FACTORS AFFECTING THE LONG-TERM COEVOLUTION OF STREPTOCOCCUS THERMOPHILUS AND ITS LYTIC PHAGE 2972

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Clustered regularly interspaced short palindromic repeats (CRISPR) and CRISPR-associated protein (Cas) systems are widely recognized as advanced genome engineering tools. Their main function in nature is to provide adaptive immunity for bacteria and archaea. They achieve this by detecting and usually cutting specific DNA or RNA sequences that match unique spacers found between CRISPR [1]. While bacteria with CRISPR-Cas systems can coevolve with phages over time in nature, laboratory studies are constrained by limited model systems. Most bacteria do not develop CRISPR-based immunity against phages or plasmids in laboratory settings or do so at exceptionally low rates detectable only by deep sequencing. To date, only *Streptococcus thermophilus* and *Pseudomonas aeruginosa* reliably evolve CRISPR immunity under laboratory conditions [2].

This study aims to deepen our understanding of how *S. thermophilus* DGCC7710 and its lytic phage adapt to one another over time, thereby potentially forming innovative genome-editing strategies. To achieve this, long-term coevolution experiments have been conducted, along with the optimization of previously used methods for bacterial cell counting.

As a result, a new factor has been suggested as highly influential for the host-virus dynamics.

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[2] J. Common, D. Morley, E. R. Westra, and S. van Houte, “CRISPR-Cas immunity leads to a coevolutionary arms race between Streptococcus thermophilus and lytic phage,” Philosophical Transactions of the Royal Society B: Biological Sciences, vol. 374, no. 1772, p. 20180098, May 2019, doi: 10.1098/rstb.2018.0098.