## Hardy-Weinberg problem set

Hardy-Weinberg Theorem states that if a population is NOT evolving then the frequencies of the alleles in the population will remain stable across generations - it is in equilibrium.

We can use the Hardy-Weinberg equation to make predictions about the relative frequency of the different alleles (as well as the associated genotypes), even if there is population growth, as long as the five conditions we discussed in class hold true. Think about what those five conditions are.......

Alternatively, Hardy-Weinberg equation can be a means to determine if a population is indeed evolving - that the allele frequencies are changing and therefore NOT at equilibrium.

The trick to using the Hardy-Weinberg equation to help evaluate the frequency of a particular allele frequency at time X, or to make a prediction about the frequency of a particular genotype/phenotype in future generations, is to go through the math is a step-by-step manner.

and there is a simple dominant recessive relationship.	}
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- 1. If 98 out of 200 individuals in a population express the recessive phenotype, what percent of the population would you predict would be heterozygotes?
- (a) I have given you information on the frequency of the homozygous recessive (or q2). So start by determining q2 and then solving for q.
- (b) Now that you have q, you can solve for p. Remember there are only two alleles in the population, so if you add the frequency of the two alleles, you have accounted for all possibilities and it must equal 1. So p + q = 1.
- (c) Now what is the formula for heterozygotes? Think back to the Hardy-Weinberg equation -- it is dealing with the genotypes of individuals in the population.
- (d) Now that you have figured out the % of heterozygotes, can you figure out the % of homozygous dominant? Does the % of homozygous dominant, heterozygotes and homozygous recessive individuals add up to 100%? If not, you have made an error. Those are the only three genotypes possible with only two alleles and a simple dominant and recessive relationship.

2. Your original population of 200 was hit by a tidal wave and 100 organisms were wiped out, leaving 36 homozygous recessive out of the 100 survivors. If we assume that all individuals were equally likely to be wiped out, how did the tidal wave affect the predicted frequencies of the alleles in the population? NOTE: assume the new population is at equilibrium -- AFTER the event - so you are comparing two populations what are at equilibrium to look for changes in allele frequencies.

Again, start with the frequency you know -- homozygous recessive. Follow the same step-by-step procedure as above. What is the frequency of homozygous recessive? What is the predicted frequency of heterozygotes? What is the predicted frequency of homozygous dominant? Given that the allele frequencies did change as the result of the tidal wave, we would say that microevolution has occurred. What do we call the phenomenon that caused this evolution? NOTE -- I am not necessarily asking the questions in the order in which you should answer them, given the step-by-step approach. 3. Lets say that brown fur coloring is dominant to gray fur coloring in mice. If you have 168 brown mice in a population of 200 mice...... What is the predicted frequency of heterozygotes? What is the predicted frequency of homozygous dominant? What is the predicted frequency of homozygous recessive? 4. If 81% of a population is homozygous recessive for a given trait...... What is the predicted frequency of homozygous dominant? What is the predicted frequency of heterozygotes?

What is the frequency of the dominant and recessive alleles in the population?

## 5. If 51% of the population carries at least one copy of the recessive allele......

What is the predicted frequency of individuals in the population that express the dominant phenotype?

What is the predicted frequency of individuals in the population that express the recessive phenotype?

<u>ANSWERS</u> -- work through the problems first! Remember to always double-check yourself by adding the frequencies of the three genotypes.