



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

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## ORAL SESSION 1

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

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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.