfax, Tunisia): The RSS1-PP1 pathway and its role in plant tolerance to abiotic stresses

15.05- 15.25 **Kirsten Krause** (The Arctic University of Norway, Norway): *Cuscuta campestris*: A plant genome under the influence of a parasitic lifestyle



15.25- 15.45 **Tzion Fahima** (University of Haifa, Israel): Cloning of the wheat YR15 resistance gene sheds light on the plant tandem kinase-pseudokinase family

15.45- 16.05 **Ana Paula Santos** (Universidade Nova de Lisboa, Portugal): Plasticity of Epigenetics and Chromatin structure: concerted strategies for enhanced plant tolerance under stress

16.05- 16.25 **Gianluca Teano** (IBENS, France): Linker histone H1 dynamics control Arabidopsis nuclear reorganization in response to light signals.

16.25-17.00 Coffee Break

17.00- 18.00 Parallel session for Core Group Meeting

17.00-18.15 Poster session

18.15-20.15 Social event: Discovering Praha by night and free evening

Wednesday 27th February

09:00-10:30 **WG4: Storage, Data management and integrative analysis**
Chair: **Stefan Grob**

09:00-09:10 Summary of WG4 activities: **Stefan Grob** (University of Zürich, Switzerland)

09:10- 09:45 Invited Speaker **Martin Mascher** (IPK Gatersleben, Germany): Hi-C in cereals: genome assembly, structural variation and chromatin organization

09:45- 10:05 **Dariusz Plewczynski** (Centre of New Technologies, Warsaw, Poland): Chromatin looping architecture of the human genome

10:05- 10:25 **Amanda Souza-Camara** (IPK Gatersleben, Germany): Polymer simulations to understand the structure and dynamics of mitotic barley chromosomes

10:25- 10:45 **Hana Simkova** (Institute of Experimental Botany, Czech Republic): Wheat rRNA gene loci resolved by chromosome sorting, optical mapping and RNA-seq

10.45- 11.15 Coffee Break

11.15- 11.45 STSM update with **David Evans** (Oxford Brookes University, UK)

11.45- 12.00 Final Update and poster prize presentation: **Célia Baroux** (University of Zürich, Switzerland)

12.00- **Buffet lunch or Packed lunch and Exit**





Poster WG3.8

SUNFLOWER REACTION TO COMBINED BROOMRAPE – DOWNY MILDEW ATTACK – PRELIMINARY STUDY

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During the evolution plants have developed a large set of defense mechanisms against pathogens. Defense responses have been studied in details in model plant species such as *Arabidopsis*. However, to complete our understanding of resistance mechanisms, it is important to study defense responses in non-model plants, such as sunflower. In our experiment we aimed to study expression of defense-related genes in the sunflower host plant during combined infection with downy mildew and broomrape and elucidate their role in sunflower reaction to attack of different pathogens.

Downey-mildew-resistant genotype was inoculated with the pathogen and planted into the broomrape inoculated soil. For gene expression analysis, leaf samples were taken at different stages from plants with combined broomrape-downy mildew infection, plants only infected with broomrape, and control plants. Expression of defense related genes is analyzed using RT-PCR, with special focus on defensin.

Acknowledgements

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Poster WG3.9

APPROACHING DWARFING PHENOTYPE IN WHEAT BY ATAC-SEQ

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Genetic manipulation of Gibberelin (GA) metabolic pathway is a successfully used method to improve agricultural features of crops. Previously generated semidwarf durum wheat cultivar Icaro has been characterized as a GA-insensitive mutant with increased degradation of GA precursor caused by significant overexpression of GA 2-oxidase. As the nucleotide sequences of the predicted ORF of GA 2-oxidase were identical in the mutant Icaro and the original tall durum wheat variety Anhinga, we hypothesize that increased gene expression of this enzyme could result from disrupted transcriptional regulation involving non-coding DNA.

Common methods to assess the regulatory landscape of a locus involve methylome and histone modification profiling, characterizing open chromatin regions in order to map DNA regulatory elements and revealing long-range interactions between promoters and cis-regulatory DNA. We plan to employ previously developed assay for transposase-accessible chromatin with high-throughput sequencing (ATAC-seq), a method in which hyperactive Tn5 transposase loaded with DNA adaptors selectively inserts the adaptors into accessible regions within living cells. Comparison of the ATAC-seq peak profiles of the GA-2 oxidase loci in the mutant semidwarf Icaro and tall Anhinga wheat varieties could help to decipher the causative variation of chromatin organization.

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