Supporting Information

Neher et al. 10.1073/pnas.1309697110



Fig. S1. Recurrent mutations with weak effects. Genetic diversity in populations with recurring mutations between a preferred and unpreferred state with weak effect is shown. (A) Pairwise coalescence time compared with the analytical predictions in the limits of large and small $N\sigma_b$. (B) Site frequency spectra (SFSs) normalized to $\Theta = 2N\mu$ (the SFSs are obtained from local coalescent trees). Different curves are colored by their respective $N\sigma_b$ values. The Bolthausen–Sznitman coalescent (BSC) curve serves as a guide to the eye because its proper normalization depends on $N\sigma_b$. (C) Decay of linkage disequilibrium (LD) measured as r^2 and normalized with its value at short distances. The *x* axis is rescaled by ξ_b . The resulting collapse demonstrates that LD extends over distances ξ_b . The grid of parameters used for simulations was $L \in [3000, 10000]$, $N \in [1000, 3000, 10000]$, $s \in [-0.001, -0.003, -0.01]$, $L\mu \in [1,3,10,30]$, and $L\rho$ logarithmically spaced between *s* and 1.0. For the analysis, simulations were filtered such that $\xi_b > 30$, $\xi_b < L/3$, and $\langle T_2 \rangle \mu < 0.5$.



Fig. 52. Beneficial mutations with fixed effect. Genetic diversity in populations with frequently sweeping beneficial mutations is shown. (A) Pairwise coalescence time compared with the analytical predictions in the limits of large and small $N\sigma_b$. (B) SFSs normalized to $\Theta = 2N\mu$ (the SFSs are obtained from local coalescent trees). Different curves are colored by their respective $N\sigma_b$ values. The BSC curve serves as a guide to the eye because its proper normalization depends on $N\sigma_b$. (C) Decay of LD measured as r^2 and normalized with its value at short distances. The x axis is rescaled by ξ_b . The resulting collapse demonstrates that LD extends over distances ξ_b . In these simulations, mutations are introduced into a random individual whenever a locus becomes monomorphic, analogous to the simulations with constant fitness variance discussed in the main text. However, in this set of simulations, the fitness variance is a fluctuating quantity. The grid of parameters used was $L \in [3000, 10000]$, $N \in [1000, 3000, 10000]$, $s \in [0.001, 0.003, 0.01]$, and $L\rho$ logarithmically spaced between s and 1.0. For the analysis, simulations were filtered such that $\xi_b > 30$ and $\xi_b < L/3$.



Fig. S3. Deleterious and beneficial mutations in an infinite sites model. Beneficial and deleterious mutations in a bona fide infinite sites model are shown. (*A*) Pairwise neutral diversity or coalesence time for simulations with beneficial (circles) and deleterious (triangles) mutations. The color of the symbols indicates the absolute effect size of mutations. (*B* and C) Corresponding SFSs for beneficial and deleterious mutations, respectively. The SFSs are obtained from histograms of the frequency of neutral polymorphisms and normalized to $\Theta = 2NU_n$, where U_n is the total neutral mutation rate. These results are obtained with a model that assumes chromosomes of length 1 that undergo exactly one cross-over per generation. The chromosomes mutate at random places in the interval [0,1]. With a probability of 0.5, mutations are neutral; otherwise, they have an effect s on fitness. We simulate a total mutation rate $U \in [10,30,100]$ with effect sizes $[3 \times 10^{-5}, 10^{-4}, 3 \times 10^{-3}]$ (positive and negative) for population sizes $N \in [1000, 3000, 10000]$. The SFSs and the neutral diversity follow the predictions of the analysis presented in the paper. LD was not investigated using this model.