

**Master 2 internship project
Year 2025-2026**

Laboratory/Institute: TIMC
Team: TrEE

Director: Alexandre Moreau-Gaudry
Head of the team: Fabien Pierrel

Name and status of the scientist in charge of the project:

J. Gaffé, MCU HDR: **yes** ☒ **no** ☐

T. Hindré, MCU HDR: **yes** ☐ **no** ☒

Address: Bâtiment J. Roget, Campus de la Merci, 38700 LA TRONCHE

Phone: 04-76-63-74-95

e-mail: joel.gaffé@univ-grenoble-alpes.fr

thomas.hindre@univ-grenoble-alpes.fr

Program of the Master's degree in Biology:

☒ Microbiology, Infectious Diseases and Immunology ☐ Biochemistry & Structure
☐ Physiology, Epigenetics, Differentiation, Cancer ☐ Neurosciences and Neurobiology

Title of the project:

Characterization of early adaptive regulatory mutations in the Long-Term Evolution Experiment with *E. coli*

Objectives (up to 3 lines):

Identification of regulatory mutations sustaining early bacterial adaptation in the LTEE.

Quantification of the impact of early adaptive mutations on the physiology of *E. coli*.

Abstract (up to 10 lines):

Bacteria exhibit extensive adaptive capacities to face environmental changes by quickly adapting their gene expression profile in response to environmental stimuli and/or by acquiring mutations that cause rewiring of gene regulatory networks. In the TrEE team, we study such adaptive regulatory mutations using the longest-running evolution experiment to date, called the Long-Term Evolution Experiment (LTEE). In this experiment, *Escherichia coli* populations have been propagated under controlled laboratory conditions for over 80,000 generations. Over time, these populations have adapted to their environment, achieving a 70% increase in fitness. We have discovered that several highly beneficial mutations, selected early in the experiment, affect global regulatory genes controlling the stringent response and/or the level of DNA topology. During this internship, we will continue to identify early adaptive mutations by analyzing metagenomic data from LTEE populations and assess their phenotypic impact, including on gene expression profiles.

Methods (up to 3 lines):

Characterization of bacterial phenotypes (stress response, fitness, DNA supercoiling)

Quantification of gene expression levels (q-RT-PCR)

Bioinformatics with metagenomic data

Up to 3 relevant publications of the team:

-Crozat *et al.* Parallel genetic and phenotypic evolution of DNA superhelicity in experimental populations of *Escherichia coli*. *Mol Biol Evol.* 2010 27(9):2113-28.

-Lamrabet *et al.* Plasticity of Promoter-Core Sequences Allows Bacteria to Compensate for the Loss of a Key Global Regulatory Gene. *Mol Biol Evol.* 2019 36(6):1121-1133.

Requested domains of expertise (up to 5 keywords):

- bacteriology and molecular biology

- Basic computational handling and analysis of metagenomic data