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Poster #12: Phage Fitness Landscapes and Butterfly Effects in Evolving Phage Populations

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Our study investigated evolutionary dynamics in *Klebsiella* bacteriophage populations, focusing on a spontaneously emerged mutant exhibiting a bulls-eye plaque morphology. Whole-genome sequencing identified point mutations in tail proteins as the genetic basis for this variant. *In vitro* competition experiments revealed that independent runs did not always produce the same winner, with phage variants reaching near-fixation in different experiments, reminiscent of butterfly-like effects where small differences cause distinct outcomes. This indicates that small changes in genetic background and variant characteristics can bias phage populations to distinct evolutionary outcomes, even in nominally identical environments.

To understand the impact of mutations on fitness landscapes, we determined attachment rates, burst sizes, and latent periods *in vitro*. While the bulls-eye plaque variant "Porky"and its parental phage "Shorty"did not differ significantly in attachment rate, both latent period and burst size were affected. Despite these differences, competitive advantage was not fixed: in some runs one phage outcompeted the other, and in others the outcome was reversed. In contrast, a third mutant ("Sporty") showed stronger attachment and consistently outcompeted both Shorty and Porky. To determine contribution of each fitness parameter, we performed simulations of the evolutionary dynamics using discrete mathematical models constrained by infection and replication parameters and found the adsorption rate to be a key fitness parameter. Our integrated approach shows how genetic mutations in phage populations can change phage fitness and illustrates the importance of sensitive variant detection methods, like deep sequencing, for quality control in phage preparations.

Reference #1

Zhanybek Selpiev, Sebastian Leptihn, Mathias Müsken, and Belinda Loh. Deciphering Shared Receptor Usage in

Reference #2

Reference #3

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