[ID: 282] Bacteriophage polysaccharide depolymerases, their role and biotechnological applications

Joana Azeredo [1], Hugo Oliveira [1], Ana Rita Costa [1], Mikhail Shneider [2], Sanna Sillankorva [1]

[1] *CEB – Centre of Biological Engineering, LIBRO – Laboratório de Investigação em Biofilmes Rosário Oliveira, University of Minho, Portugal, Braga, Portugal*
[2] *Shemyakin-Ovchinnikov Institute of Bioorganic Chemistry, Laboratory of Molecular Bioengineering, Moscow, Russia*

Several virulence factors have been identified in Gram-negative bacilli, among which the capsular structures which are suggested to be involved in the evasion of microbial defences. Although the capsule is commonly associated with bacteriophage resistance, some bacteriophages can recognize this structure as a receptor with the aid of structural polysaccharide depolymerases. Bacteriophages have then evolved along with the bacteria to recognize different types of capsules. This feature is well illustrated in phages infecting Acinetobacter spp. known to display at least 106 capsular types. We have isolated and characterized 5 novel podovirues infecting the Acinetobacter calcoaceticus-Acinetobacter baumannii (ACB) complex currently formed by six closely related species. Microbiologically, all phages produce plaques with opaque halos and have distinct narrow host ranges. Their genomes are closed related among them and to all other Acinetobacter podoviruses present in Genbank. There is only a very specific genomic pattern variation present located at the C-terminal tail fiber - depolymerase domain - that functions as a capsular depolymerase. We demonstrate that the depolymerase proteins exhibiting pectate lyase domains, specifically recognize bacterial capsular types as ligands for phage adsorption. We further demonstrate that the depolymerases act in a wide range of environmental conditions and that are high stable, probably related with their structural nature designed during evolution to endure harsh external conditions to maintain the phage infectivity. Moreover, we have characterized the anti-virulent effect of those depolymerases and proved that enzyme treated A. baumannii were no longer virulent to human lung epithelium. Overall this work demonstrates the great diversity of bacteriophage depolymerases, their role in phage infection and evolution and their possible biotechnological applications in bacteria typing and virulence reduction presenting thus a great contribution for diagnostic and treatment of infectious diseases cause by capsulated bacteria.