IMCB Invited Speaker

Speaker : **Dr. Robert Schneider**
Team Leader, Functional Genomics & Cancer,
Institute of Genetics and Molecular and Cellular Biology (IGBMC),
Strasbourg, France

Date : 4th June 2012 (Monday)

Time : 5pm - 6pm

Venue : Level 4, Creation Theatrette, Matrix., Biopolis

Host : Dr. Ernesto Guccione

Seminar :

Novel histone modifications – beyond the usual suspects

Histone modifications are central to the regulation of all chromatin-based processes. Currently, the repertoire of known modifications is far from complete and most attention is focused on modifications within the N-terminal tail of the core histones. We are very much interested in novel modifications in the core of the nucleosome and of histone H1.

Whereas the function of histone tails as highly modified "signalling platforms" is well established, currently little is known how modifications in the core of the nucleosome and how/if they regulate chromatin function. We identified a novel acetylation site on histone H3 that is positioned on the lateral surface of the nucleosomal core, in close contact with the DNA. We show that this acetylation has a major impact on regulating nucleosome dynamics. We present our data on the dynamics of this mark, its interplay and dependence on other modifications, as well as its genome-wide distribution. Importantly we have identified the enzymatic machinery setting this acetylation and its role in transcriptional regulation.

The 5. histone, the linker histone H1, has an important role in higher order chromatin structure, however it is often the "forgotten histone". Mammalians express up to eleven different H1 variants. Like core histones, histone H1 is also highly covalently modified, however the biological role of H1 modifications is largely unknown. We recently had interesting progress in unravelling the function of histone H1 acetylation. We identified a dual function of H1 acetylation in transcription: increase of H1 mobility and recruitment of general transcriptional activators. Our novel data on H1 modifications reveals that beside its role as general repressor of transcription, H1 can also act as gene specific transcription activator -through the existence of H1 variants and H1 variant specific modifications.

Understanding the function of new modifications allow us key insights into the regulation of nucleosome dynamics and how (external) signals are translated into changes in gene expression. The identification of novel pathways regulating chromatin function has the clear potential to provide us with new approaches and new therapy targets.

About the Speaker :

Robert Schneider obtained his Diploma in Biology in 1996 and his PhD in 2000 from the University of Munich, Germany. He did his postdoctoral work at the Gurdon Institute, University of Cambridge, UK in the group of Tony Kouzarides where he studied the role of histone methylation in transcription. He started his own group in 2005 at the Max Planck Institute of Immunobiology and Epigenetics in Freiburg, Germany where he focuses on novel histone modifications and their role in chromatin dynamics, cellular proliferation and differentiation. He is currently moving his laboratory to the IGBMC in Strasbourg, France.

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