Cinquième réunion du GDR Architecture et Dynamique Nucléaire (ADN)

Rapport sur les contributions

https://indico.in2p3.fr/e/gdradn2016

ID de Contribution: **0** Type: **Non spécifié**

3D nuclear positioning of IGF2 alleles and trans interactions with imprinted genes

jeudi 31 mars 2016 15:00 (30 minutes)

Summary

To explore the relationship between gene activity and nuclear position, genomic imprinting leading to parental-specific expression offers a good model. In one cell, it is possible to compare the nuclear environment of the two alleles for a given locus and search for a potential correlation between their nuclear position and expression status. Using 3D RNA-DNA FISH in porcine fetal liver cells, we focused on the imprinted region of Insulin-like growth factor 2 (IGF2), a paternally expressed gene located on porcine chromosome 2. We investigated the interchromosomal interactions implicating IGF2. Through a 2D FISH screening, imprinted genes from the Imprinted Gene Network (Varrault et al 2006) were tested for interactions in liver cells. The locus DLK1/MEG3 showed the highest rate of colocalization with IGF2. By 3D RNA-DNA FISH combined to confocal microscopy, we demonstrated a preferential implication of the expressed paternal IGF2 allele in a trans association with DLK1/MEG3 region (chromosome 7). We showed that this colocalization occurs also in fetal muscle and demonstrated that it occurs preferentially between the expressed IGF2, DLK1 and MEG3 alleles. We are extending this analysis through an interdisciplinary approach to develop large "functional mapping "studies focused on the mechanisms involved in the transcriptional regulation of genes expressed in muscle during late fetal development.

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Co-auteurs: M. ROBELIN, David (INRA); Mlle MOMPART, Florence (INRA); M. ACLOQUE, Hervé (INRA); Mme LIAUBET, Laurence (INRA); Mlle MARTI MARIMON, Maria (INRA); Mme BOUISSOU--MATET YERLE, Martine (INRA); M. FOISSAC, Sylvain (INRA); M. VOILLET, valentin (INRA)

Orateur: Mme LAHBIB-MANSAIS, Yvette (INRA)

Classification de Session: Mammifères

ID de Contribution: **1** Type: **Non spécifié**

Replication landscape of the human genome

jeudi 31 mars 2016 14:00 (30 minutes)

Summary

Despite intense investigation, human replication origins and termini remain elusive. Existing data have shown strong discrepancies. Here we sequenced highly purified Okazaki fragments from two cell types and, for the first time, quantitated replication fork directionality and delineated initiation and termination zones genome-wide. Replication initiates stochastically,primarily within non-transcribed, broad (up to 150 kb) zones that often abut transcribed genes, and terminates dispersively between them. Replication fork progression is significantly co-oriented with the transcription. Initiation and termination zones are frequently contiguous,
sometimes separated by regions of unidirectional replication. Initiation zones are enriched in open chromatin and enhancer marks, even when not flanked by genes, and often border 'topologically associating domains'(TADs). Initiation zones are enriched in origin recognition complex (ORC)-binding sites and better align to origins previously mapped using bubble-trap than lambda-exonuclease. This novel panorama of replication reveals how chromatin and transcription modulate the initiation process to create cell-type-specific replication programs.

Auteur principal: Dr HYRIEN, Olivier (IBENS)

Co-auteurs: Dr CHEN, Chun-Long (I2BC); Dr THERMES, Claude (I2BC); Dr KAHLI, Malik (IBENS); Dr SILVAIN, Maud (I2BC); Mme PETRYK, Nataliya (IBENS); Dr JASZCZYSZYN, Yan (I2BC); M. SHEN, Yimin (I2BC); Dr D'AUBENTON-CARAFA, Yves (I2BC)

Orateur: Dr HYRIEN, Olivier (IBENS)

Classification de Session: Mammifères

ID de Contribution: **2** Type: **Non spécifié**

Epigenomics in 4D: a functional role for the dynamic coupling between epigenome and chromatin organization

vendredi 1 avril 2016 12:00 (30 minutes)

