## **CHAPTER 9** Answers to Problems

**Problem 9.1.** (c). New chromosomal rearrangements resulting in heterozygous disadvantage will generally be removed by natural selection. Only in the case of small, isolated populations will genetic drift be able to fix new rearrangements.

**Problem 9.2.** One migrant per generation is not sufficient for "effective panmixia". We can see in Figure 9.5 that there is substantial spread of allele frequencies (0.1 to 0.9) in subpopulations connected by mN=1.

There is an "urban legend" in the population genetics literature that one migrant per generation between populations is sufficient to counteract the effects of genetic drift so that two populations will not diverge genetically. We once attended a conservation genetics meeting at which one of the invited speakers said that "one migrant per generation is the gold standard of panmixia" (random mating).

This misunderstanding has a sound but sometimes misunderstood foundation in the populations genetics theory. Sewall Wright demonstrated many years ago that even very little genetic exchange among populations is expected have a substantial effect. He concluded that at least one migrant per generation is sufficient to maintain the same alleles in different populations (qualitative similarity), but is not enough to maintain similar allele frequencies in populations (quantitative similarity).

We can also see in Figure 9.5 that allele frequencies will vary between subpopulations even when mN=25.

**Problem 9.3.**  $H_{\rm S} = 0.351$ ;  $H_{\rm T} = 0.461$ ;  $F_{\rm ST} = 0.289$ .

Nm = 0.8.

There is no apparent tendency for nearby populations to be genetically similar so these populations appear to conform to the expectations of the island model.

**Problem 9.4.**  $F_{\rm ST} = 0.257$ .

**Problem 9.5.** Eventually  $F_{ST}$  will be 1.000 with complete isolation.

**Problem 9.6.** (a) Just over 1400 individuals have to be sampled in order to have a 50% of detecting an excess of heterozygotes because of heterozygous advantage of 10%.

(b) There is much less power to detect a departure from Hardy-Weinberg proportions with an allele frequency of 0.1.

(c) Approximately 125 individuals have to be sampled in order to have a 50% of detecting an excess of heterozygotes because of heterozygous advantage of 30% at an allele frequency of 0.40.

**Problem 9.7.** (a) Approximately 400 individuals have to be sampled in order to have a 50% of detecting an deficit of heterozygotes because of 10% inbreeding with the default allele frequency of 0.4. In this case, changing the allele frequency has little effect on power.

(b) Approximately 800 individuals have to be sampled in order to have an 80% of detecting an deficit of heterozygotes because of 10% inbreeding.

**Problem 9.9.** Seedlings  $F_{IS} = 0.179$ ; Adults  $F_{IS} = -0.028$ .

S = 0.304.

The most likely explanation is inbreeding depression. That is the seedlings produced by selfing have greatly reduced viability as seen in Example 13.1.