How ecological interactions shape microbial mutation rates to antimicrobial resistance

A thesis submitted to the University of Manchester for the degree of Doctor of Philosophy in the Faculty of Science and Engineering. School of Natural Sciences, Department of Earth and Environment

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2024

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Abbreviations

CFU – Colony Forming Units

D – Final Population density - The estimated number of cells per ml at the end of the culture cycle

DAMP – Density-associated mutation-rate plasticity

m – Number of mutational events

MMR – Methyl-directed DNA mismatch repair

MRP – Mutation Rate Plasticity

N_0 – The initial population size of cells.

N_t – The population size at the end of the culture period

N_e – The effective population size

SIM – Stress-Induced Mutagenesis

1 Introduction

Uncovering the mechanisms behind environmentally responsive mutagenesis informs our understanding of evolution, notably antimicrobial resistance, where mutation supply can be critical (Gifford et al. 2023; Ragheb et al. 2019). Microbial mutation rates are responsive to a wide variety of environmental factors including population density (Krašovec et al. 2017), temperature (Chu et al. 2018), growth rate (Ram P. Maharjan and Ferenci 2018; Liu and Zhang 2019), stress (MacLean, Torres-Barceló, and Moxon 2013; Foster 2007), growth phase (Loewe, Textor, and Scherer 2003) and nutritional state (Ram P. Maharjan and Ferenci 2017). Such mutation rate plasticity inspires the idea of "anti-evolution drugs", able to slow the evolution of antimicrobial resistance during the treatment of an infection (Ragheb et al. 2019; Cirz et al. 2005; Domenech et al. 2020; Alam et al. 2016). Even small reductions in the mutation rate (2-5-fold) can have dramatic effects on the capacity of bacterial populations to adapt to antibiotic treatment, particularly when evolution is limited by mutation supply, as is the case for small pathogen populations (Ragheb et al. 2019).

Microbial mutation rates have an inverse association with population density across all domains of life, we have previously shown that 93% of otherwise unexplained variation in published mutation rate estimates is explained by the final population density (Krašovec et al. 2017). This density-associated mutation rate plasticity (DAMP) is a distinct phenotype from stress-induced mutagenesis, which acts via independent genetic mechanisms (Krašovec et al. 2018). Population density alters not only the rate but also the spectrum of mutations, with

significantly higher rates of AT>GC transitions seen in low density populations (Gifford et al. 2023). Density effects are likely relevant to natural populations given that population sizes and densities vary greatly, for example, *Escherichia coli* populations in host faeces can range in density by 5 orders of magnitude (**16**), and infections can be established by populations as small as 6×10^3 cells (**17**). We therefore aim to mechanistically describe the widespread phenotype of DAMP.

In order to test potential mechanisms generating DAMP, we developed and systematically assessed a computational model connecting metabolism and mutagenesis in a growing *E. coli* population. This model generates the hypothesis that the key determinants of DAMP are the production and degradation rates of reactive oxygen species (ROS). Though molecular oxygen is relatively stable it can be reduced to superoxide ($^{\bullet}O_{2-}$), hydrogen peroxide (H_2O_2) and hydroxyl radicals ($HO^{\bullet}$). These "reactive oxygen species" are strong oxidants able to damage multiple biological molecules including nucleotides and DNA (**18**). We tested the role of ROS in controlling DAMP by estimating mutation rate plasticity under different conditions of environmental oxygen and with genetic manipulations known to alter ROS dynamics. We find that the reduction in mutation rate at increased population density results from the population's increased ability to degrade H_2O_2, resulting in reduced ROS-associated mutagenesis. We show that this density effect is also experienced by cells deficient in H_2O_2 degradation when cocultured with wild-type cells able to detoxify the environment. Mutation rates therefore depend not only on the genotype of the individual but also on the community's capacity to degrade H_2O_2.

2 Results

The results show mutations.

3 Discussion

The discussion discusses mutations.

4 Summary

In summary, this book has no content whatsoever.

The slope of the below graph is 0.5

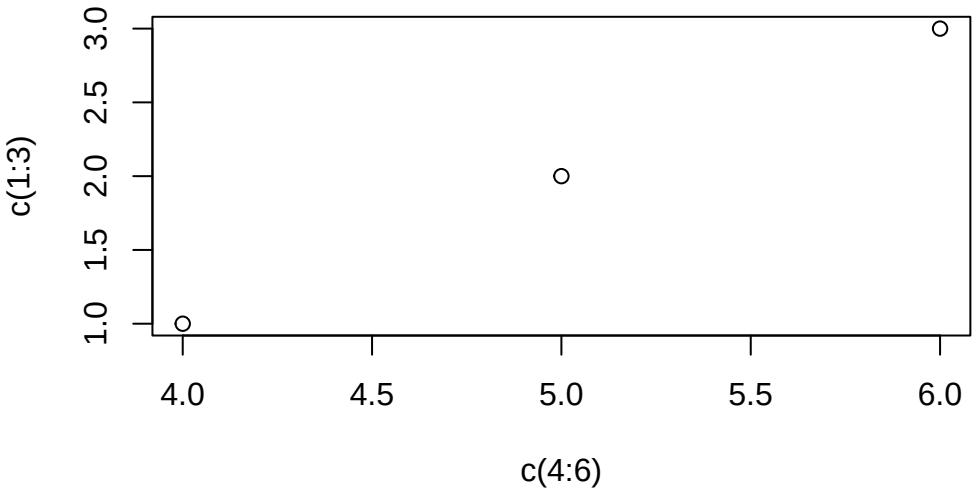

Figure 4.1: Plot of numbers

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