

P033 Effects of intragene epistasis on the benefit of sexual recombination

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Whereas spontaneous point mutation operates on nucleotides individually, sexual recombination manipulates the set of nucleotides within an allele as an essentially particulate unit. In principle, these two different scales of variation enable selection to follow fitness gradients in two different spaces: in nucleotide sequence space, and allele sequence space, respectively. Popular models for the benefit of recombination assume that the alleles manipulated by sexual recombination are mutational neighbours and thus the two spaces are coincident. However, when alleles of a gene differ by several nucleotide substitutions, models of natural selection in sexual populations must account for movement in both spaces. Here we examine scenarios where epistasis for fitness at these two scales is qualitatively different. Specifically, we assume that the genetic sequence within a gene strongly influences the fitness effect of a mutation in that gene, whereas epistatic interactions between sites in different genes are weak or absent. We find that, in cases where beneficial alleles of a gene differ from one another at several nucleotide sites, sexual populations can exhibit enormous benefit over asexual populations: not only discovering fit genotypes faster than asexual populations, but also discovering high-fitness genotypes that are effectively not evolvable in asexual populations.