COMMENTARY

Being too nice may be not too wise

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Unfortunately, it cannot be ruled out that the main point of West *et al*. (1999) is correct. Indeed, it is entirely possible that in some populations sex exists due to rapidly changing selection, while in other populations it is present as the consequence of invariant selection against deleterious mutations. Even worse, both these mechanisms (together with, God forbid, some third force) may be essential for the maintenance of sex in every population.

I do not like this possibility because such a beautiful phenomenon as sex deserves a nice, simple explanation and messy interactions of very different processes would spoil the story. Of course, this does not mean that such interactions are not, nevertheless, essential.

However, I believe that the pluralistic explanation of sex can be admitted only if all its components are shown to be (1) important and (2) individually insufficient. Before this happens, we need to keep testing the importance of these components, hoping that one of them will provide the complete explanation. I see no other way to improve our understanding of the evolution of sex.

In particular, validation/rejection of the Mutational Deterministic hypothesis is straightforward. If the genomic deleterious mutation rate U in some population is below ~ 0.8, selection against mutations cannot alone maintain sex, as long as asex enjoys the two-fold advantage. Moreover, if $U < \sim 0.2$, deleterious mutations cannot be very important, even in combination with the Red Queen. On the other hand, with $U > 1–2$, deleterious mutations maintain sex (and explain a lot of other things) alone, Red Queen or no Red Queen. Thus, only a rather narrow range of U values is consistent with the pluralistic approach.

I believe that the case of the Red Queen is similar: except for a relatively narrow grey area, changing selection is either irrelevant, or can maintain sex without any help from deleterious mutation or any other process. Testing the Red Queen is more difficult than testing the Mutational Deterministic hypothesis: while mutation rates can be (we hope) measured indoors, fluctuating selection must be measured in nature. Still, this is not impossible.

I believe that in 10 years U will be known with good confidence for a range of organisms through (1) measuring the per nucleotide mutation rate μ (for which several approaches are possible) and (2) estimating, using the comparative analysis of moderately different genomes, the total genomic number of selectively important nucleotides. Currently, we know that $\mu \approx 2 \times 10^{-8}$ in humans, implying a total diploid mutation rate > 100 (there are $\sim 3.5 \times 10^9$ nucleotides in the human haploid genome) and $U > 1$, because there is little doubt that more than 1% of human DNA is selectively important (see Kondrashov, 1998). However, there is no real problem with maintaining sex in mammals, where genome imprinting makes reversal to asex impossible.

Thus, we need to measure U in *Drosophila melanogaster*, and this is within reach, because μ can be estimated in locus-specific tests, and its genome will be sequenced soon. Only if this measurement produces $0.2 < U < 0.8$, will I accept, with regret, the pluralistic explanation of sex.

Reference

Kondrashov, A.S. 1998. Measuring spontaneous deleterious mutation process. *Genetica* **102/103**: 183–197.

West, S.A., Lively, C.M. & Read, A.F. 1999. A pluralist approach to sex and recombination. *J. Evol. Biol.* **12**: 1003–1012.

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