Summary

Cellular differentiation occurs during the development of multicellular organisms and leads to the formation of many different tissues where gene expression is modulated without modification of the genetic information. These modulations are in part encoded by chromatin-associated proteins or biochemical tags that are set down at the chromatin level directly on DNA or on histone tails. These markers are directly or indirectly involved in the local organization and structure of the chromatin fiber, and therefore may modulate the accessibility of DNA to transcription factors or enzymatic complexes, playing a fundamental role in the transcriptional regulation of gene expression. Statistical analysis of the repartition of this epigenomic information along the chromosomes have shown that genomes of higher eukaryotes are linearly partitioned into domains of functionally distinct chromatin states. In particular, experimental evidence has shown that the pattern of chromatin markers along chromosomes is strongly correlated with the 3D chromatin organization inside the nucleus. This suggests a coupling between epigenomic information and large-scale chromatin structure that could statistically quantified. Recently, using polymer physics and numerical simulations, we showed that attractive interactions between loci of the same chromatin state might be the driving forces of the folding of chromatin inside the nucleus. In this study, we assumed that the epigenomic information pre-exists to the 3D organization. However, increasing number of experimental results suggests that chromatin marks are themselves highly dynamic during cell cycle or developmental stages and that 3D organization of chromatin might play a key role in the stabilization and function of chromatin markers. We will describe our efforts to better understand the dynamical crosstalk between the epigenome and the 3D organization and we will illustrate the modularity of our framework in several biological contexts. In particular, we show that epigenomic-driven contacts and the formation of interacting compartments coupled to a reader-writer mechanism of epigenetic maintenance lead to a better and more robust control of epigenome, suggesting that 3D organization of chromosome plays a functional role at the epigenetic regulation level.

Auteurs principaux: Dr JOST, Daniel (CNRS TIMC-IMAG); Dr VAILLANT, cedric (Laboratoire de Physique ENS de Lyon CNRS)

Orateur: Dr JOST, Daniel (CNRS TIMC-IMAG)

Classification de Session: Drosophile + mammifères

ID de Contribution: **3** Type: **Non spécifié**

Polymer model of supercoiled molecules including multiple structural forms of DNA

vendredi 1 avril 2016 09:30 (30 minutes)

Summary

DNA supercoiling lies at the core of transcriptional regulation. Except for a few cases, capturing its impact in vivo remains elusive, though. Supercoiling is indeed distributed in a non-trivial way between twist, writhe (plectonemes) and change of structural forms of DNA (including denaturation) and depends, a priori, on genomic sequences. In this talk, we will present a polymer model of DNA that allows studying these properties quantitatively. We will show in particular the possibility to study the behavior of DNA sequences whose length corresponds typically to the topological microdomains that have been experimentally highlighted in *Escherichia coli* and *Salmonella typhimurium*.

Auteurs principaux: M. JUNIER, Ivan (LAPM - CNRS UMR 5163 - Université Grenoble 1 - Grenoble); LEPAGE, Thibaut (LAPM - CNRS UMR5163)

Orateur: LEPAGE, Thibaut (LAPM - CNRS UMR5163)

Classification de Session: Unicellulaires

ID de Contribution: **4** Type: **Non spécifié**

Identification et fonction des domaines chromatiniens associés au nucléole chez Arabidopsis thalianaidopsis thaliana

jeudi 31 mars 2016 16:30 (30 minutes)

Summary

The nucleolus is the site of ribosomal RNA (rRNA) genes transcription, processing and ribosome biogenesis. However, the nucleolus contains much more than rRNA genes. Using a technique designed to isolate nucleoli by Fluorescence Assisted Cell Sorting (FACS) from any plant tissue, we have identified genomic Nucleolus-Associated Domains (NADs) from Arabidopsis thaliana leaves. NADs are essentially composed of genomic regions with silent chromatin signatures. Excluding rRNA genes, NADs contain 11% of A. thaliana transposable elements and 3% of A. thaliana genes. Analyses of NADs in plant cells with affected nucleolus structure reveal how NADs composition is dependent of rRNA genes expression and the nucleolus structure. Our data also suggest a role of the nucleolus in telomere maintenance and/or protection. Finally, our analyses reveal that some NADs are composed of genes and an important fraction of them are unexpressed. Because RNA polymerase II is excluded from the nucleolus, we propose the existence of a new way to regulate gene transcription by nucleolar sequestration.

