



OPEN ACCESS

EDITED AND REVIEWED BY
Max Maurin,
Université Grenoble Alpes, France

*CORRESPONDENCE
Cecilia A. Silva-Valenzuela
✉ casilv@gmail.com

SPECIALTY SECTION
This article was submitted to
Clinical Microbiology,
a section of the journal
Frontiers in Cellular and
Infection Microbiology

RECEIVED 14 December 2022
ACCEPTED 15 December 2022
PUBLISHED 30 December 2022

CITATION
Silva-Valenzuela CA,
Molina-Quiroz RC and Sillankorva S
(2022) Editorial: Phage-bacteria
interplay: Future therapeutic
approaches against antibiotic
resistant bacteria.
Front. Cell. Infect. Microbiol.
12:1124187.
doi: 10.3389/fcimb.2022.1124187

COPYRIGHT
© 2022 Silva-Valenzuela, Molina-Quiroz
and Sillankorva. This is an open-access
article distributed under the terms of
the [Creative Commons Attribution
License \(CC BY\)](https://creativecommons.org/licenses/by/4.0/). The use, distribution
or reproduction in other forums is
permitted, provided the original
author(s) and the copyright owner(s)
are credited and that the original
publication in this journal is cited, in
accordance with accepted academic
practice. No use, distribution or
reproduction is permitted which does
not comply with these terms.

Editorial: Phage-bacteria interplay: Future therapeutic approaches against antibiotic resistant bacteria

Cecilia A. Silva-Valenzuela^{1*}, Roberto C. Molina-Quiroz ²
and Sanna Sillankorva³

¹Microbes Lab SpA Valdivia, Los Ríos, Chile, ²Stuart B. Levy Center for Integrated Management of Antimicrobial Resistance (Levy CIMAR), Tufts Medical Center and Tufts University, Boston, United States, ³International Iberian Nanotechnology Laboratory (INL), Braga, Portugal

KEYWORDS

antimicrobial resistance, phage (bacteriophage), infections, coevolution, arms-race

Editorial on the Research Topic

[Phage-bacteria interplay: Future therapeutic approaches against antibiotic resistant bacteria](#)

The antibiotic resistance crisis is a worldwide healthcare concern. World Health Organization (WHO) has projected that infections generated by multi-drug resistant (MDR) bacteria will most likely increase in the near future. This situation has encouraged scientists to develop and/or improve complementary strategies to fight this threat. In this context, bacterial viruses (bacteriophages or phages) have been proposed as a therapeutic alternative due to their specificity and different mechanism of action compared to antibiotics.

Phages are the most abundant microbial entity in the environment (reaching ~10^{e31}), and the constant interplay with their bacterial hosts shapes both phage and bacterial evolution in the so-called arms race.

This Research Topic aimed to provide an update on the impact of phage-host interactions in bacterial evolution and the cautions to consider for administering phage-based therapies. In this context, new research showing relevant aspects of phage biology during the interaction with their hosts, such as the effect of genotypic diversity and its impact on bacterial coevolution (Castledine et al.) and the dynamics of phage-bacteria coevolution in culture media was reported (Barron-Montenegro et al.). In addition, the use of CRISPR-Cas genetic scars in the host genome as a tool to understand phage-host interplay in the human microbiome (Monshizadeh et al.) and the characterization of novel phages able to infect and kill clinically relevant MDR pathogens was also highlighted (Li et al.). Altogether, these new findings increase our current understanding of phage-bacteria interactions and contribute to reinforcing the idea of a rational use of phage therapy and the identification of novel relevant aspects to consider

when using phages as an antibacterial strategy for the treatment of MDR human and foodborne pathogens.

Author contributions

All authors listed have made a substantial, direct, and intellectual contribution to the work and approved it for publication.

Funding

SS acknowledges funding by the Portuguese Foundation for Science and Technology through the individual scientific stimulus program contract (2020.03171.CEECIND).

Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Publisher's note

All claims expressed in this article are solely those of the authors and do not necessarily represent those of their affiliated organizations, or those of the publisher, the editors and the reviewers. Any product that may be evaluated in this article, or claim that may be made by its manufacturer, is not guaranteed or endorsed by the publisher.