

FIGURE 26.7. (*A*) Common diseases might be influenced by common variants that are maintained by balancing selection. In that case, it is likely that a small number of causal alleles would be involved. The diagram shows two alternative alleles that are maintained by balancing selection (*open* and *closed circles*) and that influence disease risk. Other neutral variation will also be present (*colored dots*) and, at tightly linked sites, will be in strong linkage disequilibrium with the causal allele (*red* and *blue dots*). However, for long-standing balanced polymorphisms only a very small region of genome will be influenced in this way ($r \sim \mu$ [p. 541]). (*B*) In contrast, common diseases might be influenced by many different deleterious mutations at each gene (*filled circles*): There are many ways to disrupt gene function, and so we might expect this to be typical.

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