



Jeudi 3 mars 2016 - 11h30



Jean-Paul THIERY

CNRS emeritus scientist, Paris.

Visiting Professor, National University of Singapore (NUS)

Invité par Salem Chouaïb, Inserm U.1186

«Epithelial Mesenchymal Transition in the progression of carcinoma : therapeutic implications »

Jean Paul Thiery is currently CNRS emeritus scientist in Paris and a Visiting Professor at the National University of Singapore (NUS). He was until June 2015, Professor and Head of the Biochemistry Department, School of Medicine, NUS. He also had a joint appointment as Research Director at IMCB A*STAR Singapore and was Senior Principal Investigator at the Cancer Science Institute at NUS. In 2006, he moved to Singapore from his position as Head of Translational Research at the Medical Division of the Comprehensive Cancer Center of Institut Curie, and before that, Head of the Cell Biology Department at the Institut Curie in Paris until 2003. After his PhD studies at the University of Paris, his postdoctoral research with Gerald Edelman (Nobel Laureate) at the Rockefeller University led to the discovery of N-CAM, the first intercellular adhesion molecule to be identified. His influential works include pioneering studies in cell adhesion and migration in early embryogenesis and in elucidating the roles of growth factors and adhesion signaling molecules in Epithelial-Mesenchymal Transitions (EMT). Jean Paul Thiery's current research focus is to unravel the mechanisms of invasion and metastasis of carcinoma cells. His seminal contributions to bladder carcinoma studies have led to the discovery of the molecular mechanisms underlying the formation of superficial or invasive tumors. Currently, his laboratory is focusing on oncogenomics and the creation of functional approaches to characterize breast and ovarian carcinoma with the ultimate goal to apply EMT-based therapeutic approaches. Jean Paul Thiery is an EMBO and Academia Europea member.

Jeudi 10 mars 2016 - 11h30



Thomas MERCHER

Inserm U.1170 - Gustave Roussy, Villejuif

Invité par Jean Feunteun, CNRS UMR 8200

«Genetics and models of pediatric acute megakaryoblastic leukemia»

Hematological malignancies account for approximately 45% of the pediatric cancers. Clinical features of these pediatric cancers suggest that they have different bases compared to the corresponding adult cancers. However, the precise molecular mechanisms of transformation and the bases for the exclusive association between several genetic alterations and pediatric cancers are unclear. We study acute megakaryoblastic leukemia (AML-M7 or AMKL), a subtype of AML mainly diagnosed in children generally associated with poor prognosis. For this purpose, we perform high-throughput genetic analyses to identify the genetic landscape of leukemia and functional analyses through the development of cellular and preclinical *in vivo* models. We recently identified a novel chromosomal inversion $inv(16)(p13;q24)$ in about 30% of AMKL patients. This alteration leads to the expression of a fusion protein involving two transcriptional regulators. Using molecular and functional analyses, we showed that the fusion regulates megakaryocyte lineage identity and self-renewal of hematopoietic progenitors through aberrant transcriptional programs presenting common mechanisms with other pediatric AMKL. Importantly, inhibition of fusion interaction with transcriptional cofactors through peptide interference with the nervy-homology region (NHR2) of the fusion reversed the transcriptional program, promoted differentiation and inhibited *in vivo* tumor growth of human AMKL xenografts.

Jeudi 17 mars 2016 - 11h30



Vasily OGRYZKO

CNRS UMR 8126 - Gustave Roussy, Villejuif

Invité par Jean Feunteun, CNRS UMR 8200

«What the Proteomics Platform at Gustave Roussy can do for your research?»

Proteomics is the large-scale, high-throughput study of proteins - particularly their expression levels, structures and functions -, which complements genomics by providing information on the aspects of cell biology that are difficult to study by genomics approaches, such as: post-transcriptional steps of gene regulation, post-translational modifications (PTMs) of proteins and protein-protein interactions.

The explosive growth of this field has been driven by new powerful technologies, in particular by latest developments in chromatography and mass-spectrometry, which allow us to detect and quantitatively compare thousands of proteins in a single-shot experiment.

My presentation will cover main principles of the so-called bottom-up (shotgun) proteomics that are implemented on the Orbitrap Q-exactive instrument recently installed at the Proteomics Platform at Gustave Roussy. I will also review the applications of this approach for quantitative proteomics (Stable-Isotope based and Label-Free), for the analysis of protein-protein interactions and the analysis of protein PTMs, which are currently possible at the platform.

Jeudi 24 mars & Vendredi 25 mars 2016



JOURNEES RECHERCHE à TOURS

Jeudi 31 mars 2016 - 11h30



David HYMAND

Medical oncologist -Director, developmental therapeutics
Memorial Sloan Kettering – New York

Invité par Jean-Charles SORIA, Directeur du SIRIC SOCRATE

«New clinical trial paradigms, leveraging cancer genomics in the clinic: the MSKCC precision medicine program»