## Stronger selection can slow down evolution on smooth fitness landscapes under recombination

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In population genetics, it is commonly expected that the rate of evolution is larger when selection is stronger. This is because stronger selection pressure ensures fitter genotypes created by mutation to survive. Indeed, in a weak mutation regime, it is well-known that the rate of evolution is described as  $v = 4N\mu s$  on smooth landscape, where N is the population size,  $\mu$  is the mutation rate, and s is the selection coefficient. This result clearly shows that the rate of evolution is monotonic with respect to s. This tendency is expected even in existence of clonal interference in large mutation rate, where beneficial mutations arising independently interfere with each other in asexual population. Therefore, in mutation-driven situation, the value of selection pressure maximizing the speed of evolution is infinity. However, source of genetic variation is not limited to mutation. In this paper, we show that this widely-believed story is not true for recombination-driven evolution, and evolution can slow down as selection pressure becomes stronger. Recombination is also a source of new genotypes besides mutation. Recombination between genomes mainly appears in sexual reproduction, and is beneficial in avoiding Muller's ratchet and clonal interference. Furthermore, horizontal gene transfer, which is a kind of recombination, is also considered to be main cause of evolution of prokaryotes. Here, we consider the situation where new genotypes are supplied only by recombination and migration instead of mutation, and fitness landscape is smooth. Existence of migration is necessary for constant evolution of the system, because evolution only by recombination finally homogenizes genotypes of the system. Specifically, we investigate two models. In the first model, population is divided into subpopulations, and migration occurs between subpopulations. This situation supposes that individuals of the same species with different genes are spatially distributed and migration between them starts to be allowed. In the second model, a system with a gene pool is considered, by regarding other subpopulations as a pool. This situation also models the individuals with subpopulations, but the subpopulations has adapted to their own niches and migration always decreases fitness. We numerically find that selection pressure maximizing the rate of evolution is finite in both situations.

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