## Bacteriophage-derived enzymes: from exploration to exploitation

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Bacteriophages are viruses infecting bacterial cells. During their replication cycle, these viruses cross the bacterial cell wall twice. Firstly, bacteriophages have to inject their genome across the cell wall to initiate infection. Secondly, they must exit the host cell at the end of the replication cycle to infect new host cells. The principal barrier to overcome is the polysaccharides that can either be extracellular (slime or capsules) or structural (peptidoglycan). For this, bacteriophages encode two specific enzymes, called depolymerases and endolysins, to degrade these polymers to enable either infection or lysis.
Depolymerases, are specialized enzymes that degrade polymers (e.g. slime or capsular polysaccharides) to facilitate bacteriophage access to its hosts. They can be used to strip cells from their capsules, which is the main virulence factor of most pathogens. These enzymes have also the potential to digest the slime (i.e. matrix) and control infectious biofilms, which are problematic in food and clinical settings [1].
Endolysins are enzymes that specifically cleave the bacterial rigid peptidoglycan to release progeny bacteriophages at the end of its lytic cycle. This properties make them promising antibacterial agents, able to eliminate pathogens, including antibiotic resistant bacteria, in a quick and specific manner [2].
This talk will give an overview of the identification and characterization of bacteriophage-derived depolymerases and endolysins, and how they can serve as alternatives for existing antibiotics when applied against highly virulent and multidrug resistance pathogens, like *Acinetobacter* and *Pseudomonas*, with several *in vitro* and *in vivo* examples.

[1] Pires, DP, Oliveira H, Melo LDR, Sillankorva S, Azeredo J. Bacteriophage-encoded depolymerases: their diversity and biotechnological applications. Applied Microbiology and Biotechnology. 100:2141-51, 2016.

[2] Oliveira H, Pinto G, Oliveira A, Oliveira C, Faustino M, Briers Y, Domingues L, Azeredo J. Characterization and genome sequencing of a Citrobacter freundii phage CfP1 harbouring a lysin active against multidrug-resistant isolates. *Applied Microbiology and Biotechnology*. 24:100, 2016