Séminaire de l'unité de recherche de l'institut du thorax

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Models of Human Core Transcriptional Regulatory Circuitries

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Abstract

A small set of core transcription factors (TFs) dominates control of gene expression programs in embryonic stem cells and other well-studied cell types. These core TFs are associated to "super-enhancers" and collectively regulate their own gene expression, thus forming an interconnected auto-regulatory loop that is considered the core transcriptional regulatory circuitry (CRC) for that cell type. CRCs can be predicted through integration of genomic and epigenomic data using CRCmapper (Saint-André et al., Genome Research, 2016). These CRC models should prove valuable for further investigating transcriptional regulation in development and disease. Non-coding RNAs, in particular long non-coding RNAs (lncRNAs), contribute to the CRC regulation, and some lncRNAs have been identified as major regulators of cell state transitions. However, their roles in transcriptional regulation have been poorly characterized. We are now investigating the role of lncRNAs in transcriptional circuitry rewiring upon cell state changes. This work should bring fundamental insights into lncRNA roles in gene expression regulation at the genome-wide level. It should also enable the discovery of novel regulators of cell identity that could serve as putative therapeutic targets or biomarkers of cancer progression.