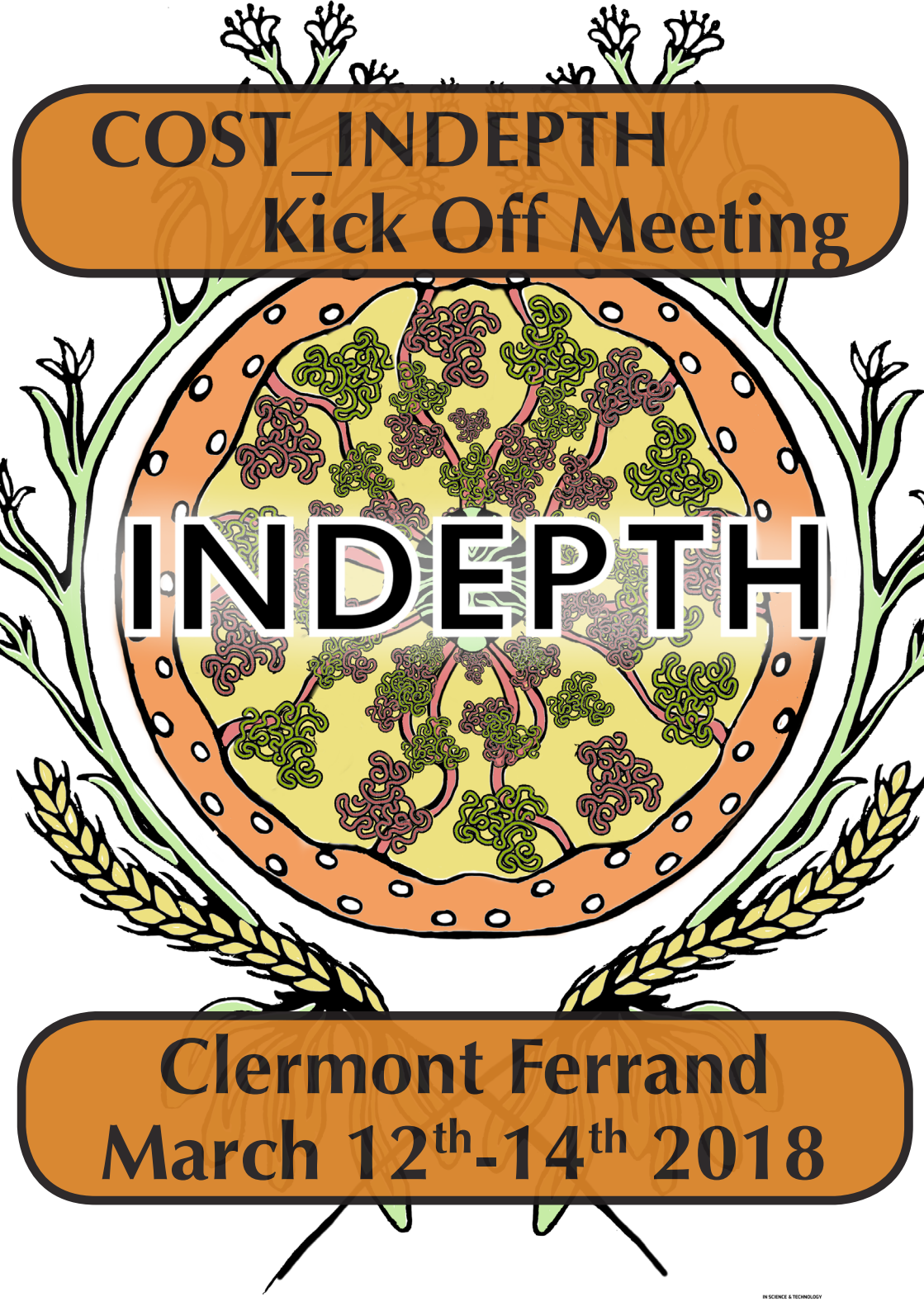
COST_INDEPTH
Kick Off Meeting



Clermont Ferrand
March 12th-14th 2018

IN SCIENCE & TECHNOLOGY

COST_INDEPTH Kickoff Meeting

Welcome to Clermont-Ferrand

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 participants to Clermont-Ferrand in the Auvergne Region. Clermont-Ferrand is famous for its very special black stone architecture in the old city centre, which is best embodied by its gothic cathedral but also because it is located in an exceptional natural environment surrounded by volcanoes.

