Quantifying the evolution of antimicrobial resistance in mixed-species communities

Supervisory team:
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Project description:
Antibiotic resistance poses formidable challenge with resistance to all but the most recently discovered antibiotics encountered in clinical and agricultural practice. Fundamental to successful deployment of antibiotics is our ability to accurately measure their efficacy. Currently this is exclusively done using microbial monocultures. Yet in nature microbes form intricate communities where multiple strains and species communicate, cooperate and compete. So why should a single-species understanding of microbial response to antibiotics completely explain resistance progression in nature? Indeed, our recent work published in Nature Ecology and Evolution (Beardmore et al 2018) demonstrates that single species antibiotic dose response is a poor predictor of multi-species community dynamics during treatment and after antibiotic withdrawal.

This project will quantify the evolution of drug-resistance in mixed-species communities using deadly human pathogens Candida albicans and Candida glabrata as a model system. Both species are commensal microbes found together in the microbiota of healthy individuals but they are also opportunistic pathogens causing life-threatening disseminated infections. These infections are difficult to diagnose and are associated with high mortality rate, ranging from 46-75% for Candidiasis in the bloodstream. Strikingly, as many people die each year from the top ten invasive fungal diseases, including candidiasis, as do from tuberculosis or malaria.

The supervisory team includes Professors Ivana Gudelj, Neil Gow, Rob Beardmore and Dr Steve Bates at Exeter and Dr Daniel Henk at Bath, and brings together a range of complementary skills including in vitro and in vivo experimental evolution, molecular biology, quantitative modeling and genomics.