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Poster #78: Adaptive trajectories of bacteriophages: Evolutionary dynamics across contrasting environments

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Bacteriophages are among the fastest-evolving biological entities, yet the early dynamics and constraints of their adaptive trajectories remain incompletely understood. This PhD project will investigate long-term phage adaptation in a controlled experimental evolution system using a Pseudomonas strain and its lytic phage, with automated serial passage enabling standardized propagation across many replicate populations and dense temporal sampling of evolutionary change.

Phage populations will be evolved under three contrasting selection regimes: differences in infection dynamics (fast- vs. slow-burst phages), spatially structured growth in biofilm-like environments, and elevated-salinity physicochemical stress. Time-resolved whole-genome sequencing will be combined with phenotypic assays (adsorption, lysis time, burst size, environmental persistence, host range, killing efficacy) to determine which early, low-frequency mutations rise to dominance, which are transient, and how genotypic change maps onto phenotype.

We hypothesize that adaptation will repeatedly target host-interaction genes, particularly tail fiber and baseplate proteins, with regime-specific shifts: biofilm selection favoring altered adsorption and recognition strategies for heterogeneous surface-associated cells, and salinity acting primarily through demographic and ecological effects on host growth and phage persistence rather than mutation supply alone. We will further test whether long-term adaptation broadens, maintains, or contracts host range, and whether such shifts trade off against phage stability or ancestral-host fitness.

By tracing evolutionary routes from early mutations to complex adaptive outcomes across environments, this project establishes a predictive framework for phage adaptability, host-phage coevolution, and the general predictability of viral evolution.

Reference #1

Reference #2

Reference #3

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