Clermont Auvergne University and the Genetics, Reproduction and Development laboratory (GReD) are very pleased to coordinate the INDEPTH challenge. INDEPTH brings together research communities to foster integrative plant research aiming to decipher the inter-related regulatory processes interpreting the genome in model and crop species with particular emphasis on the role of nuclear domains in gene expression control.

We hope that you will enjoy your stay and wish you an interesting and motivating kick-off meeting.

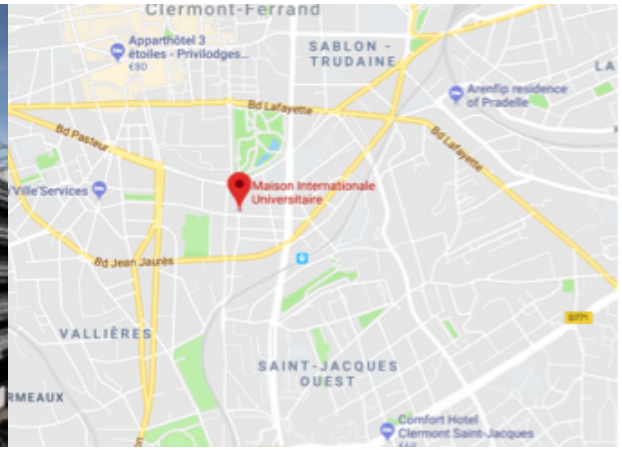
The organisers:
Aline, Claire and Christophe

COST_INDEPTH Kickoff Meeting

Meeting Information

For all meeting information please contact:
Claire Pelissier: claire.pelissier@uca.fr

The meeting will take place at:
Maison Internationale Universitaire, 9 Rue Kessler, 63000
Clermont-Ferrand (Phone: +33 4 73 29 36 00)



cost
EUROPEAN COOPERATION IN SCIENCE & TECHNOLOGY

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.

Information about GReD

GReD
génétique reproduction & développement

The GReD is a Research Unit in Clermont-Ferrand, in the Auvergne Rhône-Alpes region of France. Created in 2008, the GReD is supported by the University Clermont Auvergne (UCA), the Centre National de la Recherche (CNRS) and the Institut National de la Santé Et de la Recherche Médicale (INSERM).

UNIVERSITÉ Clermont Auvergne
cnrs advancing the frontiers
Instituts thématiques Inserm Institut national de la santé et de la recherche médicale

The GReD is situated in the Centre de Recherche Bio-Clinique (CRBC) on the campus of the Faculty of Medicine and involves around 150 researchers, teachers, students, postdocs, engineers and technicians organized in 14 research teams (https://www.gred-clermont.fr/).

Our research addresses (1) Genome dynamics and epigenetic control, (2) Reproduction and development in health and disease and (3) Endocrinology, signalling and cancer. These three research axes combine molecular and cellular biology, imaging and genetics and bridge the use of multiple model species including vertebrates, insects and plants to clinical applications to strengthen the continuum between basic and clinical research.

Axis 1 of the GReD related to the INDEPTH COST-Action aims at understanding the genetic and epigenetic programs required for development and reproduction, and how deregulation of these complex processes can result in disease.

COST_INDEPTH Kickoff Meeting

Detailed Schedule

Monday March 12th 2018

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

11:00-12:00: Arrival/Registration and Poster setup for general delegates

12:00-12:30: Welcome to the Université Clermont Auvergne (UCA) Pierre-Charles Romond (UCA Vice-president), Chantal Vaury (Head of GReD laboratory).

Official introduction to the INDEPTH COST Action:
Chair Christophe Tatout (Université Clermont Auvergne)
Vice-Chair Célia Baroux (University of Zürich)
Science Officer Ioanna Stavridou (COST programme)

12:30-13:30: Lunch

13:30-14.15: **Opening Keynote:** Daniel Schubert (Freie Universität Berlin): Chromatin Regulation At The Nuclear Envelope In Arabidopsis

14:20-17.10 **WG1:Quantitative imaging and analysis of the plant nucleus in 3D.**

14.20-14.30: Introduction: Katja Graumann (Oxford Brookes) and Dimiter Prodanov (University of Leuven)

14.30-14.50: Paul Fransz (University of Amsterdam): 3D Nuclear Organisation In *Arabidopsis thaliana*

14.50-15.05: Susan Duncan (Earlham Institute): iceFISH: a method to interrogate regulation and infer nuclear chromosome positioning in hexaploidy bread wheat

