# Understanding the evolutionary dynamics of insertion sequences in prokaryotic genomes

**Résumé**

Insertion sequences (IS) are the simplest prokaryotic transposable elements: they usually only code for a transposase, the enzyme that catalyses their movement within genomes. The transposition of IS elements within a genome can have drastic effects on gene expression that are often deleterious: as a consequence, IS are mostly considered as genomic parasites. However, IS transposition can also be a vector of adaptation. For instance, the acquisition of antibiotic resistance genes is often linked to IS movements.

Our project focuses on the evolutionary dynamics of insertion sequences in prokaryotic genomes. We combine wet lab experiments with computational work to analyze IS dynamics on different timescales. At the bench, we use molecular biology tools to study insertion site biases and experimental evolution to explore how selection sorts out insertions. Computationally, we use automated detection tools to look at the prevalence of insertion sequences in natural genomes and analyze the distribution of IS families across prokaryotic phyla. In addition, we develop evolutionary models to try to capture these distributions. One of the key questions is to determine whether purifying selection plays a role in the evolutionary dynamics of insertion sequences, or if a neutral dynamic is enough to recapitulate their distribution.

In this talk, I will present our experimental and computational strategies, as well as the first results we obtained regarding the distribution of IS across prokaryotic genomes.

**Mots-Clés:** séquences d'insertion, MGE, génomique, procaryotes, évolution