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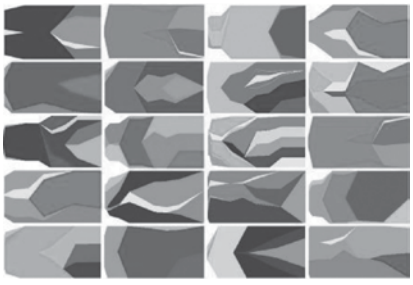
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About the cover:

Beginning with volume 43 (January 2022), the cover of *Infection Control & Hospital Epidemiology* (ICHE) will feature art inspired by or reflective of topics within the scope of the journal and their impact on patients, healthcare personnel and our society. These topics include healthcare-associated infections, antimicrobial resistance, and healthcare epidemiology. The intent is to feature original artwork that has been created by individuals who have a personal connection to one or more of these topics through their clinical work, research, or experience as a patient or an affected patient's family member, friend or advocate. The goal is to provide readers with a visual reminder of the human impact of the topics addressed in the journal and the importance of the work being done by those who read or contribute to ICHE and by all who are trying to make healthcare safer through the elimination of healthcare-associated infections.

For more information about the ICHE cover and how to submit artwork for consideration for a future cover, please visit the ICHE website: https://www.cambridge.org/core/journals/infection-control-and-hospital-epidemiology/front-covers

2025



Title: *The Dynamics of Bacterial Evolution*, 2020
Artist: Angharad Ellen Green, PhD
Medium: The artwork is made up of individual Muller plots representing *Streptococcus pneumoniae* bacteria lineages that were evolved separately within nasopharynx and lung environments. The command line program muller (v0.6.0 - https://pypi.org/project/muller/), with default parameters applied, was used to produce genotypes and trajectories tables for each of the evolved lineages. These tables were then used as inputs for ggplot2 (v3.3.2) and ggmuller (v0.5.4) in R-Studio (v4.0.2), to produce Muller plots. The individual plots were then assembled to produce the resulting artwork.

Dr. Green spoke to ICHE about her artwork.

What was the inspiration for this artwork? My postdoctoral research used an *in vivo* experimental evolution model to understand how *Streptococcus pneumoniae* (the pneumococcus) adapts to the lung and nasopharynx environments. The pneumococcus was experimentally evolved through a lung infection model and a nasopharynx infection model, producing independently evolved lung and nasopharynx lineages. We sequenced the evolved lineages and compared them to the ancestor to understand how their genomes had changed. This work also enabled us to determine how environmental differences between the upper and lower airways might shape pneumococcal adaptation and evolution. The resulting sequencing dataset was very large and complex with lots of interesting results. I wanted to use an effective method of visualising the data and Muller plots were chosen to display the evolutionary dynamics of mutations found in each evolved lineage over time. In these plots, each mutation is grouped as a genotype, which is represented by a different colour, and the blocks of colour expand when the genetic changes make the bacteria better able to survive in their local conditions. After completing the data analysis and publishing this work, I created this artwork as a memento of my postdoctoral research and I have a canvas of this work hanging in my apartment. Additionally, I wanted to demonstrate how scientific artwork can help visualise the complexities of evolution dynamics and help us to better understand bacterial processes.

What is your personnel connection to the content of ICHE? Throughout my career as a microbiologist, I have carried out research to investigate bacterial pathogenesis and antimicrobial resistance (AMR) of WHO-defined bacterial priority pathogens, such as *Pseudomonas aeruginosa*, methicillin-resistant *Staphylococcus aureus* (MRSA) and *Streptococcus pneumoniae*. I have actively promoted the importance of microbial genomic research to confront current global challenges, such as AMR and healthcare-acquired infections. I have championed microbiology research through my various roles in academia, volunteering on the Microbiology Society's Policy Committee and as a Research Manager at the Healthcare Infection Society. It is an honour for my bacterial evolution artwork to be on the cover of ICHE.

Given the scope of the journal, why is this work appropriate for the cover of *Infection Control & Hospital Epidemiology*? This artwork is made up of a collection of graphs called Muller plots, which are used to visualize how bacteria evolve when grown in diverse environments. The colours represent genetic changes that have taken place in the presence of environmental factors, such

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Cover image: *The Dynamics of Bacterial Evolution, 2020*

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as antimicrobials and the host immune system. The dynamics of evolution are complex and being able to visualise this process enables scientists to better understand bacterial processes, including the development of AMR. This artwork is appropriate for the cover of ICHE as it was created as a direct result of scientific research into how bacteria can adapt and evolve in diverse host niches to cause disease. Additionally, this artwork makes it possible for scientists to visualise the complexities of the dynamics of evolution and comprehend how bacteria adapt to different host environments.

Dr. Green is a Senior Research Data Steward in the Advanced Research Computing Centre (ARC) at UCL in London. *Her postdoctoral research at the University of Liverpool was supported by a Sir Henry Dale Fellowship, awarded by the Wellcome Trust and the Royal Society (grant number 204457/Z/16/Z) to Dr. Daniel R Neill. The research from which this artwork was derived was published in Molecular Biology and Evolution (Green AE, Howarth D, Chaguza C, et al. Pneumococcal colonization and virulence factors identified via experimental evolution in infection models. Mol Biol Evol 2023; 38: 2209-2226).*

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