15.05-15.20: Tao Dumur (Gregor Mendel Institute): Dynamic nuclear architecture in root cells during long heat stress

15.20-15.35: Célia Baroux (University of Zürich): Role of linker histones on chromatin organisation in Arabidopsis – from the nuclear level to the nanoscale

15.35-16.30: Coffee Break

16.30-16.50: Dimiter Prodanov (University of Leuven): Segmentation and classification of cells in microscopic image

16.50-17.05: Samir Omanovic (University of Sarajevo): Framework for processing 3D+time microscopy images using fusion of artificial intelligence methods and statistics

17.05-17.20: Zofia Parteka (University of Warsaw): 3D chromatin modelling from imaging data

17.20-17.35: Christophe Tatout (Université Clermont Auvergne): Linking nuclear structure and function through 3D-imaging

17:35-19:00: Parallel WG meetings (WG1-4)

19:00-21.00: Posters with drinks and hot buffet

COST_INDEPTH Kickoff Meeting

Detailed Schedule

Tuesday March 13th 2018

8:30-9.15: **Keynote Plenary:** David Evans (Oxford Brookes): Exploring the Proteins of the Plant Nuclear Envelope

9.15-11:00: **WG4: Storage, Data management and integrative analysis**

9:15-9:25: Introduction by WG4 leaders.
Björn Grüning (University of Freiburg) and Stefan Grob (University of Zürich)

9:25-9:45: Giorgio Papadopoulos (University of Montpellier): Integrative analysis of gene expression regulatory mechanisms.

9:45-10.05: Björn Gruening (University of Freiburg): The GALAXY platform for accessible, reproducible and collaborative big-data analyses

10:05-10:20: Rémy Malgouyres (Université Clermont Auvergne): WRAPSCIENCEJ: an integrative multipurpose platform for data analysis on a distributed infrastructure.

10:20-10:35: Michał Kadlof (University of Warsaw) 3D genome modelling methods that combine genomic and epigenomic data

10.35-11.05: Coffee Break

Tuesday March 13th 2018

11.05-13.00: **WG3: Structure of nuclear domains and the functional output for plant traits.**

11:05-11:15: Introduction by WG3 leaders:
Ales Pecinka (Institute of Experimental Botany) and Monica Pradillo (University Complutense of Madrid)

11.15-11:35: Christian Chevalier (Université de Bordeaux): DNA-Dependent Fruit Growth in Tomato: Nuclear Ploidy Levels and Gene Expression

11:35-11:50: David Latrasse (Institute of Plant Sciences Paris-Saclay): MAPK-triggered chromatin reprogramming by histone deacetylase in plant innate immunity

11:50-12.05: Marta Koblowska (University of Warsaw): Time-series experiment reveals new epigenetic signature and a gene regulatory network involved in early response to salinity stress in Arabidopsis T87 cells.

12.05-12:20: Nadia Fernández (University Complutense of Madrid) The nucleoporins suppressor of Auxin Resistance (SAR1) and SAR3, and chromatin: a complex affaire during meiosis

12:20-13:30:Lunch with posters

COST_INDEPTH Kickoff Meeting

Detailed Schedule

Tuesday March 13th 2018

13.30-13:50: Isabelle Colas (James Hutton Institute): Modulation of Meiotic Recombination in Barley

13:50-14:05: Danny Geelen (Ghent University): PROTEIN PHOSHATASE 2A protects sister chromatid cohesion in Arabidopsis male meiosis I by maintaining cohesin SYN1at centromeres

14:05-14.20: Ales Pecinka (Institute of Experimental Botany): Plant chromatin organiSation under ambient and stress conditions

14:20-14:35: Serena Varotto (University of Padova): Discovering the epigenetic memory of stress response in maize

14.45-17:00: Social event- Tour of Clermont-Ferrand

17:00-17.30: Coffee Break

17:30- 18:30: **Introduction to WG5: Dissemination and Training:**
Geraint Parry (Cardiff University)
Aline Probst (Université Clermont Auvergne)

18.30-19.30: Parallel Session: Core group Meeting and Poster session

19:30-20:30: Wine reception and buffet

20:30- 22:00: Brainstorming, skills matching session and STSM discusssions
Chair: David Evans.
STSM grantees: Mariamawit Ashenafi (University of Zürich) and Gianluca Teano (IBENS Paris)

Wednesday March 14th 2018

9.00-11.45: **WG2: Transcriptional regulation through association of chromatin domains with nuclear compartments**

