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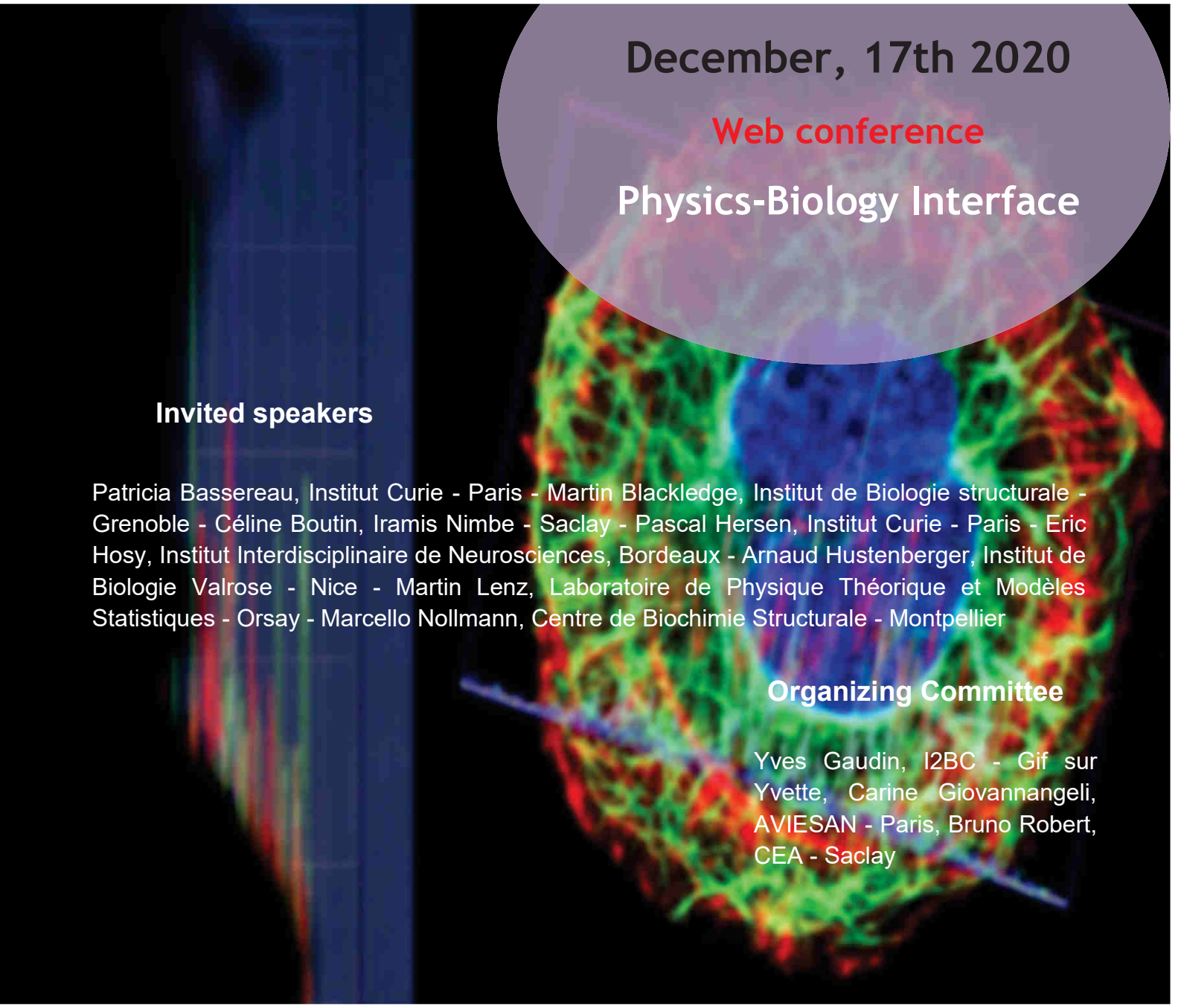
ITMO BASES MOLÉCULAIRES ET STRUCTURALES DU VIVANT