Auteur principal: Dr PONTVIANNE, Frédéric (LGDP CNRS/UPVD)

Co-auteurs: Prof. PIKAARD, Craig (Indiana University in Bloomington / HHMI); Prof. FAJKUS, Jiri (CEITEC-Central European Institute of Technology and Faculty of Science, Masaryk University); Dr SAEZ-VASQUEZ, Julio (LGDP CNRS/UPVD); Mlle CARPENTIER, Marie-Christine (LGDP CNRS/UPVD); Dr DURUT, Nathalie (LGDP CNRS/UPVD); Mme PAVLIŠTOVÁ, Veronika (LGDP CNRS/UPVD)

Orateur: Dr PONTVIANNE, Frédéric (LGDP CNRS/UPVD)

Classification de Session: Plantes

ID de Contribution: **5** Type: **Non spécifié**

Dynamic spatial genome conformation modeled from lamin-associated domains and chromosome-chromosome interactions

jeudi 31 mars 2016 14:30 (30 minutes)

Summary

Understanding how three-dimensional (3D) genome organization influences gene expression is a challenge in genome biology. Chromatin conformation is regulated by intra- and inter-chromosomal interactions and by dynamic interactions of chromatin with nuclear lamins, at the nuclear periphery and in the nuclear interior [1-3]. Chromosome-chromosome interactions are also dynamic and under the influence of stochastic and regulated processes. These premises challenge the deconvolution of individual spatial association patterns from HiC and ChIP data aggregated from millions of cells. We report a new computational strategy to infer 3D chromatin structure based on integrated modeling of lamin-associated domains (LADs) mapped by ChIP-seq of A- and B-type lamins and 3D chromosomal interactions networks identified by high-resolution HiC. The premise of our modeling are a bead-on-a-string model with beads containing topologically-associated domains (TADs), with some TADs associated with A- or B-type lamins, and others not. The modeling framework includes a scoring function incorporating HiC, LAD and nucleus shape constraints, and a set of allowed chromosome moves. The sampling method relies on a computationally-efficient Metropolis Hastings Monte Carlo algorithm. Resulting 3D models respect the notion of chromosome territories. Our models enable an elucidation of the interplay between chromosomal interactions at the nuclear periphery and in the nuclear interior. We notably identify lamin-associated TADs constitutively associated with the nuclear periphery, TADs constitutively localized in the nuclear interior, and hyper-dynamic TADs with variable spatial positioning. Integration of multiple datasets with increasingly performant computation techniques [4] will be essential to underpin the complexity of spatial genome conformation in dynamic systems such as differentiating stem cells.

[1] Lund et al. 2013. Genome Res 23, 1580-1589
[2] Lund et al. 2015. Nucleus 6, 30-39
[3] Rønningen, Shah et al. 2015. Genome Res, PMD 26359231
[4] Paulsen et al. 2015. PLoS Comput Biol 11, e1004396

Auteur principal: Prof. COLLAS, Philippe (University of Oslo)

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Orateur: Prof. COLLAS, Philippe (University of Oslo)

Classification de Session: Mammifères

ID de Contribution: **6** Type: **Non spécifié**

Effects of Hfq on the conformation and compaction of DNA.

vendredi 1 avril 2016 10:00 (30 minutes)

Summary

Hfq is a bacterial pleiotropic regulator that mediates several aspects of nucleic acids metabolism. Our recent results show that E. coli Hfq changes the mechanical properties of the double helix to compact DNA into a condensed form, its mechanism being mainly based on protein-mediated bridging of DNA segments [1].
Structurally, the E. coli Hfq is organized into two domains. An N-terminal domain, that assembles into a typical toroidal hexameric ring. A C-terminal flexible domain, that encompasses about one-third of the protein and is predicted as intrinsically disordered. We recently demonstrated that this region has the intrinsic property to self-assemble into long amyloid-like fibrillar structures [2]. The mechanisms of Hfq-CTR self-assembly and the effect of this self-assembly on DNA compaction will be presented herein.
Compaction repercussions are particularly important as they usually occur in promoters, and thus influence the transcription start and efficiency. Our results thus shed a new light on a plausible central role of Hfq in DNA transactions in general.

[1] Jiang K, Zhang C, Guttula D, et al. Effects of Hfq on the conformation and compaction of DNA. Nucleic Acids Research. 2015;43(8):4332-4341. doi:10.1093/nar/gkv268.
[2] Fortas E, Piccirilli F, Malabirade A, et al. New insight into the structure and function of Hfq C-terminus. Bioscience Reports. 2015;35(2):e00190. doi:10.1042/BSR20140128.

