

Abstract Submitted
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Quantitative evolutionary dynamics of one million barcoded lineages JAMIE BLUNDELL, Stanford University, SASHA LEVY, SUNY Stony Brook, SANDEEP VENKATARAM, DMITRI PETROV, DANIEL FISHER, GAVIN SHERLOCK, Stanford University — Evolution of large asexual cell populations underlies $\approx 30\%$ of deaths worldwide, including those caused by bacteria, parasites, and cancer. However, the dynamics underlying these evolutionary processes remain poorly understood because they involve many competing beneficial lineages, most of which never rise above extremely low frequencies. To observe these normally hidden evolutionary dynamics, we constructed a sequencing-based ultra high-resolution lineage tracking system that can monitor the relative frequencies of $\approx 500,000$ lineages simultaneously. We find that the spectrum of fitness effects of beneficial mutations is far from exponential and not even monotonic. Early adaptation is a predictable consequence of this distribution and is strikingly reproducible, but the initial small-effect mutations are soon outcompeted by rarer large-effect mutations that result in variability between replicates. Our results suggest that early evolutionary dynamics may be deterministic for a period of time before stochastic effects become important. The interplay between deterministic and stochastic effects is controlled in large part by the distribution of mutation rates to each fitness effect, which high-resolution lineage tracking is uniquely suited to measure.

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