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Physical mode of bacteria and virus coevolution PU HAN, LIANG REN NIESTEMSKI, MICHAEL DEEM, Rice University — Single-cell hosts such as bacteria or archaea possess an adaptive, heritable immune system that protects them from viral invasion. This system, known as the CRISPR-Cas system, allows the host to recognize and incorporate short foreign DNA or RNA sequences from viruses or plasmids. The sequences form what are called "spacers" in the CRISPR. Spacers in the CRISPR loci provide a record of the host and predator coevolution history. We develop a physical model to study the dynamics of this coevolution due to immune pressure. Hosts and viruses reproduce, die, and evolve due to viral infection pressure, host immune pressure, and mutation. We will discuss the differing effects of point mutation and recombination on CRISPR evolution. We will also discuss the effect of different spacer deletion mechanisms. We will describe population structure of hosts and viruses, how spacer diversity depends on position within CRISPR, and match of the CRISPR spacers to the virus population.

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