

## Seminar in Microbiology

Monday, 30<sup>th</sup> September, 2019

Salle de séminaire, E07.3347.a, CMU

**11:30 – 12:30**

**Dr. Fabien Darfeuille**



Group. Leader, Laboratoire ARNA, INSERM-CNRS, Univ. Bordeaux,  
Bordeaux, France

### **Functional analysis of type I toxin-antitoxin systems in *Helicobacter pylori***

The human bacterial pathogen *Helicobacter pylori* (*H. pylori*) is the major cause of chronic gastritis and peptic ulcers, and is associated with malignant stomach diseases. Differential RNA-seq analysis of the primary transcriptome of the human pathogen *H. pylori* revealed hundreds of cis-encoded sRNAs (Sharma et al., 2010). Whereas most of these newly identified “antisense” transcripts overlap mRNAs, some of them overlap stable RNAs such as ribosomal RNA or tRNA. Our objective is to determine whether these antisense RNAs influence the expression of their sense-strand targets and to study the underlying mechanism. We also study the regulation of these sRNAs by ribonucleases and Toxin-antitoxin (TA) systems and analyse their biological functions. We recently reported that the genome of *H. pylori* is hosting several copies of a new family of TA system. Similarly to other type I TA systems, the toxin is a small membrane protein whose production is inhibited by a small antisense RNA (antitoxin) that binds to the 5' untranslated region of the toxin mRNA.

#### **Recent publications:**

- Structural insights into the AapA1 toxin of *Helicobacter pylori*. Korkut DN, Alves ID, Vogel A, Chabas S, Sharma CM, Martinez D, Loquet A, Salgado GF, **Darfeuille F.** [Biochim Biophys Acta Gen Subj.](#) 2019
- A genetic selection reveals functional metastable structures embedded in a toxin-encoding mRNA. Masachis S, Tourasse NJ, Lays C, Faucher M, Chabas S, Iost I, **Darfeuille F.** [Elife.](#) 2019
- Maturation of atypical ribosomal RNA precursors in *Helicobacter pylori*. Iost I, Chabas S, **Darfeuille F.** [Nucleic Acids Res.](#) 2019 Jun 20;47(11):5906-5921.
- FASTBAC-Seq: Functional Analysis of Toxin-Antitoxin Systems in Bacteria by Deep Sequencing. Masachis S, Tourasse NJ, Chabas S, Bouchez O, **Darfeuille F.** [Methods Enzymol.](#) 2018
- .Type I Toxin-Antitoxin Systems: Regulating Toxin Expression via Shine-Dalgarno Sequence Sequestration and Small RNA Binding. Masachis S, **Darfeuille F.** [Microbiol Spectr.](#) 2018 Jul;6(4).
- Mechanistic insights into type I toxin antitoxin systems in *Helicobacter pylori*: the importance of mRNA folding in controlling toxin expression. Arnion H, Korkut DN, Masachis Gelo S, Chabas S, Reignier J, Iost I, **Darfeuille F.** [Nucleic Acids Res.](#) 2017.