

Antibiotic resistance evolution is studied

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Harvard University scientists say Darwinian evolution follows very few of the available mutational pathways to attain fitter proteins.

The study involved a gene whose mutant form increases bacterial resistance to a widely prescribed antibiotic by a factor of roughly 100,000.

The researchers' work indicates that of 120 five-step mutational paths that theoretically could grant antibiotic resistance, only about 10 actually endow bacteria with a meaningful evolutionary advantage.

"Just as there are many alternate routes one might follow in driving from Boston to New York, one intrinsic property of DNA is that very many distinct mutational paths link any two variants of a gene," said lead author Daniel Weinreich, a research associate in Harvard's department of organismic and evolutionary biology.

"Although this fact has been recognized for at least 35 years, its implications for evolution by natural selection have remained unexplored," Weinreich said. "Specifically, it is of great interest to determine whether natural selection regards these many mutational paths equivalently."

The research is detailed in the journal *Science*.

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