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Poster #49: Drivers and Constraints of Prophage Persistence in Natural Communities

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Prophages are widespread in nature. If their costs outweigh their benefits, they are rapidly lost from bacterial populations in vitro [1]. However, the long-term persistence and co-evolutionary trajectories of functional prophages within a bacterial host inside natural microbial communities remain poorly understood.

To answer these questions, we conducted a longitudinal cohort study over 18 months to track the *in vivo* evolution of *Escherichia coli* lysogens repeatedly isolated from human fecal samples. Whole-genome sequencing of persisting *E. coli* lineages revealed an average of 7.4 prophages per strain, with half predicted to be complete or of high quality. Across all analyzed strains, prophages were neither lost nor acquired.
In theory, the persistence and evolution of a prophage is influenced by natural compatibility between both players and subsequent compensatory adaptation. To differentiate these mechanisms, we decoupled them experimentally. We first measured baseline compatibility by transferring isolated temperate phages from the cohort strains into lab *E. coli* strains and conducting fitness assays on these non-native lysogens. Next, we will quantify the extent of compensatory adaptation by experimentally evolving these non-native lysogens in gut microcosms.

Since prophages are common in bacteria, including pathogens, investigating such evolutionary dynamics clarifies their broader ecological and medical impact.

Reference #1

Bailey, Z. M.; Igler, C.; Wendling, C. C. (2024): Prophage maintenance is determined by environment-depend

Reference #2

Reference #3

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