Auteur principal: M. MALABIRADE, Antoine (Laboratoire Léon Brillouin CEA/CNRS - Université Paris Saclay)

Co-auteurs: Dr LAVELLE, Christophe (CNRS); M. KUBIAK, Krzysztof (University Paris Sud and University of Gdansk); Dr ARLUISON, Veronique (Université Paris Diderot)

Orateur: M. MALABIRADE, Antoine (Laboratoire Léon Brillouin CEA/CNRS - Université Paris Saclay)

Classification de Session: Unicellulaires

ID de Contribution: **7** Type: **Non spécifié**

Dynamique de la méthylation de l'ADN en temps réel lors de la reproduction chez les plantes

jeudi 31 mars 2016 17:00 (30 minutes)

Summary

Cytosine methylation (mC) is an epigenetic mark playing key roles for transcriptional control and genome integrity in plants and mammals. During mammalian reproduction, DNA methylation is reprogrammed to notably facilitate the acquisition of zygotic totipotency.In plants, it is still a debate whether DNA methylation reprogramming takes place as methylome of reproductive cells is only partial. To track DNA methylation dynamics during plant reproduction, we generated genetically encoded fluorescent sensors called DYNAMET that selectively report mCG and mCHH methylation. Although global CG methylation pattern remains stable throughout male and female sporogenesis, a marked reduction of CG methylation was observed in the egg cell that was rapidly restored in the young embryo. In contrast, we detected rapid and massive loss and regain cycles of CHH methylation during male and female germline formation. Genetic analyses indicate that the DNA methyltransferase DOMAINS REARRANGED METHYLTRANSFERASE 2 (DRM2), ortholog of mammalian Dnmt3, is the key enzyme depositing CHH methylation in the egg cell, in a cell-specific, siRNA-independent manner.
Our DNA methylation reporters provide unprecedented insights into global DNA methylation dynamics at the single cell level that could potentially be used in living mammalian cells.

Auteur principal: Dr INGOUFF, Mathieu (Université de Montpellier -IRD)

Co-auteurs: Dr SELLES, Benjamin (IRD); Mme MICHAUD, Caroline (IRD); Dr GRIMANELLI, Daniel (IRD); Dr AUTRAN, Daphné (IRD); M. VAN DURME, Matthias (VIB); Dr NOWACK, Moritz (VIB)

Orateur: Dr INGOUFF, Mathieu (Université de Montpellier -IRD)

Classification de Session: Plantes

ID de Contribution: **8** Type: **Non spécifié**

Le HRS-seq : une nouvelle méthode d'analyse à haut-débit des séquences génomiques associées aux compartiments nucléaires

vendredi 1 avril 2016 12:30 (30 minutes)

Summary

Notre équipe s'intéresse à l'exploration de l'organisation de la chromatine à l'échelle supranucléosomale et à sa dynamique in vivo dans différents contextes physiologiques ou pathologiques, afin de comprendre comment ce niveau d'organisation génomique participe au contrôle et à la coordination de l'expression des gènes chez les mammifères. Nous avons montré qu'en absence de toute interaction spécifique à longue distance, l'organisation génomique à l'échelle supranucléosomale subit des contraintes qui conduisent à une modulation périodique des fréquences de contacts à l'intérieur des Domaines d'Association Topologiques (TADs) riches en gènes. Selon les loci, un repliement fonctionnel en boucle de chromatine, en lien avec les fonctions génomiques (transcription, réplication⋯), serait ensuite réalisé par des facteurs spécifiques et/ou par un recrutement à l'intérieur de compartiments nucléaires permettant un confinement de certaines régions chromatiniennes. Cependant, la plupart des compartiments nucléaires sont extrêmement difficiles à purifier et, lorsqu'elles existent, les méthodes permettant d'obtenir une vision globale des régions génomiques qui leur sont associées sont très délicates à maîtriser.

