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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.