Viruses never do as they’re told, and there’s a good reason for it: bacteria-phage coevolution as a driver of diversity

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Bacteria-phage coevolution
Bacteria-phage coevolution

Temperate phage

- Koskella & Brockhurst *FEMS Microbiol Rev* 2014
795 genomes of *Acinetobacter baumannii* → 4,122 prophages

78% of the *A. baumannii* “intact prophages” encode putative virulence genes, with an average of 1.75 virulence factors in their genomes

Bacteria-phage coevolution

Bacteriophages are viruses that infect bacteria. They play a significant role in bacterial ecosystems. The diagrams illustrate the interaction between phages and bacteria, highlighting lytic phages, which are those that enter the host cell and cause it to lyse, releasing new phages into the environment.

- Koskella & Brockhurst *FEMS Microbiol Rev* 2014
Bacteriophage coevolution

Bacterial resistance

- Koskella & Brockhurst *FEMS Microbiol Rev* 2014
Bacteria-phage coevolution

Phage counter-adaptation

Low density of anti-CRISPR phage

High density of anti-CRISPR phage

CRISPR bacteria WIN

CRISPR resistance

Immuno-suppressed

CRISPR resistance

Infection by other phage

Lysis

anti-CRISPR phages WIN

CRISPR resistance

Immuno-suppressed

Bacteria-phage coevolution

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Bacteria increase resistance to phage

Phages increase infectivity to bacteria
Bacteria-phage coevolution

Bacteria-phage coevolution

Time shift experiment

Measuring coevolution using time shift experiments

Bacteria-phage coevolution

Time shift experiment

Arms race dynamics

Fluctuating selection dynamics

Bacteriophage coevolution

Bacteriophages

Plant pathogen

Host-associated microbiome
Bacteria-phage coevolution

Bacteriophages

Host-associated microbiome

Photo credit: Design_Cells
Bacteria-phage coevolution

Phages are locally adapted

Bacteria-phage coevolution

Time shift experiment

- Koskella, *Current Biology* 2013. 23(13), 1256-1260.
Bacteria-phage coevolution
Show bacterial resistance, phage counter-adaptation

- Koskella, *Current Biology* 2013. 23(13), 1256-1260.
Bacteria-phage coevolution

Impacts on microbiome diversity
Bacteria-phage coevolution

Impacts on microbiome diversity

- Morella et al., Molecular Ecology 2018. 27(8), 2025-2038.
Bacteria-phage coevolution
Impacts on microbiome diversity

X 6 per treatment

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Bacteriophages

Plant pathogen
Bacteria-phage coevolution

...Varies depending on environment

Bacteria-phage coevolution...Varies depending on environment

Bacteria-phage coevolution

...Varies depending on environment

Bacteria-phage coevolution

...Varies depending on environment

Microbial communities are:

• Complex

• Variable (across space)

• Dynamic (across time)

• Important in shaping host phenotype
Microbial communities are:
Phages are known to:

- Complex
  - Shape composition of bacterial communities
- Variable (across space)
  - Show specific adaptations to ‘local’ bacteria
- Dynamic (across time)
  - Drive changes in composition over time
- Important in shaping host phenotype
  - Be important in shaping host phenotype
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Fluctuating selection dynamics

Prophages in *E. coli* carry genes encoding: transportation, metabolism, recombination, virulence, transcriptional regulation, and resistance (e.g., Tellurite/Colicin resistance).