

Abstract Submitted  
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**The Causality of Evolution on Different Fitness Landscapes<sup>1</sup>**

SAURABH VYAWAHARE, ROBERT AUSTIN, Princeton University, QIUCEN ZHANG, University of Illinois CU, HYUNSUNG KIM, University California Santa Cruz, JOHN BESTOSO, Princeton University — Evolution of antibiotic resistance is a growing problem. One major reason why most antibiotics fail is because of mutations on drug targets (e.g. essential enzymes). Sequencing of clinically resistant isolates have shown that multiple mutational-hotspots exist in coding regions, which could potentially prohibit the binding of drugs. However, it is not clear whether the appearance of each mutation is random or influenced by other factors. In this paper, we compare evolution of resistance to ciprofloxacin from two distinct but well characterized genetic backgrounds. By combining our recently developed evolution reactor and deep whole-genome sequencing, we show different alleles of  $\sigma_s$  factor lead to fixation of different mutations in *gyrA* gene that confer ciprofloxacin resistance to bacteria *Escherichia coli*. Such causality of evolution in different genes provides an opportunity to control the evolution of antibiotic resistance.

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