**Long non-coding RNAs in B cell differentiation: from fundamental to translational**

(Plassais Jocelyn, U1236 MICMAC, Rennes)

The aim of this project is to identify and characterize the roles of long non-coding RNAs involved in B cell differentiation. Indeed, only 2% of the genome encodes for proteins while 70% of the genome is transcribed. Long non-coding RNAs (LncRNAs) represent by far the largest fraction of non- coding genes, with numbers in humans ranging from a relatively recent estimate of ≈ 9,000 to the NONCODE database listing of 102,000. The function of the vast majority of ncRNAs is not yet known. Recently, studies showed the interest of lncRNAs in cancer and their impact on patient survival supporting the idea to explore further this part of the genome to develop potential new therapeutic strategies. The identification of some functional roles has provided a new dimension to our understanding of cellular physiology and disease pathogenesis.

My project relies on preliminary data on the transcriptional control of normal human B cell differentiation using *in vitro* model systems developed within the B-DEVIL team, which allow us to decipher the molecular events at genomic and epigenomic levels that control B cell maturation, differentiation, emergence of plasmablasts and finally, fully mature plasma cells. Using RNA-Seq data, we already identified new lncRNAs for which we observed increased expression levels during the B cell differentiation. In addition, these lncRNAs are also over-expressed in multiple myeloma cell lines. Thus, the aim of this project is now to characterize the functions of these candidate lncRNAs during the differentiation process, its interactors, and extend our knowledges to Multiple Myeloma models. For that, we developed antisense oligonucleotide approaches with GapmeRs which could represent a potential therapeutic strategy in cancers characterized by the proliferation of plasmablasts and/or tumor plasma cells.