LAB - Quantifying Evolution in a Population

AP Biology

Thus far we have seen that the frequency of phenotypes in a population can change due to selection. Do our observations mean the population is evolving? Maybe; maybe not. Alleles are shuffled each generation in sexual reproduction, and so yield different proportions of each phenotype. But what if we look at the source of the phenotype: the alleles that determine both genotype and phenotype?

In 1908, G.H. Hardy and W. Weinberg proposed that evolution could be quantified by changes in **allele frequencies.** The scientists argued that if certain conditions are met, the population’s allele frequencies remain constant from generation to generation; thus, no evolution occurs. The conditions are as follows: the breeding population is large; mating is random; no new mutations; no migration; and no selection.

Quantifying the allele frequencies allows us to see if the population is changing over time. The different alleles for a gene are represented by ***p* (dominant**) and ***q* (recessive**). The combined frequency of these two alleles in a population must equal 1 (*p* + *q =* 1.0). Additionally, the frequency of the possible allele combinations is expressed as *p*2 + 2*pq* + *q* 2 = 1.0, where *p*2 is the number of homozygous dominant, 2*pq* the number of heterozygous, and *q*2 the number of homozygous recessive.

For genes with alleles that are dominant and recessive, the value of p and q are obscured by the heterozygote phenotype. However, if we determine the number of phenotypically recessive individuals in a population, we can use the equations above to determine the frequency of each allele, as well as the frequency of each of the three genotypes in the population.

1. ***FINDING GENOTYPE FROM PHENOTYPE*** *via the Hardy-Weinberg Equation.*

The ability to perceive the taste of certain chemicals, like phenylthiocarbamide (PTC) is the result of a single dominant allele. Non-tasters are thus homozygous recessive.

* 1. Determine if you are a taster or not, via the test strip. Add your result to the class set.
  2. Calculate the **phenotypic** frequency (0.0 – 1.0) of tasters and non-tasters in the population and record.
  3. Find *q* – the recessive **allele** frequency - by taking the square root of the non-tasters frequency *(q* 2 )*.* Subtractfrom 1 to find *p*. Record.
  4. Use the above values of *p* and *q* in the H-W equation, *p* 2 + 2*pq* + *q* 2 = 1.0, to determine the genotype frequencies. Record.

1. ***SICKLE CELL SELECTION***

• The entire class will represent a breeding population. In this simulation mating will be random, and gender and genotype are irrelevant. The initial population consists of all heterozygous individuals. Accordingly the frequency for each ‘allele’ – the two colors of poker chips - is .5. Each member of the class has two of each color poker chip in a cup. The chips are the alleles in sperm or ovum the heterozygous parents potentially contribute to the offspring.

• Randomly choose a mate (gender irrelevant). The taller partner draws a chip from each cup. This is the F1 genotype for the student. Return the chips to their respective cups and have the second student draw a pair for their F1 genotype. Sort yourself by genotype as directed by the teacher. Adjust your chips to reflect your F1 genotype. Find a new mate. Repeat through the F5 generation.

• Use the class data to determine the allele frequencies for each generation by first solving for p using the following equation. Then subtract from 1.0 to find q.

2 (number *AA*) + number *Aa*

• p = ----------------------------------

2 (number of students)

**CASE I - Ideal Population** – All five conditions for H-W equilibrium are met.

**CASE II – Sickle Cell Selection in North America**

In human populations an autosomal recessive mutation causes, in the homozygous genotype, sickle cell disease. Untreated affected individuals often do not reach sexual maturity. Assume for this model that no homozygous recessive individuals survive. In which case, you and your partner try again, until each of you have genotypes that survive.

**CASE III – Sickle Cell Selection in Equatorial Ecosystems –** heterozygous individuals have greater fitness than either homozygous dominant or homozygous recessive individuals.

Despite being lethal, sickle cell remains common in equatorial populations, predominantly in sub-Saharan Africa. It turns out that heterozygous individuals produce some sickled red blood cells, which the immune system works to destroy. Since these RBC cells are equally likely to be infected with malaria in equatorial ecosystems, the immune response in the heterozygote effectively reduces the parasite load, making that individual more likely to survive both malaria and sickle cell. .

All the factors from CASE II apply except only half of the homozygous dominant individuals survive. Toss a coin to see if this offspring survives. If not, mate again until successful.

1. ***COMPUTER MODELING OF MICROEVOLUTION***

**Lab – Quantifying Evolution**

**Discussion Questions**

1. How does the context for Hardy-Weinberg differ from Mendel’s work?
2. Mendel predicted that if the number of dominant and recessive alleles were equal in a population, then the genotypes would occur in a 1:2:1 ratio. Discuss our results from Part A in light of this prediction.
3. There is some evidence that there are three phenotypes for the thiourea taste: strong taster, mild taster, and non-taster. What allele relationship is implied? Explain. Propose a reason why, based on genetics, some people really hate brussel sprouts and their ilk.
4. How likely is it that a population would be in Hardy-Weinberg equilibrium? Does the class population meet all the requirements of an ideal, non-evolving population? Justify your answer.
5. Explain both of the ‘p & q’ equations.
6. Which phenotype is the key to determining allele and genotype frequencies in a population? Explain.

