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Temperate bacteriophage populations in the human gut: culturomics and experimental insights

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While often overlooked, the most abundant entity within the gut are the viruses that infect bacteria, called bacteriophages (phages). Large-scale metagenomic and data mining efforts have uncovered an expansive diversity of phages within the human gut. However, the functional understanding of phage-host interactions and their impacts within this complex ecosystem have been limited due to a lack of cultured isolates for experimental validation. In recent work, we characterise 182 active prophages originating from 252 diverse human gut bacterial isolates using diverse induction conditions, including chemical cues, metabolites, starvation, and human cell derivatives. We found that active Bacteroidota prophages were among the most prevalent members of the gut virome, with extensive use of diversity generating retroelements and exhibiting broad host ranges. Moreover, active polylysogeny was present in 58% of studied gut lysogens and led to coordinated prophage induction. Transcriptomic analysis of selected isolates revealed fundamental information on life cycles of gut phages, including the constitutive expression of defence and counter-defence genes across both polylysogenic phages and their hosts. In this presentation, I will summarise our recent and unpublished work into the study and use of experimentally validated gut prophages, providing key insights into their diversity, biology, genetics, and function within these complex microbial communities. More broadly, this presentation will highlight the importance of experimental validation alongside genomic based computational prediction to enable further functional understanding of these commensal viruses within the human gut.

Reference #1

Reference #2

Reference #3

Author: BARR, Jeremy J. (Monash University)

Presenter: BARR, Jeremy J. (Monash University)

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