EVOLUTIONARY ECOLOGY

QUANTITATIVE AND EVOLUTIONARY ECOLOGY OF COMMUNITIES GROUP

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Towards an ecology of the bacterial pangenome: Application to antibiotic resistance genes

Bacteria are unicellular microorganisms, whose genome is composed of a single circular chromosome. They reproduce autonomously by replication to create two sister bacteria whose genome is theoretically identical (there can be replication accidents), this is a vertical gene transfer mechanism. In addition, genetic material can be exchanged between bacteria by **horizontal gene transfer**. These transfers are carried out by different mechanisms (conjugation, transduction, natural transformation) which therefore play a major role in the evolutionary trajectories of bacteria. Horizontal transfer mechanisms often involve **mobile genetic elements** (MGEs) which are entities with **evolutionary trajectories** partially independent of those of bacteria. There is a great diversity of MGEs, they can be parasites of bacterial genomes, or on the contrary be carriers of resistance genes, they can even be parasites of other MGEs or carry anti-MGE defense genes. As can be seen, MGEs have developed a wide variety of strategies in their relations (parasitism or cooperation) with their hosts but also with each other. The abundance and diversity of MGEs is characteristic of the accessory genome of bacteria, which can represent more than 80% of the total genes of certain species, the **pangenome**.

A major challenge is to better understand the eco-evolutionary dynamics of MGEs in different ecological contexts. Indeed, even if the power of genomic approaches can now describe the structuring of pangenomes as well as the diversity and abundance of MGEs, the evolutionary causes and the mechanisms behind them still escape us. Understanding the dynamics of pangenomes requires a new conceptual framework [Michael A. Brockhurst et al. *"The Ecology and Evolution of Pangenomes"*. In: Current Biology 29.20 (Oct. 2019)].

The objective of my thesis work is to enable a qualitative jump in our understanding of the dynamics of MGEs. To do so, I mobilize concepts and tools developed in the field of ecology and related to the dynamics of biodiversity. In this perspective, I consider that all the MGEs present in a bacterial population constitute a community. In this framework, the use of **biodiversity theories** (ecological niche theory and neutral biodiversity theory) should allow to evaluate the relative contribution of different processes in the dynamics of MGEs.

Finally, in my thesis work, the tools I mainly use are **mathematical models** of population dynamics (ODE models, Lotka-Volterra equations...) completed by **simulatory approaches** (C++, Python) and **statistical analysis** (R).