Host specialisms in bacterial pathogens

Supervisory team:
Main supervisor: Prof Edward Feil (University of Bath)
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Project description:

The global Covid-19 pandemic emerged due to the ability of a pathogenic agent to jump from an animal host into a human, a process known as "spillover", and this phenomenon is becoming more likely due to climate change and other anthropogenic perturbations on ecosystems and habitats. However, once a pathogen has switched from an animal to a human host, it is likely to be maladapted and show restricted capacity for human-to-human transmission. This is because each host species presents specific challenges to new pathogens, including immune defences and competition from resident species. The rapid spread of Sars-CoV-2 within the human population therefore represents an exceptional case, and host specific adaptations of pathogens typically shield humans from such large-scale zoonotic outbreaks.

Despite the importance of these host specialisms, significant knowledge gaps remain regarding the genetic basis of host adaptation and the ecological or evolutionary conditions under which specialisms are likely to be relaxed or reinforced. This project will address these questions with a focus on the important bacterial pathogen Klebsiella pneumoniae. This species, when taken as a whole, is an ecological generalist and can infect humans and multiple domesticated and wild animal species. However, evidence from large-scale genome sequencing generated in our lab has shown that different strains tend to be specialised for particular hosts, such as cows or humans. This project will pin-point the genetic changes underlying these specialisms through bioinformatics and statistical analysis of thousands of thousands of available genome sequences. These analyses will be combined with laboratory experiments to further characterise the phenotypic differences between cow and human adapted strains. The phenotypic and genomic analyses will be considered within the context of differences in diet, immunology, gut environment and microbiome between the hosts. Finally, modelling approaches will be used to illuminate how specialisms might evolve or be relaxed at a population scale under differing ecological conditions.

Expertise on comparative genomics and bioinformatics will be provided by the primary supervisor, Prof. Edward Feil, at the Milner Centre for Evolution at the university of Bath, and Prof. Sam Sheppard (also at the Milner Centre). Complimentary expertise in veterinary science and infectious disease dynamics in agricultural settings will be provided by the second supervisor, Dr Kristen Reyher, and modelling supervision will be provided by Dr Katy Turner, both of whom are at the University of Bristol Veterinary School.