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Abstract for an Invited Paper
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The size of the immune repertoire of bacteria[1]

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Some bacteria and archaea possess an adaptive immune system that maintains a memory of past infections in viral DNA elements called spacers stored in the CRISPR loci of their genomes. This memory is used to mount targeted responses against later threats, but is remarkably shallow: it remembers only a few dozen to a few hundred viruses. I will present a statistical theory of CRISPR-based immunity that quantitatively explains the depth of bacterial immune memory in terms of a trade-off with fundamental constraints of the cellular biochemical machinery. Given known cross-reactive mechanisms of CRISPR interference and primed spacer acquisition, the theory further suggests that the incorporation of phage DNA also creates a significant threat of auto-immunity. I will show that balancing viral defense against auto-immunity predicts a scaling law that relates spacer length and CRISPR repertoire size. Analysis of a publicly available database of microbial genomes shows that this scaling law is realized empirically across prokaryotes, partly through proportionate use of different CRISPR-Cas types in strains carrying multiple loci. Finally, I will demonstrate population-level selection mechanisms that can generate the observed scaling law.

[1]Simons Foundation