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Poster #76: Regulation of the lysis-lysogeny switch in temperate actinobacteriophages of Corynebacterium glutamicum ATCC 13032

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Prophages are ubiquitous elements of bacterial genomes (1). As major contributors to bacterial genetic diversity, prophages can impact host fitness and confer new phenotypes as they often encode defense systems or virulence factors (2). Intriguingly, many bacteria harbor multiple prophages –so-called polylysogens –making them valuable models to study phage-host and phage-phage interactions.

The actinobacterium Corynebacterium glutamicum ATCC 13032 harbors two cryptic prophages and the mobile genetic element CGP3. The ICE element CGP3 comprises nearly 6% (~200 kbp) of the genome and provides broad immunity against phage infection (3).

Here, we investigated the novel temperate phage CyranoPS infecting C. glutamicum. Interestingly, the attachment site of CyranoPS was found to be located within the phage repressor gene resulting in repressor truncation upon chromosomal integration. Expression of the full-length versus truncated variant of the repressor revealed that the truncated variant is indeed the active form of the protein. Using a reporter system, the master repressor was shown to promote lysogenic gene expression, while repressing the lytic promoter.

We further observed high spontaneous induction of CyranoPS yielding phage titers of up to 1E9 PFU/ml in the culture supernatant. This spontaneous induction was, however, significantly reduced in the presence of the cryptic ICE element CGP3. By mutational analysis and targeted overexpression of candidate genes, we identified two CGP3 encoded genes with a previously unrecognized role in inter-prophage competition. Together, these findings reveal how regulatory crosstalk between co-resident mobile genetic elements can modulate the lysis-lysogeny decision and thereby shape phage-host infection dynamics.

Reference #1

Touchon et al. (2016) ISME J, doi.org/10.1038/ismej.2016.47

Reference #2

Pfeifer et al. (2022) Curr Opin Microbiol, doi.org/10.1016/j.mib.2022.102230

Reference #3

Badia Roigé et al. (2026) preprint, doi.org/10.21203/rs.3.rs-9446490/v1

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