Nous présenterons ici une nouvelle méthode nommée HRS-seq, simple et directe, permettant de cartographier et d'analyser à l'échelle génomique les séquences associées aux compartiments nucléaires grâce à des traitements à haute concentration saline (HRS= High-salt Recovered Sequences) de noyaux cellulaires transcriptionnellement actifs. Nous avons appliqué la méthode HRS-seq sur un modèle de différenciation des cellules souches embryonnaires de souris en cellules de précurseurs neuraux et en neurones (collab. avec T. Bouschet/L. Journot, IGF, Montpellier, France) ainsi que sur des cellules de foies murins. Nous montrons que les HRS sont étroitement associées à des gènes fortement exprimés dont une analyse ontologique indique qu'ils sont intimement liés au type cellulaire. Parmi les HRS communes à tous les types cellulaires analysés, nous trouvons les gènes des histones, suggérant que les Corps des Loci Histones (une classe particulière de corps de Cajal) sont retenus par le test HRS. Nous trouvons aussi des séquences connues pour être associées à d'autres compartiments nucléaires tel que le nucléole (gènes des récepteurs olfactifs) et aussi peut-être les « paraspeckles » et les « nuclear speckles » (gènes Neat1 and Malat1). De plus, grâce à une analyse des données Hi-C disponible dans la littérature (collab. avec A. Cournac/J. Mozziconacci, UPMC, Paris, France), nous montrons que les HRS ont une forte probabilité de contact dans l'espace tridimensionnel du noyau.

Finalement, ces résultats nous permettent de valider notre approche expérimentale et de démontrer que la méthode HRS-seq constitue un outil simple, puissant et prometteur pour l'analyse détaillée de la composition génomique de plusieurs compartiments nucléaires et de leurs impacts sur la régulation de l'expression génique au cours de la détermination cellulaire chez les mammifères.

Auteur principal: Dr BAUDEMENT, Marie-Odile (IGMM-CNRS-UMR5535)

Orateur: Dr BAUDEMENT, Marie-Odile (IGMM-CNRS-UMR5535)

Classification de Session: Drosophile + mammifères

ID de Contribution: **9** Type: **Non spécifié**

Genome architecture and dynamics during S. cerevisiae's cell cycle.

vendredi 1 avril 2016 09:00 (30 minutes)

Summary

Improper genome organization can compromise the functional regulation of DNA related metabolic processes, and lead to chromosome instability and genomic diseases such as premature aging or cancer. Chromosome organization can notably affect the fidelity of repair pathways and promote for instance ectopic recombination between non-allelic sequences. The influence of 3D organization on genomic stability is likely to change during the cell cycle. Nevertheless, genome-wide descriptions of the dynamic reorganization of eukaryotic chromosomes during the cell cycle remain limited, preventing to fully address its impact. Working with synchronized populations of cells, we aimed at providing a comprehensive picture of the overall 3D organization of *Saccharomyces cerevisiae*'s genome during the cell cycle. We therefore capture chromosomal interactions using chromatin conformation capture experiments (Hi-C) of yeast populations synchronized in G1, S phase, G2 and different mitosis stages. The comparative analysis of chromosome organization at several time points in combination with modeling approaches provides a genomic overview of many results obtained through studies performed with imaging and genetic methods, while unveiling new aspects of genomic condensation and segregation. The high-resolution data constitutes a resource for any lab aiming at investigating DNA-related metabolic processes in light of 3D genome organization.

Auteur principal: Mlle LAZAR STEFANITA, Luciana (Institut Pasteur)

Orateur: Mlle LAZAR STEFANITA, Luciana (Institut Pasteur)

Classification de Session: Unicellulaires

ID de Contribution: **10** Type: **Non spécifié**

Predicting 3D folding of the fly epigenome

vendredi 1 avril 2016 11:30 (30 minutes)

Summary

In 2012 the first genome-wide simulation of the Yeast nucleus has been published (Wong & al, Current Biology 2012}. They have shown we can retrieve the experimental Hi-C map with a polymer brush modelling of the Yeast chromosomes. In the case of Drosophila melanogaster it has been shown (Sexton & al, Cell 2012) long genomic distance contact and specific patterns of the Hi-C map that cannot be reproduced only by chromosome territories.
Since high-throughput techniques become available, we are able to distinguish epigenetic domains with the study of regulatory proteins like in Drosophila (Filion & al, Cell 2010).
Heterochromatin can be divided in one part in which most of the genes are silenced (called black chromatin), another part associated to Polycomb like proteins that recognise H3K27me3 mark that is involved in the regulation of differentiation and development (called blue chromatin).
The third part of heterochromatin is associated with the HP1 proteins that act like a docking platform for functional proteins (Greil & al, The EMBO Journal 2007) (called green chromatin).
The last domain is the euchromatin in which most of the genes are actives (H4K4me1,2,3 gene activation marks).
We present here a chromosome-polymer model and the corresponding simulations based on the "physical epigenetic interactions"and on the Rabl initial conformation of the chromosomes of the Drosophila melanogaster epigenome 3D folding.