December, 17th 2020

Web conference

Physics-Biology Interface

Invited speakers

Patricia Bassereau, Institut Curie - Paris - Martin Blackledge, Institut de Biologie structurale - Grenoble - Céline Boutin, Iramis Nimbe - Saclay - Pascal Hersen, Institut Curie - Paris - Eric Hosy, Institut Interdisciplinaire de Neurosciences, Bordeaux - Arnaud Hustenberger, Institut de Biologie Valrose - Nice - Martin Lenz, Laboratoire de Physique Théorique et Modèles Statistiques - Orsay - Marcello Nollmann, Centre de Biochimie Structurale - Montpellier

Organizing Committee

Yves Gaudin, I2BC - Gif sur Yvette, Carine Giovannangeli, AVIESAN - Paris, Bruno Robert, CEA - Saclay

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ITMO BASES MOLÉCULAIRES ET STRUCTURALES DU VIVANT

December 17th, 2020 Physics-Biology Interface

Web conference

PYSICS-BIOLOGY INTERFACE

- 9:00am – 9:30am **Welcome**
- 9:30am – 10:10am Laser-Polarized xenon for biological applications: toward in vivo imaging - **Céline BOUTIN**, Iramis
- 10:10am – 10:50am Super-resolution microscopy to resolve the intimate organization of the synapse - **Eric HOSY**, Institut Interdisciplinaire de Neurosciences, Bordeaux
- 10:50am – 11:10am **Break**
- 11:10am – 11:50am Multiscale and multiphase organization of the transcriptome: insights from imaging and purification of endogenous RNA condensates - **Arnaud HUBSTENBERGER**, Institut de Biologie Valrose, Nice
- 11:50am – 12:30pm Complex dynamics and dynamic complexes: The essential role of intrinsic protein disorder studied by NMR spectroscopy - **Martin BLACKLEDGE,** Institut de Biologie Structurale, Grenoble
- 12:30pm – 12:45pm Elastically limited intracellular phase separation - **Pierre RONCERAY**, Princeton University, Princeton
- 12:45pm – 1:00pm Probing the role of RNA on the morphology of phase separated condensates - **Audrey COCHARD**, Ecole Normale Supérieure de Paris, Paris
- 1:00pm – 1:15pm Phasing-in protein quality control in the nucleus - **Frédéric FROTTIN**, Institute for integrative biology of the cell (I2BC), Gif-sur-Yvette
- 1:15pm – 2:00pm **Lunch time**
- 2:00pm – 2:40pm Shaping lipid membranes with proteins and actin polymers: deciphering mechanisms with reconstituted systems - **Patricia BASSEREAU**, Institut Curie, Paris
- 2:40pm – 3:20pm Elasticity from entanglements in branched actin - **Martin LENZ**, Laboratoire de Physique Théorique et Modèles Statistiques, Orsay
- 3:20pm – 3:35pm Understanding mechanotransduction through the in vitro reconstitution of actomyosin-dependent protein machineries - **Christophe LE CLAINCHE**, Institute for integrative biology of the cell (I2BC), Gif-sur-Yvette

- 3:35pm – 3:50pm — Carotenoids crystalloids in chromoplast exhibit singlet fission - **Manuel LLANSOLA-PORTOLES**, Institute for integrative biology of the cell (I2BC), Gif-sur-Yvette
- 3:50pm – 4:05pm — Experimental and Mathematical modeling of radial water transport in plants - **Yann BOURSIAC**, INRAE, Montpellier
- 4:05pm – 4:20pm — **Break**
- 4:20pm – 5:00pm — Spatial organization, dynamics and behaviour of single cells in complex communities - **Marcello NOLLMANN**, Centre de Biochimie Structurale, Montpellier
- 5:00pm – 5:40pm — Real time control of gene expression and biological circuits - **Pascal HERSEN**, Institut Curie, Paris
- 5:40pm – 5:50pm — Conclusions
- 5:50pm — **Closure**

REGISTRATION : https://physicsbiology.sciencesconf.org

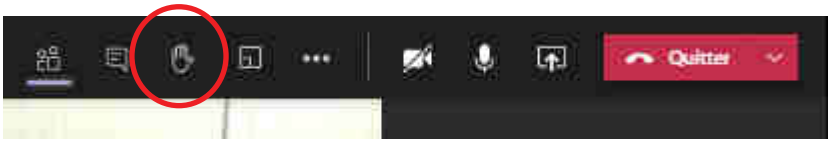
PYSICS-BIOLOGY INTERFACE

Charter of the participant and commitment

- enter first and last name when logging in

- switch off microphone and camera when not speaking

- raise your hand to ask a question or speak up (please do not use the chat for any comment)



