Fig. S1. The distribution of the time to the most recent common ancestor of three individuals (A) and four individuals (B) in a model where mutational effects are normally distributed and mutations are frequent (compare with Fig. 3). Different line styles correspond to $s = 0.01$ (solid), $s = 0.001$ (dashed), and $s = 0.0001$ (dotted), whereas the mutation rate is $\mu = 1$. For each parameter combination, random pairs are sampled at 10,000 time points $2s^{-1/2}$ generations apart.

Fig. S2. The site frequency spectrum of neutral-derived mutations in Kingman’s coalescent with constant ($\alpha = 0$) and exponentially growing population sizes ($\alpha > 0$ is the growth rate measured in units of $N^{-1}$). The genealogies are produced with the program ms (1). The black lines show the theoretical expectation for a population of constant size and a rapidly expanding population. The $x$ axis is scaled as in Fig. 4.

Fig. S3. (A) The average time to the most recent common ancestor of the whole population increases relative to the timescale of coalescence with the population size $N = ND^1$. This scaling is a well-known feature of the Bolthausen–Sznitman coalescent, where one expects $\langle T_{\text{MRCA}} \rangle = T_c \log \log N$. $\beta$ compares $\langle T_{\text{MRCA}} \rangle / T_c$ with $1 + \log \log N$, where the additional +1 is necessary to account for $T_{\text{delay}} \approx T_c$ before coalescence begins.

Fig. S4. The delay $T_{\text{delay}}$ and the coalescence timescale $T_c$ can be extracted from the Laplace transform of $P(T_2)$ for very large populations and confirm that $T_c = \frac{2D}{\sigma^2}$.

Fig. S5. Results for alternative models of adaptation, in which all mutations confer the same selective advantage $s$ and the mutation rate satisfies $\mu < s$. $A$ shows the distribution of pair coalescent times, and $B$ shows the site frequency spectra and comparison with the Bolthausen–Sznitman coalescent. The times are rescaled with the prediction for the coalescent time $\langle T_2 \rangle = s^{-1} \log(s \mu^{-1})$ by Desai et al. (1). Solid lines correspond to $\mu/s = 0.01$; dotted lines correspond to $\mu/s = 0.1$; $s = 0.01$.

Fig. 56. Results for an alternative model of adaptation, in which the selective advantage of new mutations is drawn from an exponential distribution with mean $s$, whereas the mutation rate satisfies $\mu \ll s$. A shows the distribution of pair coalescent times, and B shows the site frequency spectra and comparison with the Bolthausen–Sznitman coalescent. In the absence of a prediction for the dependence of $T_2$ on $N_s$ or $\mu s^{-1}$, we rescale times by $s = 0.01$. The mutation rate equals $\mu = 0.1 s$.

Other Supporting Information Files

*SI Appendix (PDF)*