

Title:

"The Ins-and-Outs of Cellular Senescence :

Non-Coding RNAs and beyond "

Abstract:

In this seminar we will discuss the impact the noncoding genome has on the establishment and maintenance of the senescence phenotype. We will show how microRNAs and long, noncoding RNAs in conjunction with the RNAi machinery as well as DNA-RNA binding proteins and polycomb repressor complexes help to reconfigure the epigenomic and transcriptional landscape to arrest cells in the senescent state.

Date:

29 January 2015 (Thursday)

Time:

12:00 PM to 1:00 PM

Venue:

Amphitheatre, Level 2 Duke-NUS Grad Med School 8 College Road, S169857

(Opposite Singapore General Hospital, Block 6/7)

Host: Koji ITAHANA, PhD

Assistant Professor Program in Cancer & Stem Cell Biology Duke-NUS Graduate medical School Singapore

"No registration is required." Any enquiry, please contact: Beatrice Tan (Tel: 6516 7923)



Speaker:



Oliver BISCHOF, PhD Research Director CNRS (DR2) and Group Leader Institut Pasteur

Biography:

Dr. Oliver BISCHOF obtained his PhD in biochemistry at the Max-Delbruck Institute Berlin/Germany before joining the laboratory of Judy Campisi at the LBNL in Berkeley, CA, USA. He currently is a group leader at the Pasteur Institute in Paris/France. The laboratory of Dr. Bischof has extensive experience and expertise in dissecting signaltransduction pathways, gene regulation and chromatin structure important for senescence onset and maintenance. He co-developed a novel technology, the MAR-loop ligation assay, to show that PML physically and functionally interacts with the matrix attachment regions-(MAR)-binding protein SATB1 to organize specific gene loci into a distinct higher-order chromatin loop structure and that disrupting this interaction has profound effects on gene expression. Moreover, he previously demonstrated that the RNAi machinery and the retinoblastoma suppressor protein Rb physically and functionally interact to repress Rb/E2F-target genes in senescence, a process that is now referred to as senescence-associated transcriptional gene silencing (SA-TGS). Currently, he is involved in improving a pre-existing ChIRP (Chromatin-isolation by RNA precipitation) method to analyse the chromatin binding sites of noncoding RNAs on a global scale. He has developed and continues to develop several improvements of existing chromosome conformation capture (3C) technologies.