IRN-FJFPB

Webinar « Genome dynamics and epigenetics »

June 28th, 2021

Abstracts

Main talks (20 min + 10 min)

Dr Leandro Quadrana, CR CNRS, IBENS, Paris
leandro.quadrana@bio.ens.psl.eu
https://www.ibens.ens.fr/spip.php?article277

Transposon-induced loss of DNA methylation: Some new kids on the block

Transposable elements (TEs) are typically silenced by epigenetic mechanisms, including DNA methylation in plants and mammals. In response, some TEs have evolved sophisticated mechanisms to counteract this epigenetic silencing. Kakutani's lab (the University of Tokyo) uncovered two such anti-silencing system in *Arabidopsis thaliana*, which are based on VANC proteins encoded by DNA transposons belonging to the VANDAL superfamily (Fu et al, EMBO J 2013; Hosaka et al, Nat Commun 2017). Here, I will describe our recent collaborative efforts to characterize the complete set of VANC-dependent anti-silencing systems and their target sequences in *A. thaliana*. I will also discuss the evolutionary history of this anti-silencing systems and their implications for the invasive success of this class of TEs.

Dr Sachihiro Matsunaga, Professor, University of Tokyo Pas de réponse pour diffusion des infos
sachi@edu.k.u-tokyo.ac.jp
http://park.itc.u-tokyo.ac.jp/matsunaga_lab/english/index.html
Epigenetic priming in plant regeneration

Epigenetic priming is one of the potential systems in that genes are poised for activation by external signal inputs. Although the priming does not alter the gene expression, it is considered to induce the open structure of chromatin and the poised state for future transcription. This priming is involved in stem cell differentiation, cancer development, and drug action but remains unclear in plant regeneration. We successfully identified epigenetic priming by LYSINE-SPECIFIC DEMETHYLASE 1-LIKE 3 (LDL3) that specifically eliminates H3K4me2 during the formation of callus derived from roots of *Arabidopsis thaliana*. While LDL3-mediated H3K4me2 removal does not immediately affect gene expression, it does facilitate the later activation of genes that act to form shoot progenitors after shoot induction. This finding gives insights into plant regenerative competency with epigenetic priming.

Short talks (8 min + 2 min)

1- Dr Daniel Bouyer, CR CNRS, RDP, ENS de Lyon
daniel.bouyer@ens-lyon.fr
http://www.ens-lyon.fr/RDP/epigenetique-chromatine-et-developpement/

Role of DNA methylation dynamics for reproductive success in plants

DNA cytosine methylation (5mC) is an epigenetic mark that plays critical roles in the silencing of transposable elements as well as the transcriptional regulation of genes in plants and mammals. Its active removal is an evolutionary conserved phenomenon and required for sexual reproduction in flowering plants but the molecular determinants underlying this epigenetic control are not known. Here, I will present that the DNA demethylases DEMETER (DME) and REPRESSOR OF SILENCING 1 (ROS1) act semi-redundantly in the vegetative cell of pollen to demethylate DNA and ensure proper pollen tube progression in the model plant Arabidopsis thaliana. Both demethylases target a set of pollen-specific genes, which are, at least partially, responsible for the sterility phenotype in dme and dme ros1 mutant pollen. Based on these data I will discuss the role of epigenetic regulation of reproductive genes.

2- Dr Masayuki Tsuzuki, Assistant Professor, Department of Life Sciences, Graduate School of Arts and Sciences, The University of Tokyo, Japan
mtsuzuki@bio.c.u-tokyo.ac.jp

Pervasive non-coding transcription by Pol V suggesting a genome surveillance mechanism

Non-coding transcription is a resource of functional RNAs acting on gene regulation in various molecular mechanisms. Plants have RNA-based transcriptional silencing system called RNA-directed DNA methylation (RdDM) carried out by two non-coding RNA polymerases, Pol IV and Pol V. These two polymerases are responsible for RdDM specificity on transposable element (TE) regions, however, its mechanism is not conclusive. Here, we combined a newly developed sequencing method and genomics approach to identify Pol V transcribing region. This approach revealed that Pol V transcribes more broadly than speculated, which suggests pervasive non-coding transcription. Our analysis provided a new insight about the mechanism how the specificity of RdDM is determined and a model of genome surveillance.

3- Dr Angélique Déléris, CR CNRS, Epigenetic regulation of transposable elements in Arabidopsis, Genome Biology (I2BC)
angelique.deleris@i2bc.paris-saclay.fr
https://www.i2bc.paris-saclay.fr/spip.php?rubrique224&lang=en

Investigating a non-canonical role of H3K27me3 marks at transposable elements

In plants and mammals, DNA methylation and histone H3 lysine 27 trimethylation (H3K27me3), which is deposited by the polycomb repressive complex 2, are considered as two specialized systems for the epigenetic silencing of transposable element (TE) and genes, respectively. Nevertheless, many TE sequences acquire H3K27me3 when DNA methylation is impaired, like in met1 or ddm1 Arabidopsis mutants. We have also shown that this gain of H3K27me3 observed at hundreds of TEs in the ddm1 mutant essentially depends on CURLY LEAF (CLF), one of two partially redundant H3K27 methyltransferases active in vegetative tissues. I will present the results of the analyses we performed in the double ddm1-clf mutant to study a potential role of H3K27me3 in silencing TEs in the absence of DNA methylation. I will further place these results in the context of what is known about the targetting of H3K27me3 to TEs in other organisms.

