

## CHAPTER 8 Answers to Problems

**Problem 8.2.** No, the occurrence of H-W proportions in a population does not indicate the absence of selection acting on that locus. A population may be in H-W proportions even if there is strong selection on differential fertility. In addition, strong differential survival may or may not cause a population to depart from H-W proportions (Lewontin and Cockerham 1959). Further, power to detect deviations from H-W proportions is very low; see Problem 8.9.

### Problem 8.3.

- (a)  $p^* = 0.40$
- (b)  $p^* = 1.00$
- (c)  $p^* = 0.50$
- (d)  $p^* = 0.83$
- (e)  $p^* = 1.00$

**Problem 8.4.** NOTE: It may be helpful to use *Populus* to simulate these scenarios.

- (a)  $p^* = 0$  or 1 ( $p = 0$  more likely because the more common allele is more likely to become fixed)
- (b)  $p^* = 0$  or 1 ( $p = 0$  more likely). NOTE: Perhaps surprisingly, this result is independent of the fitness advantage of the  $A_1A_1$  homozygote because this allele is recessive with regard to these fitnesses. The  $A_1$  is initially rare so that there will not be any  $A_1A_1$  homozygotes in the population. Therefore, it will most likely be lost by drift before its fitness advantage can have any effect.
- (c)  $p^* = 0$  or 1 ( $p = 0$  more likely)
- (d)  $p^* = 0$  or 1 ( $p = 1$  more likely)
- (e)  $p^* = 0$  or 1 ( $p = 1$  more likely)

**Problem 8.5.** The translocation will certainly be lost because of natural selection in the large population. However, genetic drift in the small population could result in the increase in frequency of the translocation and its eventual fixation.

**Problem 8.6.** Natural selection is more effective in large populations.

**Problem 8.8.** Dominant. As we saw in Problem 8.4b, rare recessive alleles that have even a large selective advantage will be lost by drift before they can be affected by natural selection.

**Problem 8.9.** Over 600 individuals must be sampled to have at least a 50% chance of detecting an excess of heterozygotes. The answer is dependent on allele frequencies. Even larger samples are needed when allele frequencies are greater than 0.7 or less than 0.3.