After two masters in biotechnologies and in food industry sciences in the engineer school ENSAIA in Nancy (France), **Céline Boutin** has performed her PhD in Optics and nanotechnologies at the University of Troyes in 2008. She has worked on fluorescence correlation spectroscopy applied to detect multidrug resistance on single cells. Then she worked at the CEA Saclay form 2008 to 2010 as a postdoc to develop and to study bimodal biosensors for xenon NMR and fluorescence microscopy. She got following a permanent position in the Laboratoire Structure et Dynamique par Résonance Magnétique (CEA Saclay) to continue researches on biological applications of hyperpolarized xenon NMR on cells and also on rodents. She works also on the development of 3D printing setups to do cell culture directly in the magnet under controlled conditions.

Laser-Polarized xenon for biological applications: toward in vivo imaging

Because NMR suffers from its low sensitivity, hyperpolarized 129Xe is a powerful sensor for magnetic resonance detection of molecular or biological events. This is due to the huge signal provided by the prior optical pumping step, to its exogenous and gaseous nature, its solubility in biological media and finally its wide chemical shift range. Using these properties, two approaches where the hyperpolarized noble gas is used alone as a tracer or targeted to biological receptors via functionalized host systems are developed in the lab.

Several research axes are currently explored in order to optimize its use and to arrive at a proof of concept in vivo:

1) Optimizing the optical pumping setup to produce hyperpolarized xenon

2) Studying biological events using 129Xe NMR/MRI

3) Designing and building biocompatible 3D-printed devices to study biological cells in situ

4) Exploring 129Xe MRI of rodent lungs

Eric Hosy (research director (DR2) CNRS) works at the Interdisciplinary institute for Neuroscience at Bordeaux since 12 years in the daniel choquet's group. He develops and implements super super-resolution imaging techniques that he combines with electrophysiology and modeling to decipher how glutamate receptor nanoscale organization impacts on the synaptic transmission properties at basal state and during plasticities and pathologies. Amongst his main discovery there is the invention of the uPAINT technique (2009), the specific organization of AMPAR type glutamate receptors in nanodomains which tune synaptic transmission (2013), the characterization and the modeling of the co-organization of the three main type of glutamate receptors (2020), the role of the adhesion proteins in the co-organization between the pre and the post-synaptic component (2018). He obtained in 2019 the Jansen price from académie nationale de médecine for his recent discoveries on synaptic physiology..

Super-resolution microscopy to resolve the intimate organization of the synapse

The synapse is a 1 µm size bi-partite organelle responsible of the talk between neurons. The role of glutamate receptors is to convert the chemical signal emits by the pre-synapse (glutamate release) to an electrical signal understandable by the post-synaptic neuron. Due to their relatively low affinity for glutamate and to the limited amount of glutamate, the spatiotemporal nano-organization of these receptors in post-synaptic membrane is fundamental to understand synaptic transmission and so information processing by the brain. This nanoscale sub-synaptic organization has been render accessible by the use of single particle based super-resolution microscopy, which aim to decorrelate in a time dependent manner the emission of fluorescence to obtain a single particle signal which can be fitted by Gaussian equation. These type of techniques allow to obtain a 10 nm accuracy in two color or to extract the mobility of individual proteins. All these discoveries succeed to improve our tight understanding of synaptic transmission properties.