Auteurs principaux: Dr JOST, Daniel (CNRS TIMC-IMAG); Dr CAVALLI, Giacomo (CNRS); M. CARRIVAIN, Pascal (ENS Lyon); Prof. EVERAERS, Ralph (ENS-Lyon); Dr VAILLANT, cedric (Laboratoire de Physique ENS de Lyon CNRS)

Orateur: M. CARRIVAIN, Pascal (ENS Lyon)

Classification de Session: Drosophile + mammifères

ID de Contribution: **15** Type: **Non spécifié**

Discussion libre

vendredi 1 avril 2016 13:00 (30 minutes)

Classification de Session: Drosophile + mammifères

ID de Contribution: **16** Type: **Non spécifié**

The GIP proteins, key actors at the nuclear periphery for centromere regulation in plants

jeudi 31 mars 2016 17:30 (30 minutes)

Summary

The nuclear envelope is not only a site of molecular exchange between cytoplasm and nucleoplasm through nuclear pores, but it is also functionally linked to key cellular processes such as cytoskeleton organization, 3D nuclear architecture and chromatin regulation.

In Arabidopsis cycling cells, the nuclear envelope is a site of microtubule nucleation and is also involved in nuclear movements. The presence of a nuclear plamina, considered as the human homologue of the lamina, was also related to chromocentre regulation. Chromocentres are mainly constituted of pericentromeric heterochromatin located in the close vicinity of the inner nuclear membrane. Centromeres are embedded in these chromocentres and require a tight regulation to maintain their identity, allowing further spindle fibre connexions.

We identified GCP3-Interacting Proteins (GIP1 and GIP2) and characterized their association with γ-tubulin complexes (1) as shown their human and fission yeast homologues. Besides the localization of GIPs at microtubule arrays, GIPs are also present on both sides of the nuclear envelope in plants. gip1gip2 KD mutants showed pleiotropic developmental phenotypes suggesting their involvement in various cellular functions. Indeed, these mutants are strongly affected in nuclear shaping and organization (2) as well as centromere organization (3).

We demonstrated that GIPs form a complex with CENH3 - the epigenetic marker of the centromere - using co-IP and colocalization assays with interphase nuclei. A decreased CENH3 loading was observed in the mutants beside high level of KNL2, the epigenetic regulator of CENH3 loading. This argues in favour of a role of GIPs in CENH3 loading and/or maintenance.

Centromere maintenance was also affected in the mutant where both centromeric and pericentromeric cohesion were reduced as shown by FISH experiments using specific probes on flow sorted nuclei.

Altogether, our data focused on the nuclear periphery provide a novel centromere regulatory model that needs to be further deciphered and explored in other Eukaryote organisms in which GIP proteins are conserved.

(1) Janski et al., Plant Cell, 2012

(2) Batzenschlager et al., Front. Plant Sci, 2013

(3) Batzenschlager et al., Proc. Natl. Acad. Sci. USA

Auteur principal: Dr CHABOUTÉ, Marie-Edith (CNRS-IBMP, Strasbourg)

Co-auteurs: Dr BERR, Alexandre (IBMP, CNRS Strasbourg); Prof. SCHMIT, Anne-Catherine (MP-UDS, Strasbourg); Dr HERZOG, Etienne (IBMP, UDS-Strasbourg); Dr HOULNÉ, Guy (IBMP, Strasbourg); Dr LERMONTOVA, Inna (IPK,Gatersleben); Dr FUCHS, Joerg (IPK, Gatersleben); Dr BATZENSCHLAGER, Morgane (IBMP, Strasbourg); Prof. FRANSZ, Paul (SILS, University of Amsterdam); Dr SCHUBERT, Veit (IPK, Gatersleben)

Orateur: Dr CHABOUTÉ, Marie-Edith (CNRS-IBMP, Strasbourg)

