

EVOLUTION

The routes of adaptation

Two studies that combine experimental evolution and genome resequencing have provided new insights into bacterial adaptation. One study reveals unexpected relationships between new mutations and their adaptive significance, whereas the other gives a mechanistic account of the evolution of rapid phenotype switching.

Important questions about the molecular genetic dynamics of evolution and adaptation include whether mutations accumulate gradually or in bursts, and what the consequences of these mutations are. Barrick, Yu and colleagues tracked mutations that arose and were fixed in an experimental population of *Escherichia coli* that had been growing under glucose-limiting conditions for 20 years

(40,000 generations). Genome sequencing at various time points across the first 20,000 generations showed that mutations fixed at an approximately constant rate, which is as expected for neutral mutations as they accumulate in line with the underlying mutation rate. However, the mutations that fixed were almost all beneficial — a surprising finding given that the increase in population fitness was actually slowing down during that time (see figure). In the second half of the experiment, the rate of mutation jumped up (owing to the emergence of a mutator phenotype) and indeed many neutral mutations accumulated. Although it is no secret that the genomics of adaptation are varied and complex, this work highlights that they can also be counterintuitive — especially considering that evolution was being observed in a simple, stable environment.

Trundling along over 20 years might seem like the lap of luxury to cells that face an ever-changing environment. Some bacteria deal with the unpredictable nature of their surroundings by switching randomly between different phenotypic states — a trait that, although widespread (it also occurs in the human immune system, for example) has not been experimentally proved to have an adaptive origin. This has now been achieved in another experimental

evolution study, by Beaumont and colleagues. Here, 12 replicate lines of *Pseudomonas fluorescens* were grown under conditions that repeatedly favoured the emergence of new colony morphologies. Again, genomic evolution was monitored by resequencing. In the initial rounds of selection, phenotypic adaptations arose by the traditional route of mutation and selection. However, in two of the colonies this trend was broken by the appearance of bet-hedging genotypes, which could switch rapidly between colony morphologies. Further examination of one of these two lines revealed nine mutations, of which only the most recent (a non-synonymous substitution in the metabolic gene *carB*) was sufficient to confer the bet-hedging phenotype. However, the fitness advantage of the ninth mutation was contingent on the presence of the earlier mutations.

These studies tell us that we should beware of making generalizations about the rate of genomic evolution without having a deep understanding of the system under study but that, conversely, sequencing tools can finely chart the mutation dynamics of well-defined phenomena.

Tanita Casici

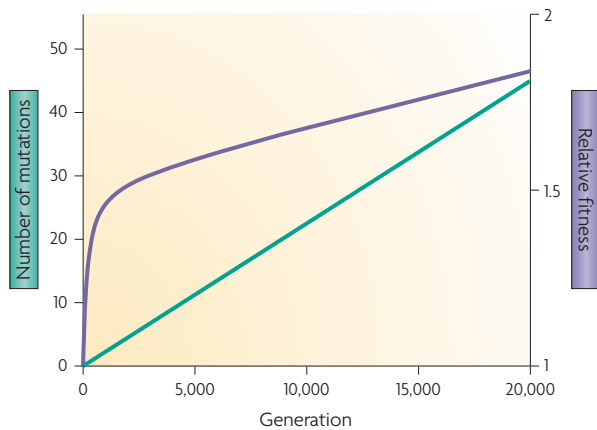


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ORIGINAL RESEARCH PAPERS Barrick, J. E., Yu, D. S. et al. Genome evolution and adaptation in a long-term experiment with *Escherichia coli*. *Nature* **461**, 1243–1247 (2009) | Beaumont, H. J. E. et al. Experimental evolution of bet hedging. *Nature* **462**, 90–93 (2009)
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