Arnaud Hubstenberger was among the very first to introduce phase transitions as a framework to study the supra-molecular organization of the cellular transcriptome (Hubstenberger et al., 2013). AH was trained as molecular and cellular biologist at l'Ecole Normale Supérieure de Lyon (France), and then obtained his PhD from Grenoble University in 2006. To study the post-transcriptional control of gene expression, AH joined Tom Evans' team in Colorado for his first post-doctoral position, where he demonstrated that RNA can condense into liquid droplets, viscoelastic hydrogels, freeze into disorganized glass-like aggregates, or harden into crystal-like solids within cells, and connected these changes in material properties to the control of mRNA translation. During a second post-doctorate in Dominque Weil's team at the Institut Biology Paris Seine, he developed a cutting edge FAPS method to purify RNA condensates, unravelling the complexity of RNA super-assemblies and their connection to transcriptome-wide control of RNA expression. In 2017, after joining the CNRS as researcher, he initiated an ATIP-AVENIR team at the Insitute of Bioogy Valrose in Nice, focusing on the multiscale multiphase organization of the transcriptome and its impact on the epigenetic control of gene expression.

Multiscale and multiphase organization of the transcriptome: insights from imaging and purification of endogenous RNA condensates

To adapt the rate of biochemical reactions to cellular activity, cells must control reactant storage and flux. Within the super-crowded environment of the cell where biomolecule concentration reaches saturation, RNAs and their regulatory proteins (RNPs) can coassemble into diverse condensates, such as translation factories or repressive bodies, whose assembly responds to cellular activity. However, we possess no quantitative nor mechanistic understanding of how condensates may control mRNA and protein local concentration and stoichiometry, and thus RNA metabolism rates. We have used mRNA translation control in C elegans oogenesis as a model to explore how the biochemistry of insoluble phases and a biophysical understanding of condensed matter are essential to fully comprehend gene expression control. Soluble mRNAs can condense into liquid or semi-liquid droplets, glass or crystal-like solid aggregates, whose material properties impact compartmentation and exchange. With hundreds and thousands of protein and RNA species co-assembling into condensates respectively, we have probed how the interplay between strong stereospecific and weak promiscuous interactions may control condensate composition and material properties. We have uncovered that condensates can regulate the cytosolic concentration and stoichiometry of RNA and their regulatory proteins and, in this way, may function as a buffering system providing robustness to cellular biochemistry. Taken together, we provide evidence that the organization of the transcriptome through phase separations is essential to maintain a tight spatiotemporal control of RNA expression during development and in the face of large environmental changes. We propose a mechanism for subcellular condensate regulation of cellular biochemistry in vivo through phase separation.

Martin Blackledge studied particle physics at the University of Manchester and was introduced to NMR at the University of Oxford where he received his D. Phil under Professor George Radda. Following a postdoc at the physical chemistry department of the ETH Zürich with Professor Richard Ernst he moved to the IBS in Grenoble where he heads the “Protein Dynamics and Flexibility by NMR” group.

The primary research interest of the Blackledge group is the study of protein dynamics by NMR spectroscopy, often combined with complementary biophysical techniques and advanced molecular simulation. His group uses NMR to characterize the role of conformational flexibility in biological function on a broad range of time and length scales, from molecular recognition dynamics in folded proteins, to dynamics of large multi-domain assemblies to the study of the fundamental biophysics underlying dynamic modes exhibited by proteins. These techniques are used to describe the conformational space sampled by highly flexible or intrinsically disordered proteins, to map their interaction trajectories at atomic resolution and to describe their role in the stabilisation of membraneless organelles. Amongst other applications these methods are applied to understand the function of highly dynamic protein assemblies involved in viral replication.

COMPLEX DYNAMICS AND DYNAMIC COMPLEXES: NMR-BASED DESCRIPTIONS OF HIGHLY FLEXIBLE PROTEINS AND THEIR ROLE IN PROTEIN FUNCTION

Serafima GUSEVA, Wiktor ADAMSKI, Aldo CAMACHO-ZARCO, Nicola SALVI, Luiza Mamigonian BESSA, Anas MALKI, Emmi MIKKOLA, Maiia BOTOVA, Damien MAURIN, Malene JENSEN, Sigrid MILLES, Rob RUIGROK & Martin BLACKLEDGE

Proteins are inherently dynamic, exhibiting conformational freedom on many timescales,1 implicating structural rearrangements that play a major role in molecular interaction, thermodynamic stability and biological function. Intrinsically disordered proteins (IDPs) that exhibit no stable three dimensional structure in their physiological forms, represent extreme examples where flexibility defines molecular function. The description of the dynamics and thermodynamics underpinning the function of IDPs is a clear example of how physics can provide new insight into complex biological processes. We use NMR spectroscopy, combined with advanced molecular modelling, to develop a unified description of the dynamics of IDPs as a function of environmental conditions,2-6 and to map these complex molecular recognition trajectories at atomic resolution, from the highly dynamic free-state equilibrium to the bound state ensemble.7

