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Coevolution of CRISPR bacteria and phage in 2 dimensions PU HAN, Physics & Astronomy, Rice University, Houston, TX, MICHAEL DEEM, Physics & Astronomy and Bioengineering, Rice University, Houston, TX — CRISPR (cluster regularly interspaced short palindromic repeats) is a newly discovered adaptive, heritable immune system of prokaryotes. It can prevent infection of prokaryotes by phage. Most bacteria and almost all archae have CRISPR. The CRISPR system incorporates short nucleotide sequences from viruses. These incorporated sequences provide a historical record of the host and predator coevolution. We simulate the coevolution of bacteria and phage in 2 dimensions. Each phage has multiple proto-spacers that the bacteria can incorporate. Each bacterium can store multiple spacers in its CRISPR. Phages can escape recognition by the CRISPR system via point mutation or recombination. We will discuss the different evolutionary consequences of point mutation or recombination on the coevolution of bacteria and phage. We will also discuss an intriguing "dynamic phase transition" in the number of phage as a function of time and mutation rate. We will show that due to the arm race between phages and bacteria, the frequency of spacers and proto-spacers in a population can oscillate quite rapidly.

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