Classification de Session: Plantes

ID de Contribution: **17** Type: **Non spécifié**

Fermeture/ouverture de bulles de dénaturation dans l'ADN en solution

vendredi 1 avril 2016 10:30 (30 minutes)

Summary

The issue of the nucleation and slow closure mechanisms of non-superhelical-stress-induced denaturation bubbles in DNA is addressed by using coarse-grained MetaDynamics simulations. A minimal mesoscopic model is proposed, where the double helix is made of two interacting bead-spring rotating strands, with a prescribed realistic torsional modulus in the duplex state. The timescales for the nucleation and closure of an approximately 10 base-pair bubble are shown to be in agreement with experimental available values, and are associated with the crossing of free-energy barriers of 22 kBT and 13 kBT, respectively, at room temperature. MetaDynamics allows us to highlight the limiting step, a collective twisting, that controls the nucleation/closure mechanism, and to access opening time scales on the millisecond range. A special amphasis will be made between these long-lived equilibrated denaturation bubbles (with a lifetime on the microsecond time-scale) and much more short-lived breathers, which survive less than a nanosecond.

Auteur principal: Prof. DESTAINVILLE, Nicolas (Univ. Toulouse III-Paul Sabatier)

Orateur: Prof. DESTAINVILLE, Nicolas (Univ. Toulouse III-Paul Sabatier)

Classification de Session: Unicellulaires

ID de Contribution: **18** Type: **Non spécifié**

The Arabidopsis thaliana mobilome and its impact at the species level

jeudi 31 mars 2016 18:00 (30 minutes)

Summary

Transposable elements are powerful motors of genome evolution yet a comprehensive assessment of the "mobilome" and its impact at the species level is lacking. Here, using genome sequencing data for 211 *Arabidopsis thaliana* accessions taken from across the globe, we uncover thousands of recent transposition events originating from almost half of the 326 transposable element families annotated in this plant species. Furthermore, we show that mobilome activity varies extensively between accessions in relation to both climate and genetic factors. Transposition often occurs near or within genes, with consequences on their expression and DNA methylation status. Remarkably, loci controlling adaptive responses to the environment such as pathogen resistance and flowering time are the most frequent transposition targets observed. Our findings reveal the pervasive, species-wide impact that a rich mobilome can have and demonstrate the importance of transposition as a recurrent source of rare alleles with large effects.

Auteur principal: Dr QUADRANA, Leandro (IBENS)

Co-auteurs: Dr SILVEIRA, Amanda (IBENS); Dr COLOT, Vincent (IBENS)

Orateur: Dr QUADRANA, Leandro (IBENS)

Classification de Session: Plantes

ID de Contribution: **19** Type: **Non spécifié**

Spatiotemporal organization and expression of the genome —a live-cell single-RNA imaging approach

jeudi 31 mars 2016 15:30 (30 minutes)

Summary

Heterogeneities in nuclear organization are present at all scales. From whole chromosomes to single loci, the genome assumes a hierarchy of reproducible but probabilistic spatial patterns in the nuclear space –defining concepts such as chromosome territories, nuclear compartments, topological domains and chromatin loops. Related to this notion of spatial heterogeneity, is the idea temporal heterogeneity, such as the fact that the transcription of many eukaryotic genes occurs non-uniformly over time as discrete bursts of transcript synthesis, and more generally the idea that the genome does not function at equilibrium and is organized and expressed in a dynamic and probabilistic fashion.

My research focuses on understanding these heterogeneities in the organization of the nucleus and the expression of the genome using a panel of approaches, from computational modeling to live-cell microscopy. In particular, we use an imaging approach (MS2 and PP7 RNA labeling) to visualize single RNAs in multiple colors in living cells. This technique allows following over time the amount of nascent transcripts from one or several gene(s) of interest as well as their position in the nuclear space. We also developed an analysis method to reveal, from the resulting time traces, the kinetic relationship and coordination between the underlying molecular processes. I will first present my earlier work on the kinetics of transcription and RNA processing, before describing the future plans for my group in studying the relationship between transcriptional regulation and the physical organization of the genome in the nuclear space.

Auteur principal: Dr COULON, Antoine (Institut Curie - CNRS)

Orateur: Dr COULON, Antoine (Institut Curie - CNRS)

Classification de Session: Mammifères