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Deciphering Host-virus Interactions: Receptor-mediated Lytic Phage Host Range in *Pseudomonas aeruginosa*

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DESCRIPTION

In the ongoing battle against bacterial infections, the emergence of antibiotic-resistant strains poses a formidable challenge. In response, bacteriophages, or phages, viruses that infect and replicate within bacteria, have garnered renewed interest as potential alternatives to antibiotics. However, the success of phage therapy hinges on understanding the intricate host-virus interactions that govern phage infectivity, particularly in the context of lytic phages targeting pathogenic bacteria such as *Pseudomonas aeruginosa*. A pivotal aspect of these interactions lies in the identification and recognition of host receptors by lytic phages, a process that dictates phage host range and infectivity. *P. aeruginosa*, a versatile opportunistic pathogen notorious for its antibiotic resistance and ability to cause severe infections in immunocompromised individuals, represents a prime target for phage therapy. Lytic phages specific to *P. aeruginosa* have been isolated and characterized for their therapeutic potential, yet the determinants of phage host range within this bacterium remain a subject of active investigation. Recent research has elucidated the critical role of host receptors in dictating lytic phage host range in *P. aeruginosa*. Phage receptors are surface molecules on bacterial cells that serve as binding sites for phage attachment and entry, facilitating the initiation of the infection process. These receptors often consist of specific bacterial surface structures, such as lipopolysaccharides (LPS), outer membrane proteins, or pilin proteins, which interact with corresponding phage tail fiber proteins or receptor-binding proteins. Studies employing molecular genetics, genomics, and structural biology have unveiled a diverse array of phage receptors in *P. aeruginosa*, each contributing to the specificity and efficiency of phage infection. For instance, LPS, a major component of the outer membrane in Gram-negative bacteria like *P. aeruginosa*, serves as a primary receptor for numerous lytic phages. Variations in LPS structure, such as O-antigen composition and modifications, can influence phage adsorption and infectivity, highlighting the role of bacterial surface diversity in shaping phage host range.

Additionally, outer membrane proteins (OMPs) and pilin proteins have been identified as alternative receptors for lytic phages infecting *P. aeruginosa*. These proteins, involved in various cellular functions including nutrient transport and adhesion, can also serve as targets for phage recognition and binding. Genetic mutations or alterations in the expression of OMPs and pilins can impact phage susceptibility, further underscoring the dynamic nature of host-virus interactions in bacterial infections. Moreover, bacteriophage-encoded receptor-binding proteins (RBPs) play a pivotal role in mediating host specificity and infectivity. RBPs are surface-exposed proteins on phage particles that recognize and bind to specific receptors on the bacterial cell surface, initiating the infection process. Structural studies have elucidated the molecular interactions between phage RBPs and bacterial receptors, providing insights into the mechanisms of phage-host recognition and attachment. Understanding the diversity and dynamics of phage receptors in *P. aeruginosa* is crucial for rational phage selection and optimization of phage therapy protocols. By characterizing the repertoire of host receptors and their interactions with lytic phages, researchers can predict phage host range, assess phage efficacy, and design tailored phage cocktails to target multidrug-resistant bacterial strains effectively.

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CONFLICT OF INTEREST

The author declares there is no conflict of interest in publishing this article.

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