Elucidating the genetic and biochemical architecture underpinning cross-kingdom interactions

Supervisory team:
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Project description:
Fungi and bacteria commonly share diverse environmental niches, such as the soil or the gastrointestinal tract of warm-blooded animals, where they coordinate their interactions via intricate signalling mechanisms. Although complex, community studies often focus on either bacteria or fungi, neglecting the fact that they do not exist in isolation. Here, we aim to identify the genetic architecture underpinning bacteria-fungi interactions and characterise bacterial compounds regulating fungal growth based on our recent finding of bacterial strains affecting fungal growth. Understanding the genetic factors driving microbial communities and characterising the mode-of-action of secreted molecules affecting fungal growth will (i) provide the research community with a rich resource of a comprehensive, genome-wide catalogue of fungal and bacterial factors affecting cross-species growth suitable for future explorations and (ii) uncover a novel antifungal compound that could be further developed in aid of fighting fungal AMR. Worldwide fungi kill as many patients as tuberculosis each year (Bongomin et al., 2017) and the lack of efficacious antifungal therapies and the rapid emergence of antifungal is contributing to mortality rates of up to 95% (Brown et al., 2012).

To elucidate the intricacies governing bacteria-fungi interactions, we will (i) conduct an in-vitro genome-scale screen identifying fungal genes modulating bacterial growth in the oral cavity, (ii) mine the genomes of soil bacteria for metabolite gene clusters, (iii) screen for bacterial compounds affecting fungal growth, and (iv) systematically characterise the mode-of-action of one of these. To achieve these aims, we will employ a suite of tools and techniques ranging from bioinformatics to classic microbiology and biochemistry, deploying three microbial species for which genetic and genomic tools exist and that can be manipulated in the laboratory, such as a genome-scale Candida albicans library and a fluorescence-labelled Staphylococcus aureus strain. These will be complemented with a collection of wild Streptomyces isolates from soils around the world. This project will profoundly impact our understanding of the genetic networks governing prokaryote – eukaryote interactions and tackle fungal AMR.

The supervisory team comprises fungal and bacterial geneticists from Bristol and Bath and a microbial bioinformatics expert. This combination will ensure a stimulating and productive environment. All supervisors have experience with graduate student supervision. A mentor at Bristol will furthermore support the trainee and facilitate their effective career development and personal growth.