Examples include the nuclear pore, where weak interactions between the nuclear transporter and highly flexible chains containing multiple ultra-short recognition motifs, facilitate fast passage into the nucleus,8 and the replication machinery of Measles virus, where we use NMR to characterize the 92 kDa complex formed between the highly disordered phosphoprotein and the nucleoprotein prior to nucleocapsid assembly.9-10 These proteins undergo liquid-liquid phase separation upon mixing and we use NMR and fluorescence to describe the molecular basis and functional advantages of this phenomenon.11 We have also used these processes to investigate the molecular basis of host adaptation of influenza polymerase, via a highly dynamic interaction.12

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[2]. Jensen et al Chem Rev 114, 6632 (2014)
[3]. Abyzov et al J.A.C.S. 138, 6240 (2016)
[4]. Salvi et al Angew Chem Int Ed. 56, 14020 (2017)
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[10]. Milles et al Science Advances eaat7778 (2018)
[11]. Guseva et al Science Advances (2020)
[12]. Camacho-Zarco et al Nature Communications (2020)

Patricia Bassereau is CNRS Director at the Institut Curie in Paris where she is the leader of the group "Membranes and cellular functions". She obtained a PhD in Soft Matter at the University of Montpellier where she started her carrier on the structure of self-assembled surfactant-based systems. After a year as a visiting scientist at the IBM Almaden Center (San Jose, USA), she moved to the Institut Curie in 1993 to work on questions related to "Physics of the cell". In 2015 she received the Suffrage Science Award (Royal Society, Medical Research Council and L'Oréal), in 2017 the Emmy Noether Distinction for Women in Physics (European Physical Society, she is Fellow of the Biophysical Society since 2018 and Elected EMBO Member since 2020. For her research, she develops a multidisciplinary approach, largely based on synthetic biology and biomimetic systems, as well as quantitative mechanical and microscopy methods to understand the role of biological membranes and of their organization in cellular functions such as intracellular trafficking, endo/exocytosis or adhesion. Additionally, she studies in vitro and in cellulo the mechanics and the generation of cellular protrusions. In parallel, she contributes to a more comprehensive physical description of biomembranes by studying the consequences of non-equilibrium transmembrane transport of ions on membrane mechanics, the relation between membrane proteins' shape and their diffusion or their lateral distribution on membranes.

Shaping lipid membranes with proteins and actin polymers: deciphering mechanisms with reconstituted systems

Cell plasma membranes are highly deformable: for instance, they are strongly curved during cell migration upon the formation of cellular protrusions (filopodia) or during internalization of components (endocytosis) where small buds form and eventually detach. These membrane-shaping processes always require the interaction with proteins and in some cases with the actin cytoskeleton. Over the years, in vitro reconstituted membrane systems combined to theoretical models have been instrumental for understanding how proteins and cytoskeleton shape cellular membranes. I will present examples from my group that illustrate how with these model membranes we have deciphered some mechanisms underlying endocytosis as well as the generation of filopodia.

Martin Lenz is a CNRS senior researcher at LPTMS on the Université Paris-Saclay campus. He develops theoretical models of intracelluar structures in close collaboration with experimentalists, from protein-membrane interactions to the cytoskeleton to protein aggregation.

Martin did his PhD at Institut Curie until 2009 working on protein-membrane interactions, then became an independent postdoc at the University of Chicago working on cytokines, the actin cytoskeleton and aggregation problems mainly with Tom Witten, Margaret Gardel and Aaron Dinner. He joined the Laboratoire de Physique Théorique et Modèles Statistiques as a CNRS reserarcher in 2012, then became a directeur de recherche in 2018. He spent sabbaticals at the Weizmann Institute of Science (2017) and MIT (2018). He received an ERC Starting Grant in 2015, among other grants. He was awarded the IUPAP Young Scientist Prize (2016), the EMBO Young Investigator Award (2016) and the Friedrich Bessel Prize (2020).

