

EVOLUTIONARY MECHANISMS PROBLEM SET (ANSWERS)

Work the following problems before you arrive at lab next week. The first four refer to the population of mice described for the computer simulations, and the remainder expand the examples and may challenge you further.

1. Assume that the frequency of the black allele in the population is 0.6, and that the population meets all of the expectations of the Hardy-Weinberg equilibrium theory. What are the expected genotype frequencies for the coat color locus in this population? Show your work.

B = black; b = white; Bb = either gray or black – we don't given information in only this question.

$$B = 0.6 = p$$

$$\text{Thus, } b = 0.4 = q$$

$$P^2 = BB = 0.36$$

$$2pq = Bb = 0.48$$

$$Q^2 = bb = 0.16$$

All add up to 1 – as a check of your math

2. If the population continues to meet the assumptions of the Hardy-Weinberg Equilibrium theory, do you expect the allele and genotype frequencies at this locus to change drastically over time? Explain your answer.

No, there are no factors causing evolution (e.g., natural selection, drift, nonrandom mating, gene flow, or mutation)

3. Now investigate the coat color locus in another large population of this mouse species. In a sample of 100 mice from this population you find 60 with black coats, 10 with gray coats, and 30 with white coats. Calculate the allele and genotype frequencies in this sample.

Total mice = 100, total # of alleles is 200

B = black, b = white

Allelic Frequencies:

$$p = \text{freq of } B = (60 \cdot 2 + 10) / 200 = 130 / 200 = 0.65$$

$$q = \text{freq of } b = (30 \cdot 2 + 10) / 200 = 70 / 200 = 0.35$$

Total = 1 – so it checks out

Genotypic frequencies:

$$BB = 60 / 100 = 0.6$$

$$Bb = 10 / 100 = 0.1$$

$$bb = 30 / 100 = 0.3$$

TOTAL = 1 – so it checks out

4. Is there evidence to suggest that evolutionary mechanisms are operating on the coat color locus in this population? (This will require you to compare your observed genotype frequencies with those predicted by Hardy-Weinberg - show your work) If so, which evolutionary mechanisms would most likely cause such deviations from Hardy-Weinberg expectations?

Predicted HW frequencies can be calculated from the allelic frequencies:

$P = 0.65, q = 0.35$
 $BB = 0.65^2 = 0.4225$
 $Bb = 2 \cdot 0.65 \cdot 0.35 = 0.455$
 $bb = 0.35^2 = 0.1225$
TOTAL = 1 – so it checks out.

These HW expected frequencies are VERY different from the frequencies observed in the population (see question #3). It appears that there may selection against the heterozygote.

5. In the plant *Phlox* the alcohol dehydrogenase (ADH) locus shows two alleles a and b. The following genotypic frequencies were found in a population; aa = 0.05, ab = 0.35, bb = 0.60. Calculate the allele frequencies.

Freq of "a" = $p = (0.05) + 0.35/2 = 0.225$
Freq of "b" = $q = (0.60) + 0.35/2 = 0.775$

6. In a sample of minnows from a local stream, three genotypes controlled by 2 alleles (a_1 & a_2) at one esterase locus showed the following numbers in the population; $a_1a_1 = 10$, $a_1a_2 = 75$, and $a_2a_2 = 15$. Are these numbers what you would expect if this population were in Hardy-Weinberg equilibrium? If not, is one microevolutionary mechanism more likely to be acting than others, based on the data?

First – calculate allelic frequencies
100 minnows thus 200 alleles in population
 $A1 = (10 + 10 + 75) / 200 = 0.475$
 $A2 = (15 + 15 + 75) / 200 = 0.525$
(answers add to 1 so we're probably correct)

Then – calculate expected HW genotypic frequencies
 $A1A1 = 0.475^2 = 0.226$
 $A1A2 = 2 \cdot 0.475 \cdot 0.525 = 0.499$
 $A2A2 = 0.525^2 = 0.276$
Add up to 1 so we're probably correct.

Then – compare observed vs expected.
Observed: $A1A1 = 10/100 = 0.1$; $A1A2 = 75/100 = 0.75$; $A2A2 = 15/100 = 0.15$
It appears there is selection against both homozygote condition and/or for the heterozygote.

7. What is the frequency of heterozygotes (Aa) in a population in which the frequency of all dominant phenotypes is 0.25 and the population is in H-W equilibrium?

