



FIGURE 15.20. Variation in evolutionary history predicts patterns of linkage disequilibrium along the genome. (A) The correlation between nucleotide diversity in regions separated by different distances. The two lines show two subsets of the single-nucleotide polymorphism data, which agree well. (B) The *red line* shows the observed linkage disequilibrium (r^2) as a function of the distance between sites. This is compared with predictions based on the sharing of evolutionary history derived from A (upper and lower bounds, *blue*). The theoretical prediction in B (*black curve*) is based on a simple model assuming constant population size and uniform recombination rates.

15.20A,B, redrawn from Reich D.E. et al., *Nat. Genet.* **32**: 135–142, © 2002 Macmillan, www.nature.com