Elasticity from entanglements in branched actin

Branched actin networks exert pushing forces in eukaryotic cells, and adapt their stiffness to their environment. To understand the microscopic underpinnings of their response, we show using high-sensitivity micromanipulation experiments, numerical simulations and theory that unlike usual crosslinked networks, branched actin is dominated by the proliferation of interfilament contacts under compression. The tree-like topology of the networks make them particularly prone to developing growth-induced entanglements, and is thus key to their active adaptive mechanics.

Marcelo Nollmann is CNRS Director at the Center of Structural Biology in Montpellier where he is the leader of the group "Mechanisms of DNA segregation and remodeling ". He obtained a Msc in Physics from the Balseiro Institute (Argentina), and a PhD in Biophysics from the Wellcome Center at the University of Glasgow (UK) where he started his career on the study of enzymes that transport, entangle and reshape the structure of DNA in cells. After a postdoc at the labs of Nick Cozzarelli, Carlos Bustamante and James Berger in UC Berkeley, he moved to the CBS in 2008 to work on developing and applying novel imaging methods to understand how DNA is organized and remodeled in the cell. He received ERC funding (Starting Grant 2011; Consolidator 2017; Proof of concept 2016, 2019) to work on eukaryotic DNA structure and develop cutting-edge microscopies. He received the 'coup d'elan' prize of Bettencourt-Schueller foundation in 2017 and the 'Etancelin' prize of the Academie de Sciences in 2019. Currently, his group focuses on the development of high-throughput and sequential imaging methods to understand how chromosomes are organized in single cells within embryos and tissues, whether this organization has a functional role in transcriptional regulation, and to characterize and understand the roles of cell and sub-cell types in tissues and complex organisms.

Spatial organization, dynamics and behaviour of single cells in complex communities

Bacteria are often portrayed as the archetypal single-cell organism. However, bacteria most often live in complex environments such as the gut or forest floors. In these environments, they display collective behaviours that suggest task specialization. We will explore this concept using microscopy-based techniques able to follow the dynamics of single bacterial cells in multi-species communities displaying complex spatial structures.

Pascal Hersen is a CNRS physicist, senior group leader and director of the Physico-Chimie Curie laboratory (UMR168, Institut Curie, PSL, CNRS, Sorbonne Université). His team develops tools in microscopy, microfabrication and synthetic biology to study the physics of living cells and specifically how information flows in cellular processes. He is a pioneer in the field of Cybergenetics, a field of research at the interface of control theory and synthetic biology which aims at taking control of cellular processes thanks to external feedback control loop, interfacing living systems with computers and machines.

Cybergenetics : Real time control of gene expression and biological circuits

Gene expression plays a central role in the orchestration of cellular processes. We recently developed an experimental platform for real-time, closed-loop control of gene expression that integrates microscopy for monitoring gene expression in live cells, microfluidics to manipulate the cells environment, and dedicated software for automated imaging, quantification and model predictive control strategy. This method implements a dynamic interaction between cells and a computer, making it possible to control precisely the level of expression of a gene for both time-constant and time-varying target profiles, at the population level, and at the single-cell level. I will discuss recent developments of this method, called Cybergenetics, on two examples: controlling the hyper-osmotic stress response in yeast and controlling a bistable synthetic circuit in bacteria.

Elastically limited intracellular phase separation

Pierre Ronceray*[1], Sheng Mao[1,2], Andrej Kosmlrj[1], and Mikko Hattaja[1]

[1]Princeton University – États-Unis
[2]Peking University – Chine

Résumé

Many intracellular bodies have been shown to be membrane-less liquid droplets that form through liquid-liquid phase separation (LLPS), both in the cytoplasm and in the nucleoplasm. In contrast to the archetypal oil-in-water demixing, the intracellular environment imposes mechanical constraints on the formation of large droplets. In the cell nucleus, in particular, the elastic response of the chromatin network has been shown to oppose LLPS. Here we theoretically consider three scenarios by which LLPS can occur in such an elastic network: (i) by cavitation of large droplets that exclude the network, (ii) by forming many mesh-size-scale microdroplets in the pores of the network, and (iii) by permeating through the network and including it in large droplets. We set forth simple criteria for which scenario is preferred, introducing a phase diagram controlled by the trade-off between elastic modulus, liquid-liquid surface tension, and liquid-network wetting properties. Our theory predicts the possibility of yet-unobserved mesh-size-limited liquid droplets in the cytoplasm and nucleoplasm.