*Table I*

*Chemical:*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Phenotype | Taster |  | Non-Taster | = equals |
| Class phenotype data |  |  |  |  |
| Phenotype frequency |  |  | (*q2)* |  |
| Allele frequency | *p=* |  | *q=* | *= 1.0* |
| Genotype | Homozygous dominant | Heterozygous | Homozygous recessive | n/a |
| Genotype frequency | *p2=* | *2pq=* | *q2=* | *= 1.0* |
| # student per genotype |  |  |  |  |

*Table I*

*Chemical:*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Phenotype | Taster |  | Non-Taster | = equals |
| Class phenotype data |  |  |  |  |
| Phenotype frequency |  |  | (*q2)* |  |
| Allele frequency | *p=* |  | *q=* | *= 1.0* |
| Genotype | Homozygous dominant | Heterozygous | Homozygous recessive | n/a |
| Genotype frequency | *p2=* | *2pq=* | *q2=* | *= 1.0* |
| # student per genotype |  |  |  |  |

*Table I*

*Chemical:*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Phenotype | Taster |  | Non-Taster | = equals |
| Class phenotype data |  |  |  |  |
| Phenotype frequency |  |  | (*q2)* |  |
| Allele frequency | *p=* |  | *q=* | *= 1.0* |
| Genotype | Homozygous dominant | Heterozygous | Homozygous recessive | n/a |
| Genotype frequency | *p2=* | *2pq=* | *q2=* | *= 1.0* |
| # student per genotype |  |  |  |  |

**Case \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_**

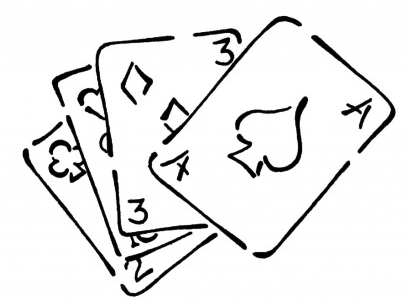
|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Self |  | Class |  | Allele | freq. |
|  |  | *AA* | *Aa* | *aa* | *p* | *q* |
| P generation data |  |  |  |  |  |  |
| F1 |  |  |  |  |  |  |
| F2 |  |  |  |  |  |  |
| F3 |  |  |  |  |  |  |
| F4 |  |  |  |  |  |  |
| F5 |  |  |  |  |  |  |

**Case \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Self |  | Class |  | Allele | freq. |
|  |  | *AA* | *Aa* | *aa* | *p* | *q* |
| P generation data |  |  |  |  |  |  |
| F1 |  |  |  |  |  |  |
| F2 |  |  |  |  |  |  |
| F3 |  |  |  |  |  |  |
| F4 |  |  |  |  |  |  |
| F5 |  |  |  |  |  |  |

**Case \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Self |  | Class |  | Allele | freq. |
|  |  | *AA* | *Aa* | *aa* | *p* | *q* |
| P generation data |  |  |  |  |  |  |
| F1 |  |  |  |  |  |  |
| F2 |  |  |  |  |  |  |
| F3 |  |  |  |  |  |  |
| F4 |  |  |  |  |  |  |
| F5 |  |  |  |  |  |  |

Modeling the Effect of the Hardy-Weinberg Conditions

AP Biology

1. From a deck of cards count out any five cards of each suit. Set aside the jokers and the rest of the cards to draw from. Shuffle your deck of 20.

*For each model, calculate the frequency of each suit in the population and record. What is the effect of the variable on the suit frequency? What is the effect of the variable on the population?*

*Always return the population to its original equilibrium before moving on to the next model.*

1. Mutation: Replace two randomly chosen cards of the population with two Jokers.
2. Migration: Remove two cards from the population and add in four cards from the deck of extras.
3. Non-random mating: Draw the top two cards of the population. If they make a ‘heterozygote’ pair, both cards remain in the population; homozygous pairs do not survive and so are removed from the population. Repeat for the entire population
4. Selection: Remove the top two cards. Assume the following dominance ranking of the suits: hearts dominant over clubs; clubs over diamonds; diamonds over spades; spades over hearts. All others are codominant. Deal out all the cards in pairs. For dominant/recessive pairs use the deck of extras to convert the pair to reflect the homozygous dominant genotype of the offspring. Do nothing with the codominant pairs.
5. Large population: Repeat step 5 but with a population twice as large to begin with by combining two decks. Calculate frequencies and record. What is the effect of population size on Hardy-Weinberg equilibrium?

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| H-W | *Hearts* | | *Clubs* | | *Diamonds* | | *spades* | | *JOKERS* | |
| CONDITION | Number | Freq. | Number | Freq. | Number | Freq. | Number | Freq. | Number | FREQ |
|  |  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |