



# Individual-based model highlights the importance of trade-offs in shaping bacteria-phage co-evolutionary dynamics

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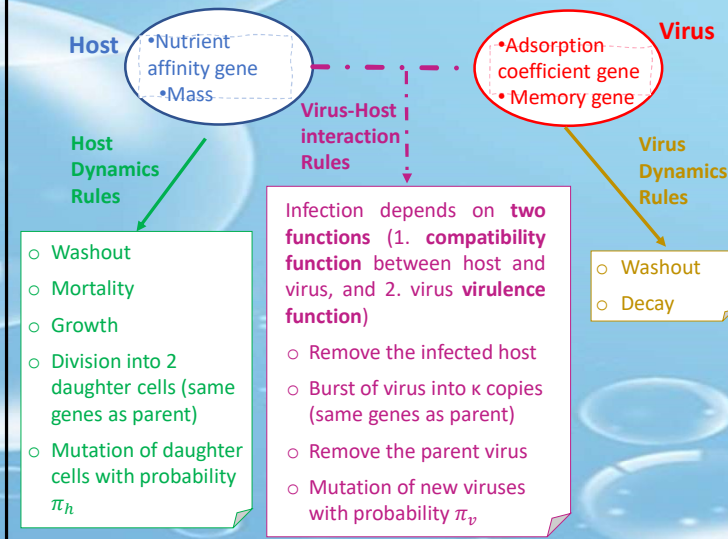
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## Introduction and Motivation

- Understanding the interactions between phage and bacteria can serve as a simple model system for understanding infectious diseases.
- Mathematical and individual based models can be helpful in:
  - analyzing rapid coevolutionary dynamics of phage and bacteria
  - understanding virus-host scenarios depending on the different infection parameters

## Method

Evolutionary Individual-based stochastic model for studying phage-bacteria interaction in a chemostat.



## Acknowledgment

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## Experimental results

The growth curves of bacterium *Escherichia coli* E28 under bacteriophage T4 infection at different Multiplicity of Infection (MOI). Growth assays (including replicates) were conducted in parallel at 37°C, 150 rpm, using the 2300 EnSpire Multilabel Plate Reader (PerkinElmer) and monitored through automated measurement of optical density at 600 nm (OD600) every 15 min. Dashed line marks the timepoint of T4 infection. Plotted values: mean ( $n = 8$ ;  $n_{\text{control}} = 11$ ).

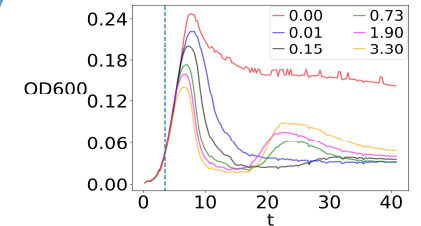


Fig 1. Infection dynamics of T4 phage and *Escherichia coli* bacteria

## Simulation Results

We report population dynamics for hosts (**H**) and viruses (**V**) and focused here on:

- Effect of MOI (ratio of virus to host numbers)
- Nutrient concentration (phosphorous)
- Constrained vs random phage-bacteria interactions
  - two virus-host **compatibility** functions: trade-off based (genotypic) and random
  - two **virulence** functions: trade-off based (genotypic) and random

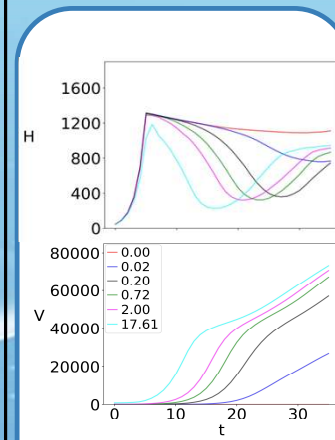


Fig 2. Effect of MOI on H and V

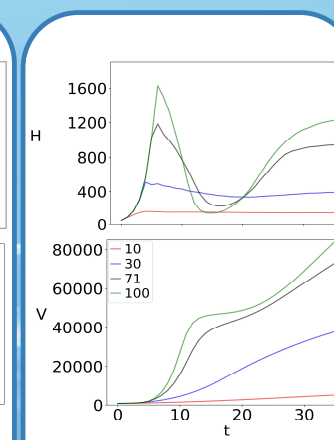


Fig 3. Effect of total phosphorous content ( $\mu\text{mol}$ )

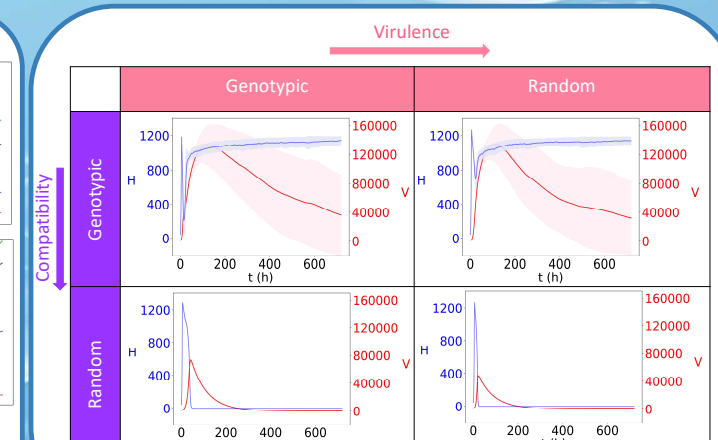


Fig 4. Importance of trade-offs in shaping biological interactions