Mots-Clés: liquid liquid phase separation, elasticity, membraneless organelles

*Intervenant

Probing the role of RNA on the morphology of phase separated condensates

Audrey Cochard*[1], Marina Garcia-Jove Navarro[1], Shunnichi Kashida[1], Dominique Weil[2], and Zoher Gueroui[1]

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[2]Compartimentation et Trafic Intracellulaire des mRNP - Institut de Biologie de Paris-Seine – CNRS : UMR7622 – France

Résumé

Membrane-less organelles are ubiquitous functional sub-units of cells that are involved in many vital functions such as RNA regulation (storage, translation and degradation), thus shaping the general gene expression output. Importantly, their dysfunction is linked to viral infection, cancer, and neurodegenerative diseases. The concept of phase separation has been proposed to explain how RNAs and proteins can condense into viscoelastic granules, named condensates. Though role of RNA-binding proteins (RBPs) in condensates has been recently investigated, the input of RNA molecules in the formation and biophysical properties of condensates remains more elusive. Studies aiming to bridge that gap have been carried out mainly using *in vitro* reconstitution experiments, because of the lack of tools allowing to work in a cellular context. By combining synthetic biology and biophysics, we have developed a novel methodology allowing the formation in cells of artificial condensates made of a synthetic protein scaffold engineered to specifically recruit exogenous RNA. Our artificial RNA-protein condensates recapitulate the hallmarks of phase-separated liquid membrane-less organelles and can be used to dissect the contribution of RNA to the biophysical properties of the condensates. We showed that the co-segregation of RNA to the condensate has a high impact on their size and number, as well as on their morphology.

Mots-Clés: Phase separated condensates

*Intervenant

Phasing-in protein quality control in the nucleus

Frédéric Frottin*[1], Florian Schueder , Shivani Tiwary , Roman Körner , Thomas Schlichthaerle , Jürgen Cox , Ralf Jungmann , F. Ulrich Hartl , and Mark S. Hipp

[1]I2BC – Institut de Biologie Integrative de la Cellule – France

Résumé

Cells have evolved protein quality control mechanisms that operate under normal growth conditions and during stress to maintain protein homeostasis (proteostasis) and prevent the formation of potentially toxic aggregates. Nuclear protein aggregates have been observed in various neurodegenerative disorders such as amyotrophic lateral sclerosis and Huntington's disease, but protein quality control in the nucleus is not well understood. Here, we used a combination of fluorescence imaging, biochemical analyses, and proteomics to investigate the fate of stress-denatured and aberrant proteins in the nucleus. We found that metastable nuclear proteins that misfold upon heat stress enter the liquid-like granular component phase of the nucleolus. The nucleolus, site a ribosome biogenesis, is a paradigm example of membraneless compartment. In the organelle, misfolded proteins associated with proteins including nucleophosmin and adopted a state of low mobility. Storage in the granular component phase effectively prevented the irreversible aggregation of misfolded protein species, allowing their extraction and refolding upon recovery from stress in a Hsp70-dependent manner. Prolonged stress or the uptake of proteins associated with neurodegenerative diseases prevented this reversibility. Our findings provide an example of how the properties of a non–membrane-bound, phase-separated compartment can be used in protein quality control, a fundamental biological function.

Mots-Clés: Protein quality control, Nucleolus, biocondensates

*Intervenant

Understanding mechanotransduction through the in vitro reconstitution of actomyosin-dependent protein machineries.

