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Hidden Complexity in Bacterial Evolution ROBERT AUSTIN, JULIA BOS, GRIGORY TARNOPOLSKIY, JOHN BESTOSO, JAMES STURM, Princeton University, HYUNSUNG KIM, NADER POURMAND, University of California Santa Cruz, ROBERT AUSTIN, Princeton University — We compare the local fitness maxima a Growth Advantage in Stationary Phase (GASP) [**?**] bacterial strain evolves in comparison to the local maxima of the parental wild-type strain. The rapid evolution of antibiotic resistance in GASP to an identical stressor, starting from a different initial phenotype and genotype, diverges from a parental wild-type strain on the fitness landscape. That is, while the GASP strain evolves a (Serine^{83} $\rightarrow$ Leucine missense mutation in *gyrA*) which is the target of the antibiotic, only 2 amino acids removed from the WT strain resistant mutant, it does not evolve the other 3 SNPS the WT strain did. Rather, it excises the prophage e14 sequence [**?**]. We show that this e14 excision profoundly changes the ability of the GASP strain to form a biofilm, revealing the hidden complexity of *E. coli* evolution to antibiotics in complex environments. We show that these profound changes in resistance to cipro do not come at a substantial fitness cost on the landscape and discuss why this makes the mutations basically irreversible.

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