

La Tronche, October, 11th, 2021

Master 2 internship in experimental evolution (Location: Grenoble)

Background: Bacterial organisms exhibit extensive adaptive capacities to face environmental changes. In the short term, transcriptional regulatory networks allow bacterial cells to quickly adapt their gene expression profile in response to environmental stimuli. In the long term, mutations causing regulatory networks rewiring can provide bacterial populations with the opportunity to colonize new environments. These networks involve two types of regulatory actors: i) transcription factors, which bind DNA and modulate transcription initiation by interacting directly with RNA polymerase; ii) nucleoid associated proteins and topoisomerases, which act indirectly by modulating DNA topology.

In our TrEE team, we study the interplay between these two types of regulatory factors using evolution experiments, and more particularly the Long-Term Evolution Experiment (LTEE) during which *Escherichia coli* populations have been propagated for more than 70 000 generations. In particular, we have found that early highly beneficial mutations affect global regulatory genes controlling DNA topology rather than genes coding more specific transcriptional factors.

Objectives: The objectives of the proposed internship are two-fold:

- To fully characterize the regulatory properties on which natural selection exerts by identifying as exhaustively as possible regulatory mutations that arose, and eventually were selected, in LTEE populations. To this end, we will leverage available metagenomic data that resume 60,000 generations of evolution for 12 independent LTEE populations.
- To quantify the impact of LTEE-selected global regulatory mutations on short term adaptative properties of *E. coli*. To this end, we will compare the propensity of reconstructed *E. coli* strains harboring or not LTEE-global regulatory mutations to circumvent environmental challenges (changes in osmotic pressure, in pH...).

Expected skills to be improved during the internship:

- Basic computational handling and analysis of metagenomic data
- Basic know-how to test for bacterial phenotypes

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