FIGURE 16.12. Distribution of coalescence times in structured populations. (*A*) The *black curve* shows the exponential distribution expected in a single panmictic population. The *blue curve* shows the distribution of times for two genes that start in the same deme, under the island model. (There are ten demes in all, and $4N_e m = 1$; time is scaled relative to $2N_e$ generations.) The chance that the two genes share a recent common ancestor is reduced, whereas the chance that they are distantly related is increased. With $4N_e m = 1$, there is about the same chance that the genes are related recently, via an ancestor in the same deme, as that they are related much more distantly. (*B*) The very long tail to the distribution can be seen more clearly on a log scale. The *red curves* in *A* and *B* show the distribution of coalescence times for two genes that are in different demes. (*C*) The distribution of coalescence times in a two-dimensional population for genes that are near each other (*upper blue points*) and that are 5σ away from each other (*lower red points*). Neighborhood size is $Nb = 5$. As for the island model, this distribution is highly skewed. For nearby genes, there is a chance ($1/2Nb = 10\%$) of common ancestry in the previous generation and a 27% chance of common ancestry within 20 generations. However, the mean coalescence time is twice the total effective number of genes in the whole population, which could be very large (e.g., 800,000 generations for a population ranging over 1000σ by 1000σ).