

COMMENTARY

Genetic polarization: unifying theories for the adaptive significance of recombination

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The paper by West, Lively and Read (1999) advocates a pluralistic approach to the adaptive significance of recombination, i.e. that a combination of models may better explain the advantage of recombination compared with any single model. This certainly makes intuitive sense since there is no *a priori* reason to expect a single benefit to recombination. The paper focuses primarily on three processes: (a) deterministic accumulation of beneficial mutations in response to chronic antagonistic coevolution (Red Queen); (b) deterministic accumulation of deleterious mutations due to mutation-selection balance (mutational load) and, to a lesser extent, (c) stochastic accumulation of deleterious mutations (Muller's ratchet). Here I provide a simple genetic argument that reinforces the authors call for a pluralistic approach, i.e. I show that the advantages to recombination based on the Red Queen, mutational load and Muller's ratchet are all a direct consequence of the same underlying genetic property that is common to all nonrecombining populations – so if one process operates they should all operate, at least under the appropriate permissive conditions.

The common property of all nonrecombining populations is the movement of new deleterious mutations among individuals within the fitness distribution of a population. Substantial heritable variance in fitness among individuals is expected in all natural populations due to recurrent deleterious mutation (in addition to other factors). When recombination is present, the combination of syngamy, segregation and intrachromosomal recombination causes new deleterious mutations to move bidirectionally to better and to worse genetic backgrounds each generation. But when recombination is absent, each new deleterious mutation is trapped in its recipient genome, moving it unidirectionally toward lower fitness. This generates a continuous 'current' of new deleterious mutations flowing within the fitness distribution from greater to lower fitness classes. Recurrent mutation causes lineages from the highest-fitness class to flux unidirectionally through the population like water down a slow-motion stream.

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Eventually all genomes in the population are multiply mutated descendants from the highest-fitness class.

To accumulate in a nonrecombining population, a new mutation must make its way to the headwaters (highest-fitness class) of this stream of decaying genomes. The only way to reach the headwaters is to be introduced (fortuitously) via mutation into the highest-fitness class, or a neighbouring high-fitness class. All other new mutations (beneficial or detrimental) are trapped in inferior genetic backgrounds and thereby deterministically eliminated. Rare reverse and compensatory mutations occasionally reverse the unidirectional flow of deleterious mutations, but this effect is miniscule, analogous to turbulence occasionally moving a pebble a short distance upstream. The term 'genetic polarization' denotes the virtual unidirectional flow of new deleterious mutations (see for review, Rice, 1996). Many hundreds of mutations of very small effect are expected to accumulate in a population from a number of sources, for example: (a) nonpreferred codon mutations (selective disadvantage $\leq 10^{-5}$, Akashi *et al.*, 1998), (b) transposable element inserts (average selective disadvantage $\approx 10^{-4}$, Charlesworth *et al.*, 1992) and (c) mutations of nonessential genes (many selection coefficients $\approx 10^{-3}$, Thatcher *et al.*, 1998). The large number of accumulated mutations causes the expected number of individuals in the highest-fitness class to be quite small (one to a few individuals). This is expected even when the genome-wide mutation rate is small (e.g. 0.1) and the population size is very large (i.e. of the order of 10^6 or higher).

Genetic polarization has two major consequences: (1) it greatly reduces the effective size of a nonrecombining population, i.e. the effective size is the number of individuals in the highest-fitness class and the neighbouring high-fitness classes (Manning & Thompson, 1984; Charlesworth, 1994; Barton, 1995), and (2) it constrains the highest-fitness class to rely solely on its own reproduction to persist, rather than being produced globally by syngamy, recombination and segregation from the population as a whole, as is the case for a recombining population (Rice, 1998).

