

Jeudi 12 mai 2016 - 11h30



Aurélien MARABELLE

Medical oncologist in the Drug Development Department (DITEP)
Clinical director of the Cancer Immunotherapy Program at Gustave Roussy

Invité par Jean Feunteun, CNRS UMR 8200

«titre à préciser..... »

Jeudi 19 mai 2016 - 11h30



Nicholas McGRANAHAN

Cancer Research UK London Research Institute, London

Invité par Eric Solary, Directeur de la Recherche

« Exploring cancer genome evolution in heterogenous tumours »

Cancer drug resistance is almost inevitable in the majority of patients with advanced metastatic tumours. Intra-tumour heterogeneity, facilitating rapid tumour evolution, is one of the main causes of tumour adaptation and resistance to cancer therapies.

In this talk I will explore how cancer genome sequencing data can shed light on diversity within tumours and the processes shaping cancer genome evolution over space and time. Harnessing both extensive multi-region and single-sequencing data we have investigated intra-tumour heterogeneity across multiple cancer types, focusing on non-small cell lung cancer. I will discuss our findings shedding light on the extent to which mutations in known driver genes, and 'actionable mutations', linked to targeted therapies, are clonal or subclonal. Tumour phylogenies and whether patterns of tumour evolution can be deciphered in these cancer types will also be explored.

Temporal dissection of mutational signatures across cancer types will be used to reveal the dynamics of mutational processes during tumour evolution. I will explore how APOBEC mediated-mutagenesis can be linked to branched tumour evolution, and the acquisition of subclonal driver events across cancer types.

Finally, the challenges and clinical implications of intra-tumour heterogeneity as well the importance of considering diversity in the context of immune-therapy will be discussed.

Jeudi 26 mai 2016 - 11h30



Céline VALLOT

Equipe ARNs non-codants, Différenciation et Développement
UMR 7216 Epigénétique et Destin Cellulaire - Université Paris Diderot

Invitée par Jean Feunteun, CNRS UMR 8200

**« Control of the X-chromosome in early steps
of human development: a matter of coating »**

In mammals, the activity of the X chromosomes has to be tightly controlled to accommodate the disequilibrium of X-linked gene dosage between males and females. X-chromosome inactivation (XCI) enables the silencing of one of the two X-chromosomes in female cells to compensate for such imbalance. XCI is triggered in mouse by the accumulation of the long non-coding RNA Xist on the chromosome, which is responsible for the silencing and heterochromatinization of the inactive X. In the lab, we are interested in how such process is set up and regulated in humans, by studying human embryonic stem cells (hESC) and human embryos. We rely on the data-mining of integrated epigenomic and transcriptomic datasets, as well as novel imaging approaches to unravel the epigenetic control of the human X chromosome in these early stages of development. We have in particular identified XACT, an X-linked lncRNA that coats active X chromosomes in hESCs and embryos. XACT appears to take part in the epigenetic plasticity of hESCs as well as in the tight control of XCI, in competition with XIST for the coating of the X chromosomes.

Vallot C, Ouimette JF, Makhlouf M, Féraud O, Pontis J, Côme J, Martinat C, Bennaceur-Griscelli A, Lalande M, Rougeulle C. Erosion of X chromosome inactivation in human pluripotent cells initiates with XACT coating and depends on a specific heterochromatin landscape, Cell Stem Cell (2015), 16(5):533-46.

Vallot C, Huret C, Lesecque Y, Resch A, Oudrhiri N, Bennaceur-Griselli, Duret L, Rougeulle C. XACT, a long non-coding transcript coating the active X chromosome in human pluripotent cells, Nat Genet. (2013), 45(3):239-41

Gustave Roussy

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