Predicting microbiome ecological resilience and resistome persistence following antimicrobial perturbation

Project ID: 3629

Supervisory team

Main supervisor: Dr Guillaume Meric (University of Bath)
Second supervisor: Dr Sion Bayliss (University of Bristol)
Other supervisors: Prof Tim Rogers (University of Bath) & Prof Paul Wigley (University of Bristol)

Host institution: University of Bath

Project description: Microbiomes are dynamic ecosystems that can be strongly altered by antimicrobial exposure. Although many studies have described changes during and immediately after treatment in various hosts, much less is known about what determines longer-term ecological recovery. Some microbial populations may resist disturbance, others may decline and recover, disappear entirely, or be replaced by genetically distinct populations. Importantly, a microbiome can also continue to change naturally over time, so recovery may not simply mean returning to its pre-treatment state. Antimicrobial exposure may additionally leave a longer-lasting evolutionary signature through changes in the resistome, even when broader community structure appears to have recovered.This project will investigate the ecological and evolutionary principles that govern microbiome resilience following antimicrobial perturbation in livestock. It will use existing longitudinal shotgun metagenomic datasets from livestock microbiomes (4 combined studies with a total of ~1,200 metagenomes spanning ~750 animals before and after antibiotics exposure), with scope to incorporate additional datasets as the project develops. By analysing independent studies within a common framework, we will ask which features of microbiome response are reproducible across different host systems, treatments and timescales.The project will first develop quantitative descriptions of disturbance and recovery, including the magnitude of perturbation, resistance to change, rate of recovery and persistence of altered states. It will then use strain-resolved metagenomics and microbial population genomics to determine what happens to individual microbial populations following treatment, and which genomic or ecological characteristics are associated with persistence, loss, recovery or replacement.Another aim will be to develop an ecological modelling framework for microbiome recovery. Rather than assuming that recovery is a return to a fixed baseline, the project will examine whether perturbed communities converge towards the trajectory expected in the absence of treatment, and whether complex responses can be summarised by a smaller number of interpretable recovery patterns or timescales. A key test will be whether relationships inferred from some experiments can predict trajectories in independent datasets.Finally, the project will examine whether the resistome follows the same recovery dynamics as the wider microbial community, and which population-level processes allow resistance determinants to persist after antimicrobial selection presumably disappears.The student will gain interdisciplinary training in microbiome bioinformatics, microbial population genomics, antimicrobial resistance and quantitative ecological modelling, while addressing a broader question in microbial ecology about microbial ecosystem resilience and the impact of perturbation.

Our aim as the SWBio DTP is to support students from a range of backgrounds and circumstances. Where needed, we will work with you to take into consideration reasonable project adaptations (for example to support caring responsibilities, disabilities, other significant personal circumstances) as well as flexible working and part-time study requests, to enable greater access to a PhD. All our supervisors support us with this aim, so please feel comfortable in discussing further with the listed PhD project supervisor to see what is feasible.