Physiological and molecular functions of long noncoding RNA loci

Current efforts to understand the genetic and molecular interactions contributing to the development and progression of diseases have focused mostly on protein coding genes, leaving the noncoding genome vastly under-explored. But a large fraction of the genome is transcribed, producing thousands of long noncoding RNAs (lncRNAs). Several lncRNAs have been found to regulate diverse regulatory processes and accumulating evidence point to lncRNA loci as risk factors frequently deregulated or mutated in a wide variety of human diseases. Yet, most studies on lncRNAs remain correlative or are mostly performed using cell line-based assays. Thus, whether lncRNAs contribute to the establishment or progression of diseases in vivo and how they may affect pathways still remains poorly characterized. I will describe our efforts to characterize the in vivo roles of lncRNAs and how we are using human genetics and mouse models combined with molecular, cellular and computational approaches to characterize their function and mechanism in development and diseases.

Note:
Prêtre d'avisser vos étudiants gradués et stagiaires postdoctoraux afin d'avoir la participation de tous.