

Mutation, Migration Problem Set Answers

1. How is the random mating (HW) model used in evaluating whether recessive genetic diseases are maintained by a balance of selection versus mutation? What does this assume? Do you think these assumptions are reasonable?

The HW model is used to predict the frequency of the recessive disease allele in the general population from the frequency of affected individuals.

All the assumptions of the HW apply, including random mating. This is potentially of concern since recessive homozygotes may not be mating at all, depending on the severity of the genetic disease. However, the frequency of affected individuals is so low that this violation of the model has very little effect on estimates of allele frequency.

2. Some genetic diseases are much more common than predicted from the mutation-selection balance model (eg, Cystic Fibrosis). What is the explanation in the case of Cystic Fibrosis? Do you think it is correct to call the CF allele a deleterious allele?

The CF allele is at high frequency due to overdominant selection for resistance to typhoid (and possibly cholera as well).

Whether the CF allele is considered a disease allele depends on the environment. Heterozygous genotypes in an environment where typhoid is endemic have high fitness, but in the US where typhoid is very uncommon today, the allele confers no selective advantage. In fact, the frequency of the CF allele would be expected to drop over time (ultimately to the frequency predicted by mutation-selection balance) due to selection against homozygous CF genotypes of low fitness. In the US then, the CF allele is a disease allele.

3. There are two populations of a species, pop1 and pop2. Migrants move from pop1 to pop2, but not vice versa. For a locus with two alleles A and a , in generation 1, the frequency of A is 0.5 in pop1 and 0.75 in pop2; in generation 2 it is 0.5 in pop1 and 0.625 in pop2.

a. What is the rate of migration, measured as the chance that a migrant allele is a first generation immigrant (assume the absence of any other evolutionary forces)?

Answer:

Using the notation developed in lecture,

Freq'cy of A in Pop1 is p_c ,

Freq'cy of A in Pop2 is p_I

$$p_I' = (1-m)p_I + mp_c$$

Substituting $p_I' = 0.625$ and $p_I = 0.75$, $m = 0.5$

b. If the rate of migration is the same in the next generation, what is the frequency of A in generation 3?

Answer:

Using $p_I'' = (1-m)^2(p_I - p_c) + p_c$ where $m = 0.5$, $p_I' = 0.5625$

Book Problems:

#9a. Increase in CF allele frequency, due to increased reproductive success.

#9b. Decrease in CF allele frequency, due to reduced heterozygote superiority.

#9c. Decrease in CF allele frequency, due to (voluntarily) decreased reproductive success.

#9d. Increase in CF allele frequency, due to increased heterozygote superiority.

#10a. Migration from the splash-zone population. The splash-zone population apparently had a much higher frequency of the Aat120 allele than did the intertidal population.

#10b. Natural selection. The frequency of the Aat120 allele declined over several generations toward the original frequency seen in the intertidal population, likely due to selective differences in the two environments.

#10c. Genetic drift. Random events can cause random deviations in allele frequencies from the expected course of evolution. This effect is stronger in small populations.

#10d. We can expect both populations to arrive at the allele frequencies seen in the original intertidal population, assuming selective pressures remain the same and there are no significantly interfering events (such as, say, pronounced genetic drift, or mutation that creates a third allele).