Department of Biomedical Engineering
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Genomic surveillance as a scalable framework for phage therapy against critically resistant bacterial pathogens



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Abstract

The rising prevalence of hospital-acquired infections caused by multidrug-resistant pathogens underscores the urgent need for innovative treatment strategies. Bacteriophage therapy has emerged as a promising alternative, yet its broader clinical implementation faces significant challenges, including the limited host range of phages and the diversity of pathogen populations. To address this barrier, we leverage large-scale phylogeographical analysis to inform the design of phage collections tailored to the dominant pathogen strain types in specific geographic regions. In our initial efforts, we analyzed the global population structure of carbapenem-resistant *Acinetobacter baumannii* and *Klebsiella pneumoniae* using tens of thousands of genome sequences from public databases and our local surveillance data covering Southeastern Europe. We found that a limited number of strain types dominate infections in each world region, although the diversity of these two species significantly differs. This limited diversity, in combination with the relative stability of the pathogen populations, enables the development of region-specific phage collections that address the majority of the infections. Overall, by leveraging genomic epidemiology, we establish a scalable framework for phage therapy, enabling the definition of phages needed for the benefit of the largest possible patient cohorts. This approach not only accelerates clinical trials and the validation of therapeutic phages for nosocomial pathogens but also provides a model for extending this strategy to other high-priority pathogens. Ultimately, this work lays the foundation for a broader healthcare impact and the seamless integration of phage therapy into routine clinical practice.

Biography

Dr. Bálint Kintsesis a Senior Research Fellow and leader of the Translational Microbiology Research Group at the HUN-REN Biological Research Centre in Szeged, Hungary. His research combines microbial genomics, experimental evolution, and functional metagenomics to understand antimicrobial resistance and advance precision bacteriophage therapy. He leads a therapeutic bacteriophage research programme focused on developing phage collections guided by genomic surveillance of multidrug-resistant pathogens. His work aims to translate insights into pathogen diversity and evolution into scalable phage-based strategies against hospital-acquired infections.

***** ALL ARE WELCOME *****

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