

MOLECULAR EVOLUTION

Sex accelerates adaptation

An analysis confirms the long-standing theory that sex increases the rate of adaptive evolution by accelerating the speed at which beneficial mutations sweep through sexual, as opposed to asexual, populations.

MATTHEW R. GODDARD

When compared with the asexual alternative of simple cloning, sex seems like a complicated way of reproducing. The need for fast and efficient reproduction lies at the heart of Darwinian natural selection, so why sex exists is a conundrum that has fascinated biologists for more than 100 years¹. In a paper online in *Nature*, McDonald *et al.*² directly confirm the long-held theory that the advantage of sex lies in its ability to expose individual mutations to the actions of natural selection.

Sex involves the shuffling (recombination) of chromosomes from parents, followed by the separation of these newly assorted chromosomes into reproductive cells called gametes, which then fuse through mating. As well as being more complicated than asexual reproduction, this mechanism risks breaking apart collections of genes that have proved to be useful. In animals, only females can give birth, and mate finding and courtship impose further challenges. Given these disadvantages, it is not immediately clear why sexual reproduction has persisted.

Some of the mutations that accrue in genomes over time affect an organism's ability

to reproduce and compete for resources (fitness). The net fitness of an individual is the sum of these accrued mutations. Conventional theories^{3,4} suggest that selection in asexually reproducing populations is affected only by this net genomic fitness.

In this scenario, when a positive mutation arises in a genome that already harbours negative mutations, the negative mutations might overwhelm the positive one, leading to the removal of the whole genome from the population by natural selection and the loss of the positive mutation. However, if a positive mutation confers a strong-enough fitness benefit to outweigh the combined value of the negative mutations, then the genome is likely to become more common over generations — possibly becoming a permanent part of (fixed in) the population owing to positive selection. Negative mutations become common by hitch-hiking with positive ones, and thus restrict population fitness. In summary, individual mutations in asexual populations may be masked from the actions of selection, because they are entangled in genomes.

Sexual populations theoretically do not have this problem^{3,4}. Recombination and the random partitioning of chromosomes allow positive mutations to become dissociated

from negative ones. By analogy, sex allows selection to pluck rubies from rubbish⁵. Furthermore, it enables positive mutations that arise in different genomes to be recombined into the same genome, rather than competing with one another as they would in an asexual population⁴. In sexual populations, many positive mutations, mostly free from hitch-hiking mutational rubbish, can become common simultaneously. This is predicted to increase the rate and extent of adaptive evolution¹.

A series of experimental-evolution studies supports the idea that sex speeds up adaptive evolution^{6–8}. However, much less work has focused on the molecular mechanisms that underpin this advantage. One study⁹ inferred that sex accelerates adaptation by separating positive mutations from negative ones, but did not directly identify the mutations that arose.

McDonald *et al.*, however, have done just that. First, they caused sexual and asexual populations of yeast (*Saccharomyces cerevisiae*) to evolve for approximately 1,000 generations in a simple laboratory environment, to which the sexual populations adapted more rapidly. Then, building on previous studies, the authors used DNA-sequencing approaches to dissect and track the various single DNA-base mutations that arose, evaluating populations at regular time points during evolution.

A similar range of mutations initially arose in all populations, some of which affected protein function, with others having no effect. The authors reasonably assumed that only those that altered protein function would affect fitness. In asexual populations, the different types of mutation all had roughly the same chance of eventually becoming fixed, indicating that selection could not discriminate between individual mutations. Fewer mutations became fixed in sexual populations. Those that did tended to alter protein function, and thus also, presumably, fitness. This observation suggests

