Host-parasite coevolution
Cooperative strategies of parasites

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Phages

- Phages are viruses infecting bacteria.
- Bacteria have evolved different resistance mechanisms against phages.
Figure: Westra et al. (2012) Annu Rev Genet.
CRISPR-Cas:
Clustered
Regularly
Interspaced
Short
Palindromic
Repeats
/ CRISPR associated
CRISPR and anti-CRISPR

- Bacteria evolved the CRISPR immune system to defend against phages.
- Phages evolved anti-CRISPRs (ACRs) to protect against CRISPR.
Figure by S. van Houte
ACR relies on cooperation of ACR-phages

- ACR-phages often die when they infect a CRISPR-resistant bacterium.
- However ACR-phages often manage to block (a part of) the CRISPR-complexes.
- A reinfecting phage can then reproduce in the CRISPR-blocked bacterium.
- When the density of ACR-phages is sufficiently high, reinfection of a CRISPR-blocked bacterium by another ACR-phage is likely.
Population structure

- In a well mixed-population at low frequencies ACR-phages cannot profit from cooperation.
- In a structured population infection of CRISPR-blocked ACR-phages is more likely.
- ACR-phage could more likely survive in structured bacterial populations.
Strong and weak ACR-phages

- There are different ACR-inhibitors.
- The affinity of different ACR-molecules to the CRISPR-complex varies.
- The probability that a strong ACR-phage can reproduce already at primary infection is higher than in weak ACR-phages.
- Strong ACR-phages have a beneficial advantage over weak ACR-phages, because they are more likely to reproduce also in CRISPR-resistant phages.
Cheaters: no-ACR-phages

- Once the CRISPR-response has been blocked in a bacterium, also phages unable to block the CRISPR-response (no-ACR-phages) can reproduce in these bacteria.
- In weak ACR-phages the CRISPR-response might be blocked only partially, so that no-ACR-phages are not likely to reproduce in the partially blocked bacteria.
- At secondary infection weak ACR-phages could block further the CRISPR-response, and therefore are likely to reproduce in CRISPR-blocked bacteria.
Interesting processes

- When do ACR-phages manage to survive in structured bacterial populations?
- If they survive (together with their host), how ACR-phages (and noACR-phages) are distributed across the bacterial population?
A model

State space

- Assume bacteria are placed on a graph (e.g. $\mathbb{Z}^2$, a random graph, an evolving graph)
- Each vertex has one of the following states
  - CRISPR-resistant bacterium ($r$)
  - CRISPR-blocked bacterium ($b$)
  - empty ($e$)
  - CRISPR-free bacterium ($f$)
- To each vertex (several) phages of type weak ACR ($w$), strong ACR ($s$), no ACR ($n$) can be associated.
A model

Dynamics

- (Phage reproduction) Each phage located at vertex \( v \) binds to the bacterium (of state \( r, b \)) at rate 1
  - If the bacterium is in state \( r \),
    - with probability \( p_{\text{rep}} \) the phage manages to replicate. The state of the bacterium is switched to \( e \) and the number of phages increases by \( B \).
    - with probability \( p_{\sup} = 1 - p_{\text{rep}} \) the CRISPR-response is suppressed, but the phage does not manage to reproduce. Then the state of the bacterium is switched to state \( b \) and the phage dies.
  - If the bacterium is in state \( b \), the phage reproduces. The state of the bacterium is switched to \( e \) and the number of phages increases by \( B \).

- (Phage movement) At rate \( \lambda_m \) phages move to a randomly chosen neighbouring vertex.

- (bacterial reproduction) At rate \( \lambda_r \) bacteria are reproducing to a free neighbouring vertex.
Interesting processes

- Consider appropriate scalings of $B$, $\lambda_m$, $p_{rep}$ and $p_{sup}$
- When do ACR-phages manage to survive in structured bacterial populations?
- If they survive (together with their host), how ACR-phages (and noACR-phages) are distributed across the bacterial population?
Thank you!

Literature