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(G) Diversity-generating host-disease coevolution with CRISPR adaptive immunity

Wednesday 8 June 2022 13:45 (15 minutes)

Bacteria are under constant threat from viruses, and some bacteria possess adaptive immune systems that provide protection through a genomic 'memory' of past viral infections. In conjunction with viral evolution, this creates a diverse population of bacteria where each cell has a unique viral genomic imprint. The fate of the bacterial population depends on the rate at which memories are updated to track evolving viruses. How does the dynamic fitness landscape generated by adaptive immunity impact population diversity and the rate of evolution? We find with a simple stochastic population dynamics model that viruses experience a changing fitness that both drives and reigns in diversity: new virus mutants that escape immune targeting have high fitness and experience selective dynamics associated with low diversity, while established virus clones experience immune targeting and lose their fitness advantage, going extinct following neutral dynamics associated with high diversity. Both diversity and the speed of evolution depend sub-linearly on viral mutation rate in contrast to a linear dependence under neutral dynamics. The effectiveness of adaptive immunity is captured by bacterial average immunity which depends inversely on diversity and is a crucial experimental observable. Average immunity determines clone fitness, population outcomes, and the durability of immune memory, which we measure in published experimental data. This work lays a theoretical foundation for understanding immunity in co-evolving populations.

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