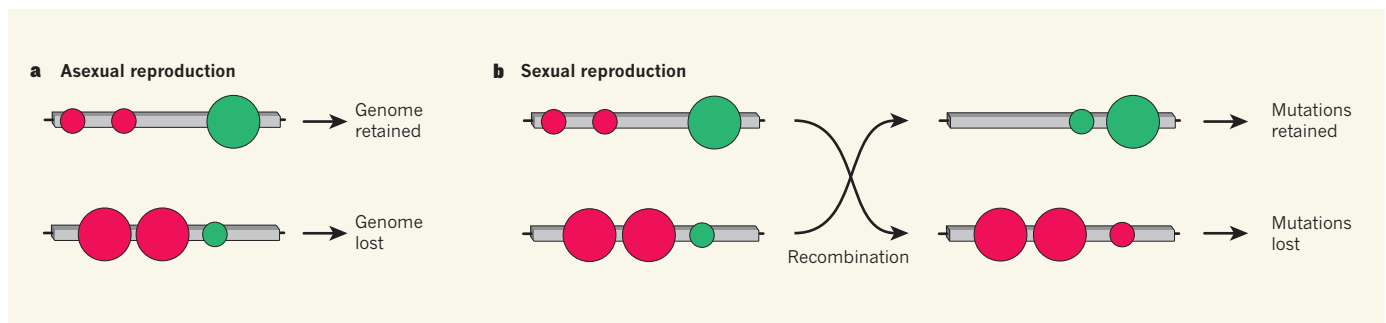


Figure 1 | Picking rubies from the rubbish. Over time, genomes accrue mutations that have either a positive (green) or a negative (red) effect on an individual's fitness (in this simple schematic, the relative benefit or cost of each mutation is indicated by size). McDonald *et al.*² compared how selection acts on mutations in asexual and sexual populations. **a**, During asexual reproduction, selection occurs on the basis of overall genome

fitness. Positive mutations may be removed from the population, and negative mutations can hitch-hike along with a positive one of greater value. **b**, During sexual reproduction, chromosomes are shuffled by recombination, changing the mutations that are grouped together in offspring. This process enables individual mutations to be independently retained or removed by selection.

that sex improved the efficiency with which selection acted on individual mutations.

To directly test the effects of specific mutations on fitness, McDonald *et al.* conducted mini-evolution experiments and tracked the change in frequency of individual mutations in the population. This key step revealed that groups of positive and negative mutations remained together in asexual populations. These groups competed with one another — some became common over generations, meaning that negative mutations persisted by hitch-hiking. By contrast, recombination meant that no groups of mutations persisted in sexual populations, and negative mutations did not become common.

These comprehensive experiments provide the long-awaited confirmation that sex accelerates adaptation by sorting the beneficial from the deleterious. Sex shuffles mutations between genomes, enabling natural selection to act on individual mutations more efficiently (Fig. 1). Selection is comparatively blind in asexual populations, because the effects of individual mutations are consistently hidden in genomes.

But McDonald and colleagues' study leaves several aspects of sexual reproduction still

to be clarified. First, the authors primarily examined changes of single DNA bases. However, mutations that duplicate, remove or rearrange whole segments of DNA are also important for adaptation. As the authors acknowledge, the effect of sex on these mutations remains to be evaluated.

Second, the study used yeast that has one copy of each chromosome, whereas most sexual species have two copies, and natural selection works slightly differently when there are two chromosomes. Third, most species inhabit complex environments, which have a variety of selection pressures whose strength varies over space and time. Although the current study elegantly shows how sex provides advantages during adaptation to simple environments, it is not clear how this translates to more-complex ones. Some work suggests that sex can also accelerate adaptation to complex environments¹⁰; however, the underlying molecular mechanisms are not known.

Finally, we do not yet know why sex arose in the first place. One theory suggests that parasitic genetic elements, which persist in genomes despite conferring no fitness benefit, might promote cell fusion and recombination¹¹. Few experiments have tested this theory,

however¹². It might well be that the evolution of sex was driven by completely different forces from those — neatly defined by McDonald *et al.* — that we now know maintain it. ■

Matthew R. Goddard is at the School of Life Sciences, University of Lincoln, Lincoln LN6 7TS, UK, and at the School of Biological Sciences, University of Auckland, New Zealand.

e-mail: mgoddard@lincoln.ac.uk

1. Burt, A. *Evolution* **54**, 337–351 (2000).
2. McDonald, M. J., Rice, D. P. & Desai, M. M. *Nature* <http://dx.doi.org/10.1038/nature17143> (2016).
3. Fisher, R. A. *The Genetical Theory of Natural Selection* (HardPress, 2013).
4. Muller, H. J. *Am. Nat.* **66**, 118–138 (1932).
5. Peck, J. R. *Genetics* **137**, 597–606 (1994).
6. Colegrave, N. *Nature* **420**, 664–666 (2002).
7. Goddard, M. R., Godfray, H. C. J. & Burt, A. *Nature* **434**, 636–640 (2005).
8. Morran, L. T., Schmidt, O. G., Gelarden, I. A., Parrish, R. C. 2nd & Lively, C. M. *Science* **333**, 216–218 (2011).
9. Gray, J. C. & Goddard, M. R. *BMC Evol. Biol.* **12**, 43 (2012).
10. Gray, J. C. & Goddard, M. R. *Ecol. Lett.* **15**, 955–962 (2012).
11. Hickey, D. A. & Rose, M. R. in *The Evolution of Sex: An Examination of Current Ideas* (eds Michod, R. E. & Levin, B. R.) 161–193 (Sinauer, 1988).
12. Giraldo-Perez, P. & Goddard, M. R. *A Proc. R. Soc. B* **280**, 20131875 (2013).