Christophe Le Clainche*[1]

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Résumé

The mechanosensitivity of focal adhesions allows cells to adapt adhesion strength to the internal force of the actomyosin cytoskeleton and to the physical properties of the extracellular matrix. The biochemical mechanisms that govern adhesion mechanosensitivity remain largely unexplored. The mechanical stretching of talin, which exposes cryptic vinculin-binding sites, controls this process. The binding of RIAM to talin could regulate this mechanism. However, the mechanosensitivity of the talin-RIAM complex has never been tested. It is also not known whether RIAM controls the force-dependent binding of vinculin to talin. To determine the mechanosensitivity, sequence and interdependence of these talin-associated reactions, we designed an in vitro microscopy assay with purified proteins. In this assay, the actomyosin force controls the binding of RIAM and vinculin to a micropatterned surface coated with talin constructs, which contain variable RIAM- and vinculin-binding sites. We demonstrate that actomyosin triggers RIAM dissociation from several talin domains. Actomyosin also provokes the sequential exchange of RIAM for vinculin on talin. Interestingly, the effect of RIAM on the force-dependent binding of vinculin to talin varies from one talin domain to another. This mechanism could allow talin to biochemically code a wide range of forces by selecting different combinations of partners.

*Intervenant

Carotenoids crystalloids in chromoplast exhibit singlet fission

Manuel Llansola-Portoles*[1], Annamaria Quaranta[2], Anja Krieger-Liszkay , Cristian Ilioaia[3], François Perreau[4], Andrew Pascal[5], Mikas Vengris[6], and Bruno Robert[7]

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Résumé

Chromoplast in plants have signaling roles to attract animals and insects. We have investigated the structure and photochemistry of carotenoids-containing chromoplast using two natural model systems displaying different properties – tomatoes and daffodil petals. Tomato chromoplasts contain lycopene crystalloids, which are responsible for red color whereas daffodil chromoplasts contain crystalloids of lutein/violaxanthin responsible for the yellow color. The absorption spectrum of lycopene crystalloids is significantly red-shifted respect to lycopene monomer whereas the absorption spectrum of lutein/violaxanthin crystalloids is not red-shifted respect to their monomeric forms. To understand this variation, we determined structural parameters using circular dichroisms and resonance Raman. The differences on the energetic pathways after photon absorption in tomato and daffodil chromoplasts were determined by transient absorption. We observed that both samples generate long-lived triplet state generated by singlet exciton fission. However, the triplet generation yield was remarkably different in both chromoplast samples, being an order of magnitude higher in tomato chromoplast than in daffodils chromoplast. This is the first time the singlet fission process has ever been shown to occur in a biological material. Our observations suggest that carotenoid

*Intervenant

crystalloids in chromoplast may have functions that are more complex. Carotenoids are the main pigments involved in photoprotection of the photosynthetic apparatus, creating energy dissipation channels. It is reasonable to hypostatize that carotenoids in chromoplast may have some photoprotective function. We are investigating currently (i) the increase of photoresistance of carotenoid in associated form and (ii) the involvement of singlet fission, which dissipates energy harmlessly and efficiently, in chromoplast photoprotection.

Mots-Clés: chromoplast, carotenoids, singlet fission, photoprotection, triplet states

Experimental and Mathematical modeling of radial water transport in plants

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[4]Techniques de lÍngénierie Médicale et de la Complexité - Informatique, Mathématiques et Applications [Grenoble] (TIMC-IMAG) – Université Joseph Fourier - Grenoble 1, Centre National de la Recherche Scientifique : UMR5525 – Domaine de la Merci - 38706 La Tronche, France

Résumé

Water transport in plant roots is of vital importance: it is a necessary transport to feed the rest of the organism in most vascular plants. To reach the xylem vessels, which ensure the long-distance transport to the aerial parts of the plant, water has first to flow across the root tissues surrounding the xylem. This flow, denoted to as radial transport, is not easily amenable to the experimentation, and has been studied mostly by measurements at a larger scale, and by models that poorly take into account cells and roots geometries.
We adopted a continuous description of stationary root radial water transport to investigate how the geometry and the permeability contrasts between root compartments affect the transport of water. We experimentally modeled the root radial section as a two-dimensional and composite porous material with variable water permeabilities. It mimics the most salient water transport features of the root anatomy and allows a direct visualization of the water pathways. We also present 2D continuous numerical simulations of the water flow, in which we systematically varied the permeabilities of the different tissues.
Our approach provides the physical premises to explain preferential sub-cellular radial routes from one cell to another and look for the subcellular pattern of structures or molecules involved in water transport.

Mots-Clés: transport equations, water, root, permeability

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