The greatly reduced effective size of a nonrecombining population, compared with its sexual counterpart, causes

a nonrecombining population to suffer the same evolutionary maladies as small isolated sexual populations: beneficial mutations accumulate more slowly and deleterious mutations accumulate more rapidly. This occurs because selection is ineffectual unless the selection coefficient (s) is greater than the reciprocal of the effective size, i.e. $s > (1/N_e)$. From this perspective the Red-Queen advantage to a recombining population is a consequence of it being able to coevolve more effectively against enemies due to an increased efficiency in recruiting new beneficial mutations (Manning & Thompson, 1983; Charlesworth, 1994; Peck, 1994).

The Muller's ratchet disadvantage to a nonrecombining population is also a consequence of its miniscule effective population size, relative to a similar but recombining population. This small effective size causes a greater portion of the spectrum of new deleterious mutations to accumulate, i.e. deleterious mutations accumulate when $s > 1/N_e$, and since N_e is far smaller for a nonrecombining population, more new mutations can and will accumulate in the absence of recombination (Manning & Thompson, 1983; Charlesworth, 1994). It is sometimes argued that Muller's ratchet does not operate in large populations, but this conclusion is a modelling artefact that occurs when the selection coefficients (s) of all mutations are defined to have the same value (e.g. set equal to the average value of s). When variable selection coefficients are permitted, with a high density of very small selection coefficients (such as those from nonpreferred codons, transposable element inserts and lesions to nonessential genes), then the expected number mutations per genome is >100 , causing the expected number of individuals in the highest extant fitness class to be one or a few individuals, and thus Muller's ratchet is expected to be ubiquitous.

The cost of the mutational load in nonrecombining vs. recombining populations also can be expressed as a direct consequence of genetic polarization. At the outset, I need to point out that I do not think that mutational load is a currency that is easily translated into the competitive ability of nonrecombining vs. recombining populations. Much of the mutational load may be expressed by selection on traits that do not directly translate into changes in the vital statistics or competitive ability of a population. For example, compensatory factors (such as increased survival of sibs when competition for parental investment is reduced by mortality within a clutch) may offset the impact of mutational load on population growth rate. As a consequence, the fact that the mutational load of one population is higher than that of another does not guarantee that the population will be competitively inferior. The major significance of mutational load occurs when it is sufficient in a nonrecombining population, but not in a recombining population, to deterministically lead to its extinction. It is this context on which I focus below.

Genetic polarization isolates the highest fitness class from the remainder of a nonrecombining population, since newly mutated individuals flow out, but not into, this class (with the exception of rare beneficial mutations in the classes neighbouring the highest-fitness class). It must therefore be maintained exclusively via its own reproduction. Assuming a Poisson distribution of new deleterious mutations, only a fraction e^{-U} (where U = the genome-wide deleterious mutation rate) do not receive new mutations, and hence the net reproductive rate of the least mutated class must be the reciprocal of this value (i.e. it must be e^U) to prevent deterministic mutation accumulation via recurrent extinction of the highest-fitness class (Kimura & Maruyama, 1966). When the net reproductive rate of the fittest class is less than e^U , then the mutation load is intolerable since the highest-fitness class is not self-sustaining and this leads to open-ended, deterministic mutation accumulation and eventual extinction. In a recombining population, the least mutated class is reconstituted each generation from the offspring produced from the population as a whole. When there is reinforcing epistasis, buffering epistasis and/or positive assortative mating for fitness (only weak levels are needed), then syngamy, segregation and recombination within the population at large builds the least mutated class faster than it would have reproduced itself via its own clonal reproduction, and recombining populations can resist open-ended deterministic mutation accumulation (i.e. tolerate a higher mutational load) at genome-wide mutations levels where their nonrecombining counterparts cannot (Rice, 1998).

In summary, the genetic polarization of nonrecombining populations guarantees the simultaneous operation of all of the processes discussed in the paper by West *et al.*: the Red Queen (unless the biotic environment is not antagonistically coevolving, which seems unlikely in any natural environment), Muller's ratchet (ubiquitous application), and mutational load (unless U is so small that the equilibrium mutational load is tolerable in both the recombining and nonrecombining populations). All populations are finite, and hence all three processes are expected to operate in all natural populations.

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