



Clinical P. Aerginosa Prophages: Insights Into Their Role Via Their Activity, Abundance, Persistence

Kyrkou, Ifigeneia; Bartell, Jennifer; Lood, Cédric; Mateo, Ana Lechuga; Marvig, Rasmus; Lavigne, Rob; Johansen, Helle Krogh; Molin, Søren

Published in:
The Danish Microbiological Society Annual Congress 2023

Publication date:
2023

Document Version
Publisher's PDF, also known as Version of record

[Link back to DTU Orbit](#)

Citation (APA):
Kyrkou, I., Bartell, J., Lood, C., Mateo, A. L., Marvig, R., Lavigne, R., Johansen, H. K., & Molin, S. (2023). Clinical P. Aerginosa Prophages: Insights Into Their Role Via Their Activity, Abundance, Persistence. In *The Danish Microbiological Society Annual Congress 2023: Abstract book* (pp. 6-6). Article 1 Danish Microbiological Society.

General rights

Copyright and moral rights for the publications made accessible in the public portal are retained by the authors and/or other copyright owners and it is a condition of accessing publications that users recognise and abide by the legal requirements associated with these rights.

- Users may download and print one copy of any publication from the public portal for the purpose of private study or research.
- You may not further distribute the material or use it for any profit-making activity or commercial gain
- You may freely distribute the URL identifying the publication in the public portal

If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

ORAL SESSION 1

[1] CLINICAL *P. AERUGINOSA* PROPHAGES: INSIGHTS INTO THEIR ROLE VIA THEIR ACTIVITY, ABUNDANCE, PERSISTENCE

Ifigeneia Kyrkou*,¹, Jennifer Bartell,² Cédric Lood,³ Ana Lechuga Mateo,⁴ Rasmus Marvig,⁵ Rob Lavigne,⁶ Helle Krogh Johansen,⁷ Søren Molin,⁸

¹ University of Copenhagen, Clinical Microbiology, Veterinary and Animal Sciences, Copenhagen, Denmark, ² University of Copenhagen, Center for Health Data Science, Copenhagen, Denmark, ³ KU Leuven, Biosystems, Leuven, Belgium, ⁴ Catholic University of Leuven, Biosystems, Leuven, Belgium, ⁵ Rigshospitalet, Center for Genomic Medicine, Copenhagen University Hospital, Copenhagen University Hospital, Rigshospitalet, Department of Genomic Medicine, Copenhagen, Denmark, ⁶ KU Leuven, Department of Biosystems, Laboratory of Gene Technology, Heverlee, Belgium, ⁷ Department of Clinical Microbiology, Copenhagen University Hospital, Clinical Microbiology, Copenhagen, Denmark, ⁸ Technical University of Denmark, Denmark

It remains unclear how much the accessory genome contributes in the complex processes of establishment and virulence of bacterial infections. *P. aeruginosa* is one of the most common opportunistic human pathogens and can establish difficult-to-eradicate infections. Genome-integrated viruses, known as prophages, are frequent components of this bacterium's large accessory genome and can contribute to the virulence of *P. aeruginosa*. However, systematic interpretations of the contributing role of prophages in the evolution and fitness of the ubiquitous *P. aeruginosa* in its diverse niches are still in their infancy. This study provides insights into these roles by exploring the activity, abundance and persistence of prophages belonging to *P. aeruginosa* from the cystic fibrosis (CF) lung. We selected a cohort of 12 CF patients with a high-resolution history of difficult-to-eradicate *P. aeruginosa* infections. Nanopore technology was used to sequence high-contiguity genomes of one early isolate per patient. Subsequently, we applied a strategy that combined bioinformatics, antibiotic-assisted inductions, lysate sequencing and genomics to identify intact prophages in the host genomes and assess their long-term survival in follow-up isolates. From these data, we observed that CF *P. aeruginosa* genomes harbour a high abundance of intact prophages which can sometimes self-induce. We identified 29 intact prophages with a wide genomic diversity and some unique prophage genomes with minimum similarity to available genomes. All induced prophages were retraced in follow-up isolates for a tested period of 4 to 9 years with minimal genomic changes. In addition to elucidating the role of prophages in *P. aeruginosa*, we expect our findings to assist in developing novel diagnostics and phage-based therapies for *P. aeruginosa* infections.