

## Laboratoire LAMBE

Laboratoire Analyse et Modélisation pour la Biologie et l'Environnement  
Université d'Evry val d'Essonne

**Séminaire le 13 avril 2018 à 14h30 – Salle Blanche LAMBE**

### **A network of protein interactions to drive splicing signals recognition.**

Manel Tari<sup>1</sup>, Valérie Manceau<sup>2</sup>, Jean de Matha Salone<sup>1</sup>, Asaki Kobayashi<sup>1</sup>, Vandana Joshi<sup>1</sup>, David Pastré<sup>1</sup> and **Alexandre Maucuer**<sup>1</sup>.

<sup>1</sup> SABNP, Univ Evry, INSERM U1204 and <sup>2</sup> INEM, Paris

Splicing of pre-mRNA in higher eucaryotes is a complex mechanism thought to involve hundreds of proteins and small RNAs. The initial step of splicing consists in the recognition of defined sequences in the pre-mRNA substrates to determine the future exon-exon junctions in the mature mRNAs. Recent exome sequencing data have revealed that splicing factors involved in this early process are highly mutated in cancers. How these mutations drive cell transformation is however still elusive.

We employ a combination of biochemical and functional assays to unravel the function of particular splicing factors in early spliceosome assembly. Recent structural data indicate that a particular type of protein-protein interaction structure is recurrent during spliceosome assembly. We purified the proteins involved in this type of interaction and characterized their respective properties. In parallel knockdown experiments combined to transcriptomic studies in cultured cells allowed to analyze their requirements for splicing events. This leads us to propose a mechanistic model important for splicing signals recognition.