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Infection Control & Hospital Epidemiology


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CONTENTS

Commentaries

- 221** Protecting patients and peers from healthcare personnel with respiratory viral infections
Michael Klompas, Theodore Pak and Chanu Rhee
- 224** Chatting new territory: large language models for infection surveillance from pilot to deployment
Julie T. Wu, Bradley J. Langford, Erica S. Shenoy, Evan Carey and Westyn Branch-Elliman

Review

- 227** Risk period for transmission of SARS-CoV-2 and seasonal influenza: a rapid review
Erin C. Stone, Devon L. Okasako-Schmucker, Joanna Taliano, Melissa Schaefer and David T. Kuhar

Original Articles

- 236** A telehealth approach to central line-associated bloodstream infection prevention activities in nursing homes: the SAFER lines program
Raveena D. Singh, Bardia Bahadori, Tom Tjoa, Mohamad N. Alsharif, Shereen Nourollahi, Justin Chang, Amarah Mauricio, Jessica Bethlahmy, Syma Rashid, Raheeb Saavedra, Isabel Y. Ashbaugh, Steven Tam and Shruti K. Gohil
- 243** Prospective, crossover, comparative study of two methods of chlorhexidine bathing
Richard Jordan Hankins, Luke Handke, Paul D. Fey, Ruth Jennifer Cavalieri, Kelly A. Cawcutt, Trevor Van Schooneveld, Elizabeth Lyden, Robin High and Mark E. Rupp
- 249** Examining the impact of clinical features and built environment on risk of hospital onset *Clostridioides difficile* infection
Priti Singh, Endia Reid, Justin Smyer, Jennifer Martin, James Odei, Courtney Hebert and David Kline
- 256** Enhancing the control of respiratory virus spread: a comprehensive approach integrating airborne virus detection, aerological investigations, and airflow modeling for practical implementation
Guillaume Mellon, Nadia Mahjoub, Fabien Metivier, Nathalie Osinski, Audrey Gabassi, Constance Delaugerre, Emmanuel Vanoli, Cyril Crawford and Jérôme Le Goff
- 266** Evaluating an urgent care antibiotic stewardship intervention: a multi-network collaborative effort
Daniel E. Park, Annie L.S. Roberts, Rana F. Hamdy, Sabrina Balthrop, Patrick Dolan and Cindy M. Liu
- 272** Prioritizing emergency department antibiotic stewardship interventions for skin and soft tissue infections using judgment analysis
Meggie Griffin, Kimberly C. Claeys, Rebecca J. Schwei, Roger L. Brown and Michael S. Pulia
- 281** Benchmarking antimicrobial use to antimicrobial resistance: a comparative study of two hospitals using current National Healthcare Safety Network (NHSN) metrics
Carlos A.Q. Santos, Sarah Y. Won, Ryan Dwyer, Caren Perez, William E. Trick and for the CDC Prevention Epicenters Program

- 289** Social mixing patterns of United States healthcare personnel at a quaternary health center: a prospective observational study
Lauren Pischel, Obianuju G Aguolu, Noureen Ahmed, Melissa M Campbell, Ryan Borg, Chelsea Duckwall, Kathryn Willebrand, Agnieska Zaleski, Elliott E Paintsil, M Catherine Muenker, Aryn A Malik, Moses C Kiti, Joshua L Warren, Samuel M Jenness, Ben A Lopman, Justin Belsky, Richard A Martinello, Inci Yildirim, Albert I Ko and Saad B Omer
- 298** Using electronic medical records in hospital simulation for infection control intervention assessment
Fardad Haghpanah, Eili Y Klein and for the CDC MInD-Healthcare Program

Concise Communications

- 305** Performance of a large language model for identifying central line-associated bloodstream infections (CLABSI) using real clinical notes
Guillermo Rodriguez-Nava, Goar Egoryan, Katherine E. Goodman, Daniel J. Morgan and Jorge L. Salinas
- 309** A head-to-head comparison of the accuracy of commercially available large language models for infection prevention and control inquiries, 2024
Oluchi J Abosi, Takaaki Kobayashi, Natalie Ross, Alexandra Trannel, Guillermo Rodriguez Nava, Jorge L. Salinas and Karen Brust
- 312** Utilizing whole genome sequencing to characterize central line-associated bloodstream infections due to *Staphylococcus epidermidis*
Chunyi Zhou, Michael Wiley, Jessica Wiley, Kelly Cawcutt, Elizabeth Grashorn, Kathie Rogers, Emily McCutchen, Peter Iwen, Paul Fey and Mark Rupp
- 316** Navigating the blood–brain barrier: enhancing blood culture practices in the neuro-ICU
Maureen Metz, Katharine Colton and Jessica Seidelman
- 319** Heterogeneity in preoperative *Staphylococcus aureus* screening and decolonization strategies among healthcare institutions
Sarah L. Bennis, Shalini Kulasingam, Patricia Ferrieri and Susan E. Kline
- 323** Facilitators of antibiotic decision-making in home-based primary care: a qualitative investigation
Rupak Datta, Eliza Kiwak, Terri Fried, Andrea Benjamin, Lynne Iannone, Sarah Krein, Warren Carter and Andrew Cohen
- 327** Evaluation of a new technology for terminal sterilization of flexible endoscopes using hydrogen peroxide gas plasma
Martin M. Varghese, Samir Memic, Maria M. Torres-Teran, Jennifer L. Cadnum, William A. Rutala and Curtis J. Donskey
- 330** A bridge over troubled water: reverse osmosis to maintain patient care in a boil water notice
Jacob Smith, Julia Fischer, Manju Mathew and Sarah Haessler

Letters to the Editor

- 333** Respiratory equality: let's stop playing favorites with COVID-19 in the healthcare setting
Catherine L. Passaretti, Werner Bischoff, Justin Chan, Daniel J. Diekema, Shira Doron, Carolee Estelle, Jesse T. Jacob, Tsun Sheng N. Ku, Surbhi Leekha, Richard A. Martinello, Vidya K. Mony, L. Silvia Munoz-Price, Rekha Murthy, Judith A. O'Donnell, David H. Priest, Mindy M. Sampson, Thomas J. Sandora, Graham M. Snyder, Michael P. Stevens, Julie E. Szymczak, Francesca Torriani, Deborah S. Yokoe and Jonas Marschall
- 335** Central line utilization reduction via weekly prospective audit and feedback using a standardized audit tool
Ken Dekitani, Meghan S. Madhusudhan, Jonathan D. Grein, Angelena R. Lopez, Isabel F. Pedraza and Michael A. Ben-Aderet

Corrigendum

- 337** Mixed-methods multicenter assessment of healthcare workers' knowledge, perceptions, and practices related to blood culture utilization in hospitalized adults – CORRIGENDUM
- 338** Incidence of surgical infection in cefazolin 3 g versus 2 g for colorectal surgery in obese patients – CORRIGENDUM

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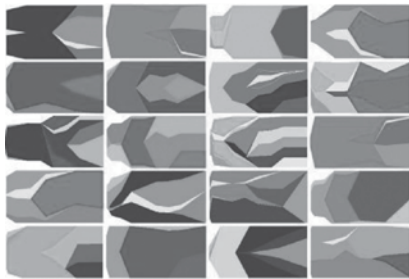
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About the cover:

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 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

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

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).