4- Ms Alice Lambolez, PhD student, RIKEN Center for Sustainable Resource Science, Japan
alice.lambolez@riken.jp

Histone modifications controlling the chronology of the wound response

(abstract not available)

5- Dr Olivier Da Ines, CR CNRS, GReD Génétique, Université Clermont Auvergne
UMR CNRS 6293 - Université Clermont Auvergne - INSERM U1103
olivier.da_ines@uca.fr
https://www.gred-clermont.fr/directory/team/en/team-05-recombination-and-maintenance-of-genome-integrity/

RAD54 is essential for RAD51-mediated repair of meiotic DSB in Arabidopsis

Homologous recombination is a universal pathway which repairs broken DNA molecules through the use of homologous DNA templates. It is both essential for maintenance of genome stability and for the generation of genetic diversity through sexual reproduction. A central step of the homologous recombination process is the search for and invasion of a homologous, intact DNA sequence that will be used as template. This key step is catalysed by the RAD51 recombinase in somatic cells and the two DNA strand-exchange proteins RAD51 and DMC1 in meiotic cells, assisted by a number of associated factors. Among these, the chromatin-remodelling protein RAD54 is a required cofactor for RAD51 in mitotic cells. Understanding of its role during meiotic recombination has however remained elusive. Using a combination of genetic and cytogenetic approaches, we show that absence of RAD54 has no detectable effect on meiotic recombination in otherwise wild-type plants but becomes essential for meiotic double strand break repair by RAD51 in absence of DMC1. We further show that this function is downstream of the meiotic role of RAD51 in supporting the activity of DMC1. Our findings have several interesting implications for the regulation of the strand invasion step during meiotic recombination in plants, and very probably also other multicellular eukaryotes.

6- Dr Hidenori Takeuchi, Designated Assitant Professor, Institute for Advanced Research, Nagoya University, Japan
hidenori.takeuchi@itbm.nagoya-u.ac.jp

Centromeric chromatin dynamics in the fertilization process of Arabidopsis

Hidenori Takeuchi[1,2], Shiori Nagahara[2], Frédéric Berger[3], Tetsuya Higashiyama[2,4,5]
[1] Institute for Advanced Research, Nagoya University, Japan
[2] Institute of Transformative Bio-Molecules, Nagoya University
[3] Gregor Mendel Institute of Molecular Plant Biology, Austria
[4] Graduate School of Science, Nagoya University
[5] Graduate School of Science, University of Tokyo

In eukaryotes, epigenetic marks including histone variants are essential for chromatin maintenance and function. During reproductive processes, some epigenetic marks are dynamically reprogrammed to establish proper chromatin states for the next generation. In flowering plants, the egg cell inside the ovule is fertilized by one of two sperm cells generally delivered by a pollen tube in a species-specific manner, and develops into a zygote and then embryo. However, it remains unclear how female and male chromatin are regulated after fertilization and what is the key for a species-specific mechanism of chromatin maintenance.

To investigate dynamics and recognition mechanisms of chromatin in the fertilization processes of flowering plants, we focus on the centromere-specific histone H3 variant, CENH3, which is commonly used for chromosome segregation during mitosis and meiosis in eukaryotes and shows diverged amino-acid sequences between species. Here, we show the dynamics of CENH3 and surrounding heterochromatin marks in zygote/embryo development of *Arabidopsis thaliana* by the live-cell imaging using multiphoton-excited fluorescence microscope and ovule culture systems. Using several mutants defective in the heterochromatin formation, we are trying to understand the regulatory network among chromatin marks and its importance in zygote/embryo development.

7- Jacinthe Azevedo-Favory, CR CNRS, Laboratoire Génomes et Développement des Plantes, UMR5096, CNRS/UPVD, Perpignan, FRANCE
jacinthe.azevedo-favory@univ-perp.fr
http://lgdp.univ-perp.fr/index.php?page=equipe-2

Exploring the role of a new plant specific WG/GW protein family in response to heat stress

AZEVEDO FAVORY Jacinthe1, ALART Emilie1. PICART Claire1, LAUDIE Michèle, PONTIER Dominique, VIGNOLS Florence3, HAKIMI Mohamed-Ali2, LAGRANGE Thierry1
1 Laboratoire Génomes et Développement des Plantes, UMR5096, CNRS/UPVD, Perpignan, FRANCE
2 Host-Pathogen Interactions and Immunity to Infections, Institute for Advanced Biosciences (IAB), UMR5309 INSERM/CNRS/Université Grenoble Alpes, Grenoble, FRANCE
3 Biochimie et Physiologie Moléculaire des Plantes, University of Montpellier, Centre National de la Recherche Scientifique, Institut National de la Recherche Agronomique, SupAgro, 34060 Montpellier, FRANCE

Plants evolved to acquire sophisticated and specialized RNA silencing pathways, leading to sequence specific regulations through Argonaute effector proteins guided by small RNAs (sRNA), targeting either DNA or RNA. Our lab contributed to the development of an original aspect highlighting the existence of an evolutionary GW-rich conserved motif in factors implicated in AGO action, and defined as "Ago hook" proteins. In order to propose a systematic, cross-species approach to the identification of Ago-hook proteins, we developed a bioinformatic screen based on the presence of a GW/WG dipeptide in a compositionally-biased environment. Among candidates identified in A. thaliana, one protein family stands out from factors previously described. This new protein family, composed of two members, is conserved among angiosperms and presents no other known functional domain. Whereas first evidences confirm their AGO-hook properties, our last breakthroughs lead to us to reconsider their role at the crossroads of RNA silencing and abiotic stress regulation pathways, thereby raising many questions at this stage of our work.