Developing bacterial GWAS beyond SNP-based diversity

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Project description:

GWAS is a cornerstone of genotype-phenotype studies in eukaryotes. It has been used only rarely for the study of bacteria, but these studies have suggested it can be a powerful approach to revealing the genetic basis for bacterial traits. Most studies in bacteria have focused on genetic variation at the level of gene content and SNPs.

Bordetella pertussis is the causative agent of whooping cough, or pertussis, a serious respiratory tract infection. For many years vaccination appeared to control the incidence of pertussis but it has become resurgent in many countries worldwide. One aspect of this resurgence is adaptation of *B. pertussis* to vaccine mediated immunity, making the understanding of the basis for *B. pertussis* variation of high importance.

B. pertussis is highly clonal. The species has remarkably low levels of genetic diversity when measured by SNPs and gene content, the traditional diversity sampled by GWAS. However recently, we, and others, have revealed that *B. pertussis* contains extensive variation at the level of genome arrangement and copy number variation (mainly duplications, but some higher copy number variants) of large genomic regions (some larger than 300kb). In addition, recent studies have identified surprising levels of phenotypic diversity among strains, even between those that are very closely related in terms of SNPs and gene content. We hypothesise that genome rearrangement and copy number variation are key drivers of BP phenotypic diversity. Here, we will develop approaches to capture genome arrangement and copy number diversity in GWAS to test our hypothesis. This would greatly extend the power of bacterial GWAS for investigating bacterial genotype-phenotype relationships and be of very wide use for the research community.

This project will involve bioinformatics and genomics as well as 'wet lab' microbiology, providing a multidisciplinary approach. The student will receive state-of-the-art training in these areas.

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 Andrew Preston, ap753@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:
Brookes et al. 2018. Emerg. Microbes. Infect. 7:81.
Ring et al. 2018. Microbial. Genom. 4: doi: 10.1099/mgen.0.000234.
Sealey et al. 2016. Infect. Genet. Evol. 40:136-143.