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FUNCTIONAL ANALYSIS OF ANTIVIRAL BREX PROTEINS

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Bacteriophages are the most abundant biological entity in the biosphere, and they are responsible for the destruction of 20-40 % of bacterial cells every day [1]. This evolutionary pressure drives the emergence of diverse bacterial defence systems, one of which is the BREX (Bacteriophage Exclusion). This system is present in about 10 % of known prokaryotic genomes, yet its detailed defence mechanism remains to be elucidated [2]. Our study focuses on the type I BREX (BREX1) system, which is encoded by a cluster of six genes: *brxA-brxB-brxC-pglZ-brxL-pglX*. This system methylates host genomic DNA at specific sequences, thereby protecting it from autoimmunity. The non-methylated DNA of bacteriophages triggers BREX1, which blocks phage proliferation (Fig. 1).

We have previously shown that deletion of certain BREX1 genes results in cytotoxicity [3]. This suggests that some BREX1 proteins are involved in the autoregulation of the immune response, while others may act as effectors that interfere with the vital process of the cell. Here, we are analysing different compositions of BREX1 proteins to find a link to their function in the cell.

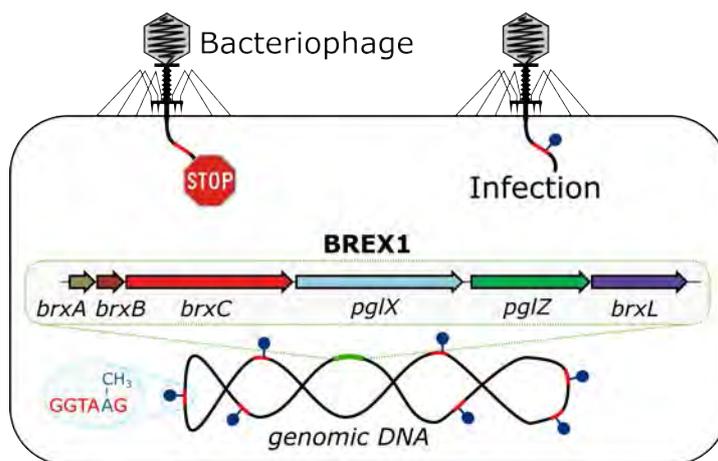


Fig. 1. The BREX1 defence system protects bacteria from bacteriophage infection.

[1] L.-C. Fortier, O. Sekulovic, Importance of prophages to evolution and virulence of bacterial pathogens

[2] T. Goldfarb et al., BREX is a novel phage resistance system widespread in microbial genomes

[3] J. Gordeeva et al., BREX system of Escherichia coli distinguishes self from non-self by methylation of a specific DNA site