Overview

My research combines experimental, mathematical, and genomic approaches to understand microbial evolution in the broadest sense. At present, this involves three lines of research.

Understanding the evolvability of resistance
This project seeks to understand why certain bacteria are more proficient at evolving antibiotic resistance than others. Through comparative experimental evolution and genomic sequencing, it aims to identify genes associated with resistance evolution in various *Pseudomonas* species, providing valuable insights into predicting and addressing antibiotic resistance. We aim to develop new genome engineering approaches to attenuating resistance by disrupting evolvability pathways. This work is funded by the BBSRC.

Antibiotic combination therapy for suppressing resistance evolution
Focused on combating antimicrobial resistance, this research explores novel combination therapies designed to prevent resistance emergence. By investigating combinations that impose significant growth penalties on bacteria, the project aims to develop effective treatments resistant to single resistance mechanisms, using experimental evolution to uncover evolutionary principles guiding combination therapy design. This work uses urinary tract infections in *Escherichia coli* as a system for exploring new treatment regimes. This work is funded through a Springboard Award from the Academy of Medical Sciences.

Evolutionary dynamics of extremophiles
This project aims to understand the adaptation of extremophilic microbes to novel environments, and better understand the role of genome replication fidelity in their evolvability. Through experimental evolution with the archaeon *Sulfolobus acidocaldarius*, we aim to reveal unexplored evolutionary processes under extreme conditions, advancing our understanding of archaean evolution and its broader implications for the evolution of the diversity of life on Earth. This work is funded through grants from NERC and the Royal Society.

Overview

Prospective applicants
If you are interested discussing the possibility of a postgraduate or postdoctoral positions, please contact me with a brief statement outlining your research interests, your research experience, and a recent CV.
Postdocs positions: Will be advertised on https://www.jobs.manchester.ac.uk/.
Technician positions: Will be advertised on https://www.jobs.manchester.ac.uk/.
PhD students: I am happy to discuss student-proposed projects with prospective students in the areas of antimicrobial resistance, evolutionary genomics, and experimental evolution. Advertised studentships will be posted on https://www.findaphd.com/phds/.
Externally-funded studentship projects
Prospective students interested in applying for externally-funded studentships should contact me regarding available funding sources.

Employment

Lecturer
Academic (Teaching and Research) Lecturer
Division of Evolution, Infection and Genomics
The University of Manchester
1 Sept 2022 → present

BBSRC Pool of Experts
Biotechnology & Biological Sciences Research Council (BBSRC)
Swindon, United Kingdom
1 Jan 2023 → present
Research outputs

Antibiotic resistance alters the ability of Pseudomonas aeruginosa to invade the respiratory microbiome

Eco-evolutionary dynamics of experimental Pseudomonas aeruginosa populations under oxidative stress
Fu, T., Gifford, D. R., Knight, C. G. & Brockhurst, M. A., 9 Nov 2023, In: Microbiology. 169, 11

Mutators can drive the evolution of multi-resistance to antibiotics

Coincidence analysis of efflux pumps in the Escherichia coli pangenome

Competition delays multi-drug resistance evolution during combination therapy

Mathematical modelling for antibiotic resistance control policy: Do we know enough?

Measuring Microbial Mutation Rates with the Fluctuation Assay
Krašovec, R., Richards, H., Gomez, G., Gifford, D. R., Mazoyer, A. & Knight, C. G., 28 Nov 2019, In: Journal of visualized experiments : JoVE. 153

Life on the frontline reveals constraints

Mutators drive evolution of multi-resistance to antibiotics

Environmental pleiotropy and demographic history direct adaptation under antibiotic selection

Identifying and exploiting genes that potentiate the evolution of antibiotic resistance

Opposing effects of final population density and stress on Escherichia coli mutation rate

Critical mutation rate in a population with horizontal gene transfer

Spontaneous Mutation Rate Is a Plastic Trait Associated with Population Density across Domains of Life
Critical Mutation Rate has an Exponential Dependence on Population Size for Eukaryotic-length Genomes with Crossover

Multicopy plasmids potentiate the evolution of antibiotic resistance in bacteria

Divergent evolution peaks under intermediate population bottlenecks during bacterial experimental evolution

Epistatic interactions between ancestral genotype and beneficial mutations shape evolvability in Pseudomonas aeruginosa

Parasite diversity drives rapid host dynamics and evolution of resistance in a bacteria-phage system

Environmental variation alters the fitness effects of rifampicin resistance mutations in Pseudomonas aeruginosa

Modelling colony population growth in the filamentous fungus Aspergillus nidulans

Awards

Projects

Evolutionary mechanisms and dynamics
Walton, C., Shultz, S., Sansom, R., Krasovec, R., Knight, C., Gilman, R., Gifford, D., Garwood, R., Chamberlain, A. & Buckley, M.

Oxford Nanopore PromethION
31/07/23 → 30/07/26