

Local genes for local bacteria: Analysing the transmission dynamics of severe campylobacteriosis in Western Africa

Lead Supervisor: Dr Ben Pascoe, Department of Biology & Biochemistry

Project description:

Diarrhoeal disease remains a major cause of child morbidity, growth faltering and mortality in low and middle income countries (LMICs), with *Campylobacter* among the most common causes. In developed countries, the primary route of infection is by consumption of contaminated meat products, but little is known about the risk factors, transmission routes and evolution of virulence in LMICs. We will sample and sequence thousands of *Campylobacter* isolates and develop machine-learning approaches to quantitative source attribution. Identification of strains, genes and individual nucleotides associated with different sources can be used to quantify the relative contribution of different reservoirs to human infection.

Candidate:

Applicants should hold, or expect to receive, a First Class or high Upper Second Class UK Honours degree (or the equivalent qualification gained outside the UK) in a relevant subject. A master's level qualification would also be advantageous.

Applications:

Informal enquiries should be directed to Dr Ben Pascoe, bp467@bath.ac.uk.

Formal applications should be made via the University of Bath's [online application form](#).

On the application form, please ensure that you quote 'Evolution Education Trust' in the Finance section and the supervisor's name and project title in the 'Your research interests' section. Should you wish to be considered for more than project, quote the projects in order of preference and upload a separate personal statement relevant to each one.

Please see our Doctoral College website for [more information on how to apply](#) for a PhD at Bath.

Application deadline: 30 April 2019.

Interviews will take place in Bath on 14 June 2019.

Anticipated start date: 30 September 2019.

References:

Pascoe et al (2017) Local genes for local bacteria: evidence of allopatry in the genomes of transatlantic *Campylobacter* populations *Molecular Ecology* 26 (17): 4497-4508

Thépault et al (2017) Genome-wide identification of host-segregating epidemiological markers for source attribution in *Campylobacter jejuni* *AEM* 83 (7): e03085-16

Pascoe et al (2015) Enhanced biofilm formation and multi-host transmission evolve from divergent genetic backgrounds in *Campylobacter jejuni*. *Environmental Microbiology* 17:(11) 4779-4789