

EVOLUTIONARY ECOLOGY

QUANTITATIVE AND EVOLUTIONARY ECOLOGY OF COMMUNITIES GROUP

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MAÎTRE DE CONFÉRENCES

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Research in progress

Reproduction of perennial plants: understanding its mechanisms and consequences at the community level

The reproduction of perennial plants is often characterized by highly fluctuating and synchronized fruiting at the population scale (masting). Our interannual monitoring of temperate oak (*Quercus* spp) reproduction, combined with modelling work, aims to better understand the proximal and evolutionary causes of masting and to propose scenarios on the future of oak regeneration in the context of climate change (ANR Program 'FOREPRO'). Masting has important cascading effects (dynamics and assemblage of perennial plant species, seed consumers -insects, birds, mammals-, up to the epidemiology of some human diseases). Explicit modeling of masting will then allow us to assess some of the ecosystem consequences of climate change in temperate forests. This program, led by our team, is developed in collaboration with two other teams of the department of evolutionary ecology (Evolutionary Ecoepidemiology, Evolutionary Biodemography), three universities (Montpellier-CNRS-, Bordeaux-INRAE-, Paris-Saclay) and the Office National des Forêts.

Team members involved: MC Bel-Venner, E Fleurot, L Keurinck, J Lobry, S Venner

The spread of antibiotic resistance genes in bacteria

Antibiotic resistance is recognized as one of the greatest current threats to human health, and mobile genetic elements (MGEs) circulating in bacterial populations and communities are the main vectors of this threat. To understand the dynamics and diversity of MGEs in bacterial pangenomes and the emergence of antibiotic resistance genes, we propose to go beyond conventional genomics by considering pangenomes as complex ecological communities. In the Ab-One program, we mobilize concepts and tools developed in community ecology using an integrative approach (monitoring of bacterial populations/communities evolving in contrasting environments -One-Health approaches-, genome-wide analyses, molecular and cellular microbiology experiments, mathematical modeling). This program is currently focused on the dynamics of MGE in *Acinetobacter baumannii*, an antibiotic-resistant microorganism classified as a priority by the WHO. Other more general approaches will illustrate the relevance of this new conceptual framework to understand the dynamics and diversity of MGEs in bacterial pangenomes. This program, co-piloted by our team and a team from CIRI (Horigene) involves the participation of 9 organizations (6 from Lyon -LBBE, CIRI, MMSB, HCL, LEM, VetAgro Sup-, Institut Pasteur (Paris), LMGM (Toulouse), Institut Robert Koch (Germany))

Team members involved: S Dray, R Tuffet, S Venner

List of publications :

<https://scholar.google.fr/citations?user=0KckCcAAAAAJ&hl=fr&oi=sra> ↗