



FIGURE 26.8. Population expansion influences allelic heterogeneity. (A) Strongly deleterious alleles (*blue*) must have originated recently, within the large current population. Therefore, many different mutations are likely to contribute. (B) More weakly deleterious alleles (*red*) tend to be older and so trace back to the smaller ancestral population. Most mutations will be lost by random drift, but those that survive will have expanded in numbers with the population as a whole. Here, two mutations are shown as contributing.