9.00-9.10: Introduction by WG2 Leaders. Stefanie Rosa (Swedish University of Agricultural Science) and Sara Farrona (University of Galway)

9.10-9.30: Frederic Pontvianne (Université de Perpignan): Elucidating the role of the nucleolus in the global chromatin organization

9.30-9.45: Martina Dvorácková (CEITEC, Masaryk University): Replication and Transcription inside the Nucleolus

9.45-10.00: Rafal Archacki (University of Warsaw): Mechanisms of transcriptional regulation by Arabidopsis chromatin remodeler BRM

10.00-10.15: Szymon Swiezewski (University of Warsaw): Antisense Transcription and its role in seed dormancy regulation

10.15-10.45: Coffee Break


COST_INDEPTH Kickoff Meeting

Detailed Schedule

Wednesday March 14th 2018

10.45-11.05: Chang Liu (University of Tübingen): Plant Lamin-Like Proteins And Non-CG Dna Methylation Mediate Specific Chromatin Tethering At The Nuclear Periphery

11.05-11.20: Lauriane Simon (Swedish University of Agricultural Science): A Potential New H3K9me2 Methyltransferase Acting In the Endosperm

11.20-11.35: Fredy Barneche (IBENS Paris): A linker histone variant drives light-controlled heterochromatin rearrangements in Arabidopsis

11.35-11.50: Stefan Grob (University of Zürich): Transgene Silencing in 3D – How a Chromosomal Knot Can Inactivate Foreign DNA Elements

11.50-12.30: Meeting Wrap up and Future Plans. Discussion lead: Christophe Tatout

12.30-13.30: Lunch and Exit

COST_INDEPTH Kickoff Meeting

Poster WG3.12

SEEDLINGS GROWTH AND TRANSCRIPTIONAL RESPONSES TO SALT AND DROUGHT STRESS OF MEDICAGO SATIVA L, MEDICAGO ARBOREA L. AND THEIR HYBRID (ALBOREA)

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Salinity and drought are major limiting factors of crops productivity worldwide. Medicago sativa L. is an important fodder crop with high nutritive value, broadly cultivated in different environments and is a moderately salt and drought tolerant species. On the other hand, Medicago arborea L. that is considered a stress tolerant species could be an important genetic resource for the improvement of tolerance of M. Sativa to both stresses.

The aim of the present study was to evaluate the seedling response of M. sativa, M. arborea and their hybrid (Alborea) to salt and drought stress. Three salt stress treatments (50 mM, 50-100 and 50-100-150 mMNaCl gradual acclimatization), two salt shock (100 and 150 mMNaCl) and water deficit treatment were applied to seedlings.

Growth rates and transcriptional profiles of NHX1, RCI2A, P5CS1, SMIKK, ZGF, AP2/EREBP genes were evaluated. M. sativa and M. arborea performed similarly good under stress. Alborea exceeded in productivity compared to its parents under normal conditions. Nevertheless, Alborea was extremely sensitive to stresses. M. sativa and M. arborea seem to regulate different components of tolerance mechanisms. Knowledge of the different parental mechanisms of salt and drought tolerance could play an important role into incorporating both mechanisms in their hybrid.

Poster WG3.13

RESPONSE OF SUGAR BEET GENOTYPES TO IN VITRO INDUCED WATER DEFICIT

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Sugar beet is one of the most important industrial crops. In many areas of sugar beet production, the water deficit during the summer significantly limits the root yield and the sugar content. Since breeding for drought tolerance is economically the most viable solution for overcoming this problem, it is necessary to understand the reaction of sugar beet genotypes to the conditions of water deficit. As part of an extensive study of sugar beet reaction to drought stress, this research was conducted with the aim to detect changes in growth parameters, proline content and the expression of candidate genes during the in vitro induced water deficit.

Sugar beet genotypes, selected for various responses to reduced water supply, were micropropagated on media with 0%, 3% and 5% polyethylene glycol (PEG) for 28 days. The number of axillary shoots was reduced, while the dry matter content increased with the severity of the PEG concentration. No differences were detected between shoot weight of controls and treatments in any genotype. Proline content in some genotypes did not change with increase of PEG concentration, while in others PEG treatments caused increase in proline content.

The selected candidate genes differed in relative gene expression among genotypes and applied PEG treatments. The results showed that investigated morphological, physiological and genetic parameters have potential to be used in the assessment of sugar beet tolerance to water deficit