So, $AA + Aa =$ all dominant phenotypes = 0.25
So, $aa = 0.75$
So, $aa = q^2$
The freq of "a" = $q = \text{square root of } 0.75 = 0.866$

Therefore, $p = 1 - 0.866 = 0.134$
 $2pq = 2 * 0.134 * 0.866 = 0.232 = \text{freq of heterozygotes}$

8. The following frequencies are known from extensive research on a large population of PTC tasters and Non-Tasters: TT = 251 individuals; Tt = 250 individuals; tt = 334 individuals

a. What are the allele frequencies of T and t?

835 total individuals, 1670 total alleles
 $p = \text{freq of T} = ((251 * 2) + 250) / 1670 = 0.45$
 $q = \text{freq of t} = ((334 * 2) + 250) / 1670 = 0.55$
 $p + q = 1$ – so it checks out.

b. What are the expected genotype frequencies?

$TT = p^2 = 0.45 * 0.45 = 0.202$
 $Tt = 2pq = 2 * 0.45 * 0.55 = 0.495$
 $tt = q^2 = 0.55 * 0.55 = .303$
all add up to 1 – so they check out.

c. What are the phenotype frequencies?

Can't really determine from information given. We don't know what's dominant. Assuming "T" is dominant, then tasters = $0.202 + 0.495 = 0.697$; t = $1 - \text{freq of T} = 0.303$

9. Suppose the following data were accumulated for the frequencies of each of three genotypes at 5 separate loci, A through E:

AA: 0.36	BB: 0	CC: 1.0	DD: 0.70	EE: 0.25
Aa: 0.48	Bb: 0.03	Cc: 0	Dd: 0.20	Ee: 0.50
Aa: 0.16	bb: 0.97	cc: 0	dd: 0.10	ee: 0.25

a. Which loci are monomorphic? **C** Which loci are polymorphic? **All the others**

b. What are the allele frequencies at each locus?

$A = 0.36 + 0.48 / 2 = 0.6$
 $a = 0.16 + 0.48 / 2 = 0.4$
 $B = 0 + 0.03 / 2 = 0.015$
 $b = 0.97 + 0.03 / 2 = 0.985$
 $C = 1.0$
 $c = 0$
 $D = 0.7 + 0.2 / 2 = 0.8$
 $d = 0.1 + 0.2 / 2 = 0.2$
 $E = 0.25 + 0.5 / 2 = 0.5$
 $e = 0.25 + 0.5 / 2 = 0.5$

c. Is there evidence that some mechanisms of evolution are acting at some loci but not others? **yes**

How can this be? – **some loci code for traits that are subject to natural selection (e.g., C, D, B) whereas others are apparently neutral to selection.**

10. Out of 100 red oaks (*Quercus rubra*) in a population, the frequency of B allele is 0.45. The other allele at the locus, a recessive allele (b), was expressed in 20

individuals. Determine: 1) observed and expected genotype frequencies, and 2) whether the pop'n is at H-W Equilibrium.

Freq of B = p = 0.45

Freq of b = q = 0.55

Observed: bb = 0.2

Expected:

BB = $0.45 \times 0.45 = 0.2025$

Bb = $2 \times 0.45 \times 0.55 = 0.495$

bb = $0.55 \times 0.55 = 0.3025$

Expected does not appear equal to the observed, so it may not be in HW equilibrium.

- a. If you conclude it's not in H-W Eq., design a study that would eliminate or confirm one evolutionary mechanisms that may be at work.

There are any number of things you could do here.

11. Challenge Question #1: In a population a locus with 3 alleles showed the following genotypic numbers in a sample; aa=0, ab=0, bb=10, ac=0, bc=35, cc=6. Calculate allele frequencies, and determine the expected genotype frequencies under H-W conditions.

51 individuals, 102 alleles in population

Allelic frequencies:

A = $0+0+0 = 0 = p$

B = $10+10+35 = 55/102 = 0.54 = q$

C = $0+35+6+6 = 0.46 = r$

Expected Genotypic Freq:

aa = 0

bb = $0.54 \times 0.54 = 0.29$

cc = $0.46 \times 0.46 = 0.21$

ab = $2 \times 0 \times 0.54 = 0$

ac = $2 \times 0 \times 0.46 = 0$

bc = $2 \times 0.54 \times 0.46 = 0.50$

Do the genotype frequencies depart from those expected by H-W? **No** What may be going on here if they don't? **No selection at this locus is a possibility**

12. Challenge Question #1: Can a population with more than 80% heterozgotes for a locus be in Hardy-Weinberg equilibrium? Less than 10%? Explain.

No, recombination will redistribute the alleles so that you can never have more than 80% or less than 10%