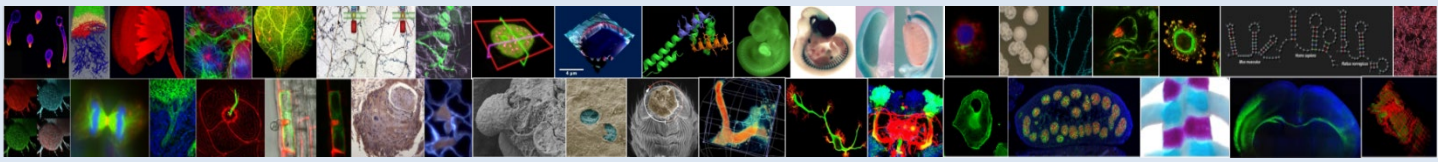
Labex SIGNALIFE Seminar series



Noncoding roles of RNA in the regulation of gene expression and genome integrity

Dr Maite Huarte
CIMA, University of Navarra, Spain

Thursday March 18th 2021, 11:00 am
Invited by Dr. Patrick Brest, Institute for Research on Cancer and Aging, Nice (IRCAN)

Webconference through Zoom
(link and access codes available through email announcement)

https://signalife.univ-cotedazur.fr/

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A major shift in our conception of genome regulation has emerged in recent years. It is now obvious that the majority of cellular transcripts do not code for proteins, and a very significant subset of them are long RNAs (lncRNAs). Many lncRNAs have been shown to be functional molecules, emerging as important regulatory molecules in tumor-suppressor and oncogenic pathways. For instance, we found that the transcription factor p53, which is crucial for the maintenance of cellular homeostasis, specifically regulates the expression of dozens of lncRNAs that constitute active components of this important tumor suppressor pathway. We found that some lncRNAs act at the chromatin level, not only influencing gene expression but also DNA replication and genomic integrity, representing a novel aspect of genome regulation and placing lncRNAs at the focal point of cancer biology. I will present our findings implicating lncRNAs in the regulation of these key aspects of the transformed phenotype of cancer cells, with particular attention to the molecular mechanisms that underlie their function.

Biosketch

Maite Huarte obtained her PhD at National Center for Biotechnology (CSIC) in Universidad Autónoma de Madrid. Her postdoctoral work was carried out first in Harvard Medical School where she identified new histone demethylase enzymes and their contribution to the epigenetic landscape of cells. In 2008 she joined John Rinn's laboratory at the Broad Institute of Harvard and MIT, where she initiated the study of long noncoding RNAs (lncRNAs) in gene regulation. Since 2011 she leads a research group at CIMA (University of Navarra) that investigates how noncoding RNAs contribute to the mechanisms of gene regulation at the epigenetic and non-epigenetic levels. To reach these goals, her team combines functional genomics with molecular and cell biology, *in vivo